Complete chloroplast genome of *Alternanthera philoxeroides* by de novo sequencing

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**ABSTRACT**

*Alternanthera philoxeroides* (Mart.) Griseb. (*Alternanthera philoxeroides*) is an important herbage species, which could provide high-quality feed for livestock and poultry breeding. This paper is the first to report the *A. philoxeroides*’s chloroplast genomes, which were detected by de novo sequencing. The results showed that the length of *A. philoxeroides*’ chloroplast genome sequence was 152,255 bp, including a large single-copy (LSC) region (84,670 bp), a small single-copy (SSC) region (17,343 bp), and two inverted repeat (IR) regions (25,121 bp). *Alternanthera philoxeroides*’ chloroplast genome encoded 132 genes including 8 rRNA, 38 tRNA, and 86 protein-coding genes. After phylogenetic and cluster analysis, *A. philoxeroides* was closest to *Amaranthaceae*, and the relationship between *Amaranthus* and *Achyranthes* was closest.

The fresh leaves of *Alternanthera philoxeroides* was been collected from Pihe National Wetland Park, Lu'an city, Anhui province, P. R. China (N:31.76\(^\circ\), E:116.49\(^\circ\)), and the fresh leaves of *Alternanthera philoxeroides* was deposited at West Anhui University (Ping Jiang, 02000137@wxc.edu.cn) under the voucher number TCVM202008280035. The Plant DNA extraction kit was used to extract the total DNA of *Alternanthera philoxeroides*. After the DNA quality meets the sequencing requirements detected by the method of micro-volume spectrophotometer and 1% agarose electrophoresis, the DNA was escorted to Beijing Zhongxingbomai Technology for sequencing using Illumina NovaSep platform. The Raw data were filtered and Get Organelle pipeline (Jin et al. 2020) was run to obtain high-quality data. The contig sequence was been assembled by SPAdes de novo software (Luo et al. 2012; Yinran et al. 2020), and the relative position of the genome in the contig sequences was acquired by the BLAT (Kent 2002) referencing the NCBI database (NC 024157.1, NC 011942.1, NC 009618.1, NC 000932.1, KC 352464.1). The Bandage tool (Wick et al. 2015) and the Geseq program (Tillich et al. 2017) were run to obtain the full-length frame diagram and annotate the chloroplast genome, respectively. The OGDRAW software (Lohse et al. 2013) was run to draw the physical map (GenBank accession number: MW285080).

Similar to other higher plants, the *Alternanthera philoxeroides* has a typical four-segment structure, including a large single-copy (LSC) region (84,670 bp), a small single-copy (SSC) region...
And the plastome sequence of *Alternanthera philoxeroides* chloroplast genome was 152,255 bp. Its GC content was 36.40% and contained 132 genes including 8 rRNA, 38 tRNA, and 86 protein-coding genes. To determine the phylogenetic status of *Alternanthera philoxeroides* in *Amaranthaceae* plants, we used two *Amaranthus*, two *Achyranthes*, three *Chenopodium*, and three *Fagopyrum* plants and 1 outgroup (*Silene*) in NCBI for phylogenetic analysis. The GTRCATX model from raxmlGUI version 1.5 b (Silvestro and Michalak 2012) performed 1000 bootstrap replicates to calculate the evolutionary relationship and drawing the phylogenetic tree. The cluster analysis results showed that *Alternanthera philoxeroides* was closest to *Amaranthaceae*, and the relationship between *Amaranthus* and *Achyranthes* was closest (Figure 1).

**Disclosure statement**

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

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**Data availability statement**

The data that support the findings of this study have send it up to Bankit (2403319) of National Center for Biotechnology Information, and provided GenBank accession number (MW285080). The associated BioProject and Bio-Sample numbers are PRJNA683712 (https://www.ncbi.nlm.nih.gov/bioproject/PRJNA683712) and SRX9689754 (https://www.ncbi.nlm.nih.gov/sra/SRX9689754), respectively.

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