The complete chloroplast genome of Polygonatum zanlanscianense (Pampanini, 1915) (Asparagaceae), an adulterants of Polygonati rhizoma

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\textbf{ABSTRACT}

\textit{Polygonatum zanlanscianense} Pamp. is a plant species of the genus \textit{Polygonatum} (Asparagaceae) distributed widely in China. The complete chloroplast genome of \textit{P. zanlanscianense} was sequenced by Illumina sequencing technology. The plastome is 155,609 bp in length with a typical quadripartite structure, including one single small copy (SSC, 18,427 bp), one large copy (LSC, 84,438 bp), and two inverted repeat regions (IRs, 26,372 bp each). The cp genome encoded 132 genes, including 38 tRNA, 8 rRNA, and 86 protein-coding genes. The overall GC content is 37.7%. The ML phylogenetic analysis based on the cp genomes indicated that the genus \textit{Polygonatum} is sister to the genus Heteropoligonatum within the tribe Polygonateae, \textit{P. zanlanscianense} is sister to \textit{P. cirrhifolium} within the genus \textit{Polygonatum}. This study provides an important theoretical foundation for varieties identification, the phylogenetic relationship of \textit{P. zanlanscianense}. Furthermore, this article takes a radical reform of \textit{Polygonati rhizoma}.

\textit{Polygonati rhizoma} is one of the most valuable medicinal and edible plants, which has been fully used by people since ancient times (Liu and Si 2018). Even now \textit{Polygonati rhizoma} has great potential for resource development and broad market prospects for its high economic and medicinal value (Zhang et al. 2019; Liu et al. 2020). However, there are many species in the genus \textit{Polygonatum}, besides it is difficult to classify and identify species (Zhao et al. 2018). In production and daily life, species of the same family are often used as the counterfeit of \textit{Polygonati rhizoma}, which seriously endangers people’s life and property safety. \textit{Polygonatum zanlanscianense} Pamp. is one of the species in the genus \textit{Polygonatum}, distributed in Gansu, Henan, Jiangsu, Hubei, Sichuan, and other provinces in China (Chen and Tamura 2000). Because of the morphology similarity between \textit{P. zanlanscianense} and \textit{Polygonati rhizoma}, the adulterants were mixed with \textit{P. zanlanscianense}. Therefore, the study of \textit{P. zanlanscianense} is conducive to the effective identification of medicinal materials and the standardization of \textit{Polygonati rhizoma} market (Wang 2020).

Chloroplast is a semi-autonomous organelle responsible for photosynthesis in green plant cells (Jansen et al. 2005). It has a stable and conserved double-stranded genome, containing four parts: large single copy (LSC), small single copy (SSC), and two inverted repeats (IRs) (Wang et al. 2012). In view of the advantages of the chloroplast genome, such as easy obtainment, moderate length, monophyletic inheritance, and relatively moderate nucleic acid replacement rate, researchers have widely used it in plant phylogeny, species identification, and genetic breeding (Zhang and Li 2011; Sheng et al. 2021).

In this study, the sample was collected from Wanyuan (107°35′23″E, 31°52′46″N) at Sichuan, China. The specimen was stored in the Herbarium of Kunming Institute of Botany, Chinese Academy of Sciences (URL: http://www.kib.ac.cn; email: jiyh@mail.kib.ac.cn, Yunheng Ji), with the voucher number JYH002. The fresh leaves of the sample were used to extract total genomic DNA using the modified CTAB method. The DNA sample was deposited in the Key Laboratory for Plant Diversity and Biogeography of East Asia, Chinese Academy of Sciences. And the sequencing library was constructed and quantified following the methods introduced by Liu et al. (2019), then sequencing was carried out using Illumina HiSeq 2500 platform. Resultant clean reads were assembled using the GetOrganelle pipeline (https://github.com/kinggerm/GetOrganelle) with \textit{P. humile} (GenBank accession no. MN218691) as the reference sequence. The assembly was edited and annotated according to the reference in Geneious V10.2. Start and stop codons and intron/exon boundaries for protein-coding genes were checked manually. The plastome sequence of \textit{P. zanlanscianense} was deposited in the NCBI GenBank database (MW800891).

The \textit{P. zanlanscianense} plastome presents a typical quadripartite structure consisting of one large single-copy region
(LSC, 84,438 bp), one small single-copy region (SSC, 18,427 bp), and a pair of inverted repeat regions (IRs, 26,372 bp each). The overall GC content is 37.70%, and the corresponding values for LSC, SSC, and IR regions are 35.70%, 31.50%, and 42.90%, respectively. The plastome encodes 132 genes (86 protein-coding genes, 38 tRNAs, and 8 rRNAs).

We used the online software: CIPRES Gateway (http://www.phylo.org/) to construct a phylogenetic tree based on the maximum likelihood method to determine the phylogenetic position of *P. zanlanscianense* (Figure 1). In this study, 17 species representing eight genera were downloaded from the genebank database, Asparagus officinalis L. (NC_034777) was taken as an outgroup. The results showed that the genus Polygonatum was closely related to Heteropolygonatum within the Tribe Polygonateae; *P. zanlanscianense* was sister to *P. cirrhifolium*, which may be related to their transitional morphology and overlapping geographical distribution.

**Disclosure statement**

The authors declare no potential conflict of interests.

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**Data availability statement**

The data that support the findings of this study are openly available in GenBank at https://www.ncbi.nlm.nih.gov, reference number [MW800891]. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA722812 SRR14270298 and SAMN18793888, respectively.

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**Figure 1.** Phylogenetic relationships of *P. zanlanscianense* with other Polygonatum species.