

## The Complete Chloroplast Genome of a Variety of *Lagenaria siceraria* var. *microcarpa* (Naud.) Hara

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**Abstract** Small gourd (*Lagenaria siceraria* var. *microcarpa* (Naud.) Hara), a cultivar of *Lagenaria* family, is an important medicinal and ornamental plants. However, there are few studies on its chloroplast (cp) genome. In this study, we characterized its complete chloroplast (cp) genome with high throughput sequencing. The circular cp genome is determined to be 157, 121 bp in length, with a long sing-copy and a small sing-copy separated by a pair of inverted repeat regions. A total of 132 genes were annotated, including 86 protein-coding genes, 37 tRNA genes, 8 rRNA genes, and 1 pseudo gene. The overall GC content of cp genome was 37.09%. The maximum likelihood tree suggested that small gourd was closely related to *Lagenaria siceraria*. These results provided an understanding of small gourd cp genome and might be useful for future genetic studies.

**Keywords** *Lagenaria siceraria* var. *microcarpa* (Naud.) Hara; Chloroplast genome; Phylogenetic analysis

## Background

The genus *Lagenaria*, well known as a member of Cucurbitaceae family, comprises *Lagenaria siceraria* [Mol.] Stand (*L. siceraria*), *L. siceraria* var. *hispida*, *L. siceraria* var. *microcarpa*, and *L. siceraria* var. *depressa*. (Ahmed and Ashiq, 2018). Numerous pharmacological activities like anticancer, antidiabetic, antihelminthics, antimicrobial, and antioxidant have been found in the extract from *Lagenaria* (Mohan et al., 2012; Attar and Ghane, 2018). These characteristics indicate *Lagenaria* plants have great medicinal values in addition to edible and ornamental values. Small gourd (*L. siceraria* var. *microcarpa* (Naud.) Hara), a variety of *Lagenaria*, originates in China. Except Aiyang Li isolated a hypoglycemic component in small gourd, there are few researches have been made on small gourd (Li, 2009). However, the genetic information like nuclear genome and chloroplast (cp) genome still remains unknown. Since plant cp plays essential roles in photosynthesis and various metabolic pathways, therefore, we firstly characterized the complete cp genome of small gourd and deposited the genome in GenBank (GenBank accession number: MT773628.1).

## 1 Results

We planted a cultivar of small gourd, in Zhuanghang Comprehensive Experiment Station, Shanghai, China (121.391429°E, 30.894732°N) and the germplasm resource (voucher specimen: LS-133) was deposited in Shanghai Academy of Agricultural Sciences. Fresh plant leaves were obtained to extract DNA. Then, the extracted DNA was sequenced by Nanjing Genepioneer Biotechnologies Inc. (Nanjing, China) on Illumina Novaseq platform. After removing low-quality reads, obtained clean reads were used to assemble the cp genome by SPAdes version 3.10.1 (Bankevich et al., 2012), and gaps were filled by Gapfiller version 2.1.1 (Boetzer and Pirovano, 2012). Blast version 2.6 (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>) was used to annotate the assembled cp genome sequence, HMMER version 3.1b2 (<http://www.hmmer.org/>) was performed to predict rRNA, and ARAGORN version 1.2.38 (<http://130.235.244.92/ARAGORN/>) was used to identify tRNA. Finally, the cp genome map was generated by OGDRAW (<https://chlorobox.mpimp-golm.mpg.de/OGDraw.html>).

Consequently, a total of 157,121 bp in size of the circular cp genome of small gourd is obtained, consisting of a large single-copy (LSC) region of 86,891 bp and a simple single-copy (SSC) region of 18,012 bp (Figure 1). The LSC and SSC are separated by two invert repeat regions (IRa and IRb) of 26,146 in each region. The overall GC content is 37.09% higher than that of IR regions (16.64%) but lower than that of LSC (55.30%). A total of 132 genes, consisting of 86 protein-coding genes, 37 tRNA genes, 8 rRNA genes, and 1 pseudo gene, are predicted. Most of the genes occur in a single copy while 7 protein-coding genes (*ndhB*, *rpl2*, *rpl23*, *rps12*, *rps7*, *rpoC*, *ycf15*, and *ycf2*), 4 rRNA genes (*rrn16*, *rrn23*, *rrn4.5*, and *rrn5*), and 7 tRNA genes (*trnA-UGC*, *trnI-CAU*, *trn-GAU*, *trnL-CAA*, *trnN-GUU*, *trnR-ACG*, and *trnV-GAC*) are duplicated. Among protein-coding genes, 8 genes (*ndhA*, *ndhB*, *petB*, *petD*, *atpF*, *rpl2*, *rps16*, and *rpoC1*) contain one intron each and *rps12* possess two introns.

