MITOCHONDRIAL DNA PART B
2022, VOL. 7, NO. 4, 658–660
https://doi.org/10.1080/23802359.2022.2062265

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PLASTOME ANNOUNCEMENT

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The complete chloroplast genome of *Laportea bulbifera* (Sieb. et Zucc.) Wedd. and its phylogenetic analysis

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ABSTRACT

The circle complete chloroplast genome of *Laportea bulbifera* (Sieb. et Zucc.) Wedd. was sequenced for the first time. The genome length of *L. bulbifera* is 150,042 bp with 36.80% of GC content. The genome consists of a large single copy (LSC) region of 82,414 bp, a small single copy (SSC) region of 17,714 bp, and two inverted repeat (IRa and IRb) regions of 24,957 bp each. A total of 129 genes were annotated, including 84 protein-coding genes, 37 tRNA genes, and 8 rRNA genes. Phylogenetic analysis was conducted by 29 species from the Rosales, the results presented a closed relationship between the species *Laportea bulbifera* and *Poikilospermum lanceolatum*.

ARTICLE HISTORY
Received 3 February 2022
Accepted 29 March 2022

KEYWORDS
Laportea bulbifera; Urticaceae; chloroplast genome; medicinal plant

Laportea bulbifera (Sieb. et Zucc.) Wedd. 1856 first mentioned. is a perennial herb of genus *Laportea* Gaudich in the Urticaceae family, it is mainly distributed in Guizhou, Yunnan, Hunan and Heilongjiang province of China and also in Japan, Russia, India, Sri Lanka, and other countries (ECFC 1995). As a traditional Chinese medicine, *L. bulbifera* mainly contains flavonoids, coumarins, volatile oils with a wide range of pharmacological effects (Zhu et al. 2011; Lin et al. 2018; Zhang et al. 2019), and has long been utilized in TCM for the treatment of RA and some other autoimmune diseases (Xiang et al. 2009; Hou et al. 2010; Luo et al. 2011; Wang et al. 2013). Despite its high medicinal value, the complete chloroplast genome of *L. bulbifera* has not been reported yet. On the other hand, because of rare plant resources of *L. bulbifera*, the protection, development, and utilization of it were severely restricted. Therefore, the chloroplast genome of *L. bulbifera* was sequenced and the phylogenetic analysis was performed without species of *Ficus auriculata*, in order to enrich gene information and promote sustainable medicinal plant resources use of *L. bulbifera*.

Fresh leaves of *L. bulbifera* were collected from Longli county, Guizhou province, China (E 106°54′52″, N 26°23′14″). The voucher specimen (voucher No. LB20210703) and total DNA samples were deposited in the Center of Herbarium, Guizhou University of Traditional Chinese Medicine (http://www.gzy.edu.cn/, Qingwen Sun, sunqingwen445@gzy.edu.cn). Total DNA was extracted from *L. bulbifera* fresh leaves using the EZNA Plant DNA extraction kit according to the manufacturer's instruction (Yingfei Biotech Co., Ltd., Shanghai, China). The genome sequence was performed on the Illumina NovaSeq Sequencing System to generate paired-end 2*150bp reads. A total of 6.43 Gb raw data was filtered by Trimmomatic (Bolger et al. 2014), then 6.41 Gb clean data was obtained. GetOrganelle (Jin et al. 2020) and CpGAVAS2 (Shi et al. 2019) were used to assemble and annotate the chloroplast genome, respectively, with the *Poikilospermum lanceolatum* chloroplast genome sequences (NC_056983.1) as reference. The annotated genome sequence was submitted to the GenBank (Accession number: OL334513).

The chloroplast genome of *L. bulbifera* is a double-stranded DNA molecule with a length of 150,042bp, it presents a typical quadripartite structure, including a large single copy (LSC) region, a small single copy (SSC) region, and two inverted repeat (IRa and IRb) regions. The LSC and SSC regions are 82,414 and 17,714bp, respectively, which are alternated by a pair of IR regions of 24,957bp each. The overall GC content of *L. bulbifera* is 36.8% (LSC, 34.4%; SSC, 30.5%; IRs, 42.9%). A total of 129 genes were annotated, including 84 protein-coding genes, 37 tRNA genes, and 8 rRNA genes. Among these genes, 6 protein coding genes (*rps12, rps7, rpl23, rpl2, ndhB*, and *ycf2*), 7 tRNA genes (*trnA-UGC, trnI-CAU, trnI-GAU, trnL-CAA, trnN-GUU, trnR-ACG*, and *trnV-GAC*), and 4 rRNA genes (*rrn16, rrn23, rrn4.5*, and *rrn5*) contain two repeating units. Furthermore, 19 genes equip with one intron, including 11 protein-coding genes (*atpF, ndhA, ndhB* × *2, petB, petD, rpl16, rpl2* × *2, rpoC1*, and *rps16*) and 8 tRNA genes (*trnA-UGC* × *2, trnG-UCC, trnI-GAU* × *2, trnK-UUU, trnL-UAA*, and *trnV-UAC*). A total of four genes contain two introns (*rps12* × *2, clpP*, and *ycf3*). In addition, two genes (*ycf1* and *rps19*) were annotated as pseudogenes.

