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MITOGENOME REPORT

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Characterization of the complete mitochondrial genome of *Pennisetum giganteum* A. Rich. (Poaceae)

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ABSTRACT

The complete mitochondrial genome of *Pennisetum giganteum*, an African species, was sequenced and characterized for the first time. The genome is 491,311 bp long and contains 53 unique genes. Phylogenetic analysis based on these genes using maximum likelihood revealed that *P. giganteum* is most closely related to Saccharum officinarum and most distantly related to *Oryza sativa*. This study provides essential genomic data that enhances the understanding of the taxonomy and evolutionary relationships of this versatile and high-yielding species.

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Introduction

Pennisetum giganteum A. Rich. (Poaceae) is a perennial C_4 grass native to Africa, widely distributed in tropical to subtropical regions due to its adaptability to warm climates (Fulkerson et al. 2007; Xing et al. 2023). As a member of the genus *Pennisetum*, *P. giganteum* has significant ecological and agricultural value, noted for rapid growth, high biomass yield, and applications in sustainable agriculture (Samson et al. 2005; Hayat et al. 2020). However, genomic resources for *P. giganteum* remain scarce, particularly for organellar genomes. While chloroplast data exist for close relatives like *Pennisetum glaucum* (Xu et al. 2019), no mitochondrial genome has been reported for any *Pennisetum* species (Zheng et al. 2023).

Mitochondrial genomes are pivotal for resolving plant phylogenies due to structural complexity and variable evolutionary rates (Zardoya 2020). In *Pennisetum*, taxonomic relationships are complicated by hybridization and polyploidization (Dos Reis et al. 2014; Xing et al. 2023). Although nuclear and chloroplast markers have been used (Xu et al. 2019; Zheng et al. 2023), mitochondrial data are critical for evolutionary insights (Shearman et al. 2016; Wu et al. 2022). Here, we present the first complete mitochondrial genome of *P. giganteum*, assembled using Illumina and Nanopore sequencing. This work addresses a genomic gap and provides foundational data for studies on mitochondrial evolution, C_4 photosynthesis (Fan et al. 2022), and phylogenetics in this key genus.

Materials and methods

Plant materials

The *P. giganteum* was used in this study. The voucher specimen was identified by researchers and deposited at the Herbarium of Henan Institute of Science and Technology, Xinxiang, China, under voucher number XM-W145 (contact: Zhengang Ru; rzgh5819@163.com). Fresh roots of *P. giganteum* were collected from the Botanical Garden of the Wheat Research Center, Xinxiang City, Henan Province, China (113°52′E, 35°30′N) by Man Zhang (Figure 1).

DNA sequencing, genome assembly, and annotation

A genomic DNA sample was isolated from the roots with a Plant Tissue Mitochondrial DNA Extraction Kit (Genmed Scientific Inc., Arlington, MA, USA) according to the manufacturer's instructions, and quality control was subsequently carried out on the purified DNA samples. The quality of DNA was assessed using Qubit3.0 and 1% agarose gel electrophoresis. Highly qualified DNA sample (OD260/280 = 1.8 ~ 2.0, >6ug) was utilized to construct the fragment library.

To obtain full-length mitochondrial genome sequences, we used both short-read (Illumina NovaSeq 6000 platform) and long-read sequencing (Nanopore sequencing platform) technologies in this study. The raw paired-end reads were trimmed and quality controlled by Trimmomatic with parameters (SLIDINGWINDOW:4:15 MINLEN:75) (Bolger et al. 2014).

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Figure 1. Morphology features of *Pennisetum giganteum*. The seedling stage of *Pennisetum giganteum* is characterized by erect plants and alternate leaves. The photos of *Pennisetum giganteum* were taken by Man Zhang at the Botanical Garden of the Center of Wheat Research of Henan Institute of Science and Technology, Xinxiang, Henan, China.

Clean data obtained through the above quality control processes was used for further analysis.

The Illumina NovaSeq 6000 short reads (6.3 Gb) were used to evaluate the complexity of the genome and correct the Nanopore long reads. First, we used ABySS 2.2.0 (Simpson et al. 2009) to perform genome assembly with multiple-kmer parameters and received the optimal results of the assembly. Secondly, blasR (Chaisson and Tesler 2012) was used to map the preliminary assembly results to the Nanopore long reads (6.3 Gb). Then, SPAdes-3.15.5 (Prjibelski et al. 2020) was used to assemble them (Nanopore and NGS data) together to construct contigs (Scaffolds). Finally, GapCloser v1.12 (Xu et al. 2020) software was applied to fill the remaining local inner gaps and correct the single-base polymorphism for the final assembly results.

