

Complete chloroplast genome of a semi-mangrove plant *Hibiscus tiliaceus* (Malvaceae)

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ABSTRACT

Hibiscus tiliaceus is a semi-mangrove species that is widely distributed in tropical and subtropical coastal areas around the world. Here, the complete chloroplast (cp) genome sequence of *H. tiliaceus* was assembled and characterized. The cp genome was 161,748 bp in length, consisting of a large single copy (LSC) region of 89,190 bp and a small single copy (SSC) region of 19,616 bp, which were separated by a pair of 26,471 bp inverted repeat (IR) regions. The overall GC content was 36.88%. A total of 131 genes, including 85 protein-coding genes, 37 tRNA genes and 8 rRNA genes were identified. Phylogenetic tree reconstructed by 15 complete cp genomes revealed that *H. tiliaceus* was sister to the congeneric species *H. cannabinus*.

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Hibiscus tiliaceus L. (Malvaceae) is a common coastal semi-mangrove plant that is widely distributed in tropical and subtropical America, Africa, Asia, Australia, and throughout the Pacific islands (Abdul-Awal et al. 2016). As a fast-growing, wind- and salt-resistant tree or larger shrub, it grows well and is abundant in littoral forests and mangrove forest margins of atolls and high islands (Feng et al. 2008). It was used for the stabilization of sand dunes, the formation of coastal windbreaks, and also as a landscape tree species inland due to its wide adaptation various eco-geographic conditions (Tang et al. 2003). In addition, it has been used as a traditional medicine for the treatment of fevers and coughs, ear infections and abscesses, postpartum disorders, and skin diseases in Asian and African countries (Vanzella et al. 2012; Abdul-Awal et al. 2016). The phylogeography and genetic diversity of *H. tiliaceus* have been assessed on the basis of variations in chloroplast (cp) DNA sequences in several previous studies (Tang et al. 2003; Takayama et al. 2006; Yang et al. 2011; Shi et al. 2020). However, the information of the complete cp genome is still lacking. Here, we report and characterize the complete cp genome of *H. tiliaceus* to further study its genetic research and resource utilization.

Fresh leaves of *H. tiliaceus* were sampled from Beilun Gulf, Guangxi, China (N21°36'50", E108°14'20"). The voucher specimen (NNU20200325) was stored in the Herbarium of Nanning Normal University. The complete genomic DNA was extracted from the fresh leaves using a modified CTAB protocol (Doyle and Doyle 1987). Complete genome sequencing was conducted by Genepioneer Biotechnologies Inc. (Nanjing, China) on the Illumina HiSeq platform. The filtered sequences were assembled using the program SPAdes assembler 3.10.0 (Bankevich et al. 2012). Annotation was

performed using GeSeq (Tillich et al. 2017) and manually corrected.

The cp genome of *H. tiliaceus* was determined to comprise a 161,748 bp double-stranded, circular DNA (GenBank accession no. MT644160), containing two inverted repeat (IR) regions of 26,471 bp, separated by large single-copy (LSC) and small single-copy (SSC) regions of 89,190 and 19,616 bp, respectively. The overall GC content of the cp genome of *H. tiliaceus* is 36.88%. The cp genome was predicted to contain 131 genes, including 85 protein-coding genes, 37 tRNA genes, and 8 rRNA genes. Six protein-coding genes, seven tRNA genes, and four rRNA genes were duplicated in the IR regions. Fifteen genes contained one intron, while three had two introns (clpP, rps12, and ycf3). The corresponding values in IR, LSC, and SSC regions are 42.7%, 34.8, and 30.8, respectively.

To identify the phylogenetic position of *H. tiliaceus*, alignment was performed on the 15 cp genome sequences using MAFFT v7.307 (Katoh and Standley 2013), and a maximum likelihood (ML) tree was constructed by RAxML v8.2.10 (Stamatakis 2014). The results indicated that *H. tiliaceus* is mostly related to the congeneric species *H. cannabinus* (Figure 1). The complete cp genome sequence of *H. tiliaceus* will provide a useful resource for facilitating its genetic research and further utilization of *Hibiscus*.

