

The complete chloroplast genome sequence of *Ziziphus attopensis* (Rhamnaceae) and its phylogenetic analysis

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ABSTRACT

Ziziphus attopensis has high medicinal value of tonic, carminative, appetizer, and muscle analgesic. To provide genetic information for further research and conservation, the complete chloroplast genome sequence of *Z. attopensis* was determined in this study. The genome was 161,342 bp in length, consisting of a large single copy region (89,035 bp), a small single copy region (19,421 bp), and a pair of inverted repeat regions (26,443 bp). In total, 129 genes were identified in *Z. attopensis* chloroplast genome, including 85 protein coding genes, eight rRNA, and 36 tRNA genes. Maximum-likelihood tree inferred from 58-gene sequences of 20 taxa supported that Rhamnaceae is sister to Elaeagnaceae and *Z. attopensis* is more closely related to *Ziziphus jujuba*.

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Ziziphus attopensis Pierre is a scandent shrub belonging to the family of Rhamnaceae (Hauenschield et al. 2016), distributed in sparse forests, thickets, up to 1500 m in Liaos and Thailand. The decoction from the bark and wood of *Z. attopensis* was suggested to be used as tonic, carminative, appetizer, and muscle analgesic. The water extract from *Z. attopensis* did not contain acute or chronic toxicities (Sireeratawong et al. 2012). In this study, the complete chloroplast genome of *Z. attopensis* was determined and analyzed.

Fresh leaves of *Z. attopensis* were collected from Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences (N21°55'53", E101°15'46") and stored in silica gel for later use. The voucher specimen (MGZ-01) was deposited at Shaanxi Xueqian Normal University. Total DNA was extracted from 2 g of leaves using Qiagen DNeasy Plant Mini Kit (Qiagen, Hilden, Germany). Sequencing was conducted on Illumina HiSeq™ 2500 platform (Illumina Inc., San Diego, CA). After removing adapter and low-quality reads, contigs were *de novo* assembled using velvet (V1.2.07) (Zerbino and Birney 2008). Complete chloroplast genome of *Z. attopensis* was annotated by PGA (Qu et al. 2019) and submitted to GenBank using Bankit (The accession number is MW201670).

Assembled chloroplast genome of *Z. attopensis* was 161,342 bp in size, which is shorter than *Ziziphus jujuba* with 161,466 bp and *Z. jujuba* cv. Dongzao with 161,493 bp (Gao et al. 2017; Ma et al. 2017). It has a typical quadripartite

circular structure including a larger single copy region with 89,035 bp, a small single copy region with 19,421 bp separated by a pair of inverted repeat sequences with 26,443 bp. A total of 129 genes were identified, including 85 protein-coding genes, eight rRNA genes, and 36 tRNA genes. Among which, five protein-coding, four rRNA, and six tRNA genes were duplicated in IR regions. Fifteen genes contain one intron (*trnK-UUU*, *rps16*, *rpoC1*, *atpF*, *trnG-UCC*, *trnL-UAA*, *trnV-UAC*, *petD*, *petB*, *rpl16*, *rpl2*, *ndhB*, *trnA-UGC*, *ndhA*, *trnI-GAU*), and three genes contain two introns (*ycf3*, *clpP*, *rps12*). *InfA* gene has been lost in *Z. attopensis* cp genome. Overall GC content of the cp genome is 36.81%, the LSC, SSC, and IR are 34.67%, 30.87%, and 42.60%, respectively.

To investigate the phylogenetic position of *Z. attopensis*, maximum-likelihood implemented in MEGA (Kumar et al. 2018) was used to construct the phylogenetic tree. As the chloroplast genome structure may be rearranged among different species, analysis was performed using 58 protein-coding genes that were present in 18 species from Rhamnaceae, Vitaceae, Celastraceae, Elaeagnaceae, and two outgroups *Nicotiana tabacum* and *Amborella trichopoda*. Result revealed that *Z. attopensis* clustered with *Z. jujuba*; five species from *Ziziphus* genus consisting of a monophyletic group, and then clustered with *Hovenia dulcis*. Rhamnaceae was resolved as sister to Elaeagnaceae (Figure 1). This study provides basic data for the research of genetic diversity and phylogeography of *Z. attopensis* population and supplies

