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Complete plastid genome sequence of *Halimodendron halodendron* (Leguminosae)

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ABSTRACT

Halimodendron halodendron (Pall.) Voss. is a deciduous shrub belonging to the genus *Halimodendron*, Leguminosae, and is mainly distributed in dry areas. This species can be used for saline-alkali soil improvement and sand fixation. The complete plastid genome of *H. halodendron* first reported here is 129,342 bp in length, and contains 110 genes, including 76 protein coding genes, 30 tRNA genes, and 4 rRNA genes. A total of 105 simple sequence repeats (SSRs) were identified in the chloroplast genome. This information will be useful for study on the evolution and genetic diversity of *Halimodendron halodendron* in the future.

Halimodendron halodendron (Pall.) Voss. is a deciduous shrub belonging to Leguminosae. It mainly grows in Xinjiang, Gansu (sandy soil of Hexi Corridor), northwestern Inner Mongolia in China, and the former Soviet Union and Mongolia also have distribution. It is usually found in desert salinized sandy soils, saline soils along riverbank, and under *Populus euphratica* forests. *Halimodendron halodendron* has significant effects on soil nitrogen fixation under arid or semi-arid conditions (Matinkhah et al. 2020). Besides, the phenols extracted from *H. halodendron* also show antibacterial and antioxidant activities (Wang et al. 2012). Therefore, it is both an ecologically and economically important plant. In this study, to obtain the new insight into the phylogeny of *H. halodendron*, we assembled and annotated the plastid genome from sequenced data.

