The complete chloroplast genome of Suaeda physophora Pall. (Chenopodiaceae)

Yanlin Hu, Xueli Ren and Jiayin Zhang

Suaeda physophora Pall. (Chenopodiaceae) is a leaf succulent shrub species with potential usefulness as fodder for the desert animal. However, the phylogeny of S. physophora is lacking. Here, we sequenced and assembled a complete chloroplast genome of S. physophora and further reconstructed the phylogeny of Chenopodiaceae. The chloroplast genome of S. physophora is 151,104 bp in length, consisting of an 18,597 bp small single-copy (SSC), an 82,845 bp large single-copy (LSC), and a pair of 24,831 bp inverted repeat (IR) regions. The genome encodes 131 genes, including 87 protein-coding genes, 36 tRNA genes, and eight rRNA genes. Phylogenetic analysis revealed that the genus Suaeda forms a monophyletic taxon, and S. physophora is closely related to S. eltonica. Chloroplast genome and phylogenetic studies provided an essential foundation for the conservation of S. physophora.
strongly suggested that the genus *Suaeda* is monophyletic, and *S. physophora* is a sister species to *S. eltonica*.

**Author contributions**

Y.H. and J.Z. designed the study. Y.H. and X.R. collected plant samples, performed bioinformatics analysis, and wrote the manuscript. J.Z. revised the manuscript. All the authors approved the final manuscript text.

**Disclosure statement**

In accordance with Taylor & Francis policy and our ethical obligation as a researcher, the authors are reporting that Y.H. and X.R. have a business interest in a company that may be affected by the research reported in the enclosed paper. The authors have disclosed those interests fully to Taylor & Francis, and they have in place an approved plan for managing any potential conflicts arising from that involvement. No other potential conflict of interest was reported by the authors.

**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](https://www.ncbi.nlm.nih.gov) under the accession no. ONS71659. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA844225, SRR19501374, and SAMN28798005, respectively.

**Funding**

The author(s) reported there is no funding associated with the work featured in this article.

**References**

Capella-Gutiérrez S, Silla-Martínez JM, Gabaldón T. 2009. trimAl: a tool for automated alignment trimming in large-scale phylogenetic analyses. Bioinformatics. 25(15):1972–1973.

Jin JJ, Yu WB, Yang JB, Song Y, dePamphilis CW, Yi TS, Li DZ. 2020. GetOrganelle: a fast and versatile toolkit for accurate de novo assembly of organelle genomes. Genome Biol. 21(1):241.

Li L, Zhang X. 2007. Germination strategies of two halophytes in Salt Desert of northwestern China. Sci China Ser D. 50(S1):115–121.

Minh BQ, Schmidt HA, Chernomor O, Schrempf D, Woodhams MD, von Haeseler A, Lanfear R. 2020. IQ-TREE 2: new models and efficient methods for phylogenetic inference in the genomic era. Mol Biol Evol. 37(5):1530–1534.

Rozewicki J, Li S, Amada KM, Standley DM, Kato K. 2019. MAFFT-DASH: integrated protein sequence and structural alignment. Nucleic Acids Res. 47(W1):W5–W10.
Schütze P, Freitag H, Weising K. 2003. An integrated molecular and morphological study of the subfamily Suaedoideae Ulbr. (Chenopodiaceae). Plant Syst Evol. 239(3–4):257–286.

Song J, Ding X, Feng G, Zhang F. 2006. Nutritional and osmotic roles of nitrate in a euhalophyte and a xerophyte in saline conditions. New Phytol. 171(2):357–365.

Song J, Feng G, Tian CY, Zhang FS. 2005. Strategies for adaptation of *Suaeda physophora*, *Haloxylon ammodendron* and *Haloxylon persicum* to a saline environment during seed-germination stage. Ann Bot. 96(3):399–405.

Tillich M, Lehwark P, Pellizzer T, Ulbricht-Jones ES, Fischer A, Bock R, Greiner S. 2017. GeSeq – versatile and accurate annotation of organelle genomes. Nucleic Acids Res. 45(W1):W6–W11.

Walker BJ, Abeel T, Shea T, Priest M, Abouelliel A, Sakthikumar S, Cuomo CA, Zeng Q, Wortman J, Young SK, et al. 2014. Pilon: an integrated tool for comprehensive microbial variant detection and genome assembly improvement. PLoS One. 9(11):e112963.

Wick RR, Schultz MB, Zobel J, Holt KE. 2015. Bandage: interactive visualization of de novo genome assemblies. Bioinformatics. 31(20):3350–3352.

Yang X, Yu H, Zhang T, Guo J, Zhang X. 2016. Arbuscular mycorrhizal fungi improve the antioxidative response and the seed production of Suaedoideae species *Suaeda physophora* Pall under salt stress. Notul Bot Horti Agrobot. 44(2):533–540.

Yuan J-F, Feng G, Ma H-Y, Tian C-Y. 2010. Effect of nitrate on root development and nitrogen uptake of *Suaeda physophora* under NaCl salinity. Pedosphere. 20(4):536–544.