

## The complete chloroplast genome of a traditional medicinal and food plant, *Polygonatum humile* (Asparagaceae, Asparagales)

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### ABSTRACT

*Polygonatum humile* (Asparagaceae) is a medicinal and food plant that is naturally distributed in the North East Asia region and East of Russia. Here we report on the complete chloroplast (cp) genome sequence of *P. humile*. The cp genome is 155,313 bp in size and includes two inverted repeat regions of 26,302 bp each, which is separated by a large single-copy region of 84,239 bp and a small single-copy region of 18,470 bp. A total of 132 genes were predicted, including 39 tRNA, 8 rRNA, and 85 protein-coding genes. Phylogenetic analysis placed *P. humile* under the subfamily Nolinoideae of the family Asparagaceae.

### ARTICLE HISTORY

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Genomic resources; Illumina sequencing; Nolinoideae; phylogenomics; rhizomatous herb

*Polygonatum humile* Fisch. ex Maxim. is a perennial rhizomatous herb belonging to the family Asparagaceae, which is naturally distributed in the North and Northeast of China, Japan, Korea, Mongolia and East of Russia (Chen and Tamura 2000). The rhizome part is often harvested to be prepared as vegetable or snack that contains nourishing nutrients and medicinal properties; while certain groups consume its sprout in the form of raw salad or as an ingredient in soup-making (Wujisguleng et al. 2012). Due to the limited distribution of this species and unsustainable harvesting by local herb collectors, the natural populations of *P. humile* is currently threatened. Although cultivation of *P. humile* is practiced, the source for cultivation relies heavily on their asexual reproductive rhizomes instead of their seeds due to difficulty in collection (Zhang et al. 2008). Due to commercial value, studies that focus on its breeding techniques and medicinal properties often overshadow the genetic information of this species. In this study, we aimed to characterize the complete chloroplast (cp) genome sequence of *P. humile* to serve as a valuable genomic resource for this important medicinal plant species.

Total genomic DNA was extracted from fresh leaves of *P. humile* planted in the greenhouse of School of Life Sciences, Sun Yat-sen University (SYSU), originally a haplotype obtained from the arboretum of Institute of Botany, Chinese Academy of Science, Beijing, China (N39°59'21", E116°12'31"). Additional dried leaf specimens were kept in the Herbarium of SYSU (SYS) under the collection number BJ-1-4001. A genomic library consisting of an insert size of 300 bp was

constructed using TruSeq DNA Sample Prep Kit (Illumina, USA) and sequencing was carried out on an Illumina HiSeq X Ten platform. The output was an 8 Gb raw data of 100 bp paired-end reads, further trimmed and assembled using NOVOPlasty (Dierckxsens et al. 2017), using the *rbcl* sequence of *P. humile* (Genbank accession number: AB009947) as the seed sequence. The assembled cp genome was annotated using DOGMA (Wyman et al. 2004) and further manually checked by comparison against the *Polygonatum stenophyllum* complete cp genome (Genbank accession number: KX822773).

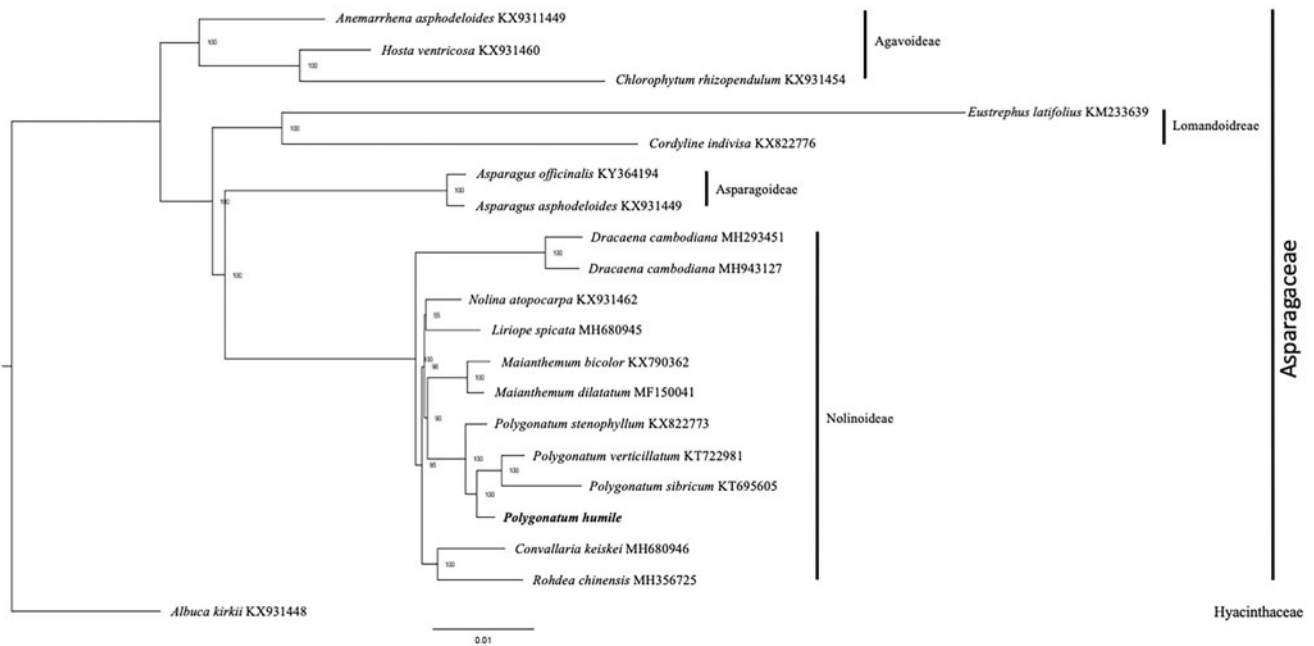
The complete cp genome of *P. humile* (Genbank accession number: MN218691) is 155,313 bp in length, displaying a quadripartite structure that contains a pair of inverted repeats (IRs: 26,302 bp each), separated by a large single-copy (LSC) region (84,239 bp) and a small single-copy (SSC) region (18,470 bp). There are 132 genes reported, including 85 protein-coding genes, 8 ribosomal RNA genes, and 39 rRNA genes. The overall GC content of the cp genome was 37.7%.

For phylogenetic analysis, a maximum-likelihood (ML) tree was constructed with 1000 bootstrap replicates using RAxML software (Stamatakis 2014). A subset of 19 species from the family Asparagaceae was included, with *Albuca kirkii* (Hacinthaceae) as outgroup. The ML analysis showed that *P. humile* is placed under the subfamily Nolinoideae of the family Asparagaceae, clustered together with other *Polygonatum* species (Figure 1). This finding could serve as valuable genomic resources in future genetic-based researches for this important medicinal plant species.

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**Figure 1.** Maximum-likelihood tree based on the complete chloroplast genome sequences of 19 species from the family Asparagaceae, with *Albuca kirkii* (Hyacinthaceae) as outgroup. Shown next to the nodes are bootstrap support values based on 1000 replicates.

## Disclosure statement

The authors report no conflict of interest.

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