

# Open-access web resources for millets, cereals & bioenergy genomics



**Welcome to FmMDB**

FmMDB is the first online marker resource developed for the model crop *Setaria italica* L., comprising a wide-range of genomic datasets that will assist plant breeders and researchers to select the most appropriate markers for marker-assisted selection in millets and bioenergy grasses.

Foxtail millet, the second largest cultivated millet species has been recently considered to be a tractable model crop for studying functional genomics, as it possesses a small genome (~515 Mb), short life-cycle, rich genetic diversity (~6,000 varieties), inbreeding nature, closely-related to several bioenergy grasses and especially, its potential abiotic stress tolerance. Moreover, the draft genome sequence information from US Department of Energy - Joint Genome Initiative and Beijing Genomics Institute, China had motivated the scientific community to

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submitted in NCBI Probe Database  
✓ The genomic and genetic SSR markers are physically mapped on to the nine chromosomes of foxtail millet and the

## Foxtail millet Marker Database (FmMDB)

<http://www.nipgr.res.in/foxtail.html>

A first comprehensive online database for information retrieval, visualization & management of large-scale marker datasets with unrestricted public access. FmMDB provides complete marker information (SSRs, eSSRs & ILPs) to the plant science community.

**Welcome to FmTFDb**

FmTFDb is the first online transcription factor database developed for the model crop *Setaria italica* L., comprising comprehensive set of transcription factors (2297 Genes) and classifies them into 55 families. Foxtail millet, the second largest cultivated millet species has been recently considered to be a tractable model crop for studying functional genomics, as it possesses a small genome (~515 Mb), short life-cycle, rich genetic diversity (~6,000 varieties), inbreeding nature and closely-related to several bioenergy grasses. Recently, the draft genome sequence was released by US Department of Energy - Joint Genome Initiative and Beijing Genomics Institute, China. Being a potential abiotic stress tolerant crop, foxtail millet is also used as model to decipher the molecular mechanism involved in tolerance towards abiotic stresses.

Recent reports on the role of transcription factors in abiotic stress tolerance (e.g. NAC, DREB) has motivated our group to identify and catalogue all the foxtail millet genes involved in transcriptional control. Promisingly, this FmTFDb will facilitate the molecular dissection of transcriptional machinery in foxtail millet, especially, identification and characterization of transcription factors controlling the expression of

**NEWS & UPDATES**  
✓ Transcription factors, particularly to drought and salinity genes as an abiotic stress tolerance and hence exploring these agronomic traits can enhance its efficiency in marker-assisted breeding as well as in genetic engineering for abiotic stress tolerance.  
✓ Recently we have performed

## Foxtail millet Transcription Factor Database (FmTFDb)

<http://59.163.192.91/FmTFDb>

FmTFDb provides free access to the 2297 FmTFs through a set of query interfaces & analysis tools, including the BLAST search, annotation query interfaces, & tools to identify enriched Gene Ontology terms & visualize physical maps.

**Welcome to FmMiRNADb**

FmMiRNADb (Foxtail millet micro RNA database) is the first online database of microRNA (miRNA) sequences, its annotation and secondary structure for the model crop *Setaria italica* L. miRNAs play a prominent role in gene regulation during multiple biological processes including stress response, through post-transcriptional control. Foxtail millet, the second largest cultivated millet species has been recently considered to be a tractable model crop for studying functional genomics, as it possesses a small genome (~515 Mb), short life-cycle, rich genetic diversity (~6,000 varieties), inbreeding nature and closely-related to several bioenergy grasses. Recently, the draft genome sequence was released by US Department of Energy - Joint Genome Initiative and Beijing Genomics Institute, China.

Being a potential abiotic stress tolerant crop, foxtail millet is also used as model to decipher the molecular mechanism involved in tolerance towards abiotic stresses such as drought and salinity. Hence, our group conducted a genome-wide investigation to identify the miRNAs and our study reported 355 mature miRNAs to be encoded by the foxtail millet genome. Further, all the 355 miRNAs were annotated and its respective

**NEWS & UPDATES**  
✓ Foxtail millet (*Setaria italica* L.) has been recently regarded as an excellent model crop to study the systems biology of millet and bioenergy grass species. [Read more](#)  
✓ FmMiRNADb is the first

## Foxtail millet miRNA Database (FmMiRNADb)

<http://59.163.192.91/FmMiRNADb>

The database encompasses complete information of 355 foxtail millet miRNAs along with a interactive physical map. Further, FmMiRNADb also contains the details of 176 miRNA-based molecular markers for genotyping & molecular breeding of millets, cereals & bioenergy grasses.

**Welcome to FmTEMDB**

Transposable elements (TE) constitute a significant fraction of plant genomes and are considered to be one of the major forces driving genome evolution. TEs have capability to change its position in the genome and called as "jumping gene" by Barbara McClintock, a renowned geneticist. Each transposition event generates new variability by creating mutations and altering cell's genome size. Retrotransposons are the class I elements which produce RNA intermediates and by the action of reverse transcriptase, they are copied into DNA and then inserted into new locations within the genome, while other TEs class II TEs, or DNA transposons move directly by a "cut and paste" mechanism. Activation of TEs in genomes generate a range of effects, including evolution, structural and functional alterations in gene expression, gene deletion and insertion. Therefore, inactivation of TEs can be crucial for the survival of the host organisms.

Foxtail millet (*Setaria italica* L.), the second largest cultivated millet species has been recently considered to be a tractable model crop for studying functional genomics, as it possesses a small genome (~515 Mb), short life-cycle, rich genetic diversity (~6,000 varieties), inbreeding nature and closely-related to several bioenergy grasses.

## Foxtail millet Transposable Elements-based Marker Database (FmTEMDB)

<http://59.163.192.91/FmTEMDB/>

The database possess the data of ~30000 foxtail millet transposable elements & 6 different types of markers useful for large-scale genotyping applications in millets, cereals & bioenergy grasses.

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