Astragalus scaberrimus Bunge 1833 is a widespread perennial herb in northern China. The plant has white flowers and white hairs on the leaves and stems. To determine the chloroplast genome, total DNA was extracted from a sample and sequenced on the Illumina HiSeq4000 platform. After sequencing, the reads of chloroplast DNA were assembled and annotated via NOVOPlasty and PGA respectively. The chloroplast genome of this plant has a circular form with a length of 123,492 bp, a 34% GC content and IR loss. After annotation, a total of 113 genes were predicted for this cp genome, comprising 79 encoded proteins, 4 rRNAs and 30 tRNAs. The evolutionary history indicates that A. scaberrimus was grouped within Astragalus and formed a clade with Astragalus laxmannii with a 100% BS support value. The complete chloroplast genome can serve as a reference for future studies on molecular biology, evolution, population genetics, taxonomy and resource protection.
common in Fabaceae, especially in Papilionoideae (Cai et al. 2008; Yi et al. 2020). A total of 113 genes were predicted for this cp genome, comprising 79 encoded proteins, 4 rRNAs and 30 tRNAs.

Phylogenetic analysis was performed on complete cp genomes of A. scaberrimus and other 29 related species in Fabaceae with two species in Polygalaceae as outgroups. The alignment was constructed by HomBlocks (Bi et al. 2018), and the evolutionary history was inferred using the maximum likelihood (ML) method by IQ-TREE 1.6.12 under the TVM + F + I + G4 model (Nguyen et al. 2015; Kalyaanamoorthy et al. 2017). Bootstrap (BS) values were calculated by UFBoot2 from 1000 replicates (Hoang et al. 2018), and the final output file was edited in MEGA X (Kumar et al. 2018). As expected, A. scaberrimus was grouped within Astragalus and formed a clade with Astragalus laxmannii with a 100% BS support value (Figure 1). The complete cp genome of A. scaberrimus can serve as a reference for future studies on molecular biology, evolution, population genetics, taxonomy and resource protection.

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

Funding
This work was supported by the High-Level Talent Foundation of Qinghai Nationalities University [grant No. 2017XJG03].

ORCID
Yupeng Guo  http://orcid.org/0000-0002-7974-4154
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/nuccore/MW654102) under the accession no. MW654102. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA725312, SRR14328337, and SAMN18875902, respectively.

References

Bi GQ, Mao YX, Xing QK, Cao M. 2018. HomBlocks: a multiple-alignment construction pipeline for organelle phylogenomics based on locally collinear block searching. Genomics. 110(1):18–22.

Cai ZQ, Guisinger M, Kim HG, Ruck E, Blazier JC, McMurtry V, Kuehl JV, Boore J, Jansen RK. 2008. Extensive reorganization of the plastid genome of Trifolium subterraneum (Fabaceae) is associated with numerous repeated sequences and novel DNA insertions. J Mol Evol. 67(6):696–704.

Delectis Florae Reipublicae Popularis Sinicae Agendae Academiae Sinicae Edita. 1993. Flora reipublicae popularis sinicae. Vol. 42. Beijing: Science Press; p. 291.

Dierckxsens N, Mardulyn P, Smits G. 2017. NOVOPlasty: de novo assembly of organelle genomes from whole genome data. Nucleic Acids Res. 45(4): e18. doi:10.1093/nar/gkw955. PMC: 28204566

Hoang DT, Chernomor O, von Haeseler A, Minh BQ, Vinh LS. 2018. UFBoot2: improving the ultrafast bootstrap approximation. Mol Biol Evol. 35(2):518–522.

Jiang ZG, Yin ZT. 1992. New taxa in the genus Astragalus L. J Hebei Normal Univ. 2:72–74.

Kalyaanamoorthy S, Minh BQ, Wong TKF, von Haeseler A, Jermiin LS. 2017. ModelFinder: fast model selection for accurate phylogenetic estimates. Nat Methods. 14(6):587–589.

Keith I, Block MD, Mark N, Mead MS. (2003). Immune System Effects of Echinacea, Ginseng, and Astragalus: A Review. INT EGRAWB CANCE R T HERAP IES. 2(3):247–267.

Kumar S, Stecher G, Li M, Knyaz C, Tamura K. 2018. MEGA X: molecular evolutionary genetics analysis across computing platforms. Mol Biol Evol. 35(6):1547–1549.

Li XX, Qu L, Dong YZ, Han LF, Liu EW, Fang SM, Zhang Y, Wang T. 2014. A review of recent research progress on the Astragalus genus. Molecules. 19(11):18850–18880.

Nguyen LT, Schmidt HA, von Haeseler A, Minh BQ. 2015. IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. Mol Biol Evol. 32(1):268–274.

Qu XJ, Moore MJ, Li DZ, Yi TS. 2019. PGA: a software package for rapid, accurate, and flexible batch annotation of plastomes. Plant Methods. 15(50).

Yang DK, Qiu J, Sheng Y. 2002. The number and karyotype analysis of chromosome of Astragalus scaberrimus. Shandong Sci. 15(4):32–34.

Yi FY, Zhan C, Wang HM, Yan XH, Ye RH, Gong Q, Qiu X, Liu QS, Sun HL. 2020. Characterization of the complete chloroplast genome sequence of Vicia costata (Fabaceae) and its phylogenetic implications. Mitochondrial DNA Part B. 5(3):3463–3464.

Zhang LZ, Fan JJ, Meng QX, Niu Y, Niu W. 2013. Caragana fabr. promotes revegetation and soil rehabilitation in saline-alkali wasteland. Int J Phytoremediation. 15(1):38–50.

Zhang ZX, Zhang L, Xu HS. 2019. Effect of Astragalus polysaccharide in treatment of diabetes mellitus: a narrative review. J Tradit Chin Med. 39(1):133–138.