The whole chloroplast genomes of 28 species in one family of Urticaceae were used for phylogenetic analysis with *Ficus auriculata* from Moraceae family as an out species (Figure 1). After sequence alignment by MAFFT (Katoh and

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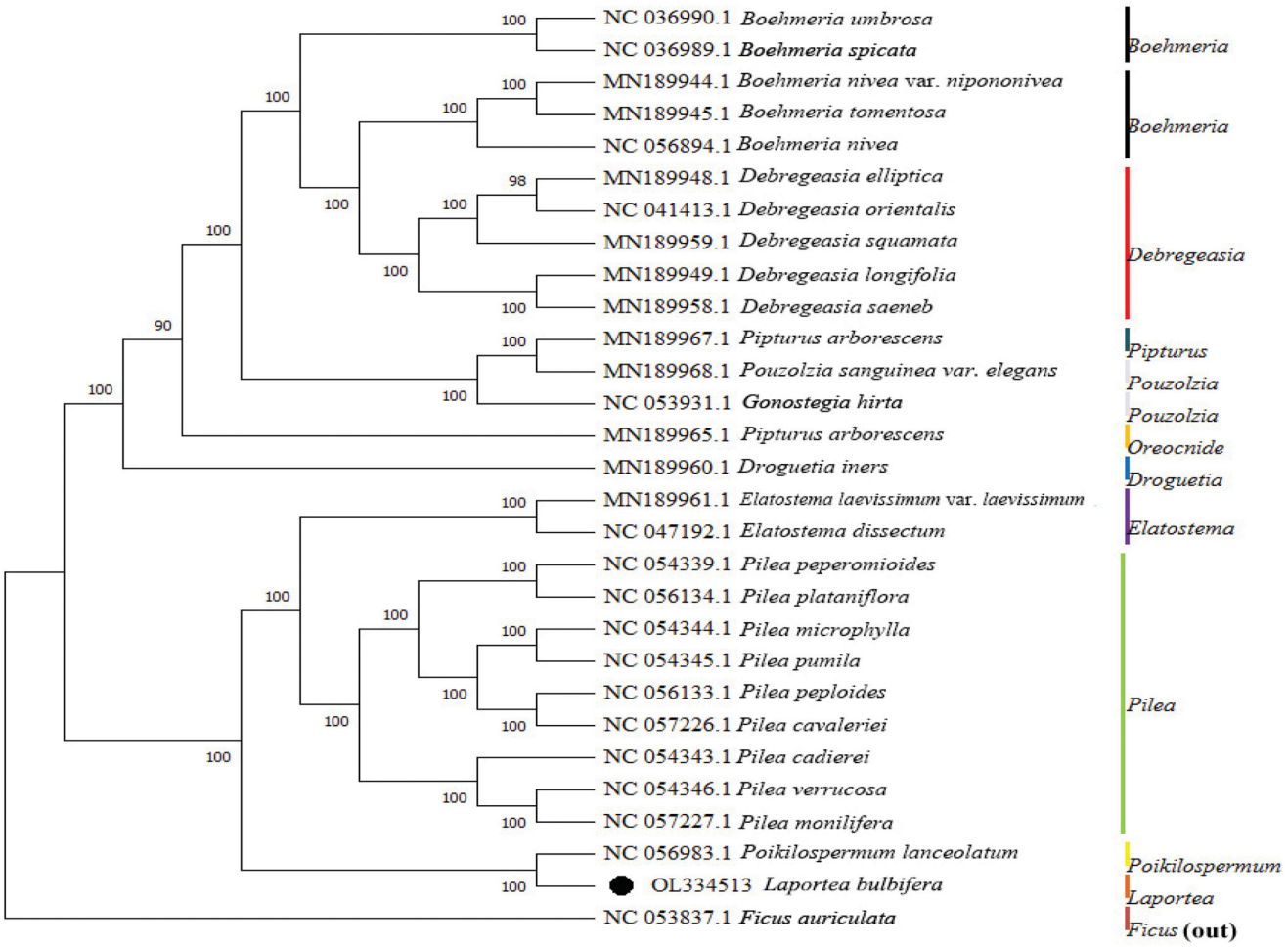

Figure 1. Phylogenetic relationships of 29 Rosales species constructed from the complete chloroplast genome sequences using maximum likelihood (ML).

Standley 2013), MEGA X (Kumar et al. 2018) was used to perform maximum likelihood (ML) tree with the Tamura Nei model. The results indicated that different species from different genera make difference, the significant factor attributes to different inner chloroplast genome construction. Previous studies showed that the genera of *Boehmeria* and *Debregeasia* species were each closely clustered into one group (Wu et al. 2018; Fu and Zhang 2021), which was consistent with our study results of phylogenetic analysis. However, the phylogenetic analysis of *Laportea* genus has not been reportedyet, its the first time to make phylogenetic analysis for *L. bulbifera* species. Present study showed that the species *L. bulbifera* from *Laportea* genus and *P. lanceolatum* from *Poikilospermum* genus of Urticaceae family showed closed relationship. These newly characterized phylogenetic analysis fruits can be used to develop markers for further study on the phylogeny and evolution of the genus *Laportea*.

Ethical approval

Research and collection of plant material was conducted according to the guidelines provided by GZY (Guizhou University of Traditional Chinese Medicine). Permission was granted by the National Natural Science Foundation of China.

Author contributions

Wenfen Xu and **Chunling Chen** planned and designed the study; **Qingwen Sun** and **Yueyun Wang** collected the plant materials; **Kaifen Sun** and **Bo Wang**: analysis of data; **Kaifen Sun**: drafting of the manuscript. All the authors agreed to be accountable for all aspects of the work.

Disclosure statement

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

Funding

This work was supported by the Excellent Young Scientific and Technological Talents Project of Guizhou Province [[2019]5658], the National Natural Science Foundation of China [81260687], Guizhou Governor Fundation Project [QSZHZ[2011]61H].

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] (https://www.ncbi.nlm.nih.gov/) under the accession no. OL334513. The associated BioProject, SRA, and BioSample numbers are PRJNA778584, SRR16853987, and SAMN22965352 respectively.

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