The complete chloroplast genome of Lagerstroemia loudonii Teijsm. & Binn. (Lythraceae), an ornamental tree with medicinal value

Bo Qin, Kaidao Sun and Xin Huang

Guangxi Key Laboratory of Special Non-wood Forest Cultivation & Utilization, Guangxi Forestry Research Institute, Nanning, China

ABSTRACT
Lagerstroemia loudonii is an ornamental tree with medicinal value. Here, we announce the first complete chloroplast genome sequence of L. loudonii. The L. loudonii chloroplast genome harbors a typical quadripartite structure with a total length of 152,372 bp, including a large single-copy (LSC) region of 84,086 bp, a small single-copy (SSC) region of 16,798 bp, and two separated inverted repeat (IR) regions of 25,744 bp each. The chloroplast genome encodes 130 genes, including 85 protein-coding genes, 37 transfer RNA (tRNA) genes, and 8 ribosomal RNA (rRNA) genes. The GC content of the whole chloroplast genome is 37.6%. Phylogenetic analysis based on complete chloroplast genomes of L. loudonii and 17 other plant species revealed that Lagerstroemia is a separate genus, and L. loudonii is closely related to L. calyculata.

KEYWORDS
Chloroplast genome; Lagerstroemia loudonii; phylogenetic analysis

CONTACT Xin Huang  hxyy82@163.com  Guangxi Key Laboratory of Special Non-wood Forest Cultivation & Utilization, Guangxi Forestry Research Institute, Nanning, China

© 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 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.
other 17 species with \textit{L. loudonii} chloroplast from NCBI, then we choose \textit{Punica granatum} (NC_035240.1) from different family and used it as outgroup. We aligned them by using MAFFT 7.037 \cite{Katoh2016} with strategy of FFT-NS-2. And we used model finder to select TVM + F + I + G4 model \cite{Kalyaanamoorthy2017} and constructed the phylogenomic tree by IQtree 2.0 \cite{Minh2020} with 1000 bootstrap and maximum likelihood method. The results of the phylogenetic analysis proposed that \textit{Lagerstroemia} is a separate genus and all the examined \textit{Lagerstroemia} species were divided into three clades. \textit{L. balansae}, \textit{L. tomentosa}, \textit{L. loudonii}, \textit{L. calyculata} and \textit{L. floribunda} formed a monophyletic clade and \textit{L. loudonii} has a close relationship with \textit{L. calyculata} (Figure 1).

**Author contributions**

HX planned and designed the research. QB and SK conducted the experiments, collected the materials, and analyzed the data. QB wrote the manuscript. HX revised the manuscript, provided advice on the experiments, and finalized the manuscript. All the authors have read and approved the final manuscript.

**Disclosure statement**

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

**Funding**

This study was supported by the Fundamental Research Funds for Guangxi Forestry Research Institute [202110], the Guangxi Key Laboratory of Special Non-wood Forest Cultivation & Utilization’s Independent Project [JA-20-01-03], and the Survey and Collection of Germplasm Resources of Woody & Herbaceous Plants in Guangxi, China [Gui-Forest-Science [2021] 34].

**Data availability statement**

The genome sequence data that support the findings of this study are openly available in GenBank of the NCBI under the accession number of NC_061954. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA791531, SRS11377984, and SAMN24292890, respectively.
References

Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, et al. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J Comput Biol. 19(5):455–477.

Doyle JJ, Doyle JL. 1987. A rapid DNA isolation procedure for small quantities of fresh leaf tissue. Phytochem Bull. 19:11–15.

Furtado CX, Srisuko M. 1969. A revision of Lagerstroemia L. (Lythraceae). Gard Bull. 24:185–335.

Gu C, Tembrock LR, Li Y, Lu X, Wu Z. 2016. The complete chloroplast genome of queen’s crape-myrtle (Lagerstroemia macrocarpa). Mitochondrial DNA B Resour. 1(1):408–409.

Kalyaanamoorthy S, Minh BQ, Wong TKF, von Haeseler A, Jermiin LS. 2017. ModelFinder: fast model selection for accurate phylogenetic estimates. Nat Methods. 14(6):587–589.

Katoh K, Standley DM. 2016. A simple method to control over-alignment in the MAFFT multiple sequence alignment program. Bioinformatics. 32(13):1933–1942.

Minh BQ, Schmidt HA, Chernomor O, Schrempf D, Woodhams MD, von Haeseler A, Lanfear R. 2020. Corrigendum to: IQ-TREE 2: new models and efficient methods for phylogenetic inference in the genomic era. Mol Biol Evol. 37(5):1530–1534.

Patel RK, Jain M. 2012. NGS QC toolkit: a toolkit for quality control of next generation sequencing data. PLOS One. 7(2):e30619.10.

Plants of the World Online. Lagerstroemia loudonii (Lythraceae). https://powo.science.kew.org/taxon/urn:lsid:ipni.org:names:553587-1.

Qu XJ, Moore MJ, Li DZ, Yi TS. 2019. PGA: a software package for rapid, accurate, and flexible batch annotation of plastomes. Plant Methods. 15:50.

Riyanti S, Dewi PS, Windyaswari AS, Azizah SAN. 2020. Alpha-glucosidase inhibitory activities of Bungur (Lagerstroemia loudonii Teijsm. & Binn.) leaves and fruits. IOP Conf Ser: Earth Environ Sci. 462(1):012042.

Wang X, Wadl PA, Pounders C, Trigiano RN, Cabrera RI, Scheffler BE, Pooler M, Rinehart TA. 2011. Evaluation of genetic diversity and pedigree within Crapemyrtle cultivars using simple sequence repeat markers. J Amer Soc Hort Sci. 136(2):116–128.