The complete chloroplast genome of the Chinese medicinal herb *Senecio scandens*

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**ABSTRACT**

*Senecio scandens* Buch.-Ham. is a crucial source of Chinese traditional medicine with antibacterial properties. In this study, we report the complete chloroplast genome sequence of *S. scandens*. The assembled chloroplast genome was 150,729 bp in length, containing two inverted repeated (IR) regions of 24,455 bp each, a large single-copy (LSC) region of 83,984 bp and a small single-copy (SSC) region of 17,835 bp. The genome encodes 133 genes consisting of 89 protein-coding genes, 36 tRNA genes, and 8 rRNA genes. The overall GC content of *S. scandens* is 37.4%, with the highest GC content of 43% in the IR region. A total of 38 simple sequence repeats are identified in the cp genome of *S. scandens*. Phylogenetic analysis demonstrated a sister relationship between *S. scandens* and *Pericallis hybrida*, indicating further revisions for the genus *Senecio*. This work provides basic genetic resources for investigating the evolutionary status and population genetics diversities for this medicinal species.

*Senecio scandens* Buch.-Ham. is a medicinal plant from family Asteraceae, which has been recorded as Senecios Scandentis Herba (Qianliguang) in Chinese Pharmacopeia. It has a climbing woody stem and usually grows on hills, mountains, woods and roadsides. *Senecio scandens* is widely used as an ingredient to produce hundreds of medicinal plantal preparations with various activities (Wang et al. 2013). Because of similar morphological characteristics, several species are easily confused with *S. scandens*. However, significant differences were found on the chemical markers even between the two species from the genus *Senecio* (Xiong et al. 2014). It is necessary to develop an effective molecular identification strategy for *S. scandens* to ensure the safety of clinical application. The aim of this study was to analyze the chloroplast genome sequence of *S. scandens*, which could provide essential information for molecular marker development and analysis of phylogenetic status of this species.

The sample of *S. scandens* was collected from Fuyang area of Zhejiang Province (30°05′2.4″N, 119°53′20.4″E) and deposited in the collection center of Zhejiang Chinese Medical University with the specific number of QLG-1919. Total genomic DNA was extracted and sequenced using the Illumina Hiseq Platform according to the previous report (Ying et al. 2019; Wang et al. 2020). The chloroplast genome of *S. scandens* was assembled by metaSPAdes with the chloroplast sequence of *Dendrosenecio brassiciformis* as reference (Nurk et al. 2017). The chloroplast was annotated using GeSqe and further confirmed by BLAST (Tillich et al. 2017). The complete cp genome of *S. scandens* was submitted to GenBank with the accession number of MT178410.

The length of the complete chloroplast genome sequence of *S. scandens* was 150,729 bp, with a large single-copy (LSC) region of 83,984 bp, a small single-copy (SSC) region of 17,835 bp, and two separated inverted repeated (IR) regions of 24,455 bp each. A total of 133 genes were identified in the cp of *S. scandens*, including 89 protein-coding genes, 36 tRNA genes, and 8 rRNA genes. The overall GC content was 37.4%, and the corresponding contents for LSC, SSC, and IR regions were 35.5%, 30.9% and 43%, respectively. The genome included 17 duplicated genes in the IR region and exhibited 52.48% protein-coding sequences. Moreover, a total of 38 small single repeats (SSR) are identified in the cp of *S. scandens*, ranging from 10 bp to 21 bp.

The complete genome sequences of *S. scandens* and other 14 representative species from the family Asteraceae were analyzed using MEGA 7.0 by maximum-likelihood (ML) method to confirm its phylogenetic position (Kumar et al. 2016). The result demonstrated that *S. scandens* clustered together with *Pericallis hybrida* and combined to form the clade II, indicating a close genetic relationship between the two species (Figure 1). In addition, the six species from genus *Senecio* did not cluster together to form a monophyletic group, but was divided into three groups, providing molecular evidences for further revisions on genus *Senecio* (Figure 1). Our results would contribute the development of...
molecular markers and further investigation on the population genetics and phylogenetics of the genus *Senecio*.

**Disclosure statement**

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

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