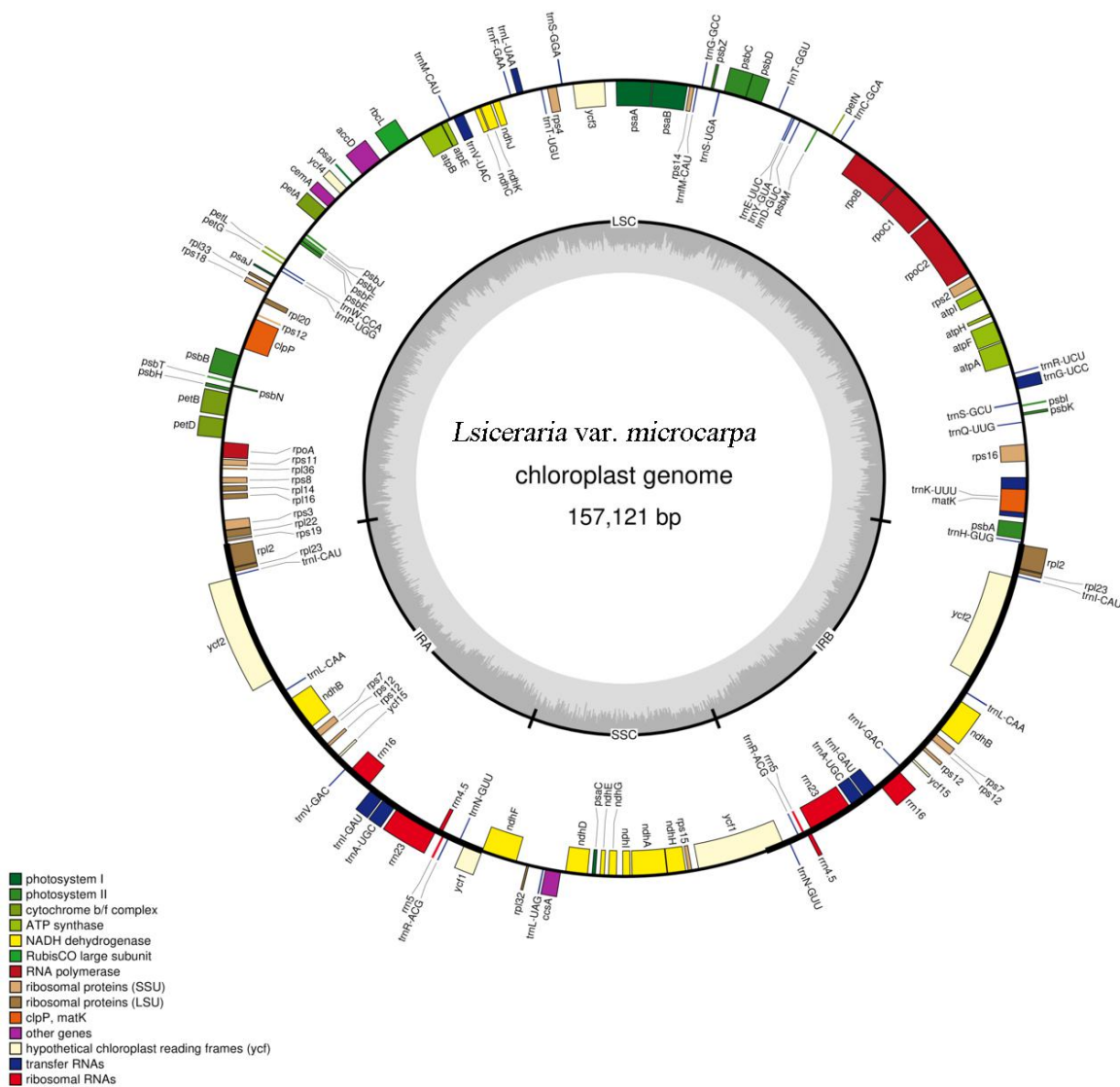


Figure 1 The cp genome map of *L.siceraria* var. *microcarpa* (Naud.) Hara.

Note: Boxes on the inside of the outermost circle represent genes clockwise transcription while boxes outside represent genes counterclockwise transcription. Dashed area in the inner circle represents GC content

To discover the phylogenic relationships of small gourd in Cucurbitaceae family, a phylogenetic analysis was performed on 11 cp genome sequencings. A multiple sequence alignment was finished by MAFFT version 7.427 (<https://mafft.cbrc.jp/alignment/software/>) (Kato and Standley, 2013), and phylogenetic tree was deduced using RAxML version 8.2.10 (<https://cme.h-its.org/exelixis/software.html>) based on the maximum likelihood (ML) with 1000 bootstrap replicates. The ML tree reveals that small gourd is most related to *L. siceraria* with 0 variation

coefficient and 100% bootstrap support value (Figure 2). Additionally, there is a small variation coefficient between small gourd and *Citullus lanatus* (Figure 2). Our discovery will provide values for future phylogenetic studies within *Lagenaria* genus.

