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MITOGENOME ANNOUNCEMENT

The complete chloroplast genome of *Tripsacum laxum* (Gramineae)

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ABSTRACT

Tripsacum laxum (Guatemalan grass) is a perennial fodder grasses, which is commonly growing in large parts of Africa for a source of livestock feed. It has a high economic value as a forage. In this study, we obtained a complete chloroplast genome of *T. laxum* by Illumina sequencing. The results showed a circular genome of 140,556 bp, including the large single copy region (LSC, 82,939 bp), the small single-copy region (SSC, 12,573 bp), and a pair of 22,522 bp inverted repeat regions (IRs). The circular genome contained 120 genes, including 74 protein-coding genes, eight ribosomal RNA genes and 38 tRNA genes. Evolutionary relationship analysis indicates that *T. laxum* is more closely related to previously reported *T. dactyloides*.

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KEYWORDS
Tripsacum laxum; chloroplast genome; phylogenetic analysis

Tripsacum laxum (Guatemalan grass) is a perennial fodder grasses, which belongs to the genus *Tripsacum* in Gramineae (http://www.iplant.cn/info/Tripsacum). This species is commonly growing in large parts of Africa for a source of livestock feed (Mwakha 1972; Topps 1986). *T. laxum* with a good adaptation can be tolerant in drought and acid, that is widely introduced as forage in other tropical regions of the world (Compere 1960; Paul et al. 2016). In recent years, *T. laxum* has also been cultivated in Southern China. Previous studies have demonstrated that it is effective for reducing run-off and soil loss (Madhu et al. 2011). The grass has important research significance and application value in the future. Hence, *T. laxum* is need to be better studied and prioritized as a considerable exploitation goal. In this study, we reported the chloroplast (cp) genome of *T. laxum*, which provided important genetic sources for molecular studying.

The fresh leaves were collected from Fujian Agriculture and Forestry University (Fuzhou, China; 26°5′16.04″N, 119°14′12.93″E). The voucher specimen of *T. laxum* was deposited in the National Engineering Research Center of Juncao Technology, Fujian Agriculture and Forestry University with specimen code FJ0623-TL01. The cp complete genomic DNA was extracted using a DNasecure Plant Kit (DP350-03) (TIANGEN, China). Therefore, we used the Illumina high-throughput sequencing to obtain the cp complete genome of *T. laxum*. The paired-end clean data were assembled by GetOrganelle kit (version 1.7.2) (Jin et al. 2020). The Geneious R21.0.1 (http://www.geneious.com/, Kearse et al. 2012) software was adopted to annotate the cp genome, while *T. dactyloides* (NC 037087.1) as reference sequences. Then, submitted to GenBank (accession number: MW387499).

The chloroplast sequence of *T. laxum* was 140,556 bp, including the large single-copy region (LSC, 82,939 bp), the small single-copy region (SSC, 12,573 bp), and a pair of 22,522 bp inverted repeat regions (IRs). The circular genome contained 120 genes, including 74 protein-coding genes (68 PCG species), eight ribosomal RNA genes (4 rRNA species) and 38 tRNA genes (21 tRNA species). The overall nucleotide composition of chloroplast genome is: 43,333 bp A (30.8%), 43,210 bp T (30.7%), 26,929 bp C (19.2%), 27,084 bp G (19.3%), and the total GC content of 38.4%.

The sequences alignments with MAFFT v7.304 (Katoh and Standley 2013) and MEGAX (Kumar et al. 2018) software was used to construct a maximum likelihood (ML) tree with 1000 bootstrap replications. The ML method based on 15 published complete chloroplast genome sequences which were downloaded from NCBI GenBank database, and constructed a phylogenetic tree (Figure 1) to confirm the relationship between *T. laxum* and other related taxa, while *Oryza rufipogon*, *Oryza sativa* were used as outgroups.

Phylogenomic analysis was conducted by RAxML v.8.2.8 (Stamatakis 2014). The ML phylogenetic analysis showed that *T. laxum* is closely related to *T. dactyloides* (NC 037087.1) in Gramineae (Figure 1).

Disclosure statement

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

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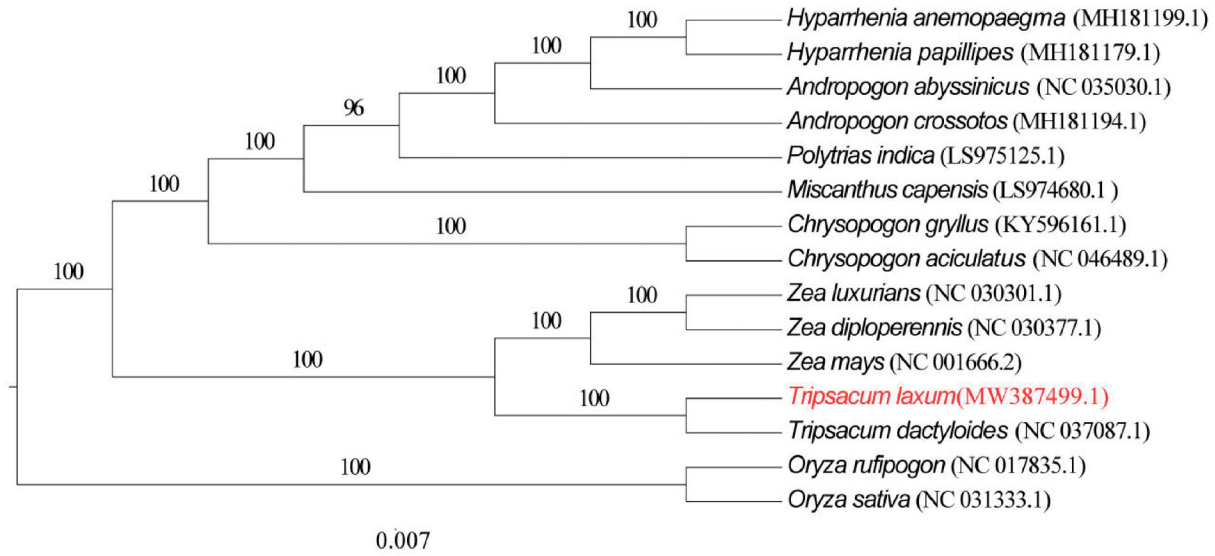

Figure 1. The maximum likelihood (ML) phylogenetic tree based on 15 complete chloroplast genomes, and *Oryza rufipogon*, *Oryza sativa were used* as outgroups.

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Data availability statement

The data that support the findings at this study have been stored in the NCBI database under accession number of MW387499 (https://www.ncbi.nlm.nih.gov/) and the NCBI SRA (BioProject: PRJNA688126) accession number of SRR13311453 (https://www.ncbi.nlm.nih.gov/sra).

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