



The complete chloroplast genome of an annual halophyte herb, *Suaeda glauca* (Amaranthaceae)

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ABSTRACT

The complete chloroplast genome (plastome) of *Suaeda glauca*, an annual halophytic herb, was determined in this study. The plastome was 149,807 bp in size, containing a large single-copy region (82,162 bp), a small single-copy region (18,191 bp), and two inverted repeats regions (24,727 bp). The overall GC content of this plastome was 36.5%. In total, 113 unique genes, including 79 protein-coding genes (PCGs), 30 tRNAs and 4 rRNAs, were annotated. Phylogenomic analysis showed that *S. glauca* was sister to other *Suaeda* species.

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Suaeda glauca; plastome; phylogenomics

Suaeda glauca (Amaranthaceae), one of the wild resources with incalculable ecological and economic benefit, is distributed in seashore salt marsh and inland of saline soil of China, Siberia, Korea and Japan (Duan et al. 2018). Like *S. salsa* (Chen et al. 2010; Song and Wang 2015), it is an annual

halophytic herb with tolerance to salt. The genus *Suaeda* have been applied as model halophytes for understanding salt tolerance (Sui et al. 2010; Yang et al. 2010; Song et al. 2011; Li et al. 2012; Cheng et al. 2014; Guo et al. 2015; Wang et al. 2015; Chen et al. 2016; Song et al. 2016; Zhou et al.

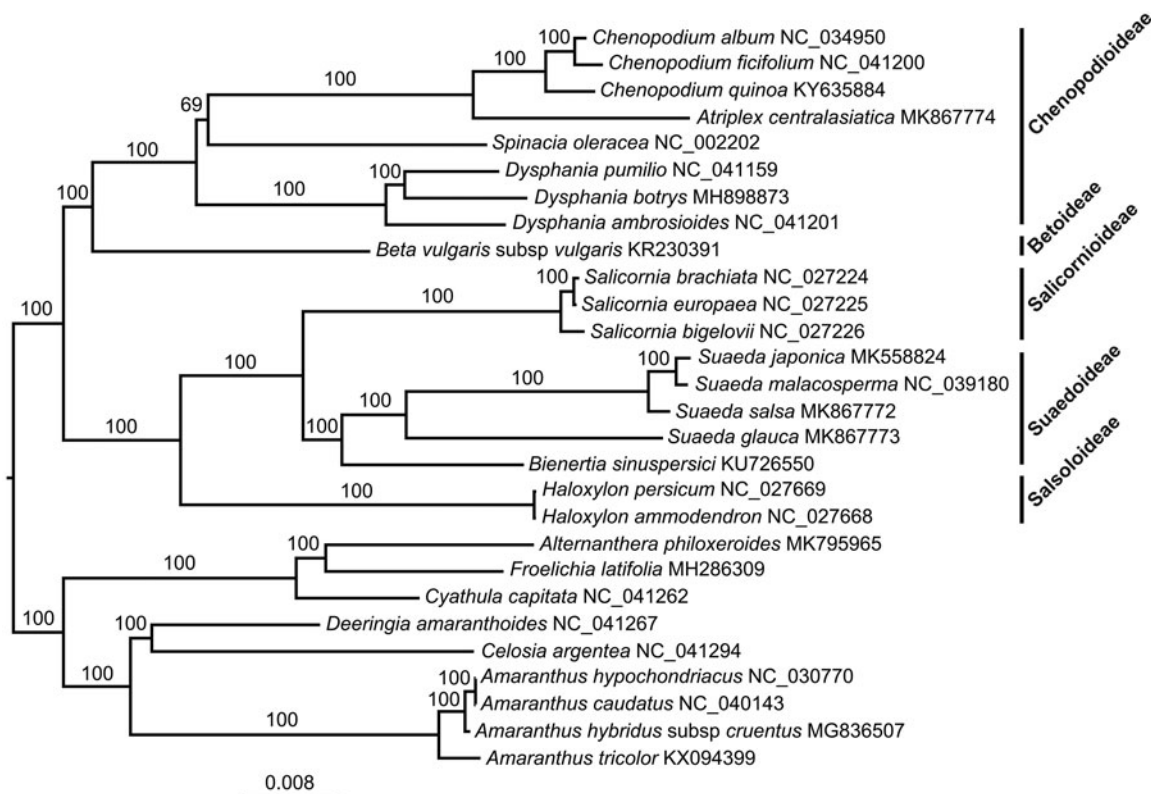




Figure 1. A maximum likelihood (ML) tree inferred from 79 plastome genes is shown. Four *Amaranthus* species, one *Celosia*, one *Deeringia*, one *Cyathula*, one *Froelichia*, and one *Alternanthera* from Amaranthaceae are used as outgroup. The numbers on branches are bootstrap support values.

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2016; Song et al. 2017; Guo et al. 2018; Liu et al. 2018). Until to now, there are 19 of *ca.* 100 *Suaeda* species reported in China (Xing 2018). As one of the 19 *Suaeda* species in China, we reported the plastome of *S. glauca* for resolving its phylogenetic position.

Fresh leaves of *S. glauca* were collected from Hekou District (Shandong, China; 38°5'N, 118°40'E). Voucher specimen (hsdwz-1) was deposited at College of Life Sciences, Shandong Normal University. Total genomic DNA was extracted by the modified CTAB method described in Wang et al. (2013). Due to limited fresh sample, the plastid DNA was not directly extracted (Liu et al. 2017). The total genomic DNA was used for library preparation and paired-end (PE) sequencing by the Illumina MiSeq instrument at Novogene (Beijing, China). The plastome was assembled using Organelle Genome Assembler (OGA) described in Qu X-J (2019). Plastome annotation was conducted with Plastid Genome Annotator (PGA; Qu et al. 2019), coupled with manual correction using Geneious v9.1.4. To determine the phylogenetic placement of *S. glauca*, a maximum likelihood (ML) tree was reconstructed using RAxML v8.2.10 (Stamatakis 2014), including tree robustness assessment using 1,000 rapid bootstrap replicates with the GTRGAMMA substitution model, based on alignment of 79 shared PCGs using MAFFT v7.313 (Katoh and Standley 2013).

The complete plastome of *S. glauca* (GenBank accession number: MK867773) was 149,807 bp in size and contained a large single-copy region (LSC: 82,162 bp), a small single-copy region (SSC: 18,191 bp), and two inverted repeats regions (IR: 24,727 bp). The overall GC content was 36.5%. In total, 113 unique genes, including 79 protein-coding genes (PCGs), 30 tRNAs and 4 rRNAs were annotated. Among them, eleven PCGs and six tRNAs contained introns, in which nine PCGs and six tRNAs contained one intron and two PCGs contained two introns. There were 18 duplicated genes in the IR. The ML phylogenetic tree showed that *S. glauca* was sister to other *Suaeda* species (Figure 1).

Disclosure statement

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