The mitochondrial genes were annotated through homology alignments and de novo prediction. Gene prediction for tRNAs was performed using tRNAscan-SE 2.0.4 (Chan and Lowe 2019) with default parameters. For rRNA and protein-coding genes (PCGs), the assembled mitochondrial genome of *P. giganteum* (query) was aligned against the complete mitochondrial genome of *Saccharum officinarum* (reference database; GenBank: LC107874) *via* BLASTn (BLAST + 2.9.0; Camacho et al. 2009). Homologous regions meeting thresholds of $\geq$80% sequence identity and $\geq$90% coverage were retained, and gene boundaries were further refined using ORFfinder (v0.4.1; Sayers et al. 2024).

Finally, the circular mitochondrial genome assembly and split gene identification were performed and validated using the Plant Mitochondrial Genomes Map (PMGmap) v2.0 (Zhang et al. 2024), a tool specialized in structural annotation based on sequence conservation and break-join modeling.

The annotated mitogenome was submitted to the GenBank database under accession number PQ768538. Then all gene models were analyzed by BLASTp (Camacho et al. 2009) against the non-redundant (NR) protein database (Sayers et al. 2024), SwissProt (The UniProt Consortium 2019), KEGG (Kanehisa and Goto 2000), Gene Ontology (GO) (The Gene Ontology Consortium 2000), and Clusters of Orthologous Groups (COG) (Tatusov et al. 2000) for functional annotation.

To validate the assembly completeness and uniformity, sequencing reads were mapped back to the mitochondrial genome using BWA-MEM v0.7.17 (Li 2013) with default parameters. The coverage depth across the genome was calculated using SAMtools v1.18 (Danecek et al. 2021) and visualized as a coverage plot (Figure S1) *via* the Integrative Genomics Viewer (IGV) v2.19.1 (Thorvaldsdóttir et al. 2013). The average coverage depth of 284.04$\times$ indicates sufficient sequencing depth to ensure high-confidence assembly and highlights uniform read distribution, which minimizes potential gaps or misassemblies (Figure S1). Coverage analysis also helps identify repetitive regions or structural variations that may challenge assembly algorithms.

Phylogenetic tree construction

To determine the molecular position of *P. giganteum* with other closely related species, phylogenetic analyses were performed using 11 complete mitochondrial genome sequences (comprising 34 PCGs, 16 tRNAs, and three rRNAs). First, global alignment was conducted with MUMmer v3.23 (Delcher et al. 2002) to identify syntenic blocks. Local alignment refinement was performed using BLAT v36 (Kent 2002) with default parameters. To ensure alignment quality, ambiguous and divergent regions were filtered using Gblocks v0.91b (Castresana 2000) under strict parameters (-t = d -b4 = 5 -b5 = h), retaining only highly conserved blocks suitable for phylogenetic inference. The best-fit nucleotide substitution model (GTR+I+G) was selected using jModelTest 2.1.10 (Darriba et al. 2012), and maximum-likelihood trees were constructed with PhyML 3.0 (Guindon et al. 2010) using 1,000 bootstrap replicates. *Oryza sativa* Japonica Group (accession BA000029.3) was selected as the outgroup, as its placement in the evolutionarily distinct Oryzoideae subfamily provides a robust phylogenetic contrast to the Panicoideae subfamily (containing *Pennisetum*), and its well-annotated mitochondrial genome is widely adopted in Poaceae studies.

The assembled mitochondrial genome (491,311 bp; GenBank ID: PQ768538) contains 34 protein-coding genes, 16 tRNA genes, and 3 rRNA genes. This circular map displays the following features from the innermost to the outermost ring: Relationships between dispersed repeats; Distribution of dispersed repeats along the genome (direct repeats shown in yellow, inverted repeats in green).

