


The complete chloroplast genome of *Agropyron desertorum* (Fisch. ex Link) Schult

Junfeng Yang^a, Wenxuan Du^b and Yongzhen Pang^{a,c} 

^aInstitute of Animal Sciences, Chinese Academy of Agricultural Sciences, Beijing, China; ^bKey Laboratory of Plant Resources and Beijing Botanical Garden, Institute of Botany, Chinese Academy of Sciences, Beijing, China; ^cUniversity of Chinese Academy of Sciences, Beijing, China

ABSTRACT

Agropyron desertorum is one of the most important fodder grasses which distributes in the temperate regions of the world. In this study, the complete chloroplast genome of *A. desertorum* was sequenced. The genome was 135,459 bp in length, with a large single-copy region of 79,617 bp, a small single-copy region of 12,760 bp, and two inverted repeat regions of 21,541 bp. The genome consisted of 132 genes, including 86 protein-coding genes, 38 tRNA genes, and 8 rRNA genes. The GC contents was 38.32%. We constructed the Maximum likelihood (ML) tree with 13 species from the Hordeinae genus, and concluded that *A. desertorum* was closely related to plant species of the *Elymus* genus in the phylogenetic tree.

ARTICLE HISTORY

Received 22 February 2021
Accepted 31 May 2021

KEYWORDS



Agropyron desertorum (Fisch. ex Link) Schult.; chloroplast genome; phylogenetic analysis

Agropyron desertorum (Fisch. ex Link) Schult. belongs to the Gramineae family, which is one of the most important grasses in the temperate regions of the world. *A. desertorum* is a wild grass with strong growth potential, high yield, soft quality and high nutrition value, which is an excellent source of forage and habitat for livestock and wildlife (Jafari et al. 2008). *A. desertorum* has strong drought resistance, cold resistance and sand fixation function, which is valued for weed control, habitat use, soil conservation and watershed management. *Agropyron desertorum* is generally adapted to sub-humid to arid climatic conditions in steppe or desert regions (Jafari et al. 2008). Due to these valuable characteristics, *A. desertorum* is suitable for the restoration and rehabilitation of rangelands in the arid and semi-arid regions (Goraghani et al. 2013; Shanjani et al. 2013). In this study, we determined the complete chloroplast genome sequences of *A. desertorum* and compared the sequence with those of other species of Hordeinae to analyze the phylogenetic relationship among them.

Seeds of *A. desertorum* was kept at the Forage Germplasm Bank at Institute of Animal Sciences of the Chinese Academy of Agricultural Sciences (Beijing, E116°29', N40°03'). The voucher specimen (FG17198) was deposited at the Herbarium of the Institute of Animal Sciences of the Chinese Academy of Agricultural Sciences, Beijing, China. After germination in the laboratory, genomic DNA from young leaves was extracted using a DNA Extraction Kit from Tiangen Bio Tech Co., Ltd (Beijing, China). The genomic DNA was broken and fragmented to 400 bp fragments by using the high-pressure

nitrogen or a Covaris machine, and these fragments were used as the template for the paired-end library. The paired-end library was constructed with Illumina TruSeq DNA Sample Preparation kit according to the Illumina TruSeq DNA Sample Preparation Guide. The sequencing was carried out on the Illumina Novaseq PE150 platform (Illumina Inc, San Diego), and 150 bp paired-end reads were generated. The software GetOrganelle v1.5 (Jin et al. 2018) was used to assemble the cleaned reads into a complete chloroplast genome with the chloroplast genome of *Alopecurus aequalis* (NC_047228.1) as reference. The chloroplast genome annotation was performed through the online program CPGAVAS2 (Shi et al. 2019) and GeSeq (Tillich et al. 2017), followed by manual correction. The assembled chloroplast genome sequence was submitted to GenBank under the accession number MW309818.

In the present study, it was found that the chloroplast genome of *A. desertorum* showed a quadripartite structure, with two reverse repeated regions (IRa and IRb) of 21,541 bp in length. The repeat regions divided the genome into two single-copy regions, SSC and LSC with 12,760 bp and 79,617 bp, respectively. The GC contents of the LSC, SSC, and IR regions individually, and of the chloroplast genome as a whole, are 39.64%, 35.72%, 36.66%, and 38.32%, respectively. It encodes a total of 132 unique genes, of which 42 are duplicated in the IR regions. Out of the 132 genes, there are 86 protein-coding genes, 38 tRNA genes, and 8 rRNA genes. Nineteen genes contained introns, and 17 (nine protein-coding and eight tRNA

CONTACT Yongzhen Pang  pangyongzhen@caas.cn  Institute of Animal Sciences, Chinese Academy of Agricultural Sciences, No. 2 Yuanmingyuan West Road, Haidian District, Beijing, 100193, China

© 2021 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group. This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0/>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