The materials of *H. halodendron* in this study were collected from Wushi County, Aksu prefecture, Xinjiang province of China (79°24.949′E, 41°12.346′N, 1322 m above sea level). The voucher specimen (TD-00549, *Halimodendron halodendron* (Pall.) Voss.) was stored in the herbarium of Tarim University, and the data related to the specimens are included in the database of wild plant germplasm resources of the Tarim basin (http://res.taru.edu.cn/, internal website, not yet open to the public; data available from the corresponding author Peipei Jiao upon reasonable request, jiaopeipei2000@126.com). The complete genomic DNA was extracted using CTAB method (Doyle et al. 1987) and sequenced using the Illumina NovaSeq 6000 platform at
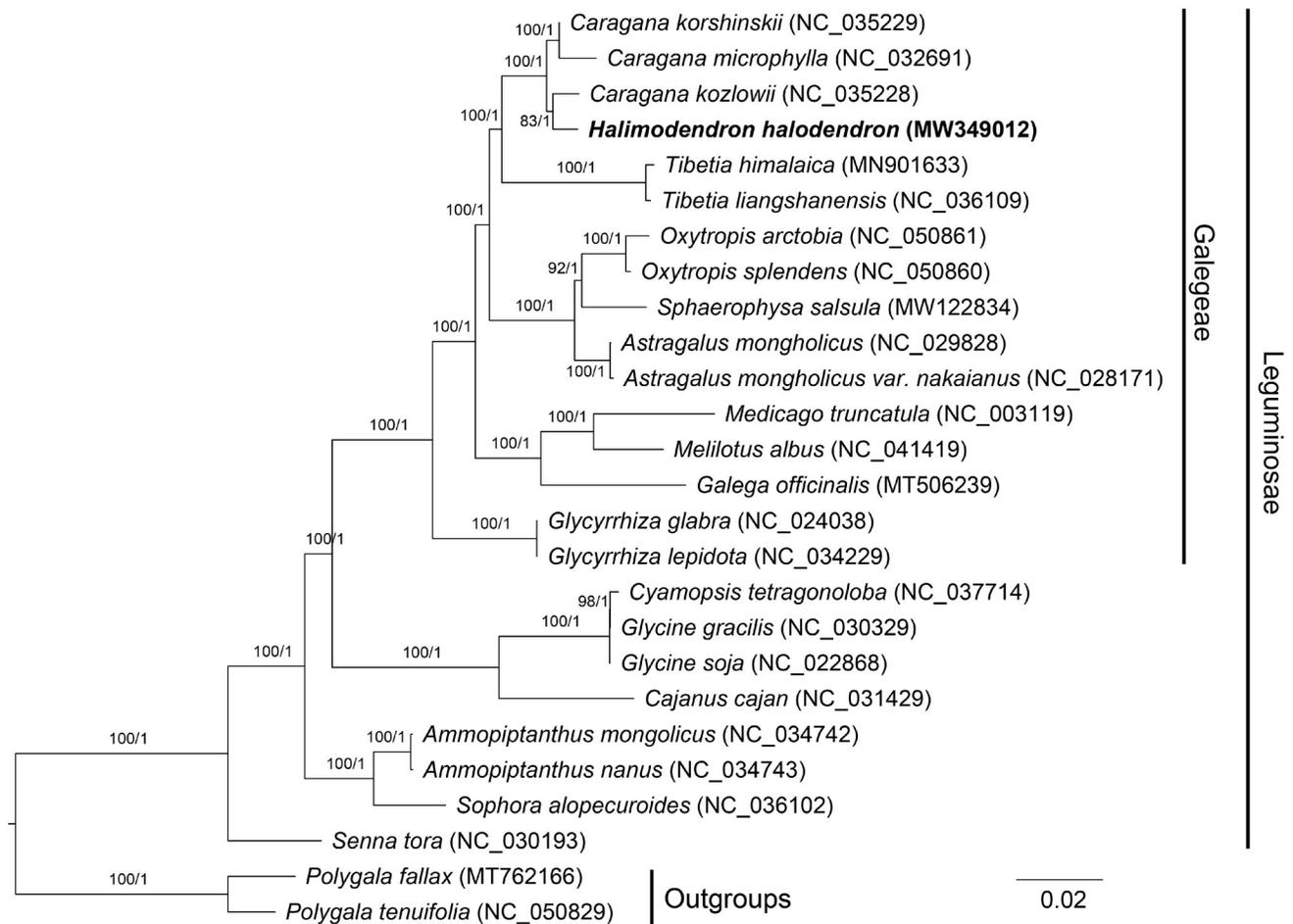
Majorbio Company (Shanghai, China). We removed low-quality sequences from the raw data (SRR13270803). The trimmed reads were assembled using GetOrganelle v1.7.3 (Jin et al. 2020). Then, the plastid gene structures were annotated using CPGAVAS2 (Shi et al. 2019) and PGA (Qu et al. 2019). The complete plastid genome was 129,342 bp (MW349012) and lost an IR region, the average GC content was 34.4%. Generally, chloroplast genomes are characterized by a quadripartite structure, with two copies of an inverted repeat (IR) separating the large (LSC) and small (SSC) single copy regions. Losing one copy of the IR in the plastid genome is a common phenomenon in some tribes among legumes, such as Carmichaelieae, Cicereae, Hedysareae, Trifolieae, Fabeae, Galegeae, and three genera of Millettieae (Palmer and Thompson 1982; Lavin et al. 1990; Liston 1995; Jansen et al. 2008). This may be a special feature of legumes in the evolutionary process. The complete plastid genomes encoded 110 functional genes, including 76 protein-coding genes, 30 tRNA genes, and 4 rRNA genes. A total of 105 SSR markers ranging from mononucleotide to hexa-nucleotide repeat motif were identified in *H. halodendron* plastid genome.

To explore the phylogenetic relationship of *H. halodendron* within Leguminosae, additional 23 species from Leguminosae were studied. With the *Polygala tenuifolia* and *Polygala fallax* as the outgroups, the phylogenetic trees were built from the whole protein-coding gene matrix by maximum-likelihood (ML) and Bayesian inference (BI) (Figure 1). The ML tree was generated using IQ-TREE v2.1.2 (Nguyen et al. 2015) based

Figure 1. Phylogenetic tree reconstructed by maximum-likelihood (ML) and Bayesian inference (BI) analysis based on the 79 plastid protein-coding genes of 26 species. Values above branches are maximum likelihood bootstrap percentages (BS)/Bayesian posterior probabilities (PP).

on the best model of TVM + F+G4 and 1000 bootstrap replicates, and BI analysis was performed in MrBayes v3.2.7 (Ronquist et al. 2012). *Halimodendron halodendron* is the only species under the genus of *Halimodendron* currently, and the phylogenetic trees indicate that *H. halodendron* was closer to the species of *Caragana kozlowii*. The information will provide the basis for the study of *H. halodendron* in the future.

Disclosure statement

No potential conflict of interest was reported by the authors.

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Data availability statement

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