

The complete chloroplast genome of *Panicum miliaceum*

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ABSTRACT

Panicum miliaceum is the most important and ancient domesticated crops in the world. The complete chloroplast genome of *P. miliaceum* was sequenced using the Illumina HiSeq platform (Illumina Inc., San Diego, CA). The chloroplast genome of *P. miliaceum* was 139,929 bp in length, with 38.60% GC content. It contains a pair of inverted repeats (IRs) (22,723 bp) which were separated by a large single copy (LSC) (81,918 bp) and a small single copy region (SSC) (12,565 bp). A total of 132 genes were annotated, which included 84 protein coding genes, 40 tRNA genes and eight rRNA genes. The neighbour-joining (NJ) phylogenetic analysis with the reported chloroplast genomes showed that *P. miliaceum* chloroplasts are most closely related to those of the Gramineae family.

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Broomcorn millet (*Panicum miliaceum*) was one of the most important and ancient domesticated crops in the world (Lu et al. 2009). They were staple foods in the semiarid regions of East Asia (China, Japan, Russia, India and Korea) and even in the entire Eurasian continent before the popularity of rice and wheat (Fuller 2006), and are still important foods in these regions today (Li & Wu 1996; Lu et al. 2009).

Chloroplasts play an important role in photosynthesis in green plants (Neuhaus & Emes 2000). The plant chloroplast genome consists of two large inverted repeats separated by a large single copy (LSC) region and a small single copy (SSC) region (Palmer 1985). The DNA sequence of the chloroplast genome can be used as a super barcode or a resource for research in phylogeography, genetic diversity and evolution. Although many members of the Gramineae are economically important and had complete chloroplast genome data available on public database on website, the common millet (*P. miliaceum*) has no its complete chloroplast sequence published.

For this study, we collected the fresh, healthy leaves from *P. miliaceum* growing in the site (39°08'N, 111°14'E), which is located near the junction between the Loess Plateau and the North China Plain at an elevation of 1086 m. DNA was extracted using CTAB-based protocol described by Gawel (1991). We sequenced the complete chloroplast genome of *P. miliaceum* with the Illumina HiSeq sequencing platform (Novogene, Beijing, China). We assembled the chloroplast genome using Mira and annotated with software CpGAVAS

(Liu et al. 2012). We determined the complete chloroplast genome sequence of *P. miliaceum* was 139,929 bp in length. The GC content was 38.6%. Chloroplasts are typically AT rich, and the GC content of the *P. miliaceum* chloroplast was similar to values previously reported for most other Gramineae species (e.g. 39.0% in *Chikusichloa aquatica*; Zhang et al. 2015). The LSC and SSC contained 81,918 bp and 12,565 bp, respectively, while the IR was 22,723 bp in length. This chloroplast genome contained 132 functional genes, including 84 protein-coding genes, 30 tRNA genes and eight rRNA genes. There were 14 protein-coding genes, 16 tRNA and all eight rRNA genes duplicated in the IR regions. The LSC region contained 60 protein-coding and 23 tRNA genes, whereas the SSC region contained 10 protein-coding and 1 tRNA genes. Fourteen genes contained one or two introns, including the protein-coding genes, *rps16*, *atpF*, *ycf3*, *petB*, *petD*, *rpl16*, *rpl2*, *ndhB*, *ndhA* and *rps12*.

The phylogenetic relationship of *P. miliaceum* to other plant families was evaluated by comparing the 29 species of Gramineae chloroplast. A neighbour-joining (NJ) analysis was performed using the software Geneious 8.0.2 (<http://www.geneious.com/>) (Figure 1). The phylogenetic tree showed that *P. miliaceum* (Gramineae) was most closely related to members of genus *Cenchrus* and the genus *Setaria* (Figure 1). The newly characterized *P. miliaceum* complete chloroplast genome will provide essential data for further study on the phylogeny and evolution of the genus *Panicum* and of the

