

## **Supplementary materials**

**Supplementary Figure S1:** Distribution of full length LTR-type retrotransposons across the nine chromosomes of foxtail millet.

**Supplementary Figure S2:** Genome-wide prediction of Full length LTR retrotransposon from foxtail genome using LTR finder software.

**Supplementary Figure S3:** BLAST analysis showing unique junction region for designing the junction based primer.

**Supplementary Figure S4:** BLAST analysis showing repetitive region in the sequence (highlighted red in color) to demarcate the junction site. Arrow shows one primer from junction site and other primer from other region of the sequence.

**Supplementary Figure S5:** PCR amplification profile of Repeat Junction Marker (a) dna13398, (b) dna16027, (c) dna19096 and (d) LINE2650. The detailed information for 24 accessions (SN. 25-48) of *Setaria italica* are listed in Supplementary Table S1.

**Supplementary Figure S6:** Multiple sequence alignment of 88 accessions of *Setaria italica* accessions along with reference genome amplified with LINE2650 primer. The detailed information for 88 accessions of *Setaria italica* are listed in Supplementary Table S1.

**Supplementary Figure S7:** Multiple sequence alignment of 11 accessions of *Setaria italica* accessions along with reference genome amplified with RJM7 primer. The detailed information for 11 accessions (RJM07:reference genome; IC480117, IC403579, cv. Prasad, cv. Lepakshi, IC403476, GS464, IC404178, IC403521, EC539248, EC539291) of *Setaria italica* are listed in Supplementary Table S1.

**Supplementary Figure S8:** Distribution of different types of nested TE subclasses.

**Supplementary Figure S9:** An un-rooted neighbor-joining tree for the 99 individuals of *Setaria italica* alongwith three wild species.

**Supplementary Figure S10:** Graphical representation showed the detection of the true number of groups  $K^*$  resulted after structure analysis.

**Supplementary Figure S11:** Bar plot of *Setaria italica* of 99 accessions were generated by STRUCTURE 2.3.4 using the admixture model with correlated allele frequencies. Groups are represented by colours.

**Supplementary Figure S12:** Tutorial of Foxtail millet Transposable Element-based Marker Database.

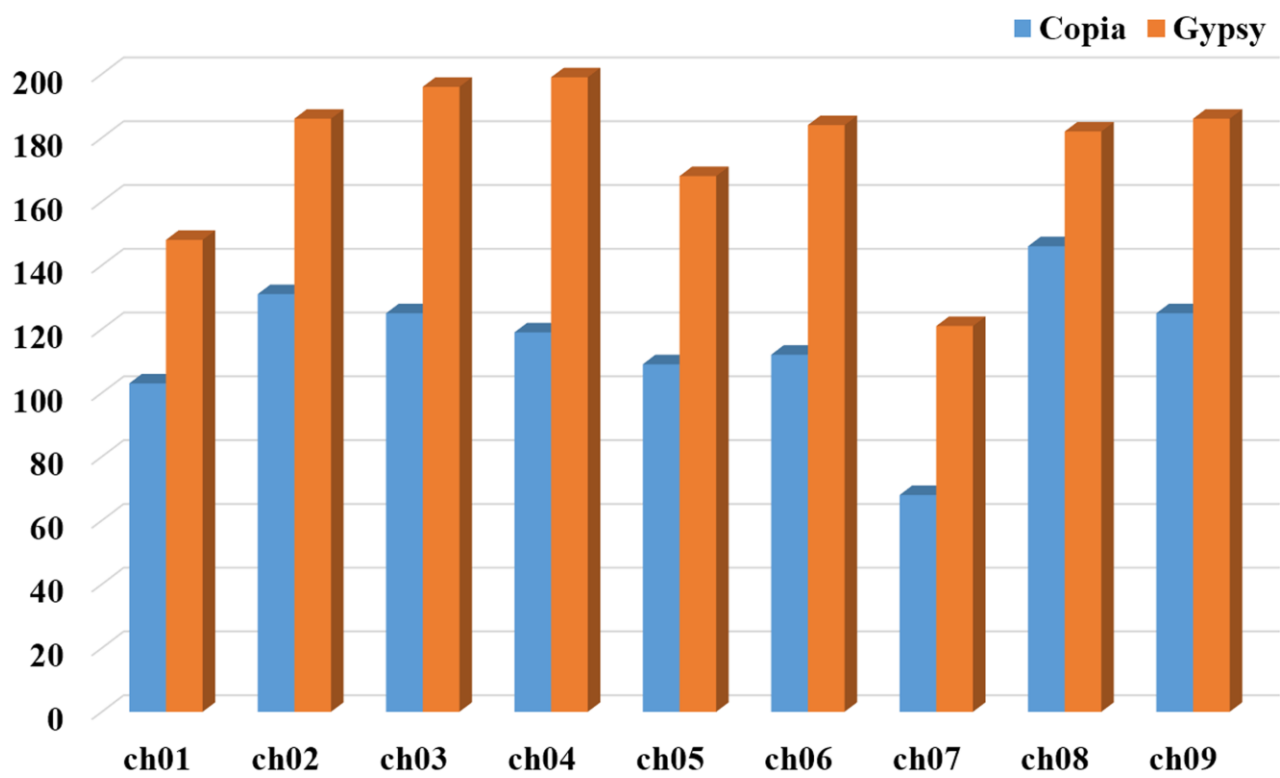
**Supplementary Table S1:** List of plant materials used in the present study

**Supplementary Table S2:** Details of *Copia*-type retrotransposons identified in foxtail millet

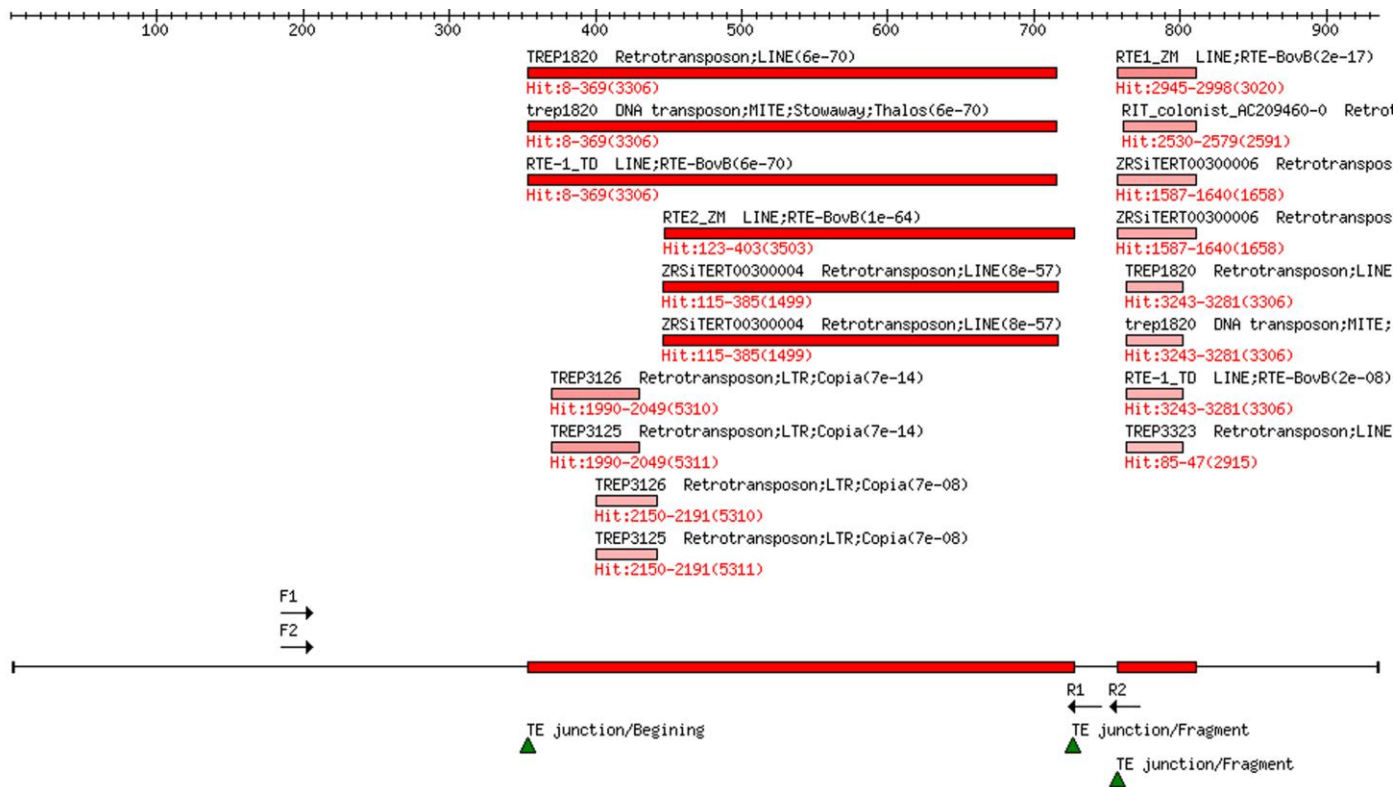
**Supplementary Table S3:** Details of *Gypsy*-type retrotransposons identified in foxtail millet