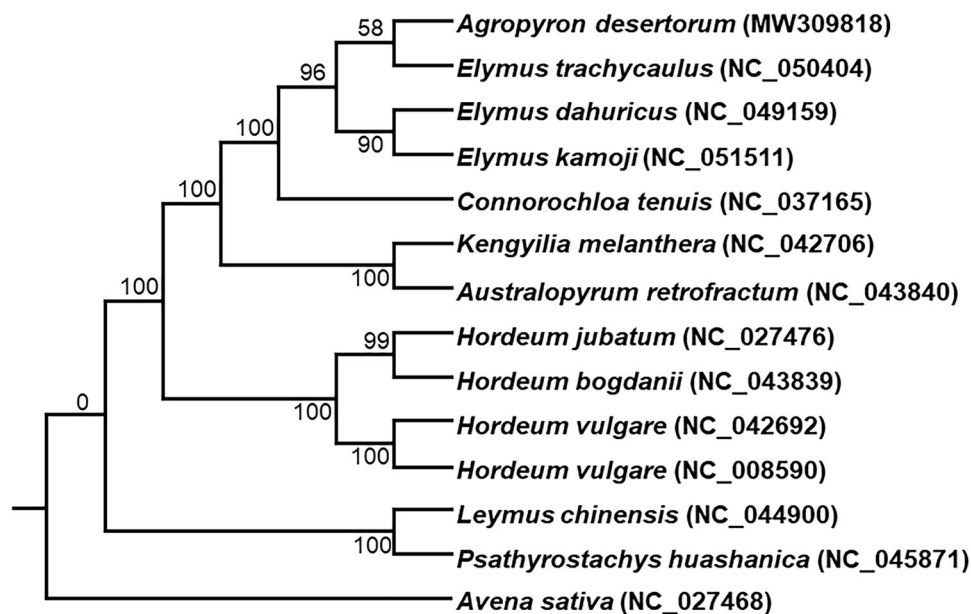


Figure 1. Phylogenetic tree constructed using maximum likelihood (ML) method based on the common protein-coding genes of 13 species of the Gramineae family, with *Avena sativa* as the out-group by using raxmlGUI1.5b and the best nucleotide substitution model: PROTGAMMALGX. Numbers above the nodes are bootstrap values based on 1000 replicates.

genes) of them contains one intron and two of them (*rps12* and *ycf3*) contain two introns.

The chloroplast genomes of 13 species from Hordeinae were downloaded from the NCBI GenBank database to infer the phylogenetic relationship of *A. desertorum*. The sequences were aligned using MAFFT v7 (Kato et al. 2019). In addition, a maximum likelihood (ML) tree based on the common protein-coding genes of 14 species, with *Avena sativa* as out-group, was constructed by using raxmlGUI1.5b (v8.2.12) (Silvestro and Michalak 2012). Phylogenetic analysis shows that *A. desertorum* is closely related to the plant species of the *Elymus* genus (e.g. *E. trachycaulus*, *E. dahuricus* and *E. kamoji*) in the phylogenetic tree (Figure 1). This study will provide important information for species identification and phylogenetic relationship in the Gramineae family, in particular for Hordeinae forage.

Disclosure statement

No potential conflict of interest was reported by the authors.

Funding

This work was supported by the Fundamental Research Funds for Central Nonprofit Scientific Institution [Y2020GH01-3 and 2020-YWF-ZX-07], and the Agricultural Science and Technology Innovation Program of China [ASTIP-IAS10].

ORCID

Yongzhen Pang  <http://orcid.org/0000-0002-2336-7476>

Data availability statement

The data that support the findings of this study are openly available in NCBI at GenBank with accession number MW309818 (<https://www.ncbi.nlm.nih.gov/nuccore/MW309818>). Raw sequencing reads used in this study was deposited in the public repository SRA with accession number SRR13495514 (<https://www.ncbi.nlm.nih.gov/sra/?term=SRR13495514>).

References

- Goraghani HRS, Heidary GA, Sardo MS. 2013. Effects of salinity and drought stresses on seed germination and seedling growth of desert wheatgrass *Agropyron desertorum*. *J Rangel Sci.* 4(1):14–22.
- Jafari AA, Seydemohammadi AR, Abdi N, Madah AH. 2008. Seed and hay production in 31 genotypes of desert wheatgrass (*Agropyron desertorum*) using drought tolerance indices. *Iran J Range Desert Res.* 15: 114–128.
- Jin JJ, Yu WB, Yang JB, Song Y, Yi TS, Li DZ. 2018. GetOrganelle: a simple and fast pipeline for de novo assembly of a complete circular chloroplast genome using genome skimming data. *bioRxiv.* 256479.
- Katoh K, Rozewicki J, Yamada KD. 2019. MAFFT online service: multiple sequence alignment, interactive sequence choice and visualization. *Brief Bioinform.* 20(4):1160–1166.
- Shanjani SP, Jafari A, Calagari M. 2013. Genetic variation among wild and cultivated *Agropyron desertorum* populations based on total protein profiles and phenotypic traits. *New Zeal J Crop Hort.* 41(3):117–134.
- Shi L, Chen H, Jiang M, Wang L, Wu X, Huang L, Liu C. 2019. CPGAVAS2, an integrated plastome sequence annotator and analyser. *Nucleic Acids Res.* 47:65–73.
- Silvestro D, Michalak I. 2012. raxmlGUI: a graphical front-end for RAxML. *Org Divers Evol.* 12(4):335–337.
- Tillich M, Lehwark P, Pellizzer T, Ulbricht-Jones ES, Fischer A, Bock R, Greiner S. 2017. GeSeq-versatile and accurate annotation of organelle genomes. *Nucleic Acids Res.* 45(W1):W6–W11.