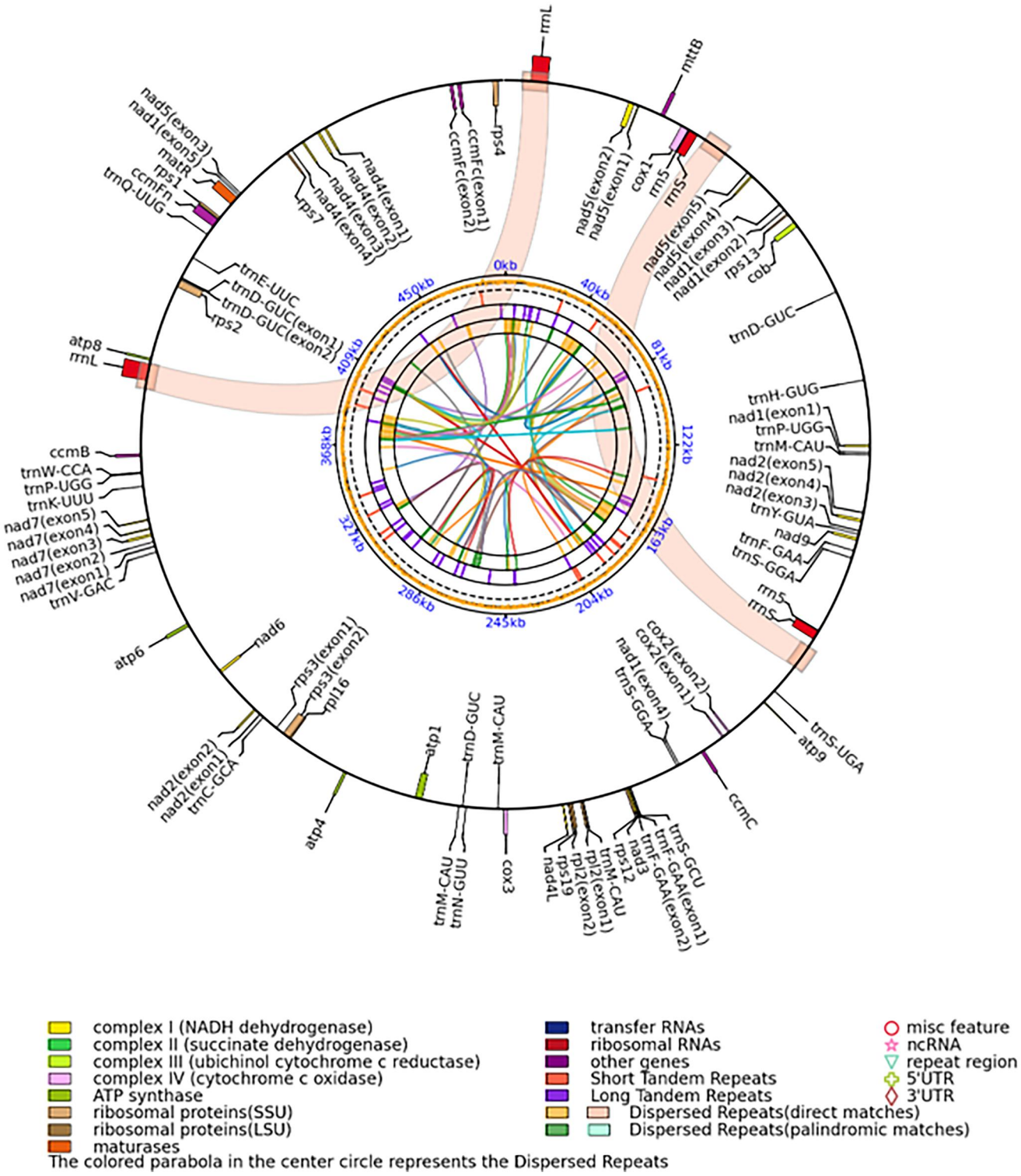

Figure 2. Mitochondrial genome map of *Pennisetum giganteum* constructed with PMGmap.

Distribution of tandem repeats; GC content across the genome; Scale axis; Genes encoded on the negative strand, genes encoded on the positive strand.

Results

The *P. giganteum* mitochondrial genome (GenBank ID: PQ768538) was assembled into a single, circular sequence with a length of 491,311 bp and a GC content of 43.81%.