**Supplementary Table S4:** Details of partially or solo *Copia*-type retrotransposons identified in foxtail millet

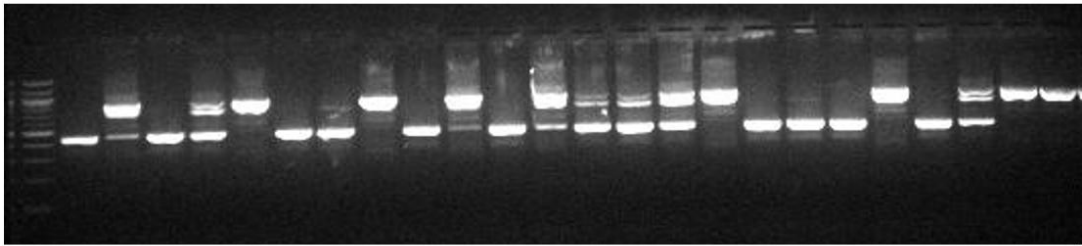
- Supplementary Table S5:** Details of partially or solo *Gypsy*-type retrotransposons identified in foxtail millet
- Supplementary Table S6:** Details of *LINEs* (Non-LTR type) identified in foxtail millet
- Supplementary Table S7:** Details of *SINEs* (Non-LTR type) identified in foxtail millet
- Supplementary Table S8:** Estimation of insertion time of *Copia*-type transposable elements
- Supplementary Table S9:** Estimation of insertion time of *Gypsy*-type transposable elements
- Supplementary Table S10:** Details of DNA transposons identified in foxtail millet
- Supplementary Table S11:** Presence of transcriptionally active *Copia*-type retrotransposons in various tissues of foxtail millet
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- Supplementary Table S20:** Details of ISBP primers designed in foxtail millet
- Supplementary Table S21:** Details of REMAP primers designed in foxtail millet
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- Supplementary Table S24:** Determination of K using Evanno's method
- Supplementary Table S25:** Summary of distribution of pure ancestral *Setaria italica* individuals
- Supplementary Table S26:** Syntenic relationships between transposable elements of foxtail millet and sorghum
- Supplementary Table S27:** Syntenic relationships between transposable elements of foxtail millet and maize
- Supplementary Table S28:** Syntenic relationships between transposable elements of foxtail millet and rice
- Supplementary Table S29:** Syntenic relationships between transposable elements of foxtail millet and *Brachypodium*



