The complete chloroplast genome of *Anisodus tanguticus*, a threatened plant endemic to the Qinghai-Tibetan Plateau

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**ABSTRACT**

*Anisodus tanguticus* is endemic to the Qinghai-Tibetan Plateau, but its wild populations are shrinking roughly, and need urgent conservation. Here, we report the complete sequence of the chloroplast genome of *A. tanguticus*. The genome was 155,764 bp in length with 129 genes comprising 84 protein-coding genes, 37 tRNA genes, and eight rRNA genes. The overall GC content of *A. tanguticus* chloroplast genome was 37.9%. Phylogenomic analysis suggested that *A. tanguticus* forms a monophyletic group with *Hyoscyamus* which shows closed relationship with the clade of *Przewalskia* and *Scopolia*.

**ANISODUS TANGUTICUS** (Maxim.) Pascher, belonging to Solanaceae, is endemic to the Qinghai-Tibetan Plateau in China (Wu and Raven 1994). As an important traditional Chinese medicine, it contains high levels of tropane alkaloids, scopolamine and scopoline, which mainly affect the parasympathetic nervous system and can be used as an anticholinergic drug for acute glomerulonephritis, rheumatoid arthritis, hemorrhagic necrotic enteritis, eclampsia, pulmonary oedema, and circulatory shock (Yang 1991). However, the populations of *A. tanguticus* is beginning to dwindle due not only to the effect of excessive collection as a medicinal species (Zheng et al. 2007) but also to the low germination rate of the seeds (He and Jia 2009). Therefore, it has been listed as a critically endangered plant in the list of wild plants under state key protection in China (http://rep.iplant.cn/prot/Anisodus%20tanguticus). In recent years, most researches concerning *A. tanguticus* mainly have been focused on its chemical composition (Guo et al. 2015), pharmacological activity (Sun and Yang 2010), genetic diversity (Zheng et al. 2007), and functional gene identification (Liu et al. 2005) and less is known about the chloroplast gene of *A. tanguticus*. In the present study, we report the completed chloroplast genome of *A. tanguticus* based on the next-generation sequencing method. To our knowledge, this is the first completed chloroplast genome of *Anisodus* genus. The chloroplast genome will contribute to molecular phylogeny, genetic improvement, conservation, and sustainable management for this threatened species.

A wild individual of *A. tanguticus* was sampled from Qinghai, China (Voucher specimen: Zhang2018050, HNWP) and its genomic DNA was isolated from the fresh leaves with the modified CTAB method. DNA sample was randomly fragmented to construct paired-end (PE) libraries according to the Illumina preparation manual (San Diego, CA, USA). Genome sequences were screened out and assembled with SPAdes (Bankevich et al. 2012). Annotation was performed with CpGAVAS (Liu et al. 2012). The annotated genomic sequence had been submitted to GenBank with the accession number MF593117.

The complete chloroplast genome of *A. tanguticus* has a total length of 155,764 bp which composed of two inverted repeats (IR, 25,882 bp) separated by a large single copy region (LSC, 86,514 bp) and a small single copy region (SSC, 17,486 bp). The GC content of its chloroplast DNA is 37.9% (LSC, 35.6%; IR, 42.9%; SSC, 31.9%). The chloroplast genome was predicted to encode 129 genes, of which, 84 were protein-coding genes, 37 were distinct tRNA genes, and eight were rRNA genes. A total of 17 genes were duplicated in the IR regions including seven tRNA, four rRNA, and six protein-coding genes.

Phylogenetic analysis was performed based on complete chloroplast genomes of *A. tanguticus* and 24 other species from Solanaceae. Meanwhile, *Lactuca sativa* (Asteraceae) was used as an outgroup. Sequences were aligned using MAFFT v7.0 (http://mafft.cbrc.jp/alignment/server/) (Kazutaka and Standley 2013), and Gblocks (Castresana 2000) was employed to remove ambiguously aligned sites. A maximum likelihood (ML) analysis was conducted on RAxML-HPC2 on XSEDE based on the GTR + G + I nucleotide substitution model as recommended by jModelTest2 with 1000 replications.

Phylogenetic analysis showed that the *A. tanguticus* forms a clade with *Hyoscyamus niger* which shows closed
relationship with the clade of *Przewalskia* and *Scopolia* (Figure 1). We expect that the chloroplast genome of *A. tanguticus* will be a valuable resource for future studies on conservation genetics, taxonomy, and phylogeny involving this particular species.

**Disclosure statement**

No potential conflict of interest was reported by the authors.

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**Figure 1.** Maximum likelihood phylogenetic tree based on 26 complete chloroplast genome sequences. The number on each node indicates the bootstrap value. Accession numbers: *Acnistus arborescens* KU306735.1; *Anisodus tanguticus* MF539117; *Capsicum chinense* KU041709.1; *Capsicum lycianthoides* KP274856.1; *Datura stramonium* JN654342.1; *Dunalia brachycantha* KP308151.1; *Eriolarynx fasciculata* KU306938.1; *Hyoscyamus niger* KP248009.1; *Iochroma loxense* KP296185.1; *Iochroma salpoanum* KU315119.1; *Lactuca sativa* AP007232; *Lycium ruthenicum* MG976805.1; *Nicotiana otophora* KU051626.1; *Nicotiana tabacum* 00544.2; *Nicotiana undulata* JN563929.1; *Physalis angulata* MH019241.1; *Physalis pruinosa* MH019243.1; *Przewalskia tangutica* KF352315.1; *Saracha punctata* KP280050.1; *Solanum bulbocastanum* DQ347958.1; *Solanum dulcamara* KY863443.1; *Solanum lycopersicum* HG975525.1; *Scopolia parviflora* KU900232.1; *Solanum tuberosum* DQ386163.2; *Vassobia dichotoma* KP294521.1.