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#### MITOGENOME ANNOUNCEMENT

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# The complete chloroplast genome sequence of Indian barnyard millet, *Echinochloa frumentacea* (Poaceae)

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#### ABSTRACT

We report the complete chloroplast genome sequence of the important nutritious millet crop Indian barnyard millet, *Echinochloa frumentacea* Link (Poaceae). The size of the circular chloroplast genome is 139593 bp in length with a typical quadripartite structure, containing pair of inverted repeats of 22618 bp, flanked by large single copy and small single copy regions of 81 839 bp, 12518 bp, respectively. Overall GC content of the genome was 38.6% and consists of 112 individual genes, including 77 protein coding genes, 30 tRNA genes, four rRNA genes and one conserved open reading frame. In addition, phylogenetic analysis with grass species has revealed that *E. frumentacea* is diverged around 1.9–2.7 million years with its close relatives, *E. oryzicola* and *E. crus-galli*.

**ARTICLE HISTORY** 

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**KEYWORDS** Chloroplast genome; *Echinochloa; E. frumentacea*; Indian barnyard millet

The chloroplast is a vital organelle genome responsible for the photosynthesis. Chloroplast genomes have non-meiotic and uni-parental inheritance mostly by maternal inheritance (Reboud & Zeyl 1994) and 120–217 kb in size with about 130 conserved genes and relatively diverse intergenic spaces (IGS) (Rivarola et al. 2011, Wang & Messing 2011, Nah et al. 2015). The chloroplast genomes have highly conserved genome structure, organization, gene order which render them as main targets to understand plant genetic diversity and evolution (Moore et al. 2010, Ye et al. 2014).

The genus *Echinochloa* belongs to the family Poaceae which consists of 50 species including two domesticated species, Indian barnyard millet or Indian sawa millet (*E. frumentacea*) and Japanese barnyard millet (*E. utilis* or *E. esculanta*) (Aoki & Yamaguchi 2008). *E. frumentacea*  $(2n=6\times=54)$  is one of the oldest domesticated millet in the semi-arid tropics of Asia and Africa (Hilu 1994) and expected to be domesticated from the hexaploid progenitor *E. colona*. It is nutritionally a rich cereal crop which serves as a food and fodder, contains vitamins, minerals, sulphur-containing amino acids and phyto chemicals even superior to the staple cereals such as rice and wheat (Yabuno 1983). Despite the above facts, the barnyard millet genome has been largely unexplored.

Here we report complete chloroplast genome of the *E. frumentacea Link* (Poaceae). Genomic DNA sample of Indian barnyard millet popular variety CO(KV)2 was obtained from Agricultural College and research Institute, Madurai, TNAU, India. Genomic DNA of the four-week old plant was used to decode the genome by Illumina MiSeq sequencing platform

with  $300 \times 2$  pair-end library. Whole genome sequences of *E. frumentacea* were assembled under CLC genome assembler to achieve the complete and error-free chloroplast genome (cpDNA) based on the guidance of our previous paper (Kim et al. 2015). The cpDNA was annotated by the Dual Organellar Genome Annotator (DOGMA) (Wyman et al. 2004) and tRNAscan-SE (Schattner et al. 2005). The cpDNA sequence with complete annotation information was deposited at GenBank database under the accession number KU242342.

The chloroplast genome has a total length of 139593 bp with a characteristic quadripartite structure, consisting of LSC region of 81839 bp, two IR regions of 22618 bp and SSC region of 12518 bp. The chloroplast genome revealed the GC content of 38.6%, was predicted to encode 112 genes, including 77 protein coding genes, 30 tRNA genes, four rRNA genes and one conserved open reading frame (ORF). Phylogenetic analysis was performed using MEGA6 based on the complete cpDNA of E. frumentacea with reported close relatives of grass or poaceae family which not only differentiated the C3 and C4 plants but also revealed the inter-and intra-species diversity in the *Echinochloa* genus (Figure 1). The molecular divergence clock analysis using the BEAST has revealed that E. frumentacea diverged with its close relatives, E. oryzicola and E. crus-galli around 1.9-2.7 million years (Drummond et al. 2012; Ye et al. 2014). This newly characterized chloroplast genome of E. frumentacea will provide a valuable resource for population and evolutionary studies of the genus Echinochloa.

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Figure 1. Phylogenetic tree based on the complete chloroplast genome sequences of *E. frumentacea* and 14 other grass species. Neighbor-joining tree was generated by MEGA6 with 1000 bootstrap replications. The molecular divergence time denoted on the node was calculated using Yule process with the reference divergence time of rice and sorghum (50 mya). The corresponding GenBank number of the cpDNA including the outgroup *Brachypodium distachyon* was denoted in the parenthesis.

## **Disclosure statement**

None of the authors report any conflict of interest. The authors alone are responsible for the content and writing of the paper.

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