

## Complete chloroplast genome sequence of *Chrysosplenium nudicaule* (Saxifragaceae)

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### ABSTRACT

*Chrysosplenium nudicaule* Bunge, Tibetan name ‘Yajima,’ growing in the highlands of China is a perennial herb belonging to the genus *Chrysosplenium* Saxifragaceae. As a traditional Chinese medicine, it has been used to treat digestive diseases for hundreds of years. The complete chloroplast genome of *Chrysosplenium nudicaule* is 152,775 bp in length and comprises two inverted repeats (IR, 25,962 bp), a large single-copy region (LSC, 83,533 bp), and a small single-copy region (SSC, 17,318 bp). It harbors 112 genes, including 78 protein-coding genes, four ribosomal RNA genes, and 30 transfer RNA genes. In addition, the *rpl32* gene was deleted. The GC content of the whole chloroplast genome is 37.54%. This chloroplast genome resource will be useful for study on the evolution and genetic diversity of *C. nudicaule* in the future.

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*Chrysosplenium nudicaule* Bunge is a small perennial herb belonging to the genus *Chrysosplenium* Saxifragaceae, and mainly distributed in the northwest and southwest mountain regions of China (Pan 1986). They grow in rock crevices ~2500–4800 m above sea level. As a traditional Chinese medicine, it has been used to treat digestive diseases for hundreds of years in Tibet (Luo et al. 2016). A variety of chemical constituents were isolated from *C. nudicaule*, such as flavonoids and 78 volatile chemical constituents (Yang et al. 2004). The flavonoid compound, 6,7,3'-trimethoxy-3,5,4'-trihydroxy flavones isolated from *C. nudicaule*, can not only induce apoptosis in human leukemia K562 cells (Wang et al. 2005) but also inhibit growth and induce apoptosis of the human stomach cancer cell line SGC-7901 (Luo et al. 2016). Recent studies have also shown that the extract of this herb had a protective effect on liver injury in mice (Zhou et al. 2019). However, there are no reports on the molecular biology of *C. nudicaule*. In this study, we assembled and annotated its complete chloroplast genome from Illumina sequencing data. Then, we reconstructed the phylogenetic tree of this genus to reveal its genetic relationships. These data will provide some genetic resources for the subsequent molecular biology studies and lay a foundation for the development of its protection and medicinal value.

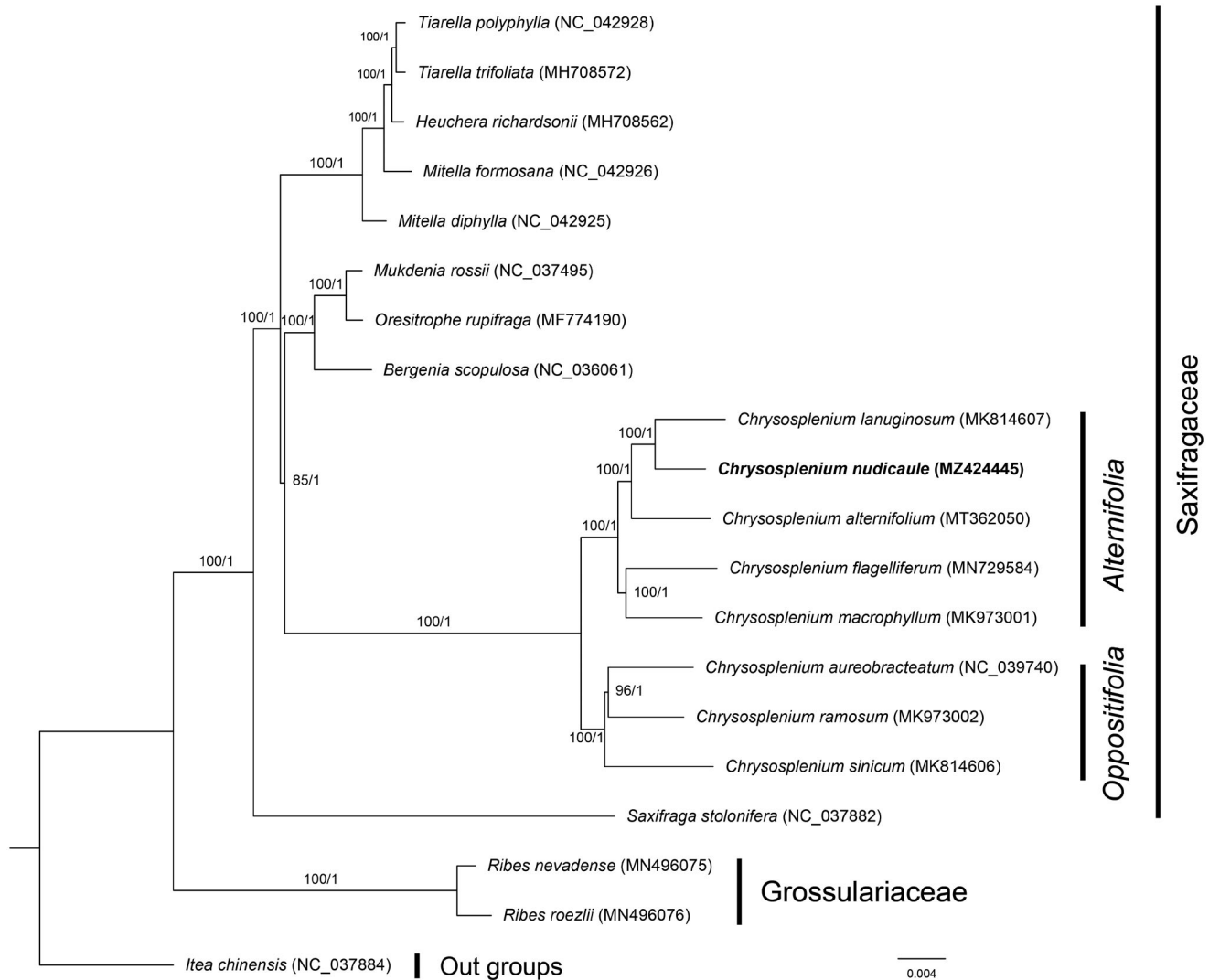
The materials of *C. nudicaule* in this study were collected from Qilian Mountain National Nature Reserve, Tianzhu County, Gansu Province of China (37°03'37"N, 102°46'05"E, 3275 m above sea level). The voucher specimens were deposited at the Herbarium of South-Central University for Nationalities (HSN). The specimen accession number is CY20210603001. The whole genomic DNA was extracted by the CTAB method (Doyle and Doyle 1987). The short-insertion library (350 bp) was constructed and then sequenced to obtain 2 × 150 bp paired-end data by using the Illumina NovaSeq 6000 platform at Majorbio Company (Shanghai, China). A total of 5 Gb raw reads were generated and low-quality sequences were filtered out. First, the clean data were quality-controlled by using FastQC v0.11.9 (<http://www.bioinformatics.babraham.ac.uk/projects/fastqc/>). Then, de novo assembly of the whole chloroplast genome by GetOrganelle v1.7.3 (Jin et al. 2020). Finally, the final assembly result is obtained, we check the accuracy of assembly results, the slimmed assembly graph and selected target assembly graph can be visualized by Bandage v0.8.1 (Wick et al. 2015) to assess the completeness of the final graph. In CPGAVAS2 (Shi et al. 2019) and PGA (Qu et al. 2019), the *C. nudicaule* chloroplast genome is annotated by using *Chrysosplenium sinicum* (MK814606) as a reference genome. The different annotations

