



The complete chloroplast genome sequence of *Trikeria hookeri*

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ABSTRACT

Trikeria hookeri is an alpine grass with significant ecological value. Here, the complete chloroplast genome sequence of *T. hookeri* using Illumina sequencing data was reported. The size of the whole cp genome was 137,696 bp in length, consisting of a pair of inverted repeats (IR 13,755 bp), a large single-copy region (LSC 81,613 bp), and a small single-copy region (SSC 28,568 bp). The *T. hookeri* chloroplast genome encodes 119 genes: 81 mRNA genes, 34 tRNA genes and 4 rRNA genes. The GC content of *T. hookeri* chloroplast genome was 38.8% and those in LSC, SSC, and IR regions were 36.9, 40.8, and 42.3%, respectively. The maximum-likelihood phylogenetic analysis demonstrated that *T. hookeri* was most closely related to *Stipa lipskyi* (NC028444) and *Stipa purpurea* (NC029390). Our findings provide fundamental information for further evolutionary and phylogenetic researches of *T. hookeri*.

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Trikeria hookeri; chloroplast genome; Poaceae; phylogenetic analysis

Poaceae is an important vegetation constituent part in alpine grassland community. The *Stipeae*, belonging to the subfamily *Pooideae*, family *Poaceae*, which is of special significance among the alpine steppe vegetation in Qinghai-Tibet plateau, which include approximately 400–500 species and 24 genera in all of the world, in which 67 species and 10 genera were distributed in China. *Trikeria hookeri* is a kind of *Stipeae*, extremely salinity-tolerant, cold-tolerant and drought-tolerant species (Khan 2003), distributed at 4300–5400 m in Qinghai and Tibet of China (Shukla and Srivastava 2020). *T. hookeri* increased the coverage of plant community, also provided food and habitation for animals. However, no studies on the plastome of *T. hookeri* have been published. In this study, we reported the complete chloroplast genome sequence of *T. hookeri* and explored its internal relationships with the family steppe.

The seeds of *T. hookeri* were collected from Zhongba county (83°30′05″E, 30°10′38″N), Shigatse, Tibet of China. A specimen was deposited at Northwest Institute of Plateau Biology, Chinese Academy of Sciences (NWIPB, Sha Xiao, xiaosa@nwipb.cas.cn) under the voucher number 0334882. In 2020, the seed was grown in light incubator, at four-leaf stage, the leaf was extracted DNA by CTAB (Dreisigacker et al. 2012) and then sequenced using the Illumina NovaSeq platform (Illumina, San Diego, CA). The raw data were used

to assemble the complete cp genome using GetOrganelle software (Jin et al. 2020), and the chloroplast genome of related species *Nassella hyalina* (GeneBank accession number NC036696) were used as the reference genome. The genome annotation was performed with the program Geneious R8 (Biomatters Ltd, Auckland, New Zealand). Finally, the complete chloroplast genome sequences of *T. hookeri* were submitted to GenBank (accession number: MW699773).

The whole chloroplast genome of *T. hookeri* cp genome is 137,696 bp in size, consisting of a pair of inverted repeats (IR 13,755 bp), a large single-copy region (LSC 81,613 bp), and a small single-copy region (SSC 28,568 bp). A total of 119 genes were annotated, containing 81 mRNA genes, 34 tRNA genes and 4 rRNA genes. The GC content of *T. hookeri* chloroplast genome was 38.8% and those in LSC, SSC, and IR regions were 36.9, 40.8, and 42.3%, respectively.

To confirm the phylogenetic location of *T. hookeri*, 11 genera of complete chloroplast genomes from Gramineae were obtained from GenBank, and the 12 complete chloroplast sequences were aligned using MAFFT (Katoh and Standley 2013). The maximum-likelihood analysis was performed by MEGA7 (Kumar et al. 2016) with bootstrap set to 1,000 (Figure 1). The phylogenetic analysis showed a strong sister relationship with *Stipa lipskyi* (NC028444) and *Stipa purpurea* (NC029390).