Disclosure statement

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

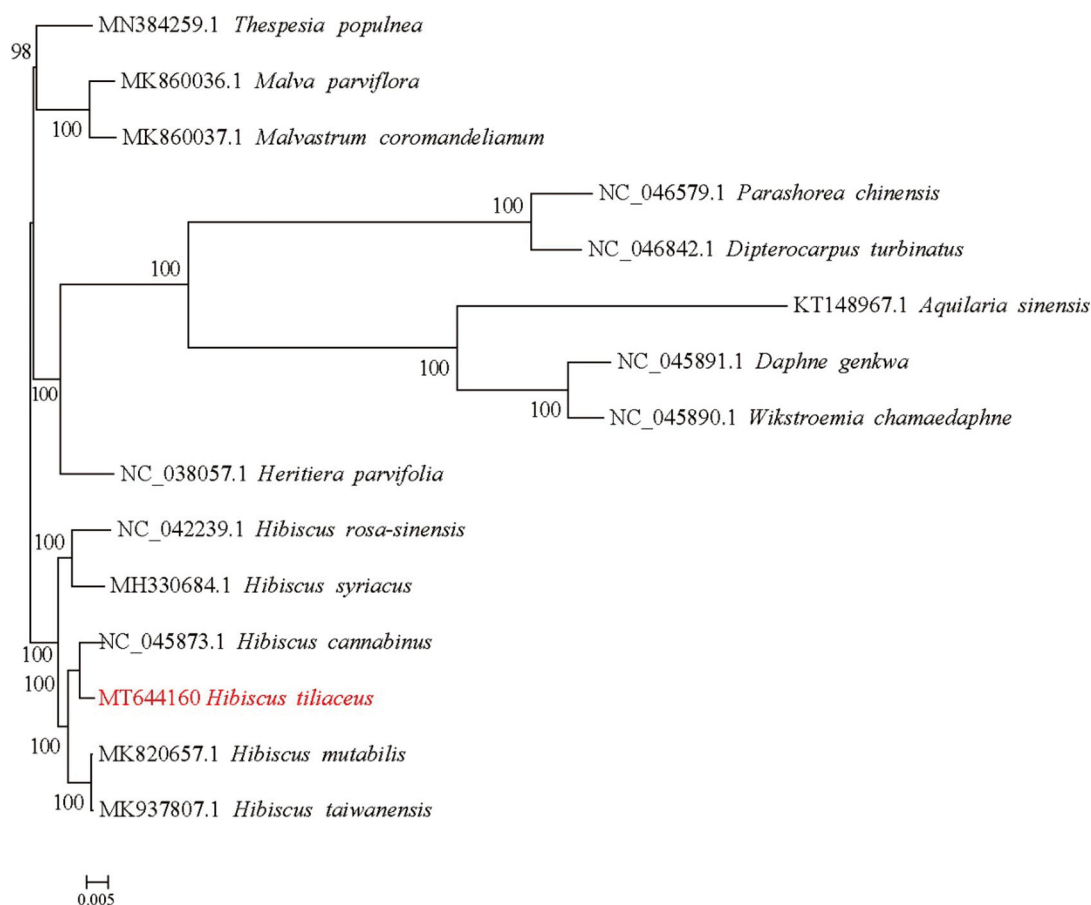


Figure 1. Phylogenetic relationship of the *H. tiliaceus* chloroplast genome with 14 previously reported complete chloroplast genomes. A total of 1000 bootstrap replicates were computed and the bootstrap support values are shown at the branches. GenBank accession numbers were shown.

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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/>) under the accession no. MT644160. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA666500, SRS7451015, and SAMN16295088, respectively.

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