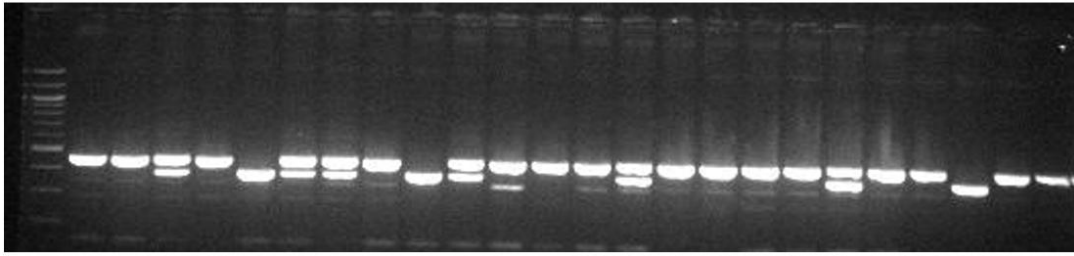




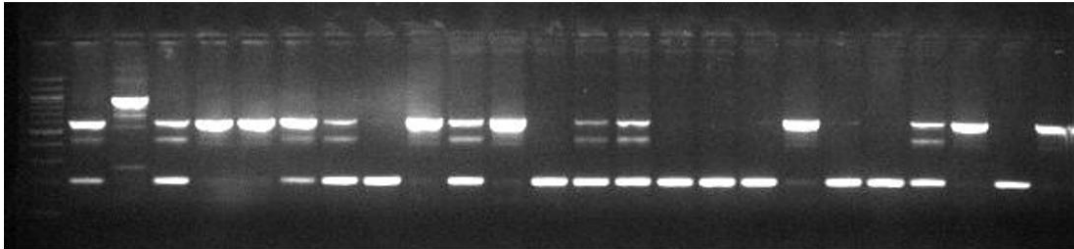




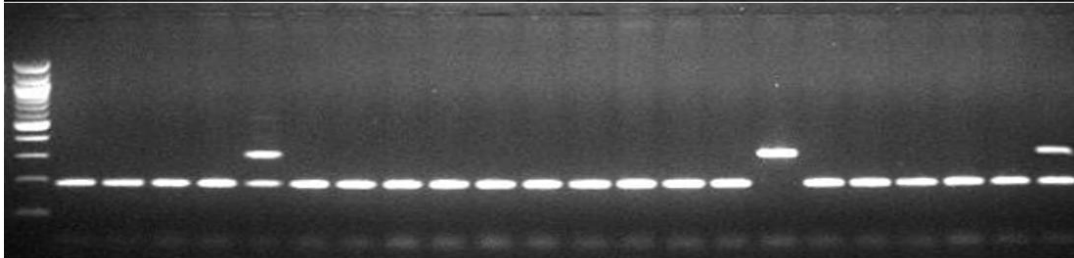
**(a) dna13398**



**(b) dna16027**



**(c) dna19096**



**(d) LINE2650**





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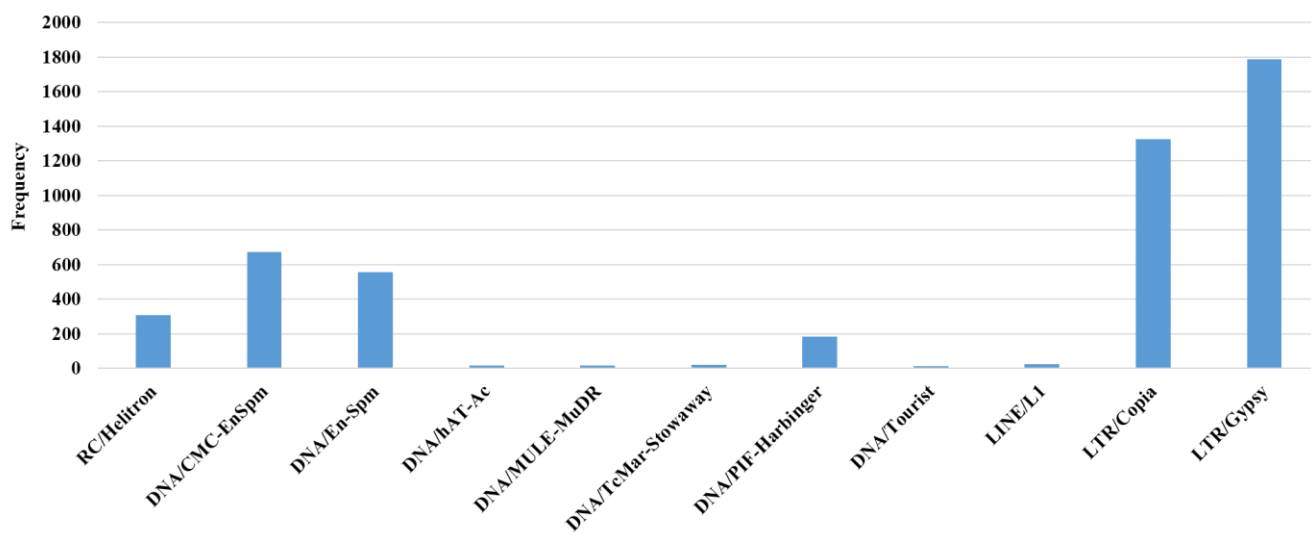
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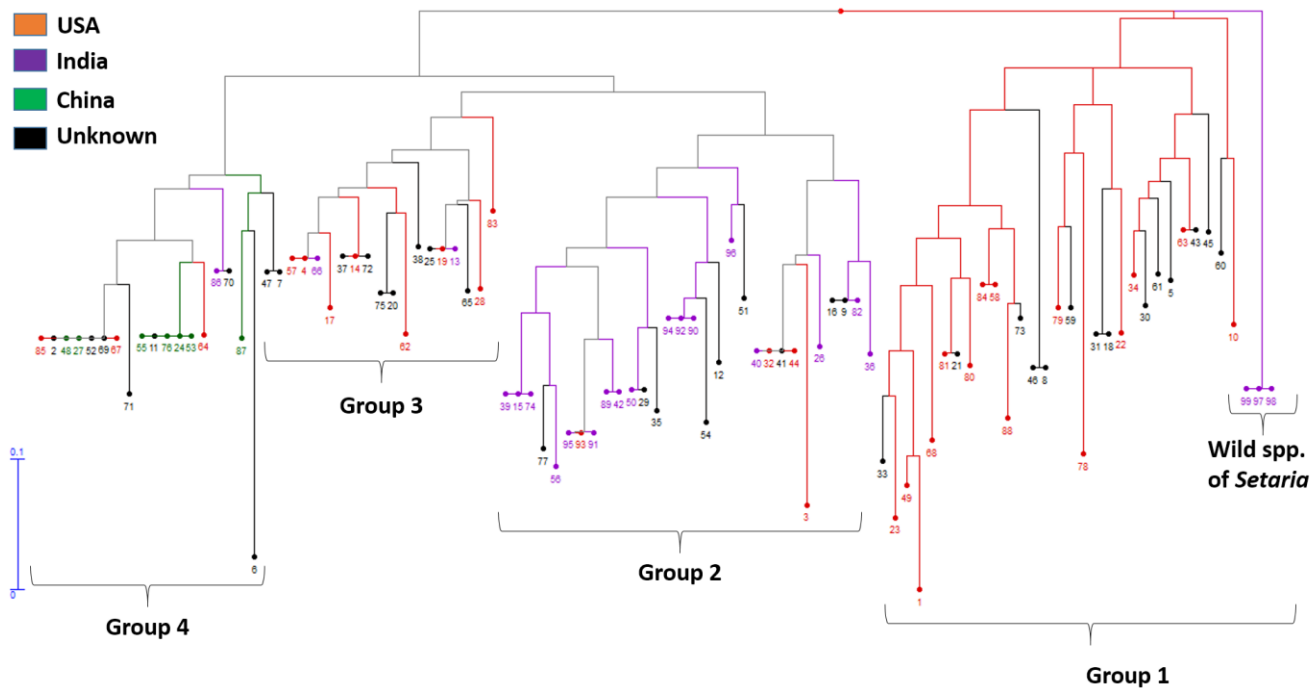
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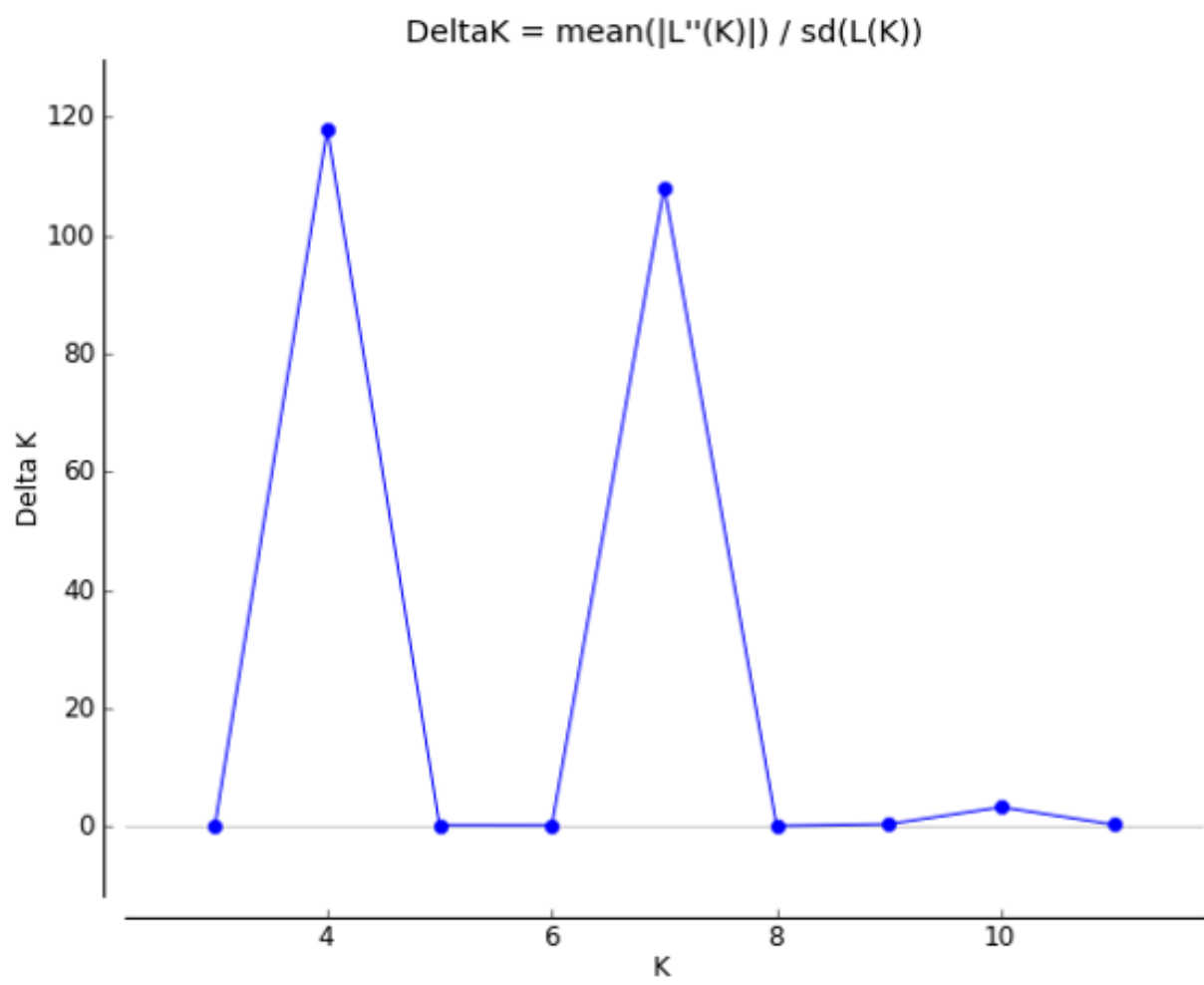
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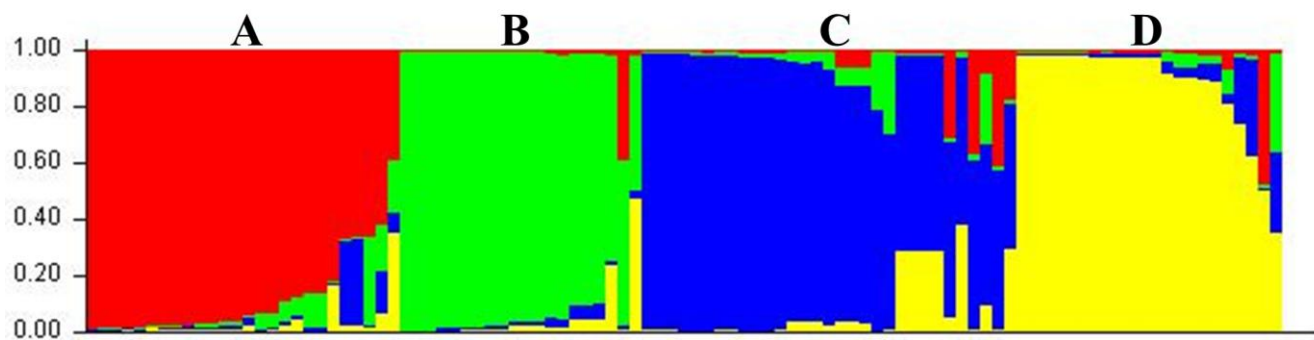
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# TUTORIAL



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## FOXTAIL MILLET TRANSPOSABLE ELEMENTS-BASED MARKER DATABASE

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### Foxtail millet Transposable Elements-based Marker Database



### 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. Recently, the draft genome sequence was released by US Department of Energy Joint Genome Initiative and

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## FOXTAIL MILLET TRANSPOSABLE ELEMENTS-BASED MARKER DATABASE

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Displays the interactive physical map

Download the complete data

Selected references for further reading



# 'SEARCH' TAB



## Search By:

TE ID:    eg: dna7423

OR

## Search By:

TE Type:    eg: Copia

OR

## Search By:

Primer Type    eg: RJM

OR

## Search By:

Chromosome:    eg: Fm03

OR

## Search By:

Chromosome:   
Between: Start:  End:    eg: Fm05, 10000 & 1000000

OR

## Search By:

TE Family:   
Chromosome:   
Between: Start:  End:    eg: Copia, Fm05, 890320, 13086892

***The 'SEARCH' tab provides the user a wide-range of search features including searching by chromosome, type of TE, type of primer, ID of TE, chromosomal location and TE family etc.***

# 'SEARCH BY TE ID'



*Search By:*

TE ID:    eg: dna7423

*Search By:*

TE Type:

*Search By:*

Primer Type

*Search By:*

Chromosome:

OR

*Search By:*

Chromosome:

Between: Start:  End:    eg: Fm05, 10000 & 1000000

OR

*Search By:*

TE Family:

Chromosome:

Between: Start:  End:    eg: Copia, Fm05, 890320, 13086892

## Transposon Details:

TE ID	dna7423	TE Type	DNA/CMC-EnSpm
Chromosome	Fm03	Start	50471905
End	50472629	Score	5
Strand	-	Physical Position	<a href="#">View</a>
Get	Primers		

# 'SEARCH BY TE ID'



Search By:

TE ID:    eg: dna7423

Search By:

TE Type:

Search By:

Primer Type:

Search By:

Chromosome:

OR

Search By:

Chromosome:

Between:

## Transposon Details:

TE ID	dna7423	TE Type	DNA/CMC-EnSpm
Chromosome	Fm03	Start	50471905
End	50472629	Score	5
Strand	-	Physical Position	<a href="#">View</a>
Get	<a href="#">Primers</a>		

## Primers Details: Part-I TE ID: dna1039

Primer Type	Junction	TE Type	TE Source	Orientation	Primer Start	Primer Len	Tm <sup>0</sup> C	GC%
ISBP	938	DNA transposon-TIR-CACTA, Unknown	trep_complete	FORWARD	899	20	59.93	50

## Primers Details: Part-II TE ID: dna1039

Primer Seq	Junctiona_spanning_loc	Insertion_type	Product_size	Primer_type	Junction	TE_Type	TE_source	Orientation
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## Primers Details: Part-III TE ID: dna1039

Start_primer	Primer_Len	Tm <sup>0</sup> C	GC%	Primer_Seq	Junctiona_spanning_loc2	Insertion_type
1215	20	60.11	45	TCCGTGTAGCAAATGTGGAA	0	Fragment

# 'SEARCH BY TE ID'



Search By:

TE ID:    eg: dna7423

Search By:

TE Type:

Search By:

Primer Type:

Search By:

Chromosome:

OR

Search By:

Chromosome:

Between:

## Transposon Details:

TE ID	dna7423	TE Type	DNA/CMC-EnSpm
Chromosome	Fm03	Start	50471905
End	50472629	Score	5
Strand	-	Physical Position	<a href="#">View</a>
Get	<a href="#">Primers</a>		

## Primers Details: Part-I TE ID: dna1039

Primer Type	Junction	TE Type	TE Source	Orientation	Primer Start	Primer Len	Tm <sup>0</sup> C	GC%
ISBP	938	DNA transposon-TIR-CACTA, Unknown	trep_complete	FORWARD	899	20	59.93	50

## Primers Details: Part-II TE ID: dna1039

Primer Seq	Junctiona_spanning_loc	Insertion_type	Product_size	Primer_type	Junction	TE_Type	TE_source	Orientation
GAGAAACCTTGGTATGCCCA	0	Fragment	317	ISBP	938	DNA transposon-TIR-CACTA, Unknown	trep_complete	REVERSE

## Primers Details: Part-III TE ID: dna1039

Start_primer	Primer_Len	Tm <sup>0</sup> C	GC%	Primer_Seq	Junctiona_spanning_loc2	Insertion_type
1215	20	60.11	45	TCCGTGTAGCAAATGTGGAA	0	Fragment

Reference  
foxtail millet  
TEMap

Fm01  
[34211]



- Mag +  
1-42,100,000 bp

# 'SEARCH BY TE TYPE'



Search By:

TE ID:

Submit

Reset

eg: dna7423

OR

Search By:

TE Type:

Submit

Reset

eg: Copia

OR

Search By:

Primer Type

Submit

OR

Search By:

Chromosome:

Submit

OR

Search By:

Chromosome:

Between: Start:  End:

Submit

Reset

eg: Fm05, 10000 & 1000000

OR

Search By:

TE Family:

Chromosome:

Between: Start:  End:

Submit

Reset

eg: Copia, Fm05, 890320, 13086892

TE Type: Copia Total TEs found: 1038

TE Type	TE ID	Get
Copia	copia235	<a href="#">More Details</a>
Copia	copia236	<a href="#">More Details</a>
Copia	copia237	<a href="#">More Details</a>
Copia	copia250	<a href="#">More Details</a>
Copia	copia251	<a href="#">More Details</a>
Copia	copia252	<a href="#">More Details</a>
Copia	copia253	<a href="#">More Details</a>
Copia	copia254	<a href="#">More Details</a>
Copia	copia255	<a href="#">More Details</a>
Copia	copia256	<a href="#">More Details</a>
Copia	copia257	<a href="#">More Details</a>

# 'SEARCH BY TE TYPE'



Search By:

TE ID:    eg: dna7423

OR

Search By:

TE Type:    eg: Copia

OR

Search By:

Primer Type

OR

Search By:

Chromosome:

OR

Search By:

Chromosome:

Between: Start:  End:    eg: Fm05

OR

TE Type: Copia Total TEs found: 1038

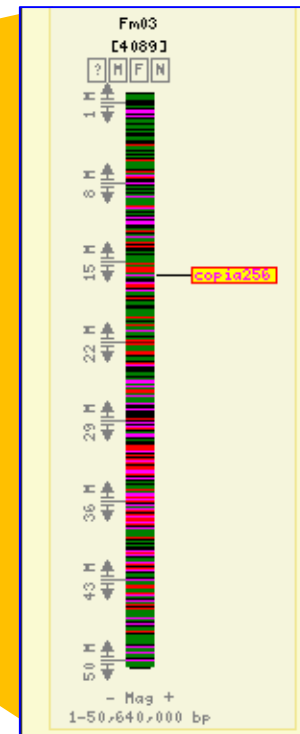
TE Type	TE ID	Get
Copia	copia235	<a href="#">More Details</a>
Copia	copia236	<a href="#">More Details</a>
Copia	copia237	<a href="#">More Details</a>
Copia	copia250	<a href="#">More Details</a>
Copia	copia251	<a href="#">More Details</a>
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Copia	copia255	<a href="#">More Details</a>
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Copia	copia257	<a href="#">More Details</a>

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Start	16160283	End	16166976
Strand	+	Score	6694
Physical Position	<a href="#">View</a>	LTR Region Similarity	6
5' -LTR Start	2147483647	5' -LTR End	16160283
5' -LTR Length	16160720	3' -LTR Start	438
3' -LTR Length	16166525	3' -LTR Length	16166976
Get	<a href="#">Primers</a>		

# 'SEARCH BY TE TYPE'

Copia Details:			
TE ID	copia256	Chromosome	Fw03
Start	16160283	End	
Strand	+	Score	
Physical Position	<a href="#">View</a>		
5'-LTR Start	2147483647	5'-LTR	
5'-LTR Length	16160720	3'-LTR	
3'-LTR Length	16166525	3'-LTR Length	
Get	<a href="#">Primers</a>		



# 'SEARCH BY TE TYPE'



Copia Details:			
TE ID	copia256	Chromosome	Fm03
Start	16160283	End	
Strand	+	Score	
Physical Position	<a href="#">View</a>		
5'-LTR Start	2147483647	5'-LTR	
5'-LTR Length	16160720	3'-LTR	
3'-LTR Length	16166525	3'-LTR Length	
Get	<a href="#">Primers</a>		



