The complete chloroplast genome of Zanthoxylum piasezkii Maxim. (Rutaceae) and its phylogenetic analysis

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ABSTRACT
Zanthoxylum piasezkii Maxim. is a widely distributed species of edible medicinal plant in China. It has been used for traditional spicy condiment and medicinal ingredients for quite a long time. In this study, the complete chloroplast genome sequence of \(Z.\) piasezkii was first reported and characterized from sequencing data. The complete chloroplast genome was determined to be 158,728 bp in length, consisting of a large single-copy (LSC) region (85,918 bp) and a small single copy (SSC) region (17,612 bp), which were separated by a pair of 27,599 bp inverted repeat (IR) regions. The chloroplast genome is predicted to contain 132 genes, including 87 protein-coding genes, 37 tRNA genes, and 8 rRNA genes. The overall GC content of cpDNA is 38.4%. The phylogenetic analysis of 12 complete chloroplast genomes reveals that \(Z.\) piasezkii is mostly related to the congeneric \(Z.\) bungeanum.
whole cp genome sequences of *Z. piasezkii* will pave the foundation for future research to understand the chloroplasts genomic information of the genus *Zanthoxylum* and conservation genetics.

**Disclosure statement**

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

**Funding**

The work was supported by the National Natural Science Foundation of China [31901324], Natural Science Foundation general Project of Chongqing Science and Technology Bureau [cstc2019jcyj-msxmX0693], and Technology Innovation and Application Development special key Project of Chongqing Science and Technology Bureau [cstc2019jxcx-gksbX0110].

**Data availability statement**

The raw sequencing data is deposited in the SRA database with the accession number SRX9591236 (https://www.ncbi.nlm.nih.gov/sra/?term=SRX9591236).

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