

The complete chloroplast genome sequence of *Opuntia sulphurea* (Cactaceae)

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ABSTRACT

Opuntia sulphurea Gillies ex Salm-Dyck 1834 (Cactaceae) acts as an invasive species due to its ability to survive in various environments. In this study, we assembled the complete chloroplast (cp) genome of *Opuntia sulphurea*, which was 122,740 bp in length. The genome contained 100 genes, including 65 protein-coding genes, 31 tRNA genes and four rRNA genes. The base composition of the chloroplast genome was 32.11% A, 17.74% G, 18.34% C, and 31.80% T, resulting in an overall G + C content of 35.39%. A phylogenetic analysis across 23 species in Caryophyllales demonstrated a close relationship between *Opuntia sulphurea* and *Opuntia quimilo*.

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Opuntia sulphurea Gillies ex Salm-Dyck 1834, which belongs to the cacti family Cactaceae, is an endemic species mainly distributed in the arid region of Argentina (Carreira et al. 2014). Commonly known as ‘prickly pear’ cacti, *O. sulphurea* has been widely used as food, forage, and medicine by natives in the western hemisphere for thousands of years (Pimienta-Barrios 1994; Casas and Barbera 2002; Panico et al. 2007). Thus, the genomic information is urgently needed to help defend the invasion of *O. sulphurea*.

Succulent stems were collected from an individual of *O. sulphurea*, which was cultivated in Minqin Desert Botanical Garden, Wuwei City, China (38°35′6.95″N, 102°58′22.68″E); Collector: Shengdan Wu (wusd@lzu.edu.cn). The specimen is deposited in the herbarium of Lanzhou University, Lanzhou, China under the voucher number MQXRZ01 (person in charge: Shengdan Wu: wusd@lzu.edu.cn). Genomic DNA was isolated using the modified CTAB method (Allen et al. 2006). The 20.45 Gb whole-genomic sequences were obtained using the Illumina HiSeq 2500 platform (Illumina, San Diego, CA). Chloroplast genome assembly was performed by using the NOVOPlasty software (Dierckxsens et al. 2016). Annotation was conducted with Plastid Genome Annotator (PGA, Qu et al. 2019).

The complete chloroplast genome of *O. sulphurea* (GenBank: MW927506) was 122,740 bp in length, and we found there are no inverted repeats (IRs) existed, which is different from the chloroplast genome of *O. quimilo* (Köhler et al. 2020). It contains 100 genes, including 65 protein-coding genes, four rRNA genes, and 31 tRNA genes. Four rRNA genes are *rrn5*, *rrn4.5*, *rrn23*, and *rrn16*.



We also constructed the phylogenetic trees with the maximum likelihood (ML, RaxML version 8) (Stamatakis 2014), and Bayesian analysis (BI, MrBayes version 3.2) (Ronquist et al. 2012) methods. The alignments were created by the MAFFT (Katoh and Standley 2013) using 23 related species of Caryophyllales including the *Gymnocarpos przewalskii* and *Portulaca oleracea* as outgroup (Figure 1). The results indicated that all 21 species from the Cactaceae were clustered together and *O. sulphurea* was most closely related to *O. quimilo*. This complete chloroplast genome can be readily used for population genomic studies of *O. sulphurea*, and such information would serve as fundamental for further research on defense to its invasion into other ecosystems.

Author contributions

S.W. collected samples; J.C., S.Z., X.D., W.T and Y.Y. conducted the analyses and interpreted the results; J.C., S.Z. and S.W. wrote the manuscript; all authors read and agreed the final version of the manuscript; S.W. designed the study.

Sampling permission statement

The plant is not listed in the List of State Key Protected Wild Plants of P.R. China (No.5 2021, by National Forestry and Grassland Administration and Ministry of Agriculture and Rural Affairs of P.R. China). Sampling was under the permission and guideline of Lanzhou University and Minqin Desert Botanical Garden.

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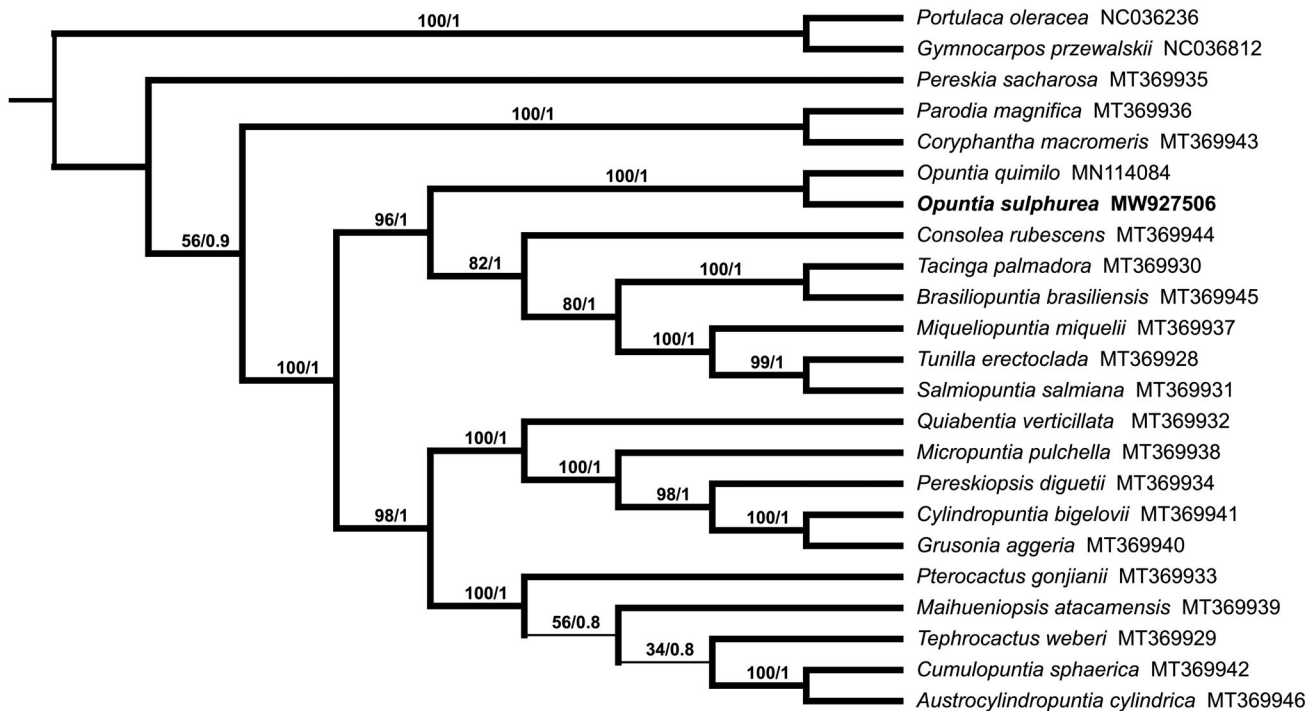


Figure 1. The phylogenetic tree based on the complete chloroplast genomes of *Opuntia sulphurea* and other 22 species of Caryophyllales, with *Portulaca oleracea* and *Gymnocarpus przewalskii* as outgroups. Numbers near the nodes represent bootstrap value and posterior probability, respectively.

Disclosure statement

The authors declare that they have no conflict interests.

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Data availability statement

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at <https://www.ncbi.nlm.nih.gov> under the accession no. MW927506. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA739272, SRS9240871, and SAMN19778433 respectively.

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