

The complete chloroplast genome of *Litsea molis* Hemsl. (Lauraceae): genome structure and phylogenetic analysis

Xin-yu Wang^a, Huan Hu^b and Dan Zhang^a

^aKey Laboratory of Medical Electrophysiology, Ministry of Education, Institute of Cardiovascular Research, Southwest Medical University, Luzhou, P. R. China; ^bInstitute of Life Sciences, Zunyi Medical University, Zunyi, P. R. China

ABSTRACT

Litsea molis Hemsl. is a precious wild aromatic oil tree species and important medicinal plant. In this study, we sequenced and characterized the chloroplast genome of *L. molis* for the first time. Its complete chloroplast genome is 152,311 bp in length, containing a large single copy region of 93,258 bp and a small single copy region of 18,917 bp separated by a pair of inverted repeat regions of 20,068 bp. The chloroplast genome contains 130 unique genes, including 85 protein-coding genes, 37 tRNA and 8 rRNA genes. Phylogenetic analysis based on chloroplast genome sequences of 36 plants from the family Lauraceae showed that *L. molis* is more closely related to species of *Lindera* genus than other genera in Lauraceae.

ARTICLE HISTORY

Received 8 June 2020
Accepted 27 June 2020

KEYWORDS

Litsea molis Hemsl.; chloroplast genome; oil species; medicine plant; phylogenetic analysis



Litsea mollis Hemsl., a traditional edible spice and medicinal plant with a long history in China, is a deciduous shrubs or small trees in the *Litsea* genus of Lauraceae. The seeds contain ca. 25% oil and are used as a main ingredient in soaps. The fruit is processed for its aromatic oil (3%–5%) (Li et al. 1982). Ingredients from volatile oil of *L. molis* can produce natural pesticides, grain and clothing anthelmintic storage agents and natural preservatives. Volatile oil in both fruit and leaf have obvious antibacterial and antifungal activity. In terms of medicinal value, the roots and fruit are used medicinally (Lin et al. 2000; Cai et al. 2019). A variety of biological activities in *L. molis* have beneficial effective on human health, such as roots and fruits can cure gas pain, strain injury, diarrhea, analgesia, schistosomiasis, allergy and disease of cardiovascular system (coronary heart disease, angina pectoris) and so on (Yang et al. 2020). However, there are very few studies on the *L. molis*, which greatly limit the development and utilization of *L. molis*. Therefore, we assembled and analyzed the complete chloroplast genome of *L. molis* for the first time, which can provide insight and evidence for its genetic background and evolution.

Fresh leaves of *L. mollis* were collected from Longquan Mountain (coordinates: CHN, 26°11'41.26''N, 107°49'10.32E''), Danzhai County, Guizhou province, China. The specimen was stored at College of life sciences, Sichuan University (specimen code LLM20001). Total genomic DNA were extracted with a modified CTAB method (Doyle and Doyle 1987) and sequencing was carried out by the Illumina pair-end technology to obtain about 5.4 Gbp of high-quality reads of *L. mollis* on the Hiseq2000 platform. Firstly, we obtained 10 million

high quality pair-end reads using Trimmomatic v0.35 (Bolger et al. 2014) and custom Perl script for *L. mollis*. With the chloroplast genome of all published Lauraceae chloroplast genomes as the reference sequences, we assembled the complete chloroplast genome from the clean reads by the GetOrganelle pipe-line (Jin et al. 2018). Secondly, we annotated the plastid genomes using PGA (Qu et al. 2019) and corrected the annotation with Geneious v11.1.5.0 (Kearse et al. 2012) and Sequin v13.70 (<http://www.ncbi.nlm.nih.gov/Sequin/>). The gene map of the chloroplast genome was generated using OGDRAW v1.3 (Greiner et al. 2019). Finally, a complete chloroplast genome of *L. mollis* was obtained and submitted to Genbank (accession number MT472628).

