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

Supplementary Table S12: Presence of transcriptionally active *Gypsy*-type retrotransposons in various tissues of foxtail millet

Supplementary Table S13: Presence of transcriptionally active non-LTR type retrotransposons (LINE) in various tissues of foxtail millet

Supplementary Table S14: Presence of transcriptionally active non-LTR type retrotransposons (SINE) in various tissues of foxtail millet

Supplementary Table S15: Presence of transcriptionally active DNA transposons in various tissues of foxtail millet

Supplementary Table S16: Details of RBIP primers designed in foxtail millet

Supplementary Table S17: Details of IRAP primers designed in foxtail millet

Supplementary Table S18: Details of RJM primers designed in foxtail millet

Supplementary Table S19: Details of RJJM primers designed in foxtail millet

Supplementary Table S20: Details of ISBP primers designed in foxtail millet

Supplementary Table S21: Details of REMAP primers designed in foxtail millet

Supplementary Table S22: Primer sequences of 134 transposable elements junction based markers validated in foxtail millet

Supplementary Table S23: The raw STRUCTURE output used for determination of true number of K

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*





100	200	300	400	500	600	700	800	900
			TREP1820 Retrot	ransposon;LINE(60	-70)		RTE1_ZM LINE;RTE	-BovB(2e-17)
			Hit (8-369(3306)				Hit +2945-2998(30)	201
			trep1820 DNA tr	ansposon;MITE;Sto	waway;Thalos(6e-	-70)	RIT_colonist_AC2	09460-0 Retrol
			Hit (8-369(3306)				Hit +2530-2579(25	01)
			RTE-1_TD LINE;R	TE-BovB(6e-70)			ZRSiTERT00300006	Retrotranspos
			Hit (8-369(3306)				Hit +1587-1640(165	(8)
			R	TE2_ZM LINE;RTE	-BovB(1e-64)		ZRSiTERT00300006	Retrotranspos
				it +123-403(3503)			Hit :1587-1640(165	(8)
			z	RSiTERT00300004	Retrotransposon;	LINE(8e-57)	TREP1820 Retrot	ransposon;LINE
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			z	RSITERT00300004	Retrotransposon;	LINE(8e-57)	trep1820 DNA tr	ansposon;MITE;
			H	it:115-385(1499)			Hit:3243-3281(3)	(06)
			TREP3126 Retr	otransposon;LTR;	Copia(7e-14)		RTE-1_TD LINE;F	TE-BovB(2e-08)
			Hit +1990-2049(5310)			Hit +3243-3281(31	061
			TREP3125 Retr	otransposon;LTR;	Copia(7e-14)		TREP3323 Retrot	ransposon;LINE
			Hit:1990-2049(5311)			Hit:85-47(2915)	
			TREP3126	Retrotransposon	LTR;Copia(7e-08	>		
			Hit:2150-	-2191(5310)				
			TREP3125	Retrotransposon	LTR;Copia(7e-08)		
			Hit:2150-	-2191(5311)				
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5

TE junction/Fragment

1	GTACAAGAAGCATTTAGGTAGTGATCCACCGATCCATTATAGTGCACTATCAAGGAGTAGCTTTATAACTTTTTTGTTTATAGGAGCATCTTTGATAGCACTACAATGTGGAAATTGCAACTCACACACTTGGATTCGTGGAATAAGTT
151	atcttccgtgtgacatcgtgtcgacatcgtgtagataatgatcatgcttctccacacccaacccatatcaaaaggccaaccaa

301	GTTTCTATTTAAGTGGTTGTGCTAGATTATTATAGAATTATTATGAACTCTACCTATGTTGTCTCAGTATAGCAGGTCCTAAGCCCTGGCAAAGGAGGAGGGTTGTGATAGGCCTGGTGAGCCAACGTTAAACCTAGCCATTGTAATGG
451	AGATGAAACCCAAGAGAAATCCGTTGGGGCGTAACCCTCTTAGCGACGCGCCATATCGGAACCCGTGTATGGTGTTAAATGGGCAAGGGCCGGGTCGTCTCCCCCTTGGTGACGTGTCGCGTTTTGAGAATGGTGTCAAGTGACC
601	AAGGATCGGGTCGTCATTTCCTTAGTGGCACGCTACATCGACGGCGGGTGTAGTGAAAAATGAGCAAGGGTCTTCACATCTCTCTC
751	TGTGGCTCTTGTTGGGTTTCAATTCTAGCCTACCCCAACTTGCTTG