## Primers Details: Part-I TE ID: copia256

Primer No	Primer Type	Junction	TE Type	TE Source	Orientation	Primer Start	Primer Len	Tm <sup>0</sup> C	GC%
1	ISBP	2688			FORWARD	2297	20	59.78	50

## Primers Details: Part-II TE ID: copia256

Primer Seq	Junctiona_spanning_loc	Insertion_type	Product_size	Primer_type	Junction	TE_Type	TE_source	Orientation
GAAGCCAATGGATCTTGAGC	0	Fragment	470	ISBP	2688			REVERSE

## Primers Details: Part-III TE ID: copia256

Start_primer	Primer_Len	Tm <sup>0</sup> C	GC%	Primer_Seq	Junctiona_spanning_loc2	Insertion_type
2766	20	59.88	40	TTGCAACATGAACAGTTGCA	0	Fragment



# 'SEARCH BY PRIMER TYPE'



Search By:

TE ID:

eg: dna7423

OR

Search By:

TE Type:

eg: Copia

OR

Search By:

Primer Type

eg: RJM

OR

Search By:

Primers Type Details: **RJM** Total Found: **712**

TE ID	Primer Type	TE Type	Get
copia1000	RJM	Copia	<a href="#">More Details</a>
copia1004	RJM	Copia	<a href="#">More Details</a>
copia1008	RJM	Copia	<a href="#">More Details</a>
copia1009	RJM	Copia	<a href="#">More Details</a>
copia1010	RJM	Copia	<a href="#">More Details</a>
copia1012	RJM	Copia	<a href="#">More Details</a>
copia1013	RJM	Copia	<a href="#">More Details</a>
copia1015	RJM	Copia	<a href="#">More Details</a>

# 'SEARCH BY PRIMER TYPE'



Search By:

TE ID:    eg: dna7423

OR

Search By:

TE Type:    eg: Copia

OR

Search By:

Primer Type    eg: RJM

OR

Search By:

Primers Type Details: RJM Total Found:712

TE ID	Primer Type	TE Type	Get
copia1000	RJM	Copia	<a href="#">More Details</a>
copia1004	RJM	Copia	<a href="#">More Details</a>
copia1008	RJM		<a href="#">More Details</a>
copia1009			<a href="#">More Details</a>

Copia Details:

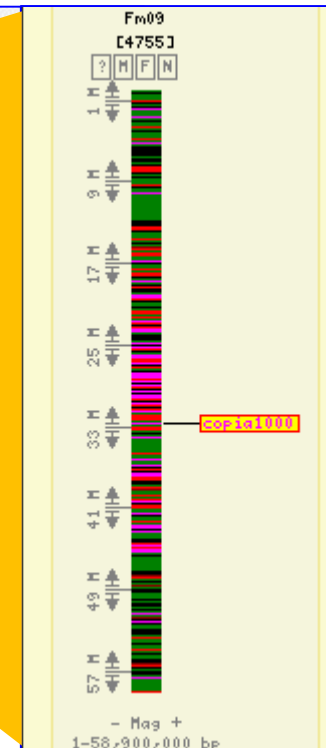
TE ID	copia1000	Chromosome	Fm09
Start	32740008	End	32748171
Strand	+	Score	8164
Physical Position	<a href="#">View</a>	LTR Region Similarity	6
5`-LTR Start	2147483647	5`-LTR End	32740008
5`-LTR Length	32741408	3`-LTR Start	1401
3`-LTR Length	32746771	3`-LTR Length	32748171
Get	<a href="#">Primers</a>		

# 'SEARCH BY PRIMER TYPE'



## Copia Details:

TE ID	copia1000	Chromosome	
Start	32740008	End	
Strand	+	Score	
Physical Position	<a href="#">View</a>		
5' -LTR Start	2147483647	5' -LTR End	
5' -LTR Length	32741408	3' -LTR Start	
3' -LTR Length	32746771	3' -LTR End	
Get	<a href="#">Primers</a>		



# 'SEARCH BY PRIMER TYPE'



## Copia Details:

TE ID	copia1000	Chromosome	
Start	32740008	End	
Strand	+	Score	
Physical Position	<a href="#">View</a>		
5'-LTR Start	2147483647	5'-LTR End	
5'-LTR Length	32741408	3'-LTR Start	
3'-LTR Length	32746771	3'-LTR End	
Get	<a href="#">Primers</a>		



## Primers Details: Part-I TE ID: copia1000

Primer No	Primer Type	Junction	TE Type	TE Source	Orientation	Primer Start	Primer Len	Tm <sup>0</sup> C	GC%
1	RJM	986	Retrotransposon-LTR-Gypsy, Unknown	trep_complete	FORWARD	972	20	62.54	55
2	RJM	1878	Unknown, Retrotransposon-LTR-Copia	trep_complete	FORWARD	1680	20	59.97	50
3	RJM	2848	Unknown, Retrotransposon-LTR-Copia	trep_complete	FORWARD	2193	19	60.76	58
4	RJM	2958	Retrotransposon-LTR-Copia, Retrotransposon-LTR-Copia	trep_complete	FORWARD	2724	20	61.04	55
5	RJM	4036	Retrotransposon-LTR-Copia, Unknown	trep_complete	FORWARD	4021	21	60.04	48
6	RJM	4036	Retrotransposon-LTR-Copia, Retrotransposon-LTR-Copia		FORWARD	3830	20	59.81	50
1	ISBP	986	Retrotransposon-LTR-Gypsy, Unknown	trep_complete	FORWARD	935	20	60.11	50
2	ISBP	1375	Retrotransposon-LTR-Gypsy, Retrotransposon-LTR-Copia	trep_complete	FORWARD	721	20	60.21	50

# 'SEARCH BY CHROMOSOME'



Search By:

TE ID:    eg: dna7423  
OR

Search By:

TE Type:    eg: Copia  
OR

Search By:

Primer Type:    eg: RJM  
OR

Search By:

Chromosome:    eg: Fm03  
OR

Search By:

Chromosome:   
Between: Start:  End:    
OR

Search By:

TE Family:   
Chromosome:   
Between: Start:  End:

Chromosome: Fm03 Total TEs found: 4089

TE Type	TE ID	Get
Copia	copia235	<a href="#">More Details</a>
Copia	copia236	<a href="#">More Details</a>
Copia	copia237	<a href="#">More Details</a>
Copia	copia250	<a href="#">More Details</a>
Copia	copia251	<a href="#">More Details</a>
Copia	copia252	<a href="#">More Details</a>
Copia	copia253	<a href="#">More Details</a>
Copia	copia254	<a href="#">More Details</a>
Copia	copia255	<a href="#">More Details</a>
Copia	copia256	<a href="#">More Details</a>
Copia	copia257	<a href="#">More Details</a>

# 'SEARCH BY CHROMOSOME'



Search By:

TE ID:    eg: dna7423  
OR

Search By:

TE Type:    eg: Copia  
OR

Search By:

Primer Type:    eg: RJM  
OR

Search By:

Chromosome:    eg: Fm03  
OR

Search By:

Chromosome:   
Between: Start:  End:    
OR

Search By:

TE Family:   
Chromosome:   
Between: Start:  End:

Chromosome: Fm03 Total TEs found: 4089

TE Type	TE ID	Get
Copia	copia235	<a href="#">More Details</a>
Copia	copia236	<a href="#">More Details</a>
Copia	copia237	<a href="#">More Details</a>
Copia	copia250	<a href="#">More Details</a>
Copia	copia251	<a href="#">More Details</a>
Copia	copia252	<a href="#">More Details</a>
Copia	copia253	<a href="#">More Details</a>
Copia	copia254	<a href="#">More Details</a>
Copia	copia255	<a href="#">More Details</a>
Copia	copia256	<a href="#">More Details</a>
Copia	copia257	<a href="#">More Details</a>

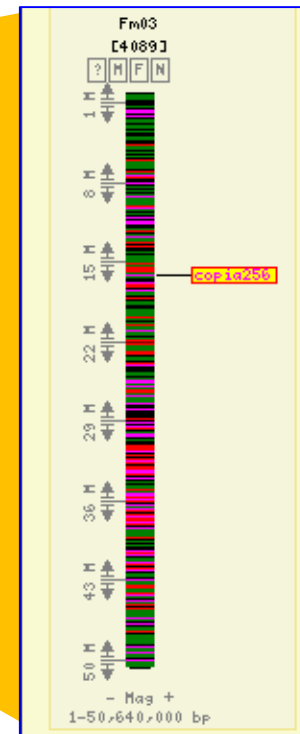
## Copia Details:

