



The complete chloroplast genome of *Polygonatum falcatum* (Asparagaceae)

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ABSTRACT: *Polygonatum falcatum* is a perennial herb distributed in East Asia. We determined the characteristics of the complete chloroplast genome in *P. falcatum* for the first time, with a *de novo* assembly strategy. The chloroplast genome was 154,579bp in length harboring 87 protein coding genes, 38 tRNA genes and eight rRNA genes. It exhibits typical quadripartite structure comprising a large single-copy (LSC) (83,528bp), a small single-copy (SSC) (18,457bp) and a pair of inverted repeats (IRs) (26,297bp). Phylogenetic analysis of 16 chloroplast genomes from Asparagaceae reveals that the genus *Polygonatum* is a monophyletic group and that *P. falcatum* is clustered together with the congener, *P. odoratum*.

Keywords: Asparagaceae, complete chloroplast genome, *Polygonatum falcatum*

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INTRODUCTION

The genus *Polygonatum* Mill. is a diverse plant group that is particularly well appreciated in East Asia for a wide array of commercial uses, including medicinal and culinary uses (Kim et al., 2014; Floden, 2017; Zhao et al., 2017). Despite the increased recognition for its value as natural resources, knowledge on the taxonomy and phylogenetic relationship among congeners has been lacking (Floden, 2014; Chao and Tseng, 2019). *Polygonatum falcatum* A. Gray (Asparagaceae) is a perennial herb distributed in forest and forest margins of Japan and Korea (Tamura, 2016; Jang, 2018). *Polygonatum falcatum* has been widely used for oriental medicines and is well-known for its ornamental values (An et al., 2006; Tomioka et al., 2008). The species has recently drawn attention, as secondary metabolites extracted from its rhizome showed potential anti-adipogenic activities (Park et al., 2012).

Chloroplast genomes provide molecular markers that are a great tool for phylogenetic analyses from species to higher rank taxa (Gitzendanner et al., 2018). There is a growing number of studies resolving problematic relationships among taxa using a whole plastome (Martin et al., 2005; Gitzendanner et al., 2018). Many *Polygonatum* species have been recently studied for their plastome identity, however, the genomic information applicable for *P. falcatum* remains absent. In the present study, we investigated the genomic architecture of the

whole chloroplast genome for *P. falcatum* using whole-genome shotgun sequencing.

MATERIALS AND METHODS

We collected young leaves of *P. falcatum* from Jeju-si, Korea (N 33°26'22.0", E 126°37'46.0"). The voucher specimen was prepared and deposited at the Herbarium of Chosun University (CHO) with the accession number *CHO0000063*.

The total genomic DNA was extracted followed by the manufacturer's protocol (QIAGEN, Hilden, Germany). After library preparation, the prepared libraries were sequenced on the Illumina HiSeq-X platform (Illumina, San Diego, CA, USA). Obtained reads were assembled with *de novo* strategy using Geneious Prime (ver. 2021.2.2) followed by Gibbs (2019). The genes were predicted with GeSeq (Tillich et al., 2017), and manually curated based on Blast search results. The simple sequence repeats were investigated with MISA with a default parameter setting (Beier et al., 2017). A circular map of the *P. falcatum* chloroplast genome was drawn by OGDRAW v. 1.3.1 (Greiner et al., 2019).

To investigate its phylogenetic relationship, the concatenated coding sequences from the entire chloroplast genome of 16 *Polygonatum* and outgroup taxa were aligned in MAFFT Online (Kato et al., 2019). All sequences except *P. falcatum* were downloaded from NCBI GenBank. We assigned

Heteropolygonatum as an outgroup following phylogenetic relationships based on a previous study (Floden and Schilling, 2018). We inferred the phylogeny using the maximum likelihood (ML) algorithm implemented in RAxML v. 4.0 with the GTR model with gamma rates (Stamatakis, 2006). For the clade support, 1,000 bootstrap replicates were used.

RESULTS AND DISCUSSION

We obtained 83 million high-quality 150 bp paired-end reads. A total of 12.6 Gb reads was assembled with *de novo* strategy. Assembled genome was 154,579 bp in length with the typical quadripartite structure comprising a large single-

copy (LSC) (83,528 bp), a small single-copy (SSC) (18,457 bp), and a pair of inverted repeats (IRs) (26,297 bp) (Fig. 1). The overall GC content was 41.68%. The chloroplast genome contained 133 genes including 87 protein-coding genes, 38 tRNA genes, and eight rRNA genes. Forty-seven simple

Table 1. Summary of simple sequence repeats (SSRs) across varying unit sizes in *P. falcatum*.