901 TTGATGACATCAGCTAGTTTATCGAATGCTTCAGG





59	• • • • • • • • • • • • • • • •	•••••		STTAGGATCTGCTACCCCATGTG	TTGAGGTGGACAAGCAACTA	TTTAGAGCCAGTACAATTGTTACA	TTGGAAAATGGGAATAGGG	
61				GTTAGGATCTGCTACCCCATGTG	TTGAGGTGGACAAGCAACTA	TTTAGAGCCAGTACAATTGTTACA	TTGGAAAATGGGAATAGGG	TC
62	•••••	•••••		STTAGGATCTGCTACCCCATGTG	TTGAGGTGGACAAGCAACTA	TTTAGAGCCAGTACAATTGTTACA	TTGGAAAATGGGAATAGGG	TCA
64 64				STTAGGATCTGCTACCCCATGTG	TTGAGGTGGACAAGCAACTA	TTTAGAGCCAGTACAATTGTTACA	TTGGAAAATGGGAATAGGG	TC
65			•••••••••••••••••••••••••••••••••••••••	GTTAGGATCTGCTACCCCATGTG	TTGAGGTGGACAAGCAACTA	TTTAGAGCCAGTACAATTGTTACA	TTGGAAAATGGGAATAGGG	TC.
66 67				STTAGGATCTGCTACCCCATGTG STTAGGATCTGCTACCCCATGTG	TTGAGGTGGACAAGCAACTA	TTTAGAGCCAGTACAATTGTTACA TTTAGAGCCAGTACAATTGTTACA	TTGGAAAATGGGAATAGGG	
68				STTAGGATCTGCTACCCCATGTG	TTGAGGTGGACAAGCAACTA	TTTAGAGCCAGTACAATTGTTACA	TTGGAAAATGGGAATAGGG	TCA
69 70		•••••		STTAGGATCTGCTACCCCATGTG	TTGAGGTGGACAAGCAACTA	TTTAGAGCCAGTACAATTGTTACA	TTGGAAAATGGGAATAGGG	
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72		• • • • • • • • • • • • • • • • • • • •		TTAGGATCTGCTACCCCATGTG	TTGAGGTGGACAAGCAACTA	TTTAGAGCCAGTACAATTGTTACA	TTGGAAAATGGGAATAGGG	TCA
73 74				STTAGGATCTGCTACCCCATGTG	TTGAGGTGGACAAGCAACTA TTGAGGTGGACAAGCAACTA	TTTAGAGCCAGTACAATTGTTACA	TTGGAAAATGGGAATAGGG	TC
75			•••••••••••••••••••••••••••••••••••••••	STTAGGATCTGCTATCCCATGTG	TTGAGGTGGACAAGCAACTA	TTTAGAGCCAGTACAATTGTTACA	TTGGAAAATGGGAATAGGG	TC
76 77				STTAGGATCTGCTACCCCATGTG STTAGGATCTGCTACCCCATGTG	TTGAGGTGGACAAGCAACTA	TTTAGAGCCAGTACAATTGTTACA TTTAGAGCCAGTACAATTGTTACA	TTGGAAAATGGGAATAGGG	
78				STTAGGATCTGCTACCCCATGTG	TTGAGGTGGACAAGCAACTA	TTTAGAGCCA <mark>GTACAATTGTTAC</mark> A	TTGGAAAATGGGAATAGGG	TC
79 80				STTAGGATCTGCTACCCCATGTG STTAGGATCTGCTACCCCATGTG	TTGAGGTGGACAAGCAACTA TTGAGGTGGACAAGCAACTA	TTTAGAGCCAGTACAATTGTTACA TTTAGAGCCAGTACAATTGTTACA	TTGGAAAATGGGAATAGGG	
87	<u>.</u>			STTAGGATCTGCTACCCCATGTG	TTGAGGTGGACAAGCAACTA	TTTAGAGCCAGTACAATTGTTACA	TTGGAAAATGGGAATAGGG	TCA
82	GTAGAGCTCTTCA	GCTCCGATGGTTATGGTATG	AGTGGACTGAAACTGATCGACCATG	GTAGGATCTGCTACCCCATGTG	TTGAGGTGGACAAGCAACTA	TTTAGAGCCAGTACAATTGTTACA	TTGGAAAATGGGAATAGGG	
84				STTAGGATCTGCTACCCCATGTG	TTGAGGTGGACAAGCAACTA	TTTAGAGCCAGTACAATTGTTACA	TTGGAAAATGGGAATAGGG	TCA
85	• • • • • • • • • • • • • • •	•••••		STTAGGATCTGCTACCCCATGTG	TTGAGGTGGACAAGCAACTA	TTTAGAGCCAGTACAATTGTTACA	TTGGAAAATGGGAATAGGG	
87				GTTAGGATCTGCTACCCCATGTG	TTGAGGTGGACAAGCAACTA	TTTAGAGCCAGTACAATTGTTACA	TTGGAAAATGGGAATAGGG	TCA
88	•••••	•••••		STTAGGATCTGCTACCCCATGTG	TTGAGGTGGