Characterization of the complete plastome of *Cyperus rotundus* L. (Cyperaceae)

Renjie Wu\(^a\), Cong Yu\(^b\) and Yang Wu\(^a\)

\(^a\)College of Life Science, Jinggangshan University, Ji’an, China; \(^b\)Institute of Physical Education, Jinggangshan University, Ji’an, China

**ABSTRACT**

*Cyperus rotundus* L. (Cyperaceae) is a sedge belonging to the family Cyperaceae and is widely distributed in tropical and warmer temperate regions worldwide. It is one of the oldest traditional medicinal herbs in China, India, Japan, and Korea. In this study, we sequenced the complete chloroplast genome of *C. rotundus* on the Illumina HiSeq Platform. The chloroplast genome is 182,986 bp in length, with a typical quadripartite structure and consisting of a pair of inverted repeat (IR) regions (35,969 bp) separated by a large single-copy (LSC) region (100,733 bp) and a small single-copy (SSC) region (10,315 bp). It was predicted to contain a total of 133 genes, with an overall GC content of 33.26%. Phylogenetic analysis suggested *C. rotundus* is sister to *Eleocharis celluosa* and *Eleocharis dulcis.*

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**CONTACT**
Yang Wu  
wuyangfenghao@126.com  
College of Life Science, Jinggangshan University, Ji’an, Jiangxi 343009, China

The complete chloroplast genome of *C. rotundus* has a typical quadripartite structure and is a circular molecule 182,986 bp in length, consisting of two inverted repeats (IR) regions of 35,969 bp, separated by large single-copy (LSC) and small single-copy (SSC) regions of 100,733 bp and 10,315 bp, respectively. The overall GC content of the chloroplast genome was 33.26%, whereas the corresponding values of the LSC, SSC, and IR regions were 30.91%, 25.11%, and 37.73%, respectively. A total of 133 genes were annotated in the sequenced *C. rotundus* chloroplast genome, containing 41 transfer RNAs, 8 ribosomal RNAs and 84 protein-coding genes. These genes belong to several categories with different functions, and 34 duplicated genes are located in the IR regions, including 14 protein-coding genes (rps3, rpl22, rps19, rpl2, rps7, ndhB, rpl32, ycf68, rps15, ndhH, ndhA, ndhI, ndhG, and rpl33), seven tRNA genes (trnH-GUG, trnM-CAU, trnL-CAG, trnL-GAU, trnA-UGC, trnR-ACG, and trnN-GUU), and four rRNA genes (rrn16, rrn23, rrn4.5, and rrn5). The transcription regulation of genes was believed to be affected by introns and exons. There are 100 unique genes, among which 16 genes contained one intron, and one gene (ycf3) contained two introns. Chloroplast genomes have been proven to be significant in reconstructing phylogenetic relationships (Hong et al. 2017). To investigate the relationship of
C. rotundus, the chloroplast genomes of C. rotundus and 8 other species from Cyperaceae were aligned using MAFFT ver. 7.307 (Katoh and Standley 2013). A phylogenetic tree (Figure 1) was constructed with the maximum likelihood method using RAxML (Stamatakis 2014). The result of the phylogenetic analysis revealed that C. rotundus is not monophyletic. The C. rotundus is sister to Eleocharis celluosa and Eleocharis dulcis. The complete plastid genome sequence of C. rotundus will provide genetic and genomic information to promote its horticulture, officinal utilization and systematics research of Cyperaceae.

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 are openly available in GenBank of NCBI at https://www.ncbi.nlm.nih.gov, reference number MT937176.

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