The complete chloroplast genome and phylogenetic analysis of *Artocarpus champeden*

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**ABSTRACT**

*Artocarpus champeden* Spreng. is a popular fruit tree, grown in tropical and subtropical regions. Besides food, *A. champeden* is also a medicinal plant with various medicinal properties. In this study, *A. champeden* chloroplast genome was sequenced, assembled, and annotated due to its rich information on species evolution and inter-species genetic relationships. The quadripartite structure of *A. champeden* complete chloroplast genome is 158,568 bp in length and comprises a large single-copy region (LSC) of 88,076 bp, a small single-copy region (SSC) of 19,028 bp, and two inverted repeat regions (IRa and IRb) of 25,732 bp. A total of 131 genes were annotated, including 85 protein-coding genes, 37 tRNA genes, eight rRNA genes, and one pseudogene. Phylogenetic analysis revealed a close relationship between *A. champeden* and *A. heterophyllus*. In addition, the study provides abundant genomic information for future phylogenetic studies of *A. champeden* and the Moraceae family.

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Chloroplast genome sequences of 22 species (Figure 1) of Moraceae family were downloaded from GenBank and used to study the phylogeny of *A. champeden*. Multiple sequence alignment was performed using MAFFT (Katoh and Standley 2013), the jModelTest 2.1.7 (David 2008) software was employed to analyze nucleotide substitutions model under the Akaike Information Criterion (AIC), the GTR $+$ G $+$ I model was selected for nucleotide and the maximum-likelihood analysis was conducted with RAxML8.2.4 (Stamatakis 2014). *Eriobotrya malipoensis*, which belongs to the Rosaceae family, was the out-group, and the node support was estimated from the results of 1000 bootstrap replicates. The phylogenetic analysis revealed a close relationship between *A. champeden* and *A. heterophyllus* (Figure 1). This study provides abundant genomic information for future phylogenetic studies of the Moraceae family.

**Disclosure statement**

No potential competing interest was reported by the authors.

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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. MT900597. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA703082, SRR13781753, and SAMN18011290 respectively.

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Figure 1. Maximum-likelihood tree based on the complete chloroplast genome sequences of *A. champeden* and 21 other species of the Moraceae family. *Eriobotrya malipoensis*, which belongs to the Rosaceae family is the out-group.
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