

The complete chloroplast genome of *Mimosa pudica* and the phylogenetic analysis of mimosoid species

Xiaoyue Yang^a, Xiyou Qian^b and Zefu Wang^c

^aState Key Laboratory of Grassland Agro-Ecosystem, School of Life Sciences, Lanzhou University, Lanzhou, People's Republic of China;

^bHeilongjiang Institute of Forestry Monitoring and Planning, Harbin, People's Republic of China; ^cKey Laboratory of Bio-Resource and Eco-Environment of Ministry of Education, College of Life Sciences, Sichuan University, Chengdu, People's Republic of China

ABSTRACT

Mimosa pudica, a typical sensitive plant, belongs to *Mimosa* (Fabaceae). It is well known for the rapid plant movement. In this study, we determined the complete chloroplast genome of *M. pudica* using the Illumina reads. The complete chloroplast genome of *M. pudica* is 163,237 bp in length, comprising a large single-copy region (LSC) of 92,045 bp, a small single-copy region (SSC) of 18,786 bp, and a pair of inverted repeats (IRs) of 26,203 bp each. The genome contained 129 encoded genes in total, including 84 protein-coding genes, eight ribosomal RNA genes, and 37 transfer RNA genes. The overall GC content of the *M. pudica* chloroplast genome is 35.53%. We reconstructed the phylogenetic relationships for 19 mimosoid species. It was revealed that *M. pudica* was closely related to *Piptadenia communis*.

ARTICLE HISTORY

Received 30 July 2018

Accepted 31 August 2018

KEYWORDS

Complete chloroplast genome; *Mimosa pudica*; phylogenetic analysis; mimosoid species

Mimosa pudica (*Mimosa*, Fabaceae) is a typical sensitive plant. It is well known for the rapid plant movement and often grown for people's curiosity. A recent study has reported the *de novo* genome of *M. pudica* (Griesmann et al. 2018); however, its complete chloroplast genome has not been analyzed or provided for further study. Herein, we assembled and annotated the complete chloroplast genome of *M. pudica*, and performed a phylogenetic analysis including 19 species of mimosoid clade.



We downloaded ~20G high-quality Illumina reads of *M. pudica* (NCBI accession # SRR5313988) using the fastq-dump software. The individual for sequencing was collected in DC Smith greenhouse, University of Wisconsin, MI, and the sample was stored at Toulouse Henry Gaussien Botanical Garden in France with the accession number FR-0-TOU-D18001N (Griesmann et al. 2018). The reads were used to assemble the complete chloroplast genome with the software NOVOPlasty v2.5.9 (Dierckxsens et al. 2017) and GapCloser (Luo et al. 2012). We performed the annotation with the software Plann (Huang and Cronk 2015) and Sequin (NCBI website). Finally, we obtained a chloroplast genome of *M. pudica*. The genome has been submitted to GenBank under the accession number of MH671330.

The complete chloroplast genome of *M. pudica* is 163,237 bp in length, containing a large single-copy (LSC) region with of 92,045 bp, a small single-copy (SSC) region of 18,786 bp, and a pair of inverted repeats (IRA and IRB) with a length of 26,203 bp each. The GC content of *M. pudica*

chloroplast genome is 35.53% in total. The SSC region has lower GC content (29.84%) than the LSC (32.68%) and IR (42.59%) regions. The chloroplast genome of *M. pudica* contains 129 genes, including 84 protein-coding genes (PCG), eight ribosomal RNA (rRNA) genes, and 37 transfer RNA (tRNA) genes. Most genes are single copy; however, 17 genes (six PCGs, four rRNA genes, and seven tRNA genes) are duplicated in the IR regions.

To infer the phylogenetic position of *M. pudica* and estimate the phylogenetic relationships of mimosoid clade, we reconstructed a phylogenetic tree including 19 mimosoid species (including *M. pudica*) based on their complete chloroplast genomes. *Senna occidentalis* (*Senna*, Fabaceae), a species of cassia clade, was used as an outgroup. First, we extracted the coding sequences (CDS) from 76 protein-coding genes (PCGs), which were shared by all of 20 species. For each gene, PRANK (Löytynoja and Goldman 2008) was used to align the sequences. Then, each pair of the aligned sequences was concatenated into a supermatrix. The software RAXML (Stamatakis 2014) was performed to construct the phylogenetic tree with 100 bootstrap replicates. The ML tree revealed *M. pudica* was closely related to *Piptadenia communis* (*Piptadenia*, Fabaceae) with strongly support (Figure 1).

Above all, we provide a valuable genomic information of *M. pudica*. The phylogenetic tree we reconstructed could yield a better understanding for us about the mimosoid species.

CONTACT Zefu Wang  wzf09@lzu.edu.cn  Key Laboratory of Bio-Resource and Eco-Environment of Ministry of Education, College of Life Sciences, Sichuan University, Chengdu 610065, People's Republic of China

© 2018 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.



Figure 1. Maximum-likelihood (ML) tree based on the concatenated data of 76 PCGs sequences of *Mimosa pudica* and 19 other species. Numbers in the nodes are the bootstrap values. Their accession numbers are as follows: *Pararchidendron pruinosum*: NC_035348.1, *Archidendron lucyi*: NC_034988.1, *Paraserianthes lophantha*: LN885334.1, *Acacia ligulata*: NC_026134.1, *Acacia dealbata*: NC_034985.1, *Samanea saman*: NC_034992.1, *Albizia odoratissima*: NC_034987.1, *Inga leiocalycina*: NC_028732.1, *Pithecellobium flexicaule*: NC_034991.1, *Faidherbia albida*: NC_035347.1, *Senegalia laeta*: NC_036736.1, *Piptadenia communis*: NC_034990.1, *Parkia javanica*: NC_034989.1, *Vachellia flava*: NC_036734.1, *Dichrostachys cinerea*: NC_035346.1, *Leucaena trichandra*: NC_028733.1, *Prosopis glandulosa*: KJ468101, *Adenantha microsperma*: NC_034986.1, *Senna occidentalis*: MF358692.1.

Disclosure statement

No potential conflict of interest was reported by the authors.

References

- Dierckxsens N, Mardulyn P, Smits G. 2017. Novoplasty: de novo assembly of organelle genomes from whole genome data. *Nucleic Acids Res.* 4:e18.
- Griesmann M, Chang Y, Liu X, Song Y, Haberer G, Crook MB, Billault-Penneteau B, Lauressergues D, Keller J, Imanishi L, et al. 2018. Phylogenomics reveals multiple losses of nitrogen-fixing root nodule symbiosis. *Science.* 13:361.
- Huang DI, Cronk QCB. 2015. Plann: a command-line application for annotating plastome sequences. *Appl Plant Sci.* 3:1500026.
- Löytynoja A, Goldman N. 2008. Phylogeny-aware gap placement prevents errors in sequence alignment and evolutionary analysis. *Science.* 320: 1632–1635.
- Luo R, Liu B, Xie Y, Li Z, Huang W, Yuan J, He G, Chen Y, Pan Q, Liu Y, et al. 2012. Soapdenovo2: an empirically improved memory-efficient short-read de novo assembler. *GigaScience.* 1:1–6.
- Stamatakis A. 2014. RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics.* 30: 1312–1313.