Unit size	Number of SSRs
1	42
2	4
3	1

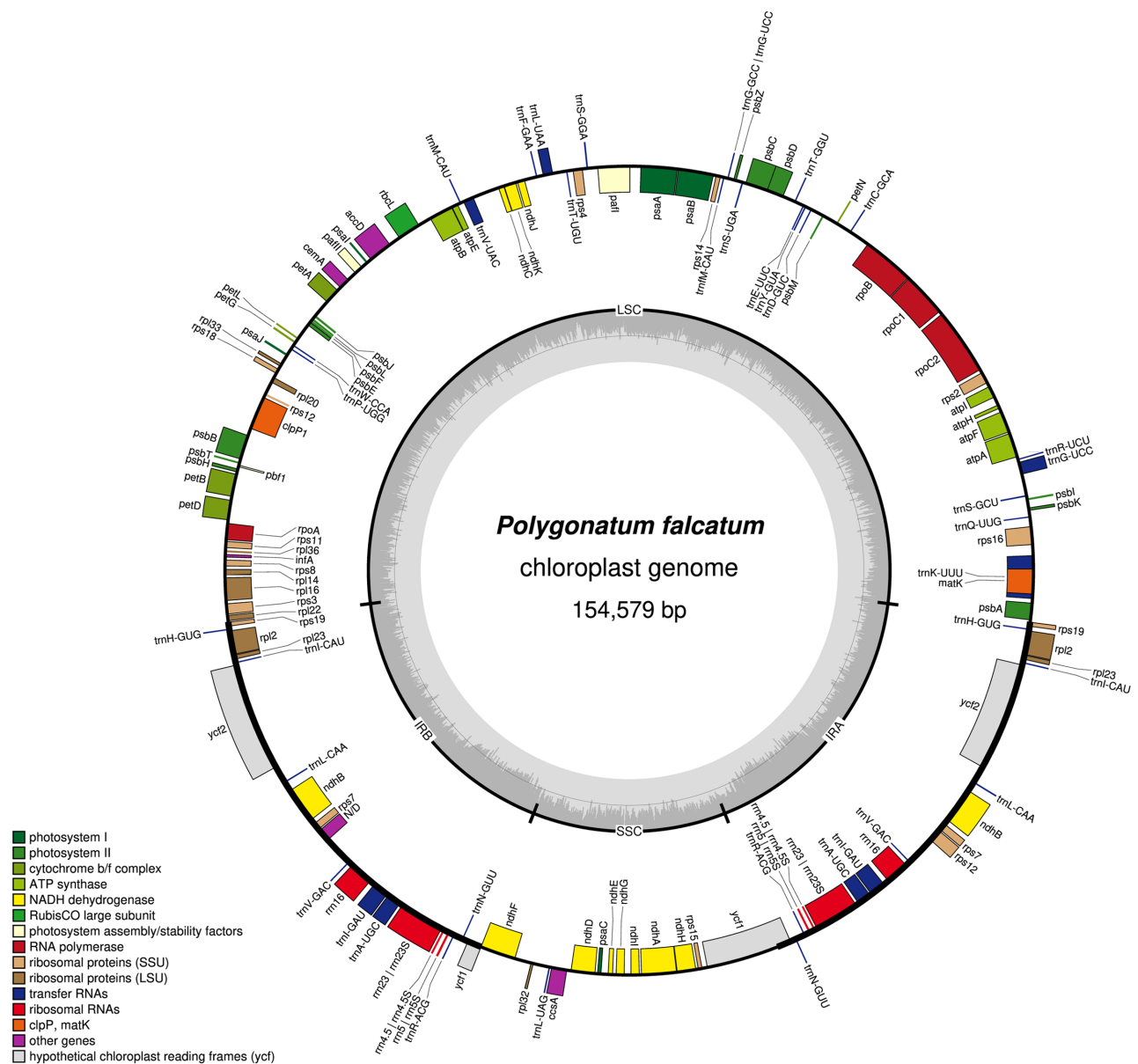


Fig. 1. Chloroplast genome annotations of a *Polygonatum falcatum* drawn by OGDRAW v. 1.3.1.

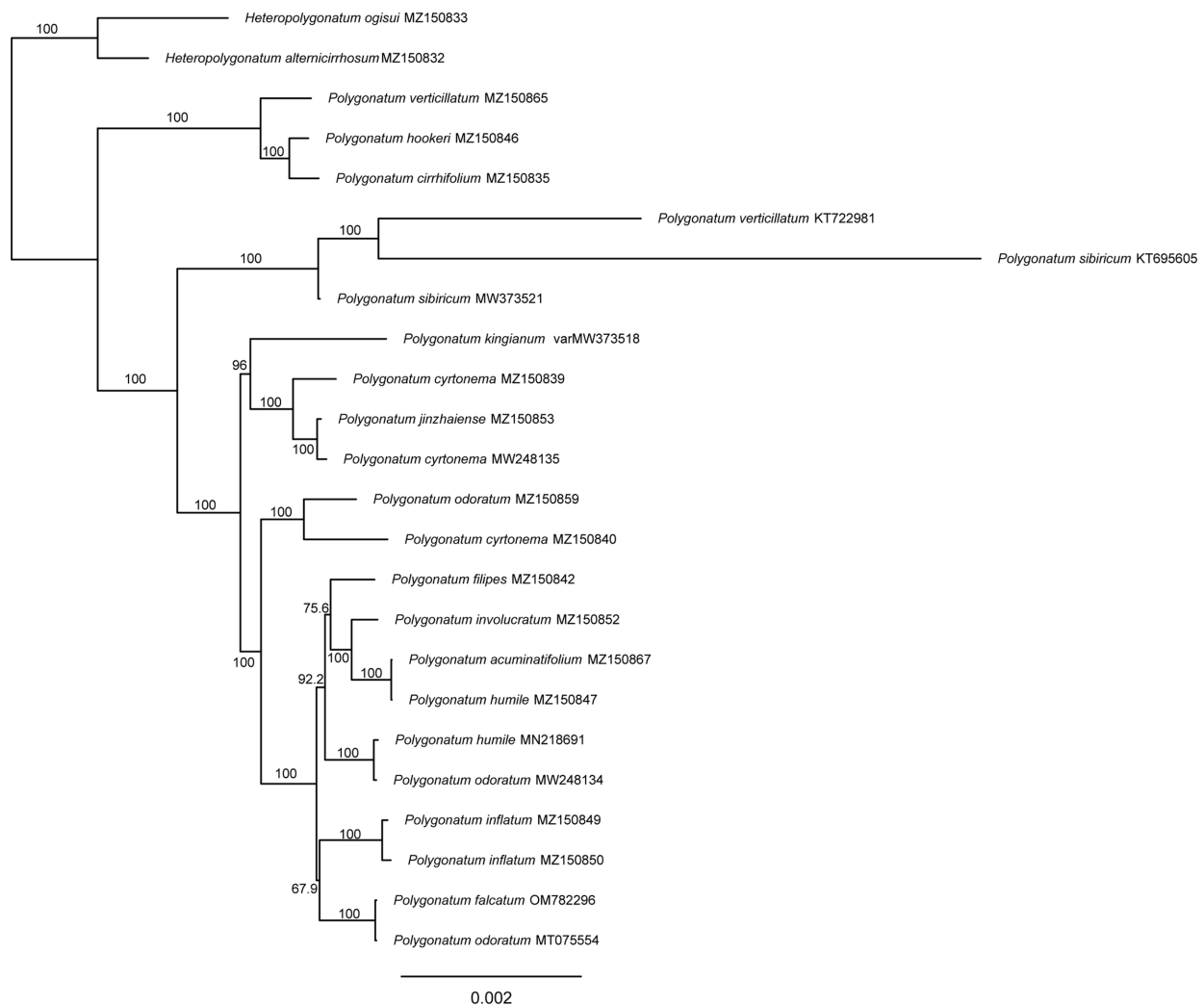


Fig. 2. Maximum-likelihood (ML) tree based on chloroplast genome sequences of 14 species of *Polygonatum*. Numbers on the nodes indicated the bootstrap support value (>50%).

sequence repeats were identified in the cp genome, most of which were mono-nucleotide repeats (Table 1). The complete chloroplast genome sequence of *P. falcatum* was deposited in GenBank with the accession number OM782296. The associated BioProject and Bio-Sample numbers are PRJNA809136 and SAMN26148647, respectively.

In our phylogenetic analysis based on the whole chloroplast genomes, 14 species of *Polygonatum* formed a monophyletic group (BP=100) with strong support on the ML tree (Fig. 2). The taxa that failed to form a monophyletic group in the ML tree (*P. cyrtonema*, *P. odoratum*, and *P. verticillatum*) are morphologically diverse and show broad distribution (Mehra and Pathania, 1960; Jeffrey, 1980; Floden and Schilling, 2018; Chen and Tamura, 2000). The result is somewhat consistent with the former phylogenetic studies which revealed high molecular variation that might in part be due to cryptic diversity unexplored (Meng et al., 2014; Floden and Schilling, 2018).

The ML tree also indicated that *P. falcatum* is most closely related to *P. odoratum* (Fig. 2). Further study might be required to fully resolve the phylogenetic relationship within the genus.

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CONFLICTS OF INTEREST

The authors declare that there are no conflicts of interest.

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