TE ID	copia256	Chromosome	Fm03
Start	16160283	End	16166976
Strand	+	Score	6694
Physical Position	<a href="#">View</a>	LTR Region Similarity	6
5'-LTR Start	2147483647	5'-LTR End	16160283
5'-LTR Length	16160720	3'-LTR Start	438
3'-LTR Length	16166525	3'-LTR Length	16166976
Get	<a href="#">Primers</a>		

# 'SEARCH BY CHROMOSOME'

Copia Details:

TE ID	copia256	Chromosome	Fm03
Start	16160283	End	
Strand	+	Score	
Physical Position	<a href="#">View</a>		
5'-LTR Start	2147483647	5'-LTR	
5'-LTR Length	16160720	3'-LTR Start	
3'-LTR Length	16166525	3'-LTR Length	
Get	<a href="#">Primers</a>		

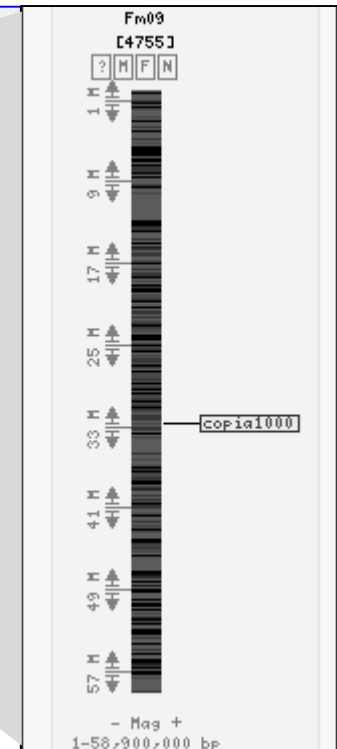


# 'SEARCH BY PRIMER TYPE'



## Copia Details:

TE ID	copia1000	Chromosome	
Start	32740008	End	
Strand	+	Score	
Physical Position	<a href="#">View</a>		
5'-LTR Start	2147483647	5'-LTR End	
5'-LTR Length	32741408	3'-LTR Start	
3'-LTR Length	32746771	3'-LTR End	
Get	<a href="#">Primers</a>		



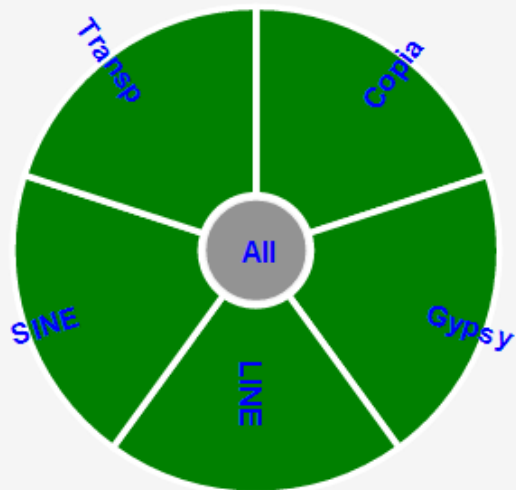
## Primers Details: Part-I TE ID: copia1000

Primer No	Primer Type	Junction	TE Type	TE Source	Orientation	Primer Start	Primer Len	Tm <sup>0</sup> C	GC%
1	RJM	986	Retrotransposon-LTR-Gypsy, Unknown	trep_complete	FORWARD	972	20	62.54	55
2	RJM	1878	Unknown, Retrotransposon-LTR-Copia	trep_complete	FORWARD	1680	20	59.97	50
3	RJM	2848	Unknown, Retrotransposon-LTR-Copia	trep_complete	FORWARD	2193	19	60.76	58
4	RJM	2958	Retrotransposon-LTR-Copia, Retrotransposon-LTR-Copia	trep_complete	FORWARD	2724	20	61.04	55
5	RJM	4036	Retrotransposon-LTR-Copia, Unknown	trep_complete	FORWARD	4021	21	60.04	48
6	RJM	4036	Retrotransposon-LTR-Copia, Retrotransposon-LTR-Copia		FORWARD	3830	20	59.81	50
1	ISBP	986	Retrotransposon-LTR-Gypsy, Unknown	trep_complete	FORWARD	935	20	60.11	50
2	ISBP	1375	Retrotransposon-LTR-Gypsy, Retrotransposon-LTR-Copia	trep_complete	FORWARD	721	20	60.21	50

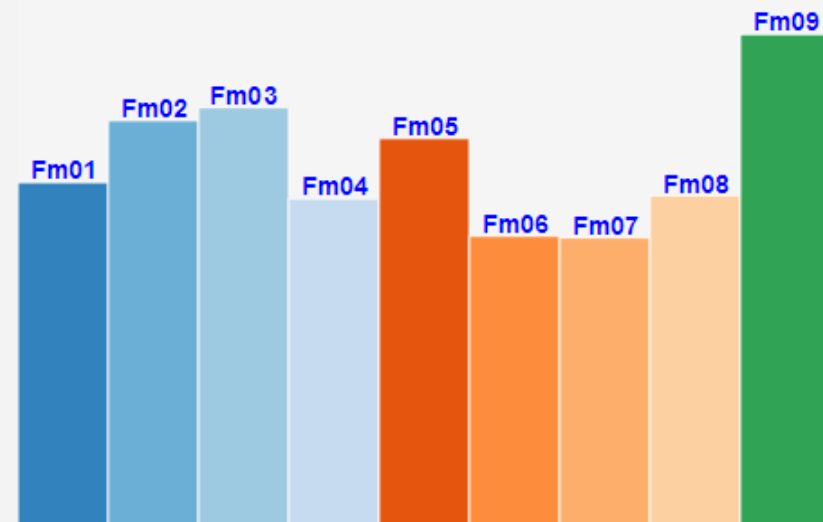


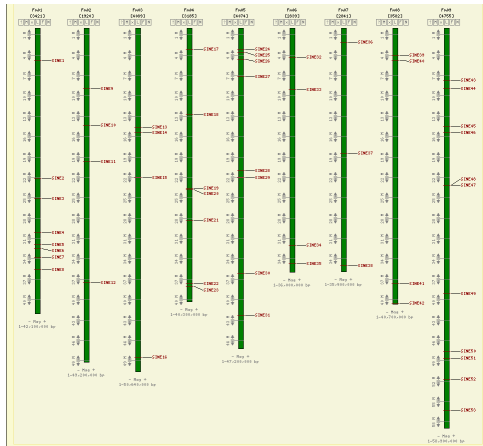
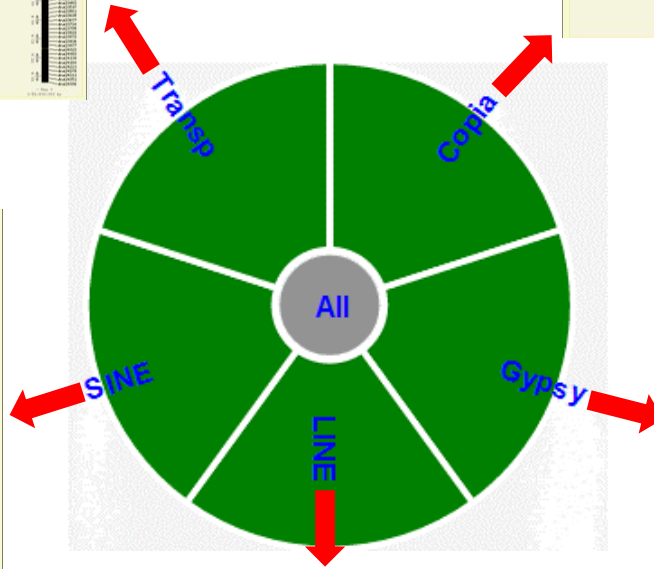
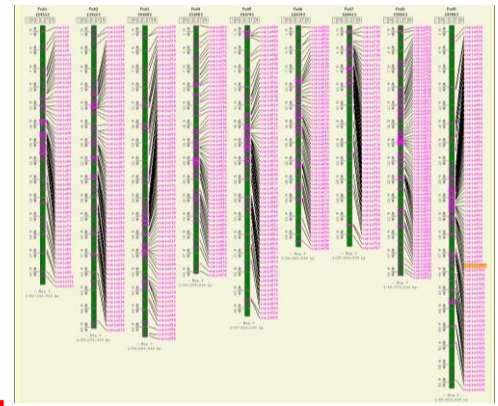
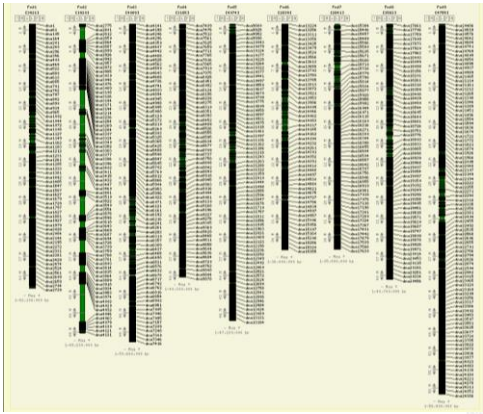
# 'MAP' OPTION

Map-I: TE Type wise

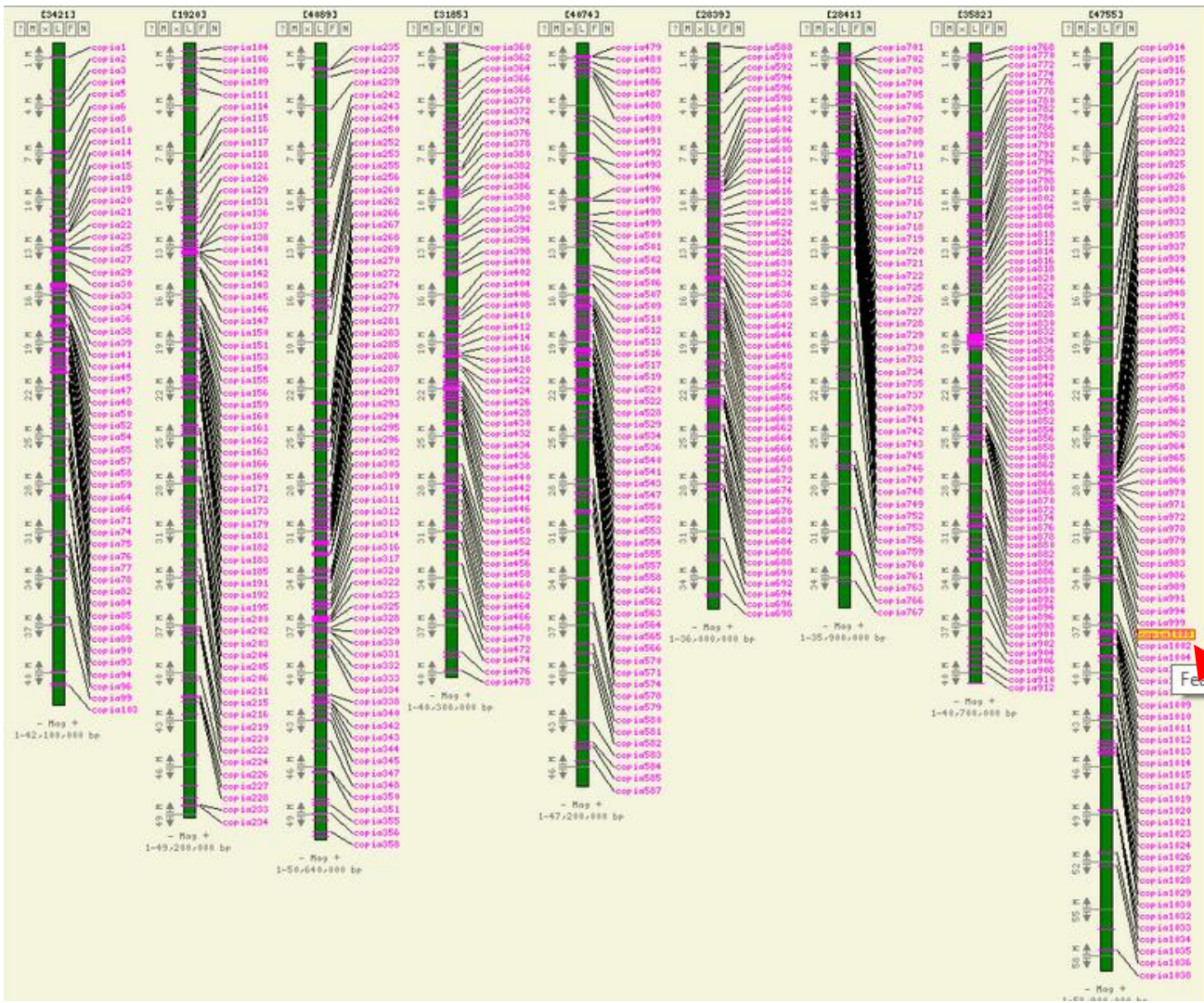


Map-II: Chromosome wise





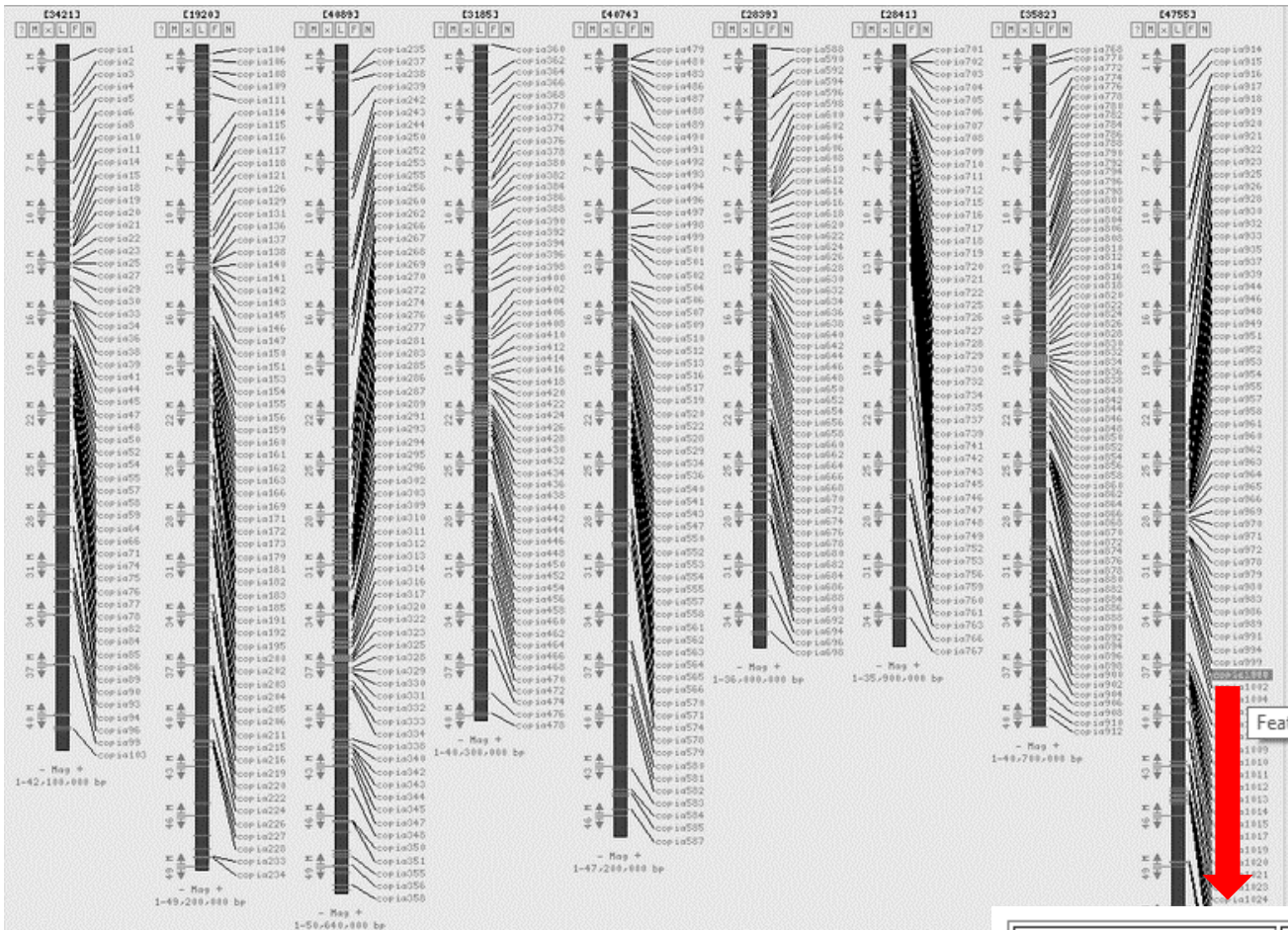
# HOW TO VIEW THE DETAILS



Feature Details: copia1000 [copia1000]