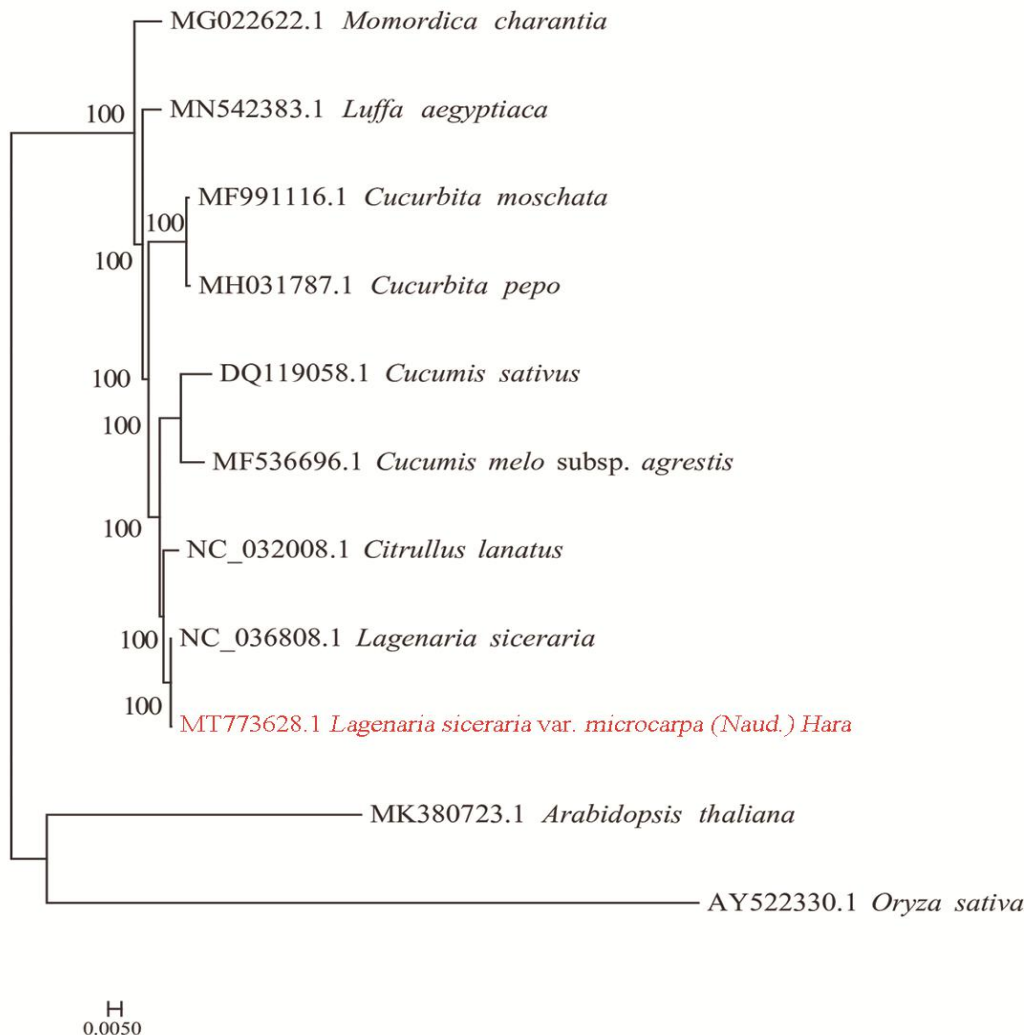


Figure 2 The phylogenetic tree of small gourd and 10 other species using whole cp genomes

Note: The bootstrap support values and GenBank accession numbers were shown at the branches

## 2 Availability of Data and Material

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/nucleotide/MT773628.1/>) under the accession No. MT773628.1. The associated BioProject, SRA, and Bio-Sample numbers are PRJN668886, SRR12824716, and SAMN16427048, respectively.

### Authors' contributions

Zhaohui Zhang planted the small gourd for cp genome sequencing. Dandan Xi wrote this manuscript. Jie Zhao, Xiaofeng Li, Lu Gao, Chunhong Chen, and Yuying Zhu helped to prepare samples and perform the statistical analysis. Hongfang Zhu designed the study and helped to write the manuscript. All authors read and approved the final manuscript.

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### Conflicts of interest

No potential conflict of interest was reported by the authors

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