The complete chloroplast genome of *L. mollis* is 152,311 bp in length, containing a pair of inverted repeat (IR) regions of 20,068 bp, a large single copy region of 93,258 bp, and a small single copy region of 18,917 bp. The chloroplast genome of *L. mollis* contains 130 unique genes, including 85 protein-coding genes, 37 tRNA genes, and 8 rRNA genes (4 rRNA species). Among these genes, 94 of them exist as single copy, but 4 protein-coding genes (i.e. *ndhB*, *rps7*, *ycf12*, and *ycf68*), 6 tRNA genes (i.e. *trnA-UGC*, *trnI-GAU*, *trnL-CAA*, *trnN-GUU*, *trnR-ACG*, *trnV-GAC*), and 4 rRNA genes (i.e. 4.5S, 5S, 16S and 23S rRNA) present in double copies. In general, the overall GC content of the whole chloroplast genome is 39.2%, whereas the corresponding values of the LSC, SSC, and IR regions are 37.95%, 33.95%, and 44.40%, respectively.

To further investigate its phylogenetic position, *Cupressus gigantea* was used as the outgroup, the phylogenetic analysis

CONTACT Dan Zhang  dan_huang_pai@sina.com  Key Laboratory of Medical Electrophysiology, Ministry of Education, Institute of Cardiovascular Research, Southwest Medical University, No. 319 Section 3, Zhongshan Road, Luzhou City, Sichuan Province

© 2021 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group.

This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0/>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

