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PLASTOME ANNOUNCEMENT

Phylogenetic relationship and characterization of the complete chloroplast genome of *Laggera crispata*, a folk herbal medicine plant in China

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ABSTRACT

Laggera crispata, an herbaceous plant, has been used in Chinese medicines as anti-inflammatory, analgesic, and anti-viral. In this study, the complete chloroplast (cp) genome sequence of *L. crispata* was first reported. The cp genome of *L. crispata* is 155522 bp in length, with two inverted repeats (IR) regions of 25042 bp, the large single copy (LSC) region of 84198 bp and the small single copy (SSC) region of 21240 bp. 128 genes were predicted, including 87 protein-coding genes, 37 tRNA genes, and 8 rRNA genes. The phylogenetic analysis suggested that *L. crispata* is more closely related to *Pluchea pteropoda* and *P. indica* with solid bootstrap values belonging to the subfamily *Inuleae* of Asteraceae.

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Laggera crispata; complete chloroplast genome; phylogenetic analysis

Laggera crispata (Vahl) Hepper & J. R. I. Wood, 1983. is a perennial herbaceous of Asteraceae (Ahmed et al. 1998), widely distributed in China, India, and Africa. The aerial parts of *L. crispata* were used in traditional medicine to treat respiratory virus infection, sore throat, bronchitis, and fever (Lu et al. 2014; Kambiré et al. 2020). So far, most of the studies on *Laggera* and its related genus have focused on chemical compositions, morphological taxonomy, and molecular phylogeny (Liu et al. 2006; Luo 2014; Tokuma et al. 2019; Wang et al. 2019). However, there are no genomic resources for the genus of *Laggera*. Therefore, we sequenced the cp genomes of *L. crispata*, characterized the genome features, and presented phylogenetic for the first time based on molecular evidence for the genus, which will provide helpful information to understand the genome phylogenetic relationship of the Asteraceae.

The fresh leaves collected from the Dapingdi mountain (N 25°40′11.71″, E 99°57′29.30″) in Yangbi counties, Yunnan province, China. This article is licensed under the Regulations of Yunnan Province on biodiversity protection and approved by Yangbi counties (Yunnan Province, China), Dali University (Yunnan province of China). And specimen was deposited at the herbarium of Dali University (http://yxy.dali.edu.cn/yhxy, Baozhong Duan, bzduan@126.com) under the voucher number HBGP0707. The genomic DNA was extracted using the Plant Genomic DNA kit (Tiangen, Beijing, China), and sequenced using the Illumina NovaSeq system (Illumina, San Diego, CA, USA). GetOrganelle conducted Denovo genome assembly (Jin et al. 2020). On this genome, 18,361,645 reads were assembled with a 1300 × coverage, and the annotated using GeSeq with default sets (Michael et al. 2017). The complete cp genome of *L. crispata* was submitted to the GenBank database (Accession Number: OK323148).

The complete cp genome sequence of *L. crispata* is 155,522 bp in length, with a large single-copy (LSC) region of 84,198 bp, a small single-copy (SSC) region of 21,240 bp, and a pair of inverted repeats (IR) regions of 25,042 bp. The overall GC content of the whole cp genome is 37.4%. A total of 128 genes were annotated in this plastome, including 87 protein-coding genes, 37 tRNA genes, and 8 rRNA genes. To reveal the phylogenetic position of *L. crispata* with other members in Asteraceae, 25 complete cp genomes of related species were downloaded from the NCBI database. The sequences were aligned by MAFFT v7.307 (Katoh and Standley 2013). *Adenophora stricta* (NC012303) and *A. racemosa* (MT036223) were served as the outgroup. The maximum likelihood (ML) trees were reconstructed with IQ-tree using default parameters which are 1000 iterations, 1000 replications, and best-fit model selection. As illustrated in Figure 1, all clades were supported robustly (>99%). Asteraceae is a sister group to Campanulaceae. Remarkably, *L. crispata* was clustered together with *Pluchea indica* and *P. pteropoda,* and then were clustered together with *Inula hupehensis* and *I. helianthus-aquatilis.* Therefore*, Laggera* is most closely related to *Pluchea* and *Inula*, and all three belong to *Tr. Inuleae*. In the present study, the phylogenetic relationship of *L. crispata* with genomic data was uncovered for the first time, which

