**PLASTOME ANNOUNCEMENT**

**Complete sequence of Cynanchum rostellatum (Apocynaceae: Asclepiadoideae) chloroplast genome and its phylogenetic analysis**

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**ABSTRACT**

*Cynanchum rostellatum* (Turcz.) Liede and Khanum 2016 is a perennial herbaceous twining vine that is widely distributed in Japan, South Korea, the United States of America, and China. In this study, the complete chloroplast (cp) genome of *C. rostellatum* was sequenced using the Illumina platform and assembled for the first time. This plastome has a circular structure with a length of 160,641 bp. The GC content of the plastome was 37.82%. The cp genome contained 113 unique genes, including 79 protein-coding, 30 transfer RNA, and four ribosomal RNA genes. Phylogenetic analysis based on the complete cp genome sequences of the Asclepiadoideae subfamily showed that *C. rostellatum* was closely related to *C. bungei* in the genus *Cynanchum*. These results provide useful information for both phylogenetic research and the utilization of *C. rostellatum*.

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GAU) contained one intron, and two genes (clpP and ycf3) contained two introns.

To elucidate the evolutionary relationship of *C. rostellatum*, the cp genomes of 21 Asclepiadoideae species were downloaded from the NCBI GenBank database. We aligned the plastomes using MAFFT and constructed a maximum likelihood (ML) tree (Figure 1) using RAxML (v.8.2.9), using the GTRGAMMA model with 1000 rapid bootstrap replicates (Cui et al. 2020). Our plastome phylogeny showed that *C. rostellatum* is most closely related to *C. bungei* in the genus *Cynanchum*. *Cynanchum rostellatum* and seven *Cynanchum* species were clustered into one branch indicating that *C. rostellatum* was likely placed in the *Cynanchum* genus, and not in *Metaplexis*, during taxonomic classification. In conclusion, the cp genome of *C. rostellatum* provides a theoretical basis for a better understanding of the evolutionary patterns and for improving its taxonomic classification.

**Ethical approval**

No permission was necessary in this study for the sample collection. *Smilax moranensis* is widely distributed in North China and is not listed as a national key protected plant.

**Authors’ contributions**

N. Cui designed and conceived this work; L.X. Pei collected the samples and carried out the experiment; B.Y. Ji and S.N. Shu analyzed the data and wrote the first version of the manuscript; All authors read, revised, and approved the final manuscript.

**Disclosure statement**

The authors declare that there is no potential conflict of interest exists.

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**Data availability statement**

The complete chloroplast genome of *Cynanchum rostellatum* assembled here is available in the GenBank of NCBI (https://www.ncbi.nlm.nih.gov/genbank, accession no. OL689165). The associated BioProject, BioSample and SRA numbers are PRJNA785091, SAMN23527168 and SRR17082022, respectively.

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