The mitochondrial genome of *P. giganteum* includes 34 PCGs, 16 tRNA genes, and three rRNA genes (Figure 2, Table S1). Most of the PCGs have an ATG start codon, except for nad1 and nad4L, which have an ACG start codon. There are two types of termination codons in the PCGs: TAA and TAG, which correspond to 15 and 19 genes, respectively. Among the PCGs, eight were *cis*-spliced genes, six of which contained one intron (*ccmFc*, *cox2*, *rpl2*, *rps3*, *trnD-GUC*, *trnF-GAA*), one contained three introns (*nad4*), and one contained

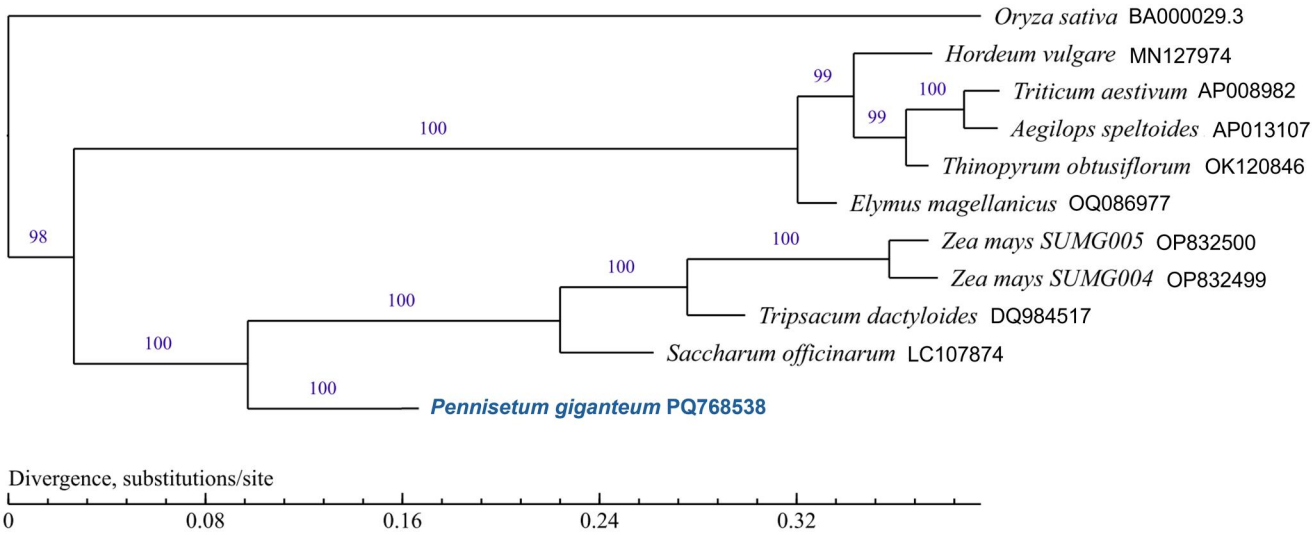

Figure 3. The maximum likelihood (ML) phylogenetic tree was constructed using the complete mitochondrial genome of 11 species. The following sequences were used: *Pennisetum giganteum* (GenBank: PQ768538), *Oryza sativa* Japonica Group (GenBank: BA000029.3; Notsu et al. 2002), *Hordeum vulgare* (GenBank: MN127974), *Triticum aestivum* (GenBank: AP008982; Ogihara et al. 2005), *Aegilops speltoides* (GenBank: AP013107), *Thinopyrum obtusiflorum* (GenBank: OK120846; Wu et al. 2022), *Elymus magellanicus* (GenBank: OQ086977; Chen et al. 2023), *Zea mays* voucher SUMG 004 (GenBank: OP832499), *Zea mays* voucher SUMG 005 (GenBank: OP832500), *Tripsacum dactyloides* (GenBank: DQ984517), *Saccharum officinarum* (GenBank: LC107874; Shearman et al. 2016). The phylogenetic tree was rooted with the outgroup (*Oryza* sativa), with branch lengths scaled to substitutions per site. Numbers next to each node indicate bootstrap support values.

four introns (*nad7*). *nad1*, *nad2*, and *nad5* were *trans*-spliced genes, all of which contained four introns (Figure S2).

The 16 tRNAs ranged from 68 to 89 bp in length. *rrn5*, *rrnL*, and *rrnS* genes were 120 bp, 3535 bp, and 1967 bp in length, respectively. There were 17 gene duplications, including 9 PCGs, five tRNA genes, and three rRNA genes.