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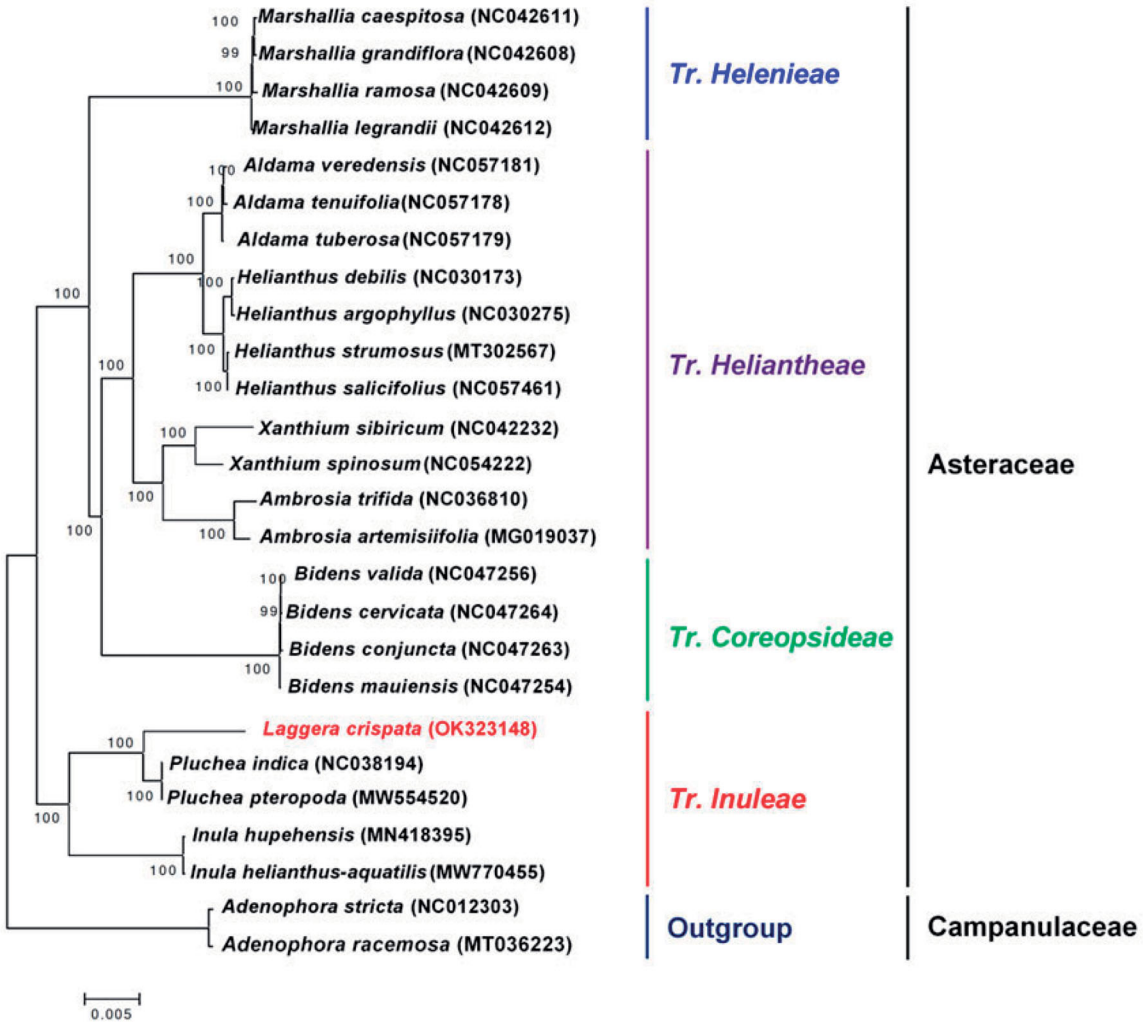

Figure 1. Phylogenetic analysis of 24 species and two taxa as outgroups based on cp genome sequences by RAxML, bootstrap support value near the branch.

will provide helpful information for phylogenetic and evolutionary analyses in Asteraceae.

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Author contributions

Zhongyu Zhou analyzed the data, prepared figures, written original draft preparation, and approved the final draft; Tingting Pu Collect materials and analyzed the data; Baozhong Duan performed the experiments and interpretation of data for the work; Manchang Zhang designed the experiments, reviewed and edited.

Disclosure statement

No potential conflicts of interest and would be responsible for the content were declared by the authors.

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Data availability statement

The data that support the findings of this study are openly available in the NCBI GenBank database at (https://www.ncbi.nlm.nih.gov) with the accession number is no. OK323148., which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA767266, SRR16114975, and SAMN21895587, respectively.

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