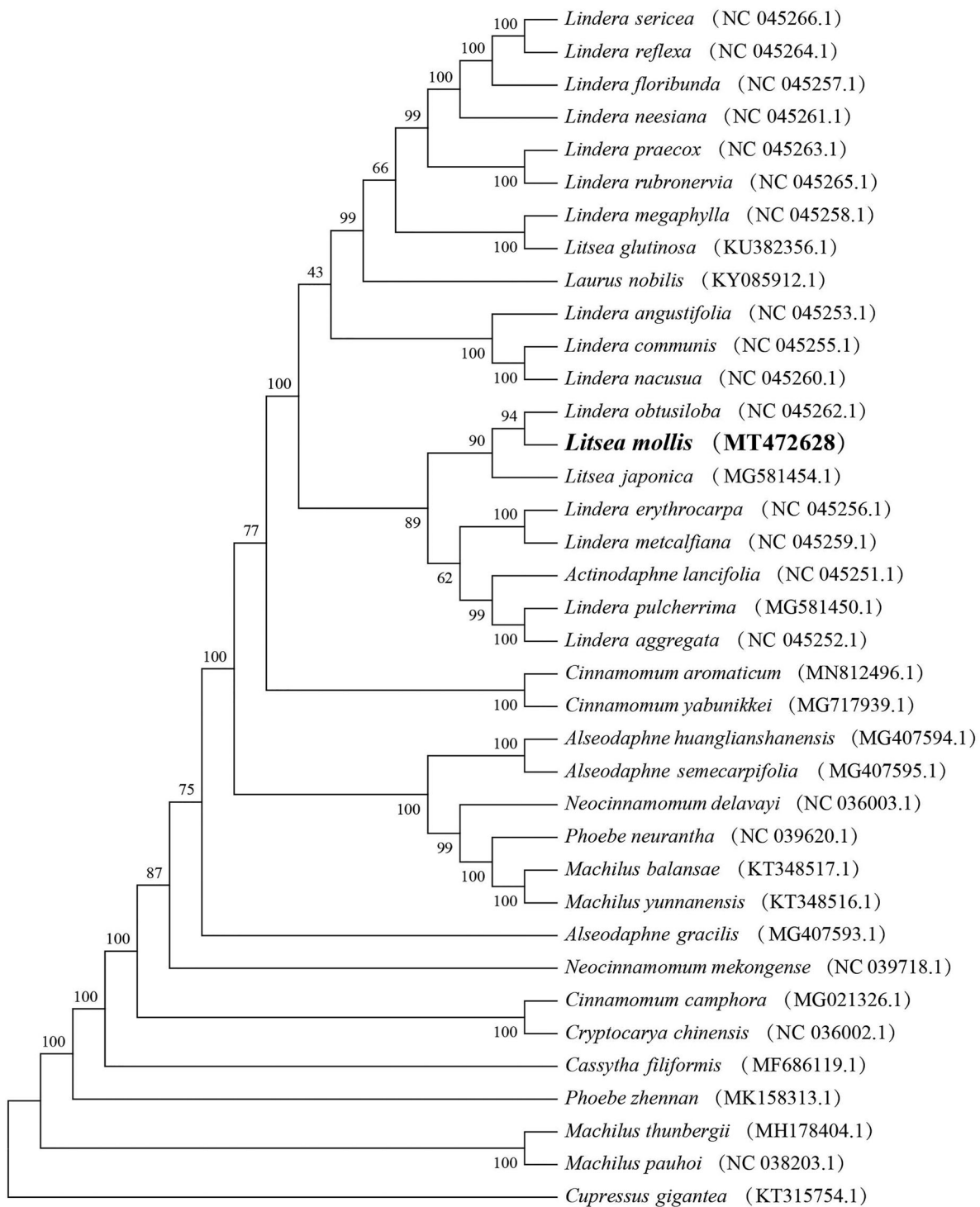


Figure 1. Phylogenetic relationships based on complete chloroplast genome sequences from *L. mollis* and other members of from Lauraceae (All the sequences were downloaded from NCBI GenBank).

of 36 plastid genomes from published species of Lauraceae were analyzed using MEGA7.0 (with 1,000 bootstrap replicates) (Kumar et al. 2016). The result indicated that *L. mollis* is more closely related to species of *Lindera* genus than other genera in Lauraceae (Figure 1).

Disclosure statement

No potential conflict of interest was reported by the authors.

Funding

This work was supported by the National Natural Science Foundation of China Scientific and Technical Project of Zunyi City [Zunyi-KHSZ-2018-17] [No. 31860104].

Data availability statement

The data that support the findings of this study is openly available in Genbank at [<https://www.ncbi.nlm.nih.gov/genbank/>], reference number MT472628.

References

- Bolger AM, Lohse M, Usadel B. 2014. Trimmomatic: a flexible trimmer for Illumina sequence data. *Bioinformatics*. 30(15):2114–2120.
- Cai X, Wang X, Chen Y, Wang Y, Song DF, Gu Q. 2019. A natural biopreservative: antibacterial action and mechanisms of Chinese *Litsea mollis* Hemsl. extract against *Escherichia coli* DH5 α and *Salmonella* spp. *J Dairy Sci*. 102(11):9663–9673.
- Doyle J, Doyle J. 1987. A rapid DNA isolation procedure for small quantities of fresh leaf tissue. *Phytochem Bull*. 19(1):11–15.
- Greiner S, Lehwark P, Bock R. 2019. OrganellarGenomeDRAW (OGDRAW) version 1.3.1: expanded toolkit for the graphical visualization of organellar genomes. *Nucleic Acids Res*. 47(W1):W59–W64.
- Jin J, Yu W, Yang J, Song Y, Yi T, Li D. 2018. GetOrganelle: a simple and fast pipeline for de novo assembly of a complete circular chloroplast genome using genome skimming data. *bioRxiv*. 256479.
- 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.
- Kumar S, Stecher G, Tamura K. 2016. MEGA7: molecular evolutionary genetics analysis version 7.0 for bigger datasets. *Mol Biol Evol*. 33(7):1870–1874.
- Li X, Bai P, Li Y, Li S, Wei F, Wei Y, Yang X. 1982. *Flora of China*. Vol. 31. Beijing: Sciences Press; p. 282.
- Lin C, Su J, Zeng L. 2000. Analysis of the chemical constituents of the essential oil from the leaves of *Litsea mollis* Hemsl. *Chin Pharm J*. 35(3):156–156.
- Qu X, Moore M, Li D, Yi T. 2019. PGA: a software package for rapid, accurate, and flexible batch annotation of plastomes. *Plant Methods*. 15(1):50.
- Yang Y, Liang M, Yang Y, Zheng F, Wang X, Yu A. 2020. Optimization of a headspace solid-phase microextraction method for the gas chromatography-mass spectrometry analysis aroma compounds of *Litsea mollis* Hemsl. immature fruit. *Food Sci. Technol*. 40(5):1–8 [http://dx. doi. org/10.1590/fst.20319](http://dx.doi.org/10.1590/fst.20319).