The complete chloroplast genome sequence of *Artemisia ordosica*

Ke Lu\(^a\), Wei Mao\(^c\), Zhongyu Du\(^{a,b}\), Yiming He\(^a\), Cheng Fan\(^a\), Kai Zhang\(^a\), Lijun Wang\(^c\), Guoming Liu\(^c\) and Yizhong Duan\(^a\)

\(^a\)Shaanxi Key Laboratory of Ecological Restoration in Northern Shaanxi Mining Area, Yulin University, Yulin, China; \(^b\)Breeding Base for State Key Laboratory of Land Degradation and Ecological Restoration in Northwest China, Ningxia University, Yinchuan, China; \(^c\)Yulin Municipal Health Commission, Yulin, China

**ABSTRACT**

*Artemisia ordosica* is one of the important plants in succession of psammophytes in sandy (desert), it is a high ecological, economic and scientific research value. The chloroplast is photosynthetic organelles that provide energy for green plants. In this study, we reported the complete chloroplast (cp) genome sequence of *A. ordosica*, which were assembled using high-throughput sequencing technology. The results showed that the total cpDNA genome of *A. ordosica* is 151,209 bp in length, consisting of a large single copy (LSC) region of 82,980 bp, a small single copy (SSC) region of 18,303 bp, and a pair of inverted repeat regions (IRa and IRb, 24,963 bp each). Among all genes, the content of GC is 37.4%. The LSC, SSC, and IRs are 58.44%, 12.10%, and 33.02% of the *A. ordosica* cpDNA genome length respectively. Furthermore, the genome contained a total of 113 genes, comprising 79 protein-coding genes, 4 rRNA genes, and 29 tRNA genes. A phylogenetic analysis based on 21 cpDNA genomes suggested that the *A. ordosica* is closely related to *A. scoparia*.

**Introduction**

*Artemisia ordosica* belongs to *Artemisia* of Compositae, which is an important and unique sand-fixing semi-shrub plant in China (Zhang et al. 2003). *A. ordosica* has rich nutritional value and high medicinal value. (Xiao et al. 2016). At present, many scientists have done a lot of research on the ecology and the determination of chemical components (Zhong et al. 2016; Hao et al. 2019). However, the characteristics of the complete chloroplast genome of *A. ordosica* has not been elucidated. Therefore, the fresh leaves of *A. ordosica* were used to analyze the cpDNA genome by the high-throughput sequencing technology in this study. We hope to provide some help for the study of *A. ordosica* in the future.

**Materials and methods**

Fresh *A. ordosica* leaves were collected in Gudimao Village, Qinhe Town, Yuyang District, Yulin City, Shaanxi Province, China (E 109°41'10.71", N 38°18'19.61"; Height:1,080 m above sea level) in September 2019. The specimen of *A. ordosica* was saved at the Herbarium (Accession Number: 20190901Y01) of College of Life Sciences, Yulin University, Shaanxi Province, China. Total DNA was extracted from the fresh leaves according to a modified cetyltrimethyl ammonium bromide (CTAB) method (Doyle and Doyle 1987). The subsequent high-throughput sequencing was completed with the IlluminaHiSeq Ten system, with the *Artemisia frigida* (NC020607) cpDNA genome was used as the reference sequence to annotate. The *A. ordosica* cpDNA genome was annotated with Geneious program (Kearse et al. 2012) after its sequence was aligned with the reference cpDNA genome. The OGDRAW online was used to visualize the *A. ordosica* cpDNA genome (Lohse et al. 2013). The cpDNA genome sequences were aligned using MAFFT (Katuta et al. 2002). We used the MEGA 7.0 program (Kumar et al. 2016) to construct a phylogenetic tree with the cpDNA sequences from 20 other plants according to the Neighbour-joining (NJ) method, with a bootstrap value of 1000. The annotated *A. ordosica* cpDNA genome sequence has been deposited into the GenBank database (accession number: MN932370).

**Results**

The cpDNA genome of *A. ordosica* was 151,209 bp in length, similar with the chloroplast structure of most other plants, with a typical quadripartite structure (Shinozaki et al. 1986; Chao, et al. 2017). The genome contains a pair of inverted repeat regions (IRa and IRb, 24,963 bp each) separated by a large single copy region (LSC, 82,980 bp) and a small single copy region (SSC, 18,303 bp). Among all genes, the content of GC is 37.4%. The LSC, SSC and IR regions accounted for 58.44%, 12.10%, and 33.02% of the cpDNA genome of *A. ordosica*, respectively. Furthermore, a total of 113 gene

**CONTACT**

Yizhong Duan duanyizhong2006@163.com Shaanxi Key Laboratory of Ecological Restoration in Northern Shaanxi Mining Area, Yulin University, Yulin 719000, China

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species were annotated for *A. ordosica*, including 79 protein-coding genes, 4 rRNA genes, and 29 tRNA genes.

We constructed a phylogenetic tree based on 21 cpDNA genome sequences, with the *Erodium absinthoides* (NC026847) and *Erodium chrysanthum* (NC027065) cpDNA genome serving as an outgroup (Figure 1). We aligned all 21 cpDNA genome sequences using MAFFT. The result showed that the *A. ordosica* (MN932370) is closely related to *A. Scoparia* (MN385624).

**Disclosure statement**

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

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**Figure 1.** Phylogenetic tree constructed based on 21 species of chloroplast genome sequences. Accession numbers: *Artemisia scoparia* (MN385624); *Artemisia frigida* (NC026067); *Artemisia montana* (NC025910); *Artemisia maritima* (MK532038); Centaurea diffusa (NC024286); *Taraxacum mongolicum* (NC031396); *Parthenium argentatum* (NC013553); *Praxelis clematidea* (NC023833); *Platycodon grandiflorus* (NC035624); *Salvia japonica* (NC035233); *Leonurus japonicus* (NC038062); *Dendrobiurn officinale* (NC024019); *Lilium brownii* var. (KX347245); *Iris sanguinea* (NC029227); *Artemisia annua* (MF623173); *Glycyrrhiza uralensis* (KURB62308); *Medicago sativa* (KU321683); *Ginkgo biloba* (NC016986); *Erodium absinthoides* (NC026847); *Erodium chrysanthum* (NC027065); *Artemisia ordosica* (MN932370).