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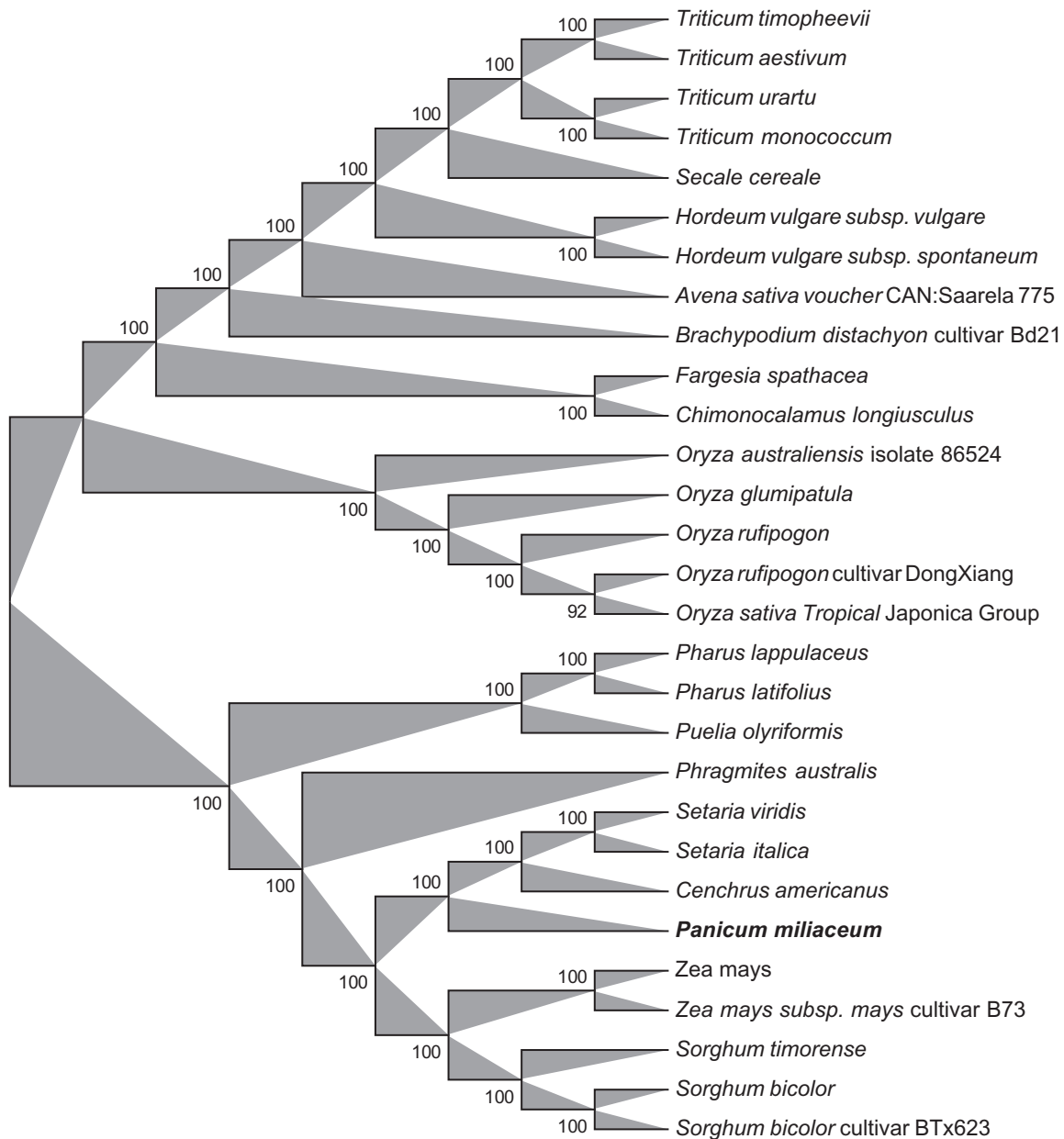


Figure 1. Phylogenetic relationships among 28 whole chloroplast genomes of Gramineae family. The 29 species can be divided into two independent clades. Bootstrap support values are given at the nodes. Chloroplast genome accession number used in this phylogeny analysis: *Triticum timopheevii*: NC024764; *Triticum aestivum*: KC912694; *Triticum urartu*: NC021762; *Triticum monococcum*: NC021760; *Secale cereale*: NC021761; *Hordeum vulgare* subsp. *vulgare*: KC912689; *Hordeum vulgare* subsp. *spontaneum*: KC912688; *Avena sativa* voucher CAN:Saarela 775: NC027468; *Brachypodium distachyon* cultivar Bd21: EU325680; *Fargesia spathacea*: NC024716; *Chimonocalamus longiusculus*: NC024714; *Oryza australiensis* isolate 86524: NC024608; *Oryza glumipatula*: KM881640; *Oryza rufipogon*: NC017835; *Oryza rufipogon* cultivar DongXiang: KF562709; *Oryza sativa* Tropical Japonica Group: KT289404; *Pharus lappulaceus*: NC023245; *Pharus latifolius*: NC021372; *Puelia olyrififormis*: NC023449; *Phragmites australis*: NC022958; *Setaria viridis*: NC028075; *Setaria italica*: KJ001642; *Cenchrus americanus*: KJ490012; *Zea mays*: NC001666; *Zea mays* subsp. *mays* cultivar B73: KF241981; *Sorghum timorense*: NC023800; *Sorghum bicolor*: NC008602; *Sorghum bicolor* cultivar BTx623: EF115542. Bold and italic were the sample as *Panicum miliaceum* in this study.

Gramineae, for molecular breeding, and potentially for genetic engineering.

Disclosure statement

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of this article.

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