

The complete chloroplast genome of the medicinal plant *Lysimachia mauritiana* (Lamarck, 1792)

Yoonkyung Lee^a, Narae Yun^a, Junghyun Kang^b, Sangho Choi^a and Jin-Hyub Paik^a

^aInternational Biological Material Research Center, Korea Research Institute of Bioscience and Biotechnology, Daejeon, Republic of Korea;

^bNatural Medicine Research Center, Korea Research Institute of Bioscience and Biotechnology, Cheong-ju, Republic of Korea

ABSTRACT

Lysimachia mauritiana Lam. (Primulaceae) is known as a medicinal plant with anti-tumor and anti-viral effects. In this study, we reported the first complete chloroplast genome sequence of *L. mauritiana*. The total length of the complete chloroplast genome was 152,691 bp, comprising a small-single copy region (SSC) of 17,928 bp, a large-single copy region of 83,811 bp, and a pair of inverted repeat regions of 25,476 bp. It contained 114 genes comprising 80 protein-coding genes, four rRNA, and 30 tRNA genes. The phylogenetic analysis showed that a chloroplast genome of *L. mauritiana* was a sister to a monophyletic clade, including *L. christinae*, *L. congestiflora*, *L. hemsleyana*. Our study will help to provide basic information for further studies on phylogenetics and population genetics.

ARTICLE HISTORY

Received 14 January 2022

Accepted 12 March 2022

KEYWORDS

Lysimachia mauritiana;
Primulaceae; chloroplast
genome; phylogenetic
analysis

Lysimachia mauritiana (Lamarck, 1792) is a medicinal plant belonging to the genus *Lysimachia* (Primulaceae). The plant extract of this species has known as a good source with anti-tumor and anti-viral effects (Yasukawa and Takido 1987; Bae and Song 2017). The plant is a biennial herb distributing coastlines in East Asia, the Philippines, Micronesia, Polynesia, and the Indian Ocean islands (Iwatsuki et al. 1993; Hu and Kelso 1996; Kono et al. 2013). Until recently, the chloroplast genome of this species has not been reported. In this study, we determined the complete chloroplast genome of *L. mauritiana* and investigated its phylogenetic position in the family Primulaceae.

Fresh leaves of *L. mauritiana* was collected from Byeonsan-myeon, Buan-gun, Jeollabuk-do in Korea (N 35°39'22", E 126°29'41") and the voucher specimen (voucher number KRIB0088806, Jin-Hyub Paik, jpaik@kribb.re.kr) was deposited in International Biological Material Research Center (IBMRC), Korea Research Institute of Bioscience & Biotechnology (KRIBB). *L. mauritiana* is not an endangered or protected species, and we did not collected from private or protected area that required permission. Ethics approval for this study was obtained from the Institutional Bioethics Committee of KRIBB.

The total genomic DNA of this plant was extracted using modified CTAB methods (Healey et al. 2014) and sequenced by Illumina HiSeqXten platform (San Diego, CA). The raw data were filtered using Trimmomatic v.0.36 (Bolger et al. 2014), and the filtered data were assembled using the chloroplast genome of *L. coreana* (NC_026197.1) as the reference with Geneious Prime (v.2021.1.1; Kearse et al. 2012). Finally, the

chloroplast genome was annotated using Geneious Prime (v.2021.1.1; Kearse et al. 2012) and GeSeq (Tillich et al. 2017) based on the chloroplast genome of *L. coreana* (NC_026197.1), and the complete chloroplast genome of *L. mauritiana* was submitted to GenBank (accession number: OK491633).

The complete chloroplast genome of *L. mauritiana* determined in this study has 152,691 bp in length, which contains a large-single copy region (LSC) of 83,811 bp, a small-single copy region (SSC) of 17,928 bp, and a pair of inverted repeat regions (IRs) of 25,476 bp. The chloroplast genome includes a total of 114 genes comprising 80 protein-coding genes, four rRNA, and 30 tRNA genes.

The phylogenetic analysis was performed with 14 accessions of Primulaceae deposited on Genbank, including a chloroplast genome of *L. mauritiana* determined in this study and an outgroup taxa from the genus *Myrsine* (MN167883.1 and MN177700.1). The sequences of these chloroplast genomes were aligned using MAFFT alignment v.7 (Katoh and Standley 2013; <http://mafft.cbrc.jp/alignment/server/index.html>). We selected TVM + F + I + G4 as the best model using ModelFinder module (Kalyaanamoorthy et al. 2017) in IQ-tree v.1.6.3 (Nguyen et al. 2015), and the maximum likelihood phylogenetic tree was reconstructed using in IQ-tree v.1.6.3 (Nguyen et al., 2015) with 1000 bootstrap replicates.

A Maximum-likelihood tree (Figure 1) shows that each genus is a highly supported monophyletic group (bootstrap support value = 100%). A chloroplast genome of *L. mauritiana* is a sister to a monophyletic clade including *L. christinae*, *L. congestiflora*, and *L. hemsleyana* with a high bootstrap

CONTACT Yoonkyung Lee  yoonyk@kribb.re.kr; Jin-Hyub Paik  jpaik@kribb.re.kr  International Biological Material Research Center, Korea Research Institute of Bioscience and Biotechnology, Daejeon, Republic of Korea

© 2022 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-NonCommercial License (<http://creativecommons.org/licenses/by-nc/4.0/>), which permits unrestricted non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

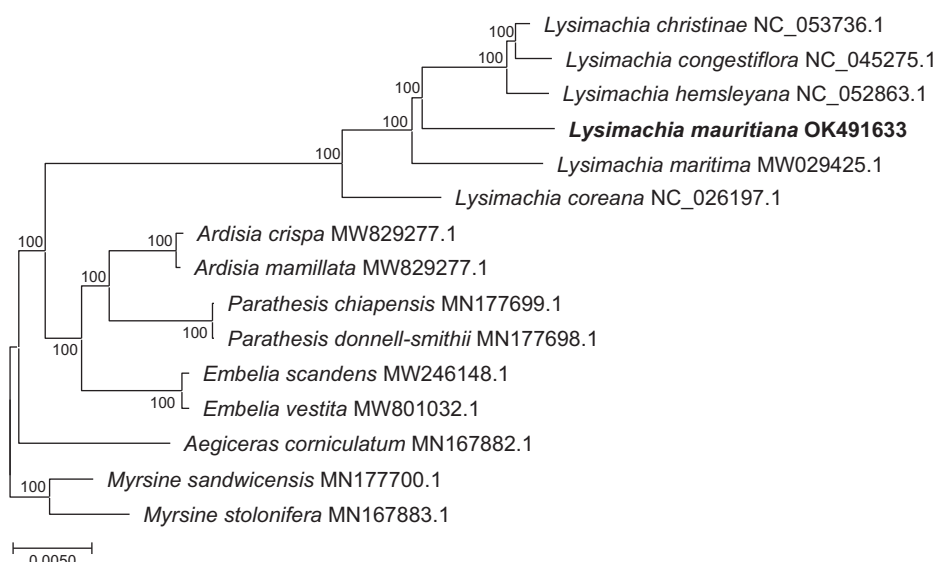


Figure 1. A Maximum-likelihood tree using 15 chloroplast genomes from Primulaceae, including a chloroplast genome of *Lysimachia mauritiana* determined in this study and an outgroup taxon (*Myrsine stolonifera*). The numbers near the nodes indicate bootstrap values.

value (bootstrap support value = 100%). Our study will provide basic information to understand the evolution and diversification of *L. mauritiana*.

Author contributions

Conceptualization: YL, SC, JP; Resources: NY, JK, SC, JP; Performed the experiments: YL, JK; Formal analysis: YL, NY, JK; Writing: YL; All authors reviewed the manuscript.

Disclosure statement

No potential conflict of interest was reported by the authors.

Funding

This work was supported by the KRIBB Initiative Program [KGM4582221] of the Republic of Korea.

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. OK491633. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA791132, SRR17284494, and SAMN24255752 respectively.

References

- Bae S, Song YJ. 2017. Inhibition of varicella-zoster virus replication by an ethanol extract of *Lysimachia mauritiana*. *Mol Med Rep.* 15(6): 3847–3851.
- Bolger AM, Lohse M, Usadel B. 2014. Trimmomatic: a flexible trimmer for Illumina sequence data. *Bioinformatics.* 30(15):2114–2120.
- Healey A, Furtado A, Cooper T, Henry RJ. 2014. Protocol: a simple method for extracting next-generation sequencing quality genomic DNA from recalcitrant plant species. *Plant Methods.* 10(1): 21–28.
- Hu CM, Kelso S. 1996. Primulaceae. In: Wu ZY, Raven PH, Hong DY, editors. *Flora of China*. Vol. 15. Myrsinaceae through Loganiaceae. Beijing (China)/St. Louis (MI): Science Press/Missouri Botanical Garden Press; p. 39–189.
- Iwatsuki K, Yamazaki T, Boufford DE, Ohba H. 1993. *Flora of Japan*. Vol IIIa. Tokyo: Kodansha Ltd.
- Kalyanamoorthy S, Minh BQ, Wong TKF, von Haeseler A, Jermini LS. 2017. ModelFinder: fast model selection for accurate phylogenetic estimates. *Nat Methods.* 14:587–589.
- 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.
- Kono Y, Hoshi Y, Setoguchi H, Yokota M, Oginuma K. 2013. Widespread cytotypic variation, cytogeography and dynamic analysis of *Lysimachia mauritiana* (Primulaceae) on Takarajima Island in the Ryukyu Archipelago of Japan. *Chromosom Bot.* 8(3):47–52.
- 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.
- 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.
- Yasukawa K, Takido M. 1987. A flavonol glycoside from *Lysimachia mauritiana*. *Phytochemistry.* 26(4):1224–1226.