The complete mitogenome of *Chrysopogon zizanioides* (L.) Roberty (Poaceae), with its phylogenetic analysis

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**ABSTRACT**

Vetiver grass (*Chrysopogon zizanioides*), is a perennial and tussock C4 grass from the genus *Chrysopogon* of Poaceae, which has been widely used as a natural and inexpensive resource for multifarious environmental applications. The complete mitogenome of *C. zizanioides* was 551,622 bp in length, containing 40 protein-coding genes (PCGs), 19 transfer RNA genes (tRNAs), and six ribosomal RNA genes (rRNAs). All PCGs started with ATG and stopped with TNN (TAA, TAG, and TGA). The overall nucleotide composition is: 28.2% A, 28.2% T, 21.7% G, and 21.9% C, with a biased A + T content of 56.4%. Phylogenetic analysis using 14 PCGs of 22 species showed that *C. zizanioides* display a close relationship with *Saccharum officinarum* (LC107874) and *Sorghum bicolor* (DQ984518) in Poaceae.

**Introduction**

*Chrysopogon zizanioides* (L.) Roberty, is a perennial and tussock C4 grass from the genus *Chrysopogon* of Poaceae, which has been widely cultivated in the tropics and subtropics of the world (Yaseen et al. 2014; Sigmon et al. 2017). *C. zizanioides* is a miracle grass that can tolerate extreme climatic and soil variations, which has been widely used as a natural and inexpensive resource for multifarious environmental applications, including conservation and detoxification of degraded soil and water and also for mitigation of flood and landslide disasters (Kemper 1993; Adams et al. 2004; Chakrabarty et al. 2015). To date, there have been more than 256 mitogenomes from land plants that have been curated or identified using tRNAscan-SE v2.0 (Bleasby and Waterhouse 1998). Moreover, the narrow genetic and genomic resources of *C. zizanioides* also obviously limited our understanding of this important C4 grass at the genome level. In this study, we first determined the complete mitogenome sequences of *C. zizanioides* using Illumina next-generation sequencing technology, and performed an analysis of the phylogenetic relationships among other 21 species with the available mitogenome data deposited in GenBank.

**Materials and methods**

The fresh leaves of *C. zizanioides* ‘Xiangnan 1’ were collected from Nanyang City, Henan Province, China (112°52′E, 33′00″N). The specimen was deposited at the Collaborative Innovation Center of Water Security for Water Source Region of Mid-line of South-to-North Diversion Project of Henan Province under the voucher number NYNU_C1102986400A, Nanyang Normal University, China (Jibao Chen, 2589425750@qq.com). Whole genome sequencing was conducted on Illumina HiSeq 3000 sequencing platform with 350 bp paired-end (Biomarker Technologies Corporation, Beijing, China). The mitogenome assembly of *C. zizanioides* was performed according to Lloyd Evans et al. (2019) using the reference mitogenome dataset of *S. officinarum* (LC107874) and *S. bicolor* (DQ984518). All mitochondrial protein-coding genes (PCGs), transfer RNA (tRNA), and ribosomal RNA (rRNA) genes were initially annotated using Blann. PCGs were further predicted or modified using NCBI ORFFinder and annotated by BLASTP searches against the NCBI NR. tRNAs were also predicted or identified using tRNAscan-SE v2.0 (Blesaby and Wootton 1990; Huang and Cronk 2015; Chan and Lowe 2019). The phylogenetic tree was reconstructed using the Bayesian analysis (BI) and maximum-likelihood (ML) analyses. The best-fit model of nucleotide substitution for sequences with the Bayesian information criterion (BIC) was determined by jModelTest 2.0.2 (Darriba et al. 2012). The Bayesian phylogenetic analysis was performed using MrBayes 3.2.5 (Ronquist et al. 2012). ML analysis was conducted using RAxML with the GTR + G + I model (Stamatakis 2014). Bootstrap values were calculated using 1000 replicates to assess node support.

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Results and discussion

The complete sequence size of *C. zizanioides* mitogenome was 551,622 bp in length (GenBank accession no. MN635785), which is well within the size range observed in the completely assembled other Poaceae mitogenomes. The overall nucleotide composition is: 28.2% A, 28.2% T, 21.7% G, and 21.9% C, with a biased A + T content of 56.4%. It presents a typical gene set of 40 PCGs, 19 tRNA genes, and six rRNA genes. All PCGs started with the conventional initiation codon of ATG, 22 of them used TAA, 10 PCGs (*atp9*, *ccmC*, *ccmFN*, *cob*, *mttB*, *matR*, *nad7*, *rps1*, and *rps3*) used TAG, and eight PCGs (*atp1*, *ccmB*, *ccmFC*, *cox3*, *nad4*, *rps2*, *rps12*, and *rps13*) used TGA as the termination codon. All 19 tRNAs could fold into a classical cloverleaf structure except for *trnY*-GTA, *trnS*-GCT, and *trnS*-TGA, with their length ranging from 71 bp (*trnC-GCA*) to 91 bp (*trnS-TGA*). The lengths of *rrn5*, *rrn18*, and *rrn26* were 118 bp, 1960 bp, and 3516 bp, including the *rrn5* and *rrn18* existed in a cluster.

The nucleotide sequences of 14 PCGs were used to understand the phylogenetic relationships of *C. zizanioides* with other 21 species using the ML method. Phylogenetic relationships obtained using the ML method were identical to those obtained using the BI analysis. The consensus topology of phylogenetic trees for 22 species extremely highly support that *C. zizanioides*, *S. officinarum*, and *S. bicolor* are a sister group (Figure 1).

Disclosure statement

No potential conflict of interest was reported by the authors.

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Data availability statement

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI athttps://www.ncbi.nlm.nih.gov/ under the accession no. MN635785. The associated BioProject, SRA, and BioSample numbers are PRJNA752393, SRR15371682, and SAMN20594899, respectively.

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Figure 1. Phylogenetic relationships between *C. zizanioides* and 21 other species based maximum-likelihood method. All GenBank accession numbers of each species were listed in the phylogenetic tree. *Phoenix dactylifera* (NC_016740) and *Cocos nucifera* (NC_031696) were used as outgroup.
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