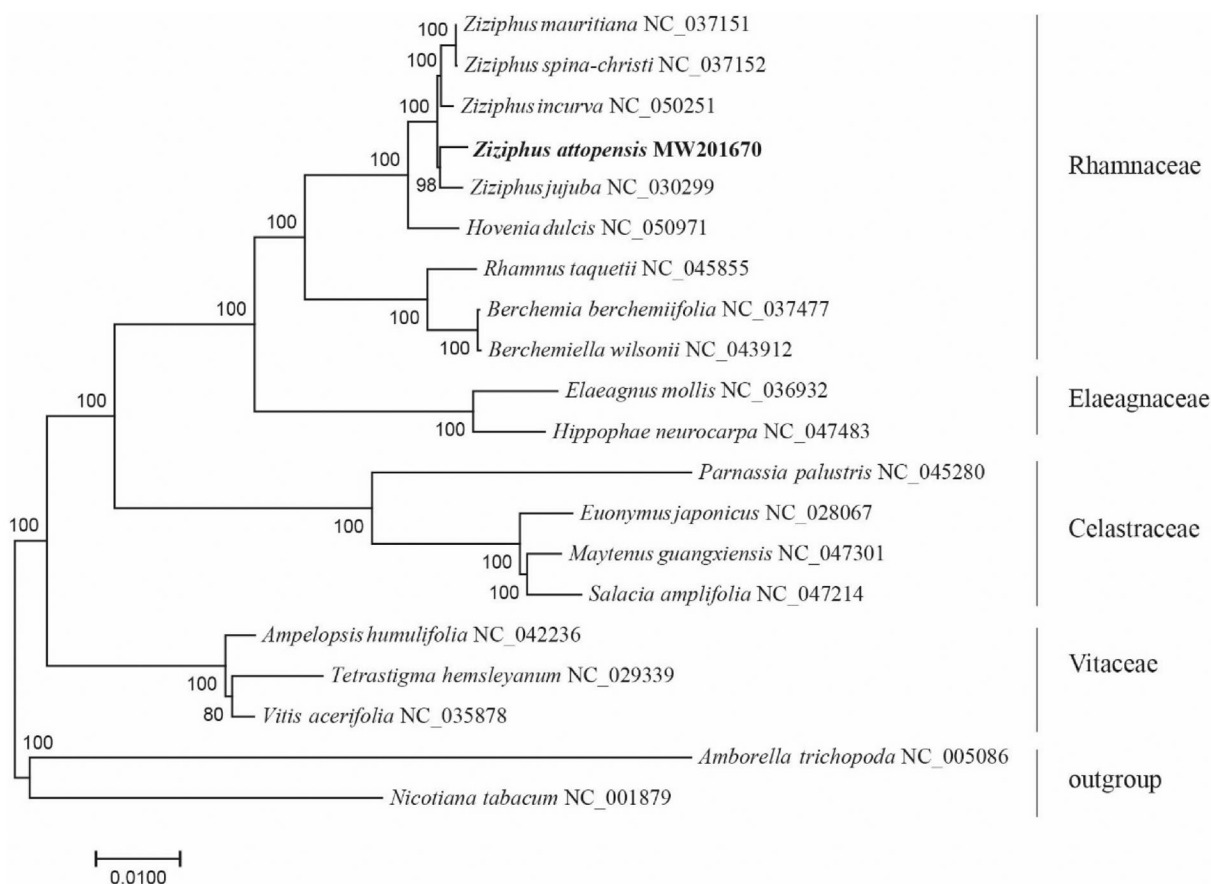


Figure 1. Phylogenetic tree constructed based on 58 common protein-coding genes of 20 species. Bootstrap values are shown near the nodes. Scale in substitution per site.

evidence for the phylogeny of Rhamnaceae in aspect of molecular data.

number MW201670. The raw sequence data were deposited successfully with registered number of SRR13442540.

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Disclosure statement

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

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Data availability statement

The data that newly sequenced in this study are available in the NCBI GenBank database (<https://www.ncbi.nlm.nih.gov>) under accession

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