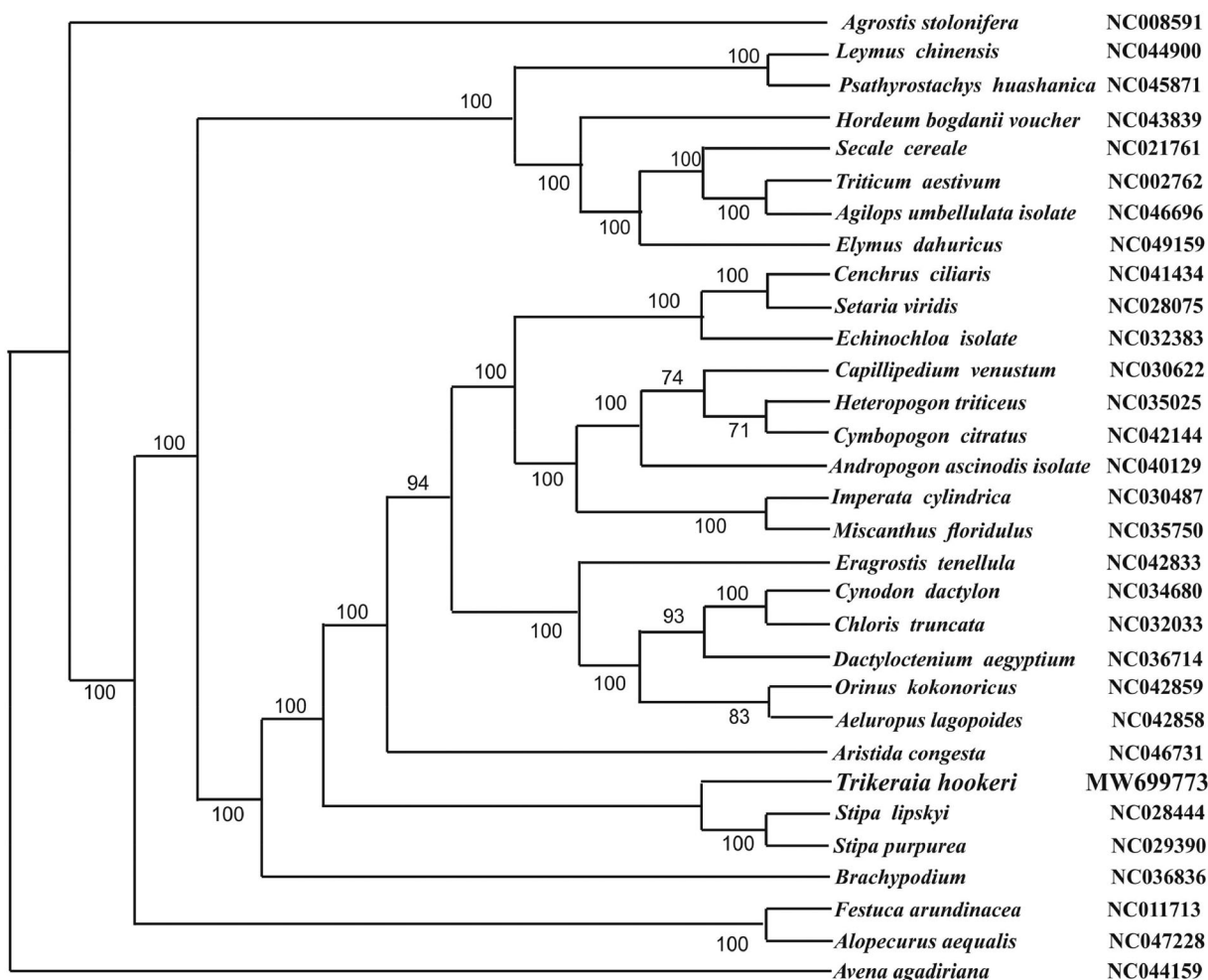


Figure 1. The maximum likelihood tree based on 30 complete chloroplast genome sequences. All the sequences were downloaded from NCBI GenBank. Bootstrap support values are given at the nodes.

Disclosure statement

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

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Data availability statement

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at (<https://www.ncbi.nlm.nih.gov/>) under

the accession no. MW699773. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA671634, SAMN16539309, and SRR12888103, respectively.

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