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Data Article

Illumina sequencing of the chloroplast genome of common ragweed (*Ambrosia artemisiifolia* L.)Erzsébet Nagy^a, Géza Hegedűs^b, János Taller^a,
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ARTICLE INFO

Article history:

Received 7 July 2017

Received in revised form

21 September 2017

Accepted 4 October 2017

Available online 7 October 2017

Keywords:

Illumina sequencing

Chloroplast genome

cpDNA

Common ragweed

Ambrosia artemisiifolia

ABSTRACT

Common ragweed (*Ambrosia artemisiifolia* L.) is the most widespread weed and the most dangerous pollen allergenic plant in large areas of the temperate zone. Since herbicides like PSI and PSII inhibitors have their target genes in the chloroplast genome, understanding the chloroplast genome may indirectly support the exploration of herbicide resistance and development of novel control methods. The aim of the present study was to sequence and reconstruct for the chloroplast genome of *A. artemisiifolia* and establish a molecular dataset. We used an Illumina MiSeq protocol to sequence the chloroplast genome of isolated intact organelles of ragweed plants grown in our experimental garden. The assembled chloroplast genome was found to be 152,215 bp (GC: 37.6%) in a quadripartite structure, where 80 protein coding genes, 30 tRNA and 4 rRNA genes were annotated in total. We also report the complete sequence of 114 genes encoded in *A. artemisiifolia* chloroplast genome supported by both MIRA and Velvet *de novo* assemblers and ordered to *Helianthus annuus* L. using the Geneious software.

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Specifications Table

Subject area	<i>Biology</i>
More specific subject area	<i>Chloroplast genome of common ragweed</i>
Type of data	<i>Table, figure</i>
How data was acquired	<i>2 × 300 Illumina MiSeq sequencing</i>
Data format	<i>Raw reads in FASTAQ, complete cp genome in FASTA</i>
Experimental factors	<i>5 g young leaves were collected from young about 20 cm tall plants, and incubated for 48 h at 4 °C in dark</i>
Experimental features	<i>Complete chloroplast genome of <i>Ambrosia artemisiifolia</i></i>
Data source location	<i>Keszthely-city, Hungary</i>
Data accessibility	<i>Information and complete data are accessible in the NCBI under BioProject and BioSample ID: PRJNA383307, SAMN06761249. The raw reads are available in Fastq format in the NCBI SRA database at the following link https://trace.ncbi.nlm.nih.gov/Traces/sra/sra.cgi?run=SRR6050242. Complete chloroplast genome is available in GenBank under accession number: MF362689; https://www.ncbi.nlm.nih.gov/nucleotide/MF362689</i>

Value of the data

- Common ragweed is one of the most aggressive invasive weed species and the most dangerous pollen allergenic plant in large areas of the temperate zone.
- Understanding the chloroplast genome of this species may indirectly support chemical control of it, since a large part of herbicides have their target genes in the chloroplast genome e.g. triazine-derivatives [1], diphenylethers [2] or the redox active Paraquat [3].
- The reported data mean an important source for further chloroplast derived investigations like phylogenetic, photosynthetic or oxidative metabolism studies of the species.

1. Data

Intact chloroplasts were isolated from young leaves of *Ambrosia artemisiifolia*. Followed by cpDNA isolation and sequencing. The raw reads are available in Fastq format in the SRA database under the accession SRR6050242. The assembled chloroplast genome and annotated genes are available through NCBI nucleotide (MF362689).

2. Experimental design, materials and methods

2.1. Plant material and isolation of cpDNA

Seeds of an *A. artemisiifolia* plant grown in our experimental garden were sown on peat, and plants were grown in pots under greenhouse conditions.

In total, 5 g leaf tissue was collected from young, about 20 cm tall plants. To avoid high level starch accumulation the harvested leaves were incubated in Parafilm-sealed Petri dishes for 48 h at 4 °C in dark before chloroplast preparation. Chloroplast was isolated using the Chloroplast Isolation kit (Sigma-Aldrich, USA) according to the instructions of the manufacturer. The intact chloroplasts were

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