The complete chloroplast genome of *Youngia gracilipes* (Asteraceae)

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**ABSTRACT**

The complete chloroplast genome of *Youngia gracilipes* was identified. Here, we sequenced and annotated complete chloroplast genome of *Youngia gracilipes*. The whole genome length is 152,811 bp, including a large single-copy (LSC) region with length of 84,337 bp, a small single-copy (SSC) region with length of 18,392 bp, a pair of inverted repeat (IR) regions with length of 25,041 bp. A total of 114 unique genes was found, of which 80 protein-coding genes, 30 tRNA genes, and 4 rRNA genes. Simultaneously, molecular phylogenetic analysis suggested that *Youngia gracilipes* was the closest to *Youngia japonica*.

The genus *Youngia* Cass. have ca. 30 species, mainly distributed in East Asia (Shih and Kilian 2011; Babcock and Stebbins 1937). It highly diversified in China, and many new species were discovered recently, such as *Pseudoyoungia baaxingensis*, *Youngia jiulongensis*, and *Youngia zhengyiana* (Chen 2018; Peng et al. 2017; Deng et al. 2014). *Youngia gracilipes* is characterized by the longest outer phyllary being about one-third of the inner and no crested or corniculate appears at inner phyllaries (Shih 1997; Shih and Kilian 2011). This species was classified into a new genus *Pseudo Youngia* by Maity and Maiti (2010). However, subsequent pollen morphological and molecular studies did not support the isolation of this new genus (Shih and Kilian 2011; Peng et al. 2013; Peng et al. 2014; Deng et al. 2014). In addition, *Y. gracilipes* grows in alpine meadows at an altitude of 2700–4800 m (Shih and Kilian 2011), which makes specimen collection difficult. This species was found in a recent field scientific expedition. *Y. gracilipes* was not used in recent Asteraceae phylogenetic study of plastome genome (Lin et al. 2019). Therefore, we reported the complete plastome genome of *Y. gracilipes* and reconstructed phylogenetic tree with related species for the convenience of a detailed study of the phylogeny.

The materials of molecular experiments of *Y. gracilipes* were collected from Têo Zong, Gansu Province, China (N34°15′/79′9″ and E103°06′52.35″). The voucher specimens were deposited in KUN (Herbarium, Kunming Institute of Botany, Kunming, China). The filtered clean reads were assembled using NOVOPlasty version 3.3 (Dierckxsens et al. 2017) with sequence of Ribulose-1,5-bisphosphate (RuBP) as a seed for starting. The complete chloroplast genome was annotated using Plastid Genome Annotator (PGA) (Qu et al. 2019). The annotated *Amborella trichopoda* and *Soroseries umbrella* plastome sequences were used as references, and all annotated results were manually corrected in Geneious version 9.0.2 (Kearse et al. 2012). At last, the assembled sequence was submitted to NCBI with annotations (NCBI accession number: MT267485).

The complete chloroplast genome of *Y. gracilipes* is 152,811 bp in size, which is divided into four parts by two inverted repeat (IR) sequences, containing an LSC region (84,337 bp), and SSC region (18,392 bp), and a pair of IR regions (25,041 bp). The GC content of whole genome is 37.8%. In addition, the values of LSC region, SSC region, and IR region are 35.9, 31.5, and 43.3%, respectively. A total of 114 unique genes were identified, including 80 protein-coding genes, 30 tRNA genes, and 4 rRNA genes. Among these, 12 protein-coding genes (ndhA, rps12, ndhB, rpl2, rpl16, petD, petB, clpP, ycf3, atpF, rpoC1, and rps16) and 6 tRNA genes (trnA-UGC, trnL-GAU, trnV-UAC, trnL-UAA, trnG-UCC, and trnK-UGU) are intron-containing genes.

The phylogenetic status was confirmed by maximum likelihood (ML) method with 77 shared CDS sequences. All sequences including 19 species (Lv et al. 2020) from the Cichorieae were aligned using MAFFT version 7.308 (Katoh et al. 2002). The GTR+G+I was selected as best-fit model of DNA evolution by jModelTest version 2.1.10 (Darriba et al. 2012). Phylogenetic tree was reconstructed using RAxML version 8.2.10 (Alexandros 2014) with 1000 bootstrap replicates. Figtree version 1.4.4 (Rambaut 2018) was used to view the phylogenetic tree. Ultimately, the phylogenetic analysis results indicated that *Y. gracilipes* was the closest to *Youngia japonica* with 100% bootstrap values (Figure 1).
Data availability

The data that support the findings of this study are available in GenBank at [https://www.ncbi.nlm.nih.gov/genbank/], reference number [MT267485].

Disclosure statement

No potential conflict of interest was reported by the author(s).

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