MITOCHONDRIAL DNA PART B
2021, VOL. 6, NO. 10, 2847–2848
https://doi.org/10.1080/23802359.2021.1970640

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MITOGENOME ANNOUNCEMENT

Characterization and phylogenetic analysis of the complete plastome of *Amaranthus retroflexus* L. (Amaranthaceae), an annual weeds

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ABSTRACT

The complete plastome of *Amaranthus retroflexus* L., a field weed, was identified in this study. The genome size was 150,710 bp and consists of a large single-copy (LSC: 83,892 bp) region, a small single-copy (SSC: 18,100 bp) region, and two inverted repeats (IRs: 24,359 bp) regions. GC content was 36.6%. A total of 113 genes were identified, including 79 protein-coding genes, four rRNA genes, and 30 tRNA genes. Twenty chloroplast genomes from Amaranthaceae were selected to reconstruct phylogenetic tree and the result supported that *A. retroflexus* was sister to *A. hypochondriacus* and *A. caudatus*.

ARTICLE HISTORY
Received 9 June 2021
Accepted 14 August 2021

KEYWORDS
Amaranthus retroflexus; plastome; phylogeny

Amaranthus retroflexus L. is a monoecious annual herb within Amaranthaceae, widely distributed all over the world. *A. retroflexus* is native to North America, it is dramatically expanded its distribution throughout the China for the past decades (Weber et al. 2008). This weed is a prolific seed producer and seriously endangers the growth of crops in farmland (Francischini et al. 2014). The *A. retroflexus* increasingly develop resistance due to extensively use of herbicides (Robertson 1985; Li et al. 2004; Powles and Yu 2010). This study reported the *A. retroflexus* complete plastome, which would provide a fundamental genetic resources for weeds prevention and analyzing its phylogenetic position.

Fresh leaves of *A. retroflexus* were collected from Changdao District (Shandong, China; 37°91′ N, 120°73′ E). A specimen was deposited at Herbarium of College of Life Sciences, Shandong Normal University (Shou-Jin Fan, Email: fansj@sdnu.edu.cn) under the voucher number 20120. Total genomic DNA was extracted using a modified CTAB method (Zhang et al. 2019; Guo et al. 2020). The library preparation and paired-end (PE) sequencing of total genomic DNA were conducted by the Illumina Novaseq platform at Novogene (Beijing, China). Organelle Genome Assembler (OGA, https://github.com/quxiaojian/OGA) was used to do plastome assembling. Annotation was accomplished with Plastid Genome Annotator (PGA, https://github.com/quxiaojian/PGA) (Qu et al. 2019). Manual annotation correction was performed through Geneious v9.1.4 (Kearse et al. 2012). In order to determine the phylogenetic position of *A. retroflexus*, a maximum-likelihood (ML) tree was reconstructed by RAxML v8.2.10 (Stamatakis 2014) using 1000 bootstrap replicates with GTRCAT model based on 73 protein-coding genes after alignment using MAFFT v7.313 (Katoh and Standley 2013).

The complete plastome of *A. retroflexus* (GenBank accession number: MW646089) was 150,710 bp in length, and comprised a large single-copy (83,892 bp) region, a small single-copy (18,100 bp) region, and a pair of inverted repeats (IRs, 24,359 bp) regions. The GC content of this plastome was 36.6%. The GC content of IR regions is 42.6%, higher than LSC (34.5%) and SSC (30.2%) regions. A total of 113 unique genes were encoded, including 79 PCGs, 30 tRNAs, and four rRNAs. There are genes with two copies, including *ndh*B, *rpl*2, *rpl*23, *rps*12, *rps*7, *rrn*16, *rrn*23, *rrn*4.5, *rrn*5, *trn*A-UGC, *trn*I-CAU, *trn*L-CAA, *trn*N-GUU, *trn*R-ACG, *trn*V-GAC, and *ycf*2. The ML phylogenetic tree showed that *A. retroflexus* was sister to *A. hypochondriacus* and *A. caudatus* (Figure 1). In conclusion, the plastome of *A. retroflexus* provides significant DNA molecular data for further phylogenetic and evolutionary analysis for *Amaranthus*.

