Complete chloroplast genome sequences of *Lagotis yunnanensis* (Scrophulariaceae): an Endangered species endemic to the Hengduan Mountains region

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**ABSTRACT**

*Lagotis yunnanensis* is a perennial plant in the Scrophulariaceae family with a high value of medicinal in Tibetan medicine. In this study, we assembled and characterized the complete chloroplast genome of *L. yunnanensis* as a resource for future studies on this species. The chloroplast genome was 152,789 bp in size, with a large single-copy (LSC) region of 83,642 bp, a small single-copy (SSC) region of 17,795 bp, separated by two inverted repeat (IR) regions of 25,676 bp each. A total of 131 genes were predicted. Phylogenetic analysis showed a close relationship between *L. yunnanensis* and *Veronicastrum sibiricum* with 100% bootstrap value.

*Lagotis yunnanensis* W. W. Smith is a perennial plant of the genus *Lagotis* that is distributed in alpine grasslands at high altitudes of 3350–4700 m in northwestern Yunnan, Tibet, and northwestern Sichuan (Editorial Committee of Flora of China 1979). It has been used in Tibetan folk medicine for the treatment of fever, hypertension, acute and chronic hepatitis (Zhu 1979). It has been used in Tibetan medicine. In this study, we reported the complete chloroplast genome of *L. yunnanensis* as a resource for future studies on this species. The chloroplast genome was 152,789 bp in length and a typical circular structure comprising a pair of inverted repeats (IR) of 25,676 bp divided by a large single copy (LSC) region of 83,642 bp and a small single copy (SSC) region of 17,795 bp. The whole genome contained 131 genes, including 86 protein-coding genes, 8 ribosomal RNA genes, and 37 tRNA genes. The general GC content was 38.4% in the whole sequence, while the corresponding values of the LSC, SSC, and IR regions are 36.6%, 32.8%, and 43.3%, respectively.

The complete chloroplast genome of *L. yunnanensis* (GenBank Accession No. MN752238) was 152,789 bp in length and a typical circular structure comprising a pair of inverted repeats (IR) of 25,676 bp divided by a large single copy (LSC) region of 83,642 bp and a small single copy (SSC) region of 17,795 bp. The whole genome contained 131 genes, including 86 protein-coding genes, 8 ribosomal RNA genes, and 37 tRNA genes. The general GC content was 38.4% in the whole sequence, while the corresponding values of the LSC, SSC, and IR regions are 36.6%, 32.8%, and 43.3%, respectively.

To determine the phylogenetic position of *L. yunnanensis*, a phylogenetic analysis was performed using the complete chloroplast genome of *L. yunnanensis* with those from seven Plantaginaceae species (including four from the genus *Plantago*, three from other genus) and Scrophulariaceae species (including four from the genus *Scrophularia*). *Orobanche* and *Pedicularis* (Orobanchaceae) were used as outgroups. All of the plastomes were aligned using MAFFT v.7 (Katoh and Standley 2013), and the RAxML (Stamatakis 2014) inference was performed using the GTR model with support for branches evaluated by 1000 bootstrap replicates. The phylogenetic tree showed that *L. yunnanensis* is sister to *Veronicastrum sibiricum* (Figure 1). Our data can provide a useful resource for the conservation genetics of *L.*
yunnanensis as well as for the phylogenetic studies of Scrophulariaceae.

Disclosure statement
No potential conflict of interest was reported by the authors.

Funding
This work was supported by the major project of science and technology in Yunnan Province [2018ZF010-1], the major project of science and technology in Yunnan Province [2017ZF002], and special subsidies for public health services of “Fourth Chinese Materia Medica Resources Survey” [DSS, MOF. No 43/2018].

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