The complete chloroplast genome sequences of Dolichandrone spathacea (L. F.) K. Schum., a semi-mangrove plant

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Abstract

Dolichandrone spathacea (L. F.) K. Schum. is an excellent tree species for coastal protection forests. In this study, the complete chloroplast genome sequence of D. spathacea was obtained through high-throughput sequencing. The length of chloroplast genome was 159,156 bp in length, containing a large single-copy region (LSC) of 86,053 bp, a small single-copy region (SSC) of 12,635 bp, and a pair of inverted repeats (IRA and IRb) regions of 30,234 bp. The chloroplast genome with 37.95% GC content, contained 134 genes, including 90 protein-coding genes, 8 rRNA genes, and 36 tRNA genes. Phylogenetic analysis with the reported chloroplast sequences shows that D. spathacea is more closely related to Spathodea campanulata.

Key words

Dolichandrone spathacea; Bignoniaceae; chloroplast genome; phylogenetic analysis; semi-mangrove plant

Automatic annotation of the chloroplast genomes was generated by CpGAVAS2 (Shi et al. 2019). The draft annotations given by CpGAVAS2 were then manually corrected using the Artemis software and other plastid genomes for comparison (Rutherford et al. 2000).

The chloroplast genome of D. spathacea (Genbank accession no. MW173028) was a circular molecular genome with a size of 159,156 bp in length, 86,053 bp of a large single-copy (LSC) and 12,635 bp of small single-copy (SSC) regions were separated by 30,234 bp of inverted repeat (IR) regions. It contained 134 genes (90 protein-coding genes, 8 rRNA genes, and 36 tRNA genes). The overall GC content of the chloroplast genome was 37.95% and those in the LSC, SSC, and IR regions were 36.18%, 33.30%, and 41.43%, respectively.

In order to understand the phylogenetic relationship between D. spathacea and related taxa, the complete chloroplast of 15 species belonging to the Bignoniaceae family and two outgroups was used for phylogenetic analysis, they were downloaded from the NCBI GenBank database and aligned by MAFFT version 7.037 (Kazutaka Katoh, Japan) (Katoh et al. 2002). Phylogenetic relationship was inferred from maximum likelihood (ML) and Bayesian inference (BI) based on complete genome sequences. BI was performed with MrBayes version 3.2.7 (Ronquist et al. 2012) under the GTR + G + I model with 10,000 bootstrap and ML method was performed with IQ-TREE under the TVM + F + R4 model with 1000 bootstrap values in the PhyloSuite version 1.2.2 (Zhang et al. 2020). Two results gave the same topologies. The tree showed that D. spathacea was closely related to Spathodea campanulata (MN106255) which also belongs to the

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Paleotropical alliance (Figure 1) (Olmstead et al. 2009). In this article, we first reported the complete chloroplast genome of *D. spathacea*, which will provide fundamental genetic resources for studying this important species as well as resolving its phylogenetic evolution.

**Disclosure statement**

The authors have declared that there are no competing interests.

**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. MW173028. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA703408, SRR13757104, and SAMN18016863, 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.

Katoh K, Misawa K, Kuma KI, Miyata T. 2002. MAFFT: a novel method for rapid multiple sequence alignment based on fast Fourier transform. Nucleic Acids Res. 30(14):3059–3066.

Lin P. 2001. A review on the mangrove research in China. J Xiamen Univ (Natural Sci). 40:592–603.

Olmstead RG, Zjhra ML, Lohmann LG, Grose SO, Eckert AJ. 2009. A molecular phylogeny and classification of Bignoniaceae. Ann J Bot. 96(9):1731–1743.

Ronquist F, Teslenko M, van der Mark P, Ayres DL, Darling A, HёOhna S, Larget B, Liu L, Suchard MA, Huelsenbeck JP. 2012. MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. Syst Biol. 61(3):539–542.

Rutherford K, Parkhill J, Crook J, Horsnell T, Rice P, Rajandream MA, Barrell B. 2000. Artemis: sequence visualization and annotation. Bioinformatics. 16(10):944–945.

Shi LC, Chen HM, Jiang M, Wang LQ, Wu X, Huang LF, Liu C. 2019. CPGAVAS2, an integrated plastome sequence annotator and analyzer. Nucleic Acids Res. 47(W1):W65–W73.

Tian GH, Li M, Yang XB, Liao BW, Liu WH, Lei ZS. 2011. Study on Introduction of Dolichandrone spathacea on Qi-ao Island. J Anhui Agr Sci. 39(16):9618–9619.

Yu H, Tardivo L, Tam S, Weiner E, Gebreab F, Fan C, Svzrikapa N, Hizroane-Kishikawa T, Rietman E, Yang X, et al. 2011. Next-generation sequencing to generate interactome datasets. Nat Methods. 8(6):478–480.

Zhang D, Gao FL, Jakovic I, Zhou C, Zheng J, Li WX, Wang GT. 2020. PhyloSuite: an integrated and scalable desktop platform for streamlined molecular sequence data management and evolutionary phylogenetics studies. Mol Ecol Resour. 20(1):348–355.