Disclosure statement

No potential conflict of interest was reported by the authors.

Funding

The study was financially supported by Shandong Provincial Agricultural Elite Varieties Project [2019LZGC017].

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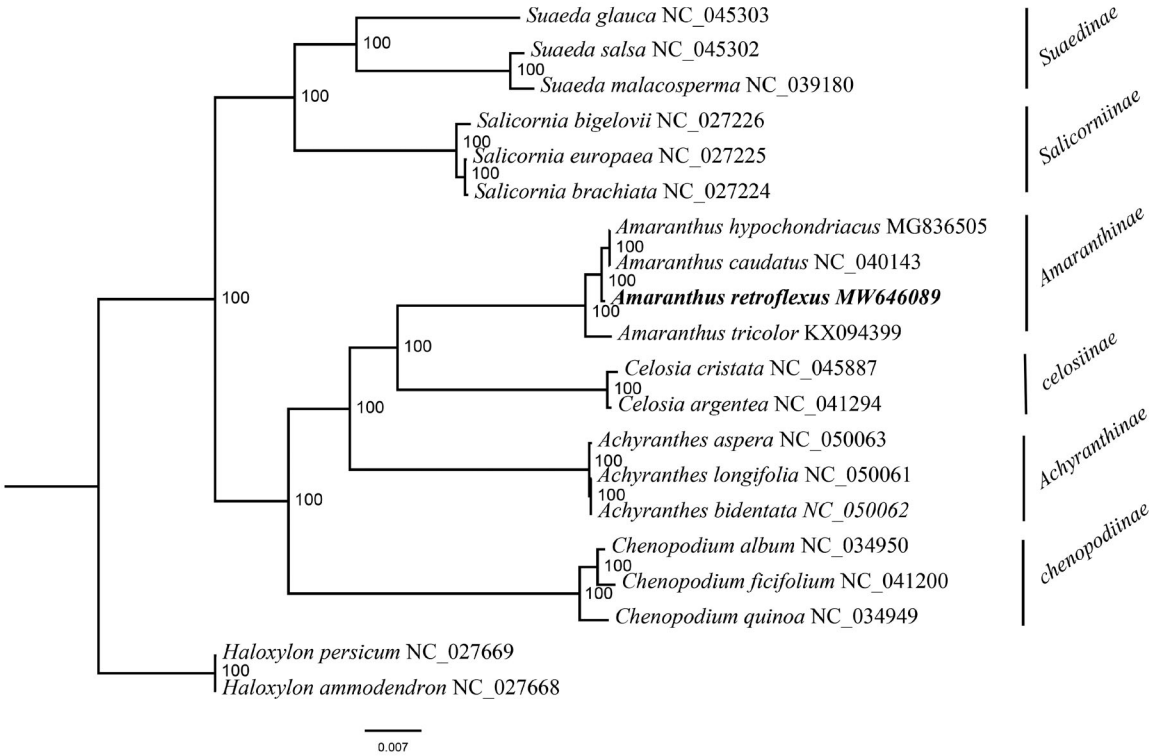

Figure 1. A maximum-likelihood (ML) phylogenetic tree based on 20 Amaranthaceae species is shown. Bootstrap support values are shown as numbers next to branches.

Data availability statement

The data that support the findings of this study are openly available in GenBank of NCBI, reference number MW646089. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA718096 (http://www.ncbi.nlm.nih.gov/bioproject/718096), SRR14089437 (https://www.ncbi.nlm.nih.gov/sra/PRJNA718096), and SAMN18522283 (https://www.ncbi.nlm.nih.gov/sra/PRJNA718096), respectively.

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