The complete chloroplast genome sequence of medicinal plant, *Sedum oryzifolium*

Jing Li and Dongling Chen

Zhang Zhongjing School of Chinese Medicine, Nanyang Institute of Technology, Nanyang, PR China

**ABSTRACT**

The complete chloroplast genome sequence of *Sedum oryzifolium* was characterized from Illumina pair-end sequencing. The chloroplast genome of *S. oryzifolium* was 149,609 bp in length, containing a large single-copy region (LSC) of 80,825 bp, a small single-copy region (SSC) of 13,126 bp, and two inverted repeat (IR) regions of 27,829 bp. The overall GC content is 30.55%, while the corresponding values of the LSC, SSC, and IR regions are 63.5%, 68.3%, and 60.2%, respectively. The genome contains 116 complete genes, including 78 protein-coding genes (58 protein-coding gene species), 30 tRNA genes (18 tRNA species) and 8 rRNA genes (4 rRNA species). The Neighbour-joining phylogenetic analysis showed that *S. oryzifolium* and *Sedum sarmentosum* clustered together as sisters to other *Sedum* species.

**Introduction**

Plants have been important footstones of a complex traditional medical system that has produced some of the most important drugs that still exist today. *Sedum oryzifolium* is a species of herbaceous perennials within the family Crassulaceae (Hou et al. 2018). *S. oryzifolium* has high ecological and economic value with high levels of intraspecific genetic diversity. *S. oryzifolium* has wide geographic distribution, high intraspecific polymorphism, adaptability to different environments, combined with a relatively small genome size. Consequently, *S. oryzifolium* represents an excellent model for understanding how different evolutionary forces have sculpted the variation patterns in the genome during the process of population differentiation and ecological speciation (Neale and Antoine 2011). Moreover, we can develop conservation strategies easily when we understand the genetic information of *S. oryzifolium*. In the present research, we constructed the whole chloroplast genome of *S. oryzifolium* and understood many genome variation information about the species, which will provide beneficial help for population genetics studies of *S. oryzifolium*.

The fresh leaves of *S. oryzifolium* were collected from Xin Jiang (88°31’N, 43°19’E). Fresh leaves were silica-dried and taken to the laboratory until DNA extraction. The voucher specimen (SORM001) was laid in the Herbarium of Nanyang Institute of Technology and the extracted DNA was stored in the −80°C refrigerator of the Key Laboratory of School of Biological and Chemical Engineering. We extracted total genomic DNA from 25 mg silica-gel-dried leaf using a modified CTAB method (Doyle 1987). The whole-genome sequencing was then conducted by Biodata Biotechnologies Inc. (Hefei, China) with Illumina HiSeq platform. The Illumina HiSeq 2000 platform (Illumina, San Diego, CA) was used to perform the genome sequence. We used the software MITObim 1.8 (Hahn et al. 2013) and metaSPAdes (Nurk et al. 2017) to assemble chloroplast genomes. We used *S. sarmentosum* (GenBank: JX427551) as a reference genome. We annotated the chloroplast genome with the software DOGMA (Wyman et al. 2004), and then corrected the results using Geneious 8.0.2 (Campos et al. 2016) and Sequin 15.50 (http://www.ncbi.nlm.nih.gov/Sequin/).

The complete chloroplast genome of *S. oryzifolium* (GenBank accession number NC_027837) was characterized from Illumina pair-end sequencing. The chloroplast genome of *S. oryzifolium* was 149,609 bp in length, containing a large single-copy region (LSC) of 80,825 bp, a small single-copy region (SSC) of 13,126 bp, and two inverted repeat (IR) regions of 27,829 bp. The overall GC content is 30.55%, while the corresponding values of the LSC, SSC, and IR regions are 63.5%, 68.3%, and 60.2%, respectively. The genome contains 116 complete genes, including 78 protein-coding genes (58 protein-coding gene species), 30 tRNA genes (18 tRNA species) and 8 rRNA genes (4 rRNA species).

We used the complete chloroplast genomes sequence of *S. oryzifolium* and 9 other related species of *Sedum* and *Adromischus cristatus* as outgroup to construct phylogenetic tree. The 10 chloroplast genome sequences were aligned with MAFFT (Katoh and Standley 2013), and then the Neighbour-joining tree was constructed by MEGA 7.0 (Kumar et al. 2016).
et al. 2016). *S. oryzaifolium* and *Sedum sarmentosum* clustered together as sisters to other *Sedum* species (Figure 1).

**Disclosure statement**

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

**Data availability statement**

The data that support the findings of this study are openly available in National Center for Biotechnology Information (NCBI) at https://www.ncbi.nlm.nih.gov, accession number NC_027837.

**References**

Campos FS, Kluge M, Franco AC, Giorgio A, Valdez FP, Saddi TM, Brito WMED, Roehe PM. 2016. Complete genome sequence of porcine parvovirus 2 recovered from swine sera. Genome Announc. 4(1): e01627–e01615.

Doyle J. 1987. A rapid DNA isolation procedure for small quantities of fresh leaf tissue. Phytochem Bull. 19(1):11–15.

Hahn C, Bachmann L, Chevreux B. 2013. Reconstructing mitochondrial genomes directly from genomic next-generation sequencing reads—a baiting and iterative mapping approach. Nucleic Acids Res. 41(13): e129–e129.

Hou Z, Wang Z, Ye Z, Du S, Liu S, Zhang J. 2018. Phylogeographic analyses of a widely distributed *Populus davidiana*: further evidence for the existence of glacial refugia of cool-temperate deciduous trees in northern East Asia. Ecol Evol. 8(24):13014–13026.

Katoh K, Standley DM. 2013. MAFFT multiple sequence alignment software version 7: improvements in performance and usability. Mol Biol Evol. 30(4):772–780.

Kumar S, Stecher G, Tamura K. 2016. MEGA7: Molecular Evolutionary Genetics Analysis version 7.0 for bigger datasets. Mol Biol Evol. 33(7): 1870–1874.

Neale DB, Antoine K. 2011. Forest tree genomics: growing resources and applications. Nat Rev Genet. 12(2):111–122.

Nurk S, Meleshko D, Korobeynikov A, Pevzner PA. 2017. metaSPAdes: a new versatile metagenomic assembler. Genome Res. 27(5):824–834.

Wyman SK, Jansen RK, Boore JL. 2004. Automatic annotation of organelar genomes with DOGMA. Bioinformatics. 20(17):3252–3255.