This study analyzed the phylogenetic relationships of 11 species using the complete mitochondrial genome sequence (Figure 3). As designated a priori for phylogenetic contrast, Oryza sativa Japonica Group (BA000029.3) formed a distinct basal branch serving as the outgroup. *P. giganteum* is most closely related to *S. officinarum* (LC107874), followed by *Tripsacum dactyloides* (DQ984517), *Zea mays* voucher SUMG 004 (OP832499), and *Zea mays* voucher SUMG 005 (OP832500). The above five species are grouped into one clade. Another large clade also contains five species: *Elymus magellanicus* (OQ086977), *Thinopyrum obtusiflorum* (OK120846), *Aegilops speltoides* (AP013107), *Triticum aestivum* (AP008982), and *Hordeum vulgare* (MN127974). Results from distant species are presented as supplementary references, with core conclusions drawn from intra-Panicoideae relationships.

Discussion and conclusion

Compared to animal mitochondria, plant mitochondrial genomes exhibit greater structural complexity and variability. Consequently, research has predominantly focused on chloroplasts, leaving many plant mitochondrial genomes unresolved (Zardoya 2020). This study presents the first complete assembly and annotation of the mitochondrial genome of *P. giganteum*, marking the first reported mitochondrial genome for any species within the genus *Pennisetum*.

The assembly and annotation of the *P. giganteum* mitochondrial genome (491,311 bp) provide critical insights into its genomic architecture. Its moderate GC content (43.81%) aligns closely with mitochondrial genomes of other Poaceae species, such as *S. officinarum* (43.9%) and *Zea mays* (43.9%), suggesting conserved compositional stability among C_4 grasses (Clifton et al. 2004; Xing et al. 2023; Li et al. 2025). Notably, the presence of atypical start codons (e.g. ACG for *nad1*) mirrors findings in *Elymus magellanicus* (Chen et al. 2023) and *Saccharum* species (Zhou et al. 2022), highlighting potential evolutionary constraints in mitochondrial gene regulation.

Mitochondrial PCGs exhibit significantly slower evolutionary rates, particularly in synonymous substitutions (Wu et al. 2020). This high conservation makes them suitable for resolving deep-level phylogenetic relationships, contrasting with chloroplast genomes better suited for lower taxonomic ranks (Lan et al. 2024).

The coexistence of *cis*-spliced and *trans*-spliced genes underscores intricate RNA processing in *P. giganteum*, aligning with mitochondrial genome plasticity observed in other polyploid grasses (Guo et al. 2020). This characterization provides foundational insights into its potential role in supporting C_4 photosynthetic evolution.

Phylogenetic analysis revealed *P. giganteum*'s closest relationship with *S. officinarum* (a C_4 grass), consistent with morphological and ecological similarities, while showing marked divergence from C_3 species like *O. sativa*. This mitochondrial genome serves as a crucial reference for resolving taxonomic uncertainties, studying polyploid mitochondrial evolution, and developing molecular markers. These findings establish a foundation for future investigations into C_4 plant mitochondrial-chloroplast interactions and stress tolerance genetics. Integrating mitogenomic data with nuclear and chloroplast genomes will enhance understanding of adaptive evolution in this genus.

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Conceptualization: MZ, XC, XW; Formal analysis: KF, HW, JY, XC; Writing – original draft: MZ, XW; Writing – review & editing: MZ, XW; All authors read and approved of the final manuscript.

Ethical approval

The plant samples used in this study were non-protected species. Sample collection was carried out in strict compliance with local and Chinese regulations. No ethical approval was required for this study.

Author contributions

CRediT: **Man Zhang**: Conceptualization, Writing – original draft, Writing – review & editing; **Xiaojun Wu**: Conceptualization, Writing – original draft, Writing – review & editing; **Kaiqiang Fang**: Formal analysis; **Haobo Wang**: Formal analysis; **Junchao You**: Formal analysis; **Xiangdong Chen**: Conceptualization, Formal analysis.

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 at (https://www.ncbi.nlm.nih.gov/), reference number PQ768538. The associated BioProject, Bio-Sample, and SRA numbers are PRJNA1196327, SAMN45421721, SRR31666584 (Nanopore) and SRR31666585 (NovaSeq), respectively.

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