**CLICK ON THE TE OF INTEREST**

# HOW TO VIEW THE DETAILS



Feature Details: copia1000 [copia1000]

<b>Name:</b>	copia1000
<b>View:</b>	on Map
<b>View:</b>	<a href="#">More Details</a>

# VIEWING THE DETAILS



Name:	copia1000
View:	on Map
View:	<a href="#">More Details</a>

**Copia Details:**

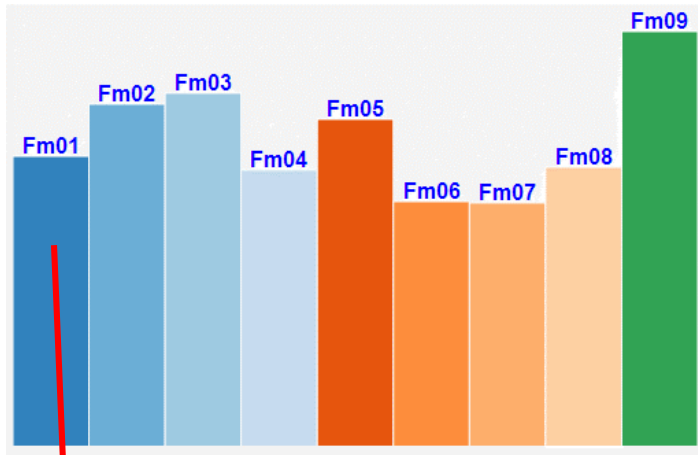
TE ID	copia1000	Chromosome	
Start	32740008	End	
Strand	+	Score	
Physical Position	<a href="#">View</a>		
5' -LTR Start	2147483647	5' -LTR	
5' -LTR Length	32741408	3' -LTR	
3' -LTR Length	32746771	3' -LTR Le	
Get	<a href="#">Primers</a>		

**Primers Details: Part-I TE ID: copia1000**

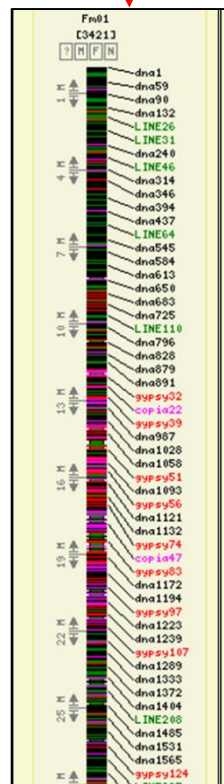
Primer No	Primer Type	Junction	TE Type	TE Source	Orientation	Primer Start	Primer Len	Tm <sup>0</sup> C	GC%
1	RJM	986	Retrotransposon-LTR-Gypsy, Unknown	trep_complete	FORWARD	972	20	62.54	55
2	RJM	1878	Unknown, Retrotransposon-LTR-Copia	trep_complete	FORWARD	1680	20	59.97	50
3	RJM	2848	Unknown, Retrotransposon-LTR-Copia	trep_complete	FORWARD	2193	19	60.76	58
4	RJM	2958	Retrotransposon-LTR-Copia, Retrotransposon-LTR-Copia	trep_complete	FORWARD	2724	20	61.04	55
5	RJM	4036	Retrotransposon-LTR-Copia, Unknown	trep_complete	FORWARD	4021	21	60.04	48
6	RJM	4036	Retrotransposon-LTR-Copia, Retrotransposon-LTR-Copia		FORWARD	3830	20	59.81	50
1	ISBP	986	Retrotransposon-LTR-Gypsy, Unknown	trep_complete	FORWARD	935	20	60.11	50
2	ISBP	1375	Retrotransposon-LTR-Gypsy, Retrotransposon-LTR-Copia	trep_complete	FORWARD	721	20	60.21	50



# Comparative map



TE-marker based comparative mapping data is available for visualization with sorghum, maize, rice and *Brachypodium*



Map Options | Redraw | Reset

Map Set	Add Maps Left	foxtail millet-TEMap (Reference Set)	Add Maps Right
Min. Correspondences			
Align Vertically	<input type="checkbox"/>		
Stack			
Maps		Fm01	
Start		1	
Stop		42100000.00	
Magnification		Original	
Flipped	<input type="checkbox"/>		

hint: To save time, select the desired options before redrawing the map.  
  (Hide Map Menu)

Feature Options  
 Correspondence Options  
 Display Options  
 Advanced Options

Comparative Maps (Right Side)

Add Map Set

No Map Set Selected

Min. Correspondences:

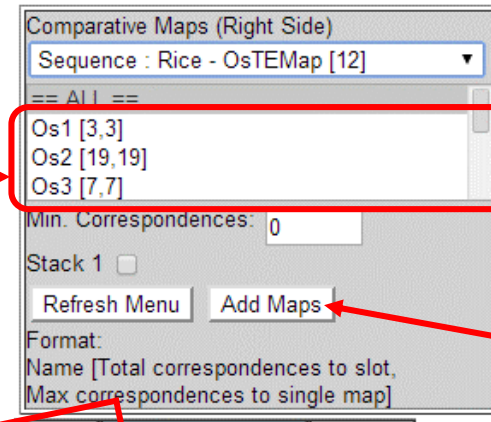
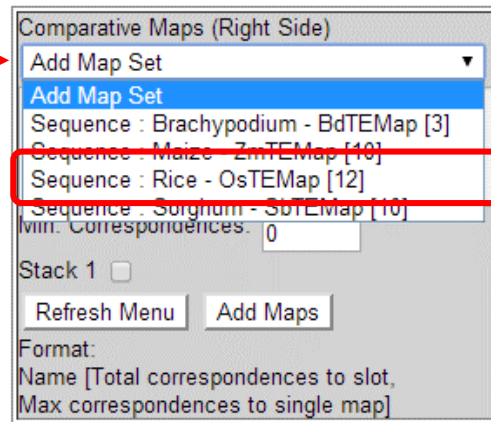
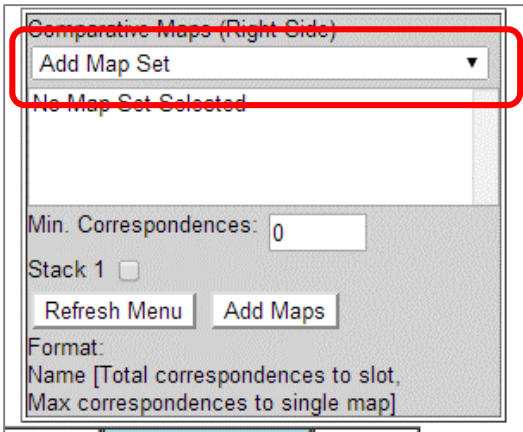
Stack 1

Format:  
 Name [Total correspondences to slot,  
 Max correspondences to single map]

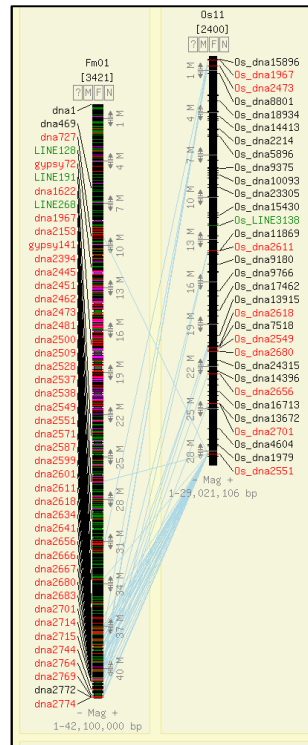
# Comparative map



NIPGR



Select the chr. of interest & click 'Add Maps'



The Syntenic TEs are displayed in RED and the blue lines indicate the orthologs



# Download Data



The complete TE & marker data of foxtail millet are available for download in this section.

Download Data		
Type of TE	TE Data	Primers
<b>Copia</b>	<a href="#">Download</a>	<a href="#">Download</a>
<b>Gypsy</b>	<a href="#">Download</a>	<a href="#">Download</a>
<b>LINE</b>	<a href="#">Download</a>	No Primers
<b>SINE</b>	<a href="#">Download</a>	No Primers
<b>Transposon</b>	<a href="#">Download</a>	<a href="#">Download</a>