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**Figure 1.** Phylogenetic tree reconstructed by maximum-likelihood (ML) and Bayesian inference (BI) analysis based on the 78 plastid protein-coding genes of 20 species. Values above branches are maximum likelihood bootstrap percentages (BS)/Bayesian posterior probabilities (PP).

of protein-coding sequences were confirmed using BLASTx in NCBI. The length of the complete chloroplast genome of *C. nudicaule* (MZ424445) was 152,775 bp with an average GC content of 37.54%. The complete chloroplast genome has a typical quadripartite structure, including a large single-copy (LSC) region of 83,533 bp, a small single-copy (SSC) region of 17,318 bp separated, and two inverted repeated regions of 25,962 bp. The chloroplast genome harbors 112 genes, including 78 protein-coding genes, 30 transfer RNA genes, and four ribosomal RNA genes. Notably, the *rpl32* gene was absent in the complete chloroplast genome of *C. nudicaule*, which also lacked in some other species of *Chrysosplenium* L.

To further investigate the phylogenetic relationship of *C. nudicaule* within Saxifragaceae, the complete chloroplast genomes of nine species from Saxifragaceae, two species from Grossulariaceae and one species from Iteaceae were obtained from the GenBank database, with the *Itea chinensis* as the outgroups, the phylogenetic trees were built from the 78 protein-coding gene matrixes by maximum-likelihood (ML) and Bayesian inference (BI) (Figure 1). The ML tree was generated using IQ-TREE (Nguyen et al. 2015) based on the best model of TVM + F + R2 with 1000 bootstrap replicates, and

BI analysis was performed in MrBayes v3.2.6 (Ronquist et al. 2012). As shown in the phylogenetic tree (Figure 1), we can see that the eight species of *Chrysosplenium* were clustered into a clade. In addition, they are divided into two major branches corresponding to the two subgenera (*Alternifolia* and *Oppositifolia*), and the result is consistent with those of Wu et al. (2020). *Chrysosplenium nudicaule* belongs to the Subgen. *Alternifolia*, and has a close relationship with the *Chrysosplenium lanuginosum*. These studies will provide some references for the phylogeny, evolution, development, and utilization of *Chrysosplenium* in the future.

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## 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. MZ424445. The associated 'BioProject,' 'SRA,' and 'Bio-Sample' numbers are PRJNA739074, SRR14861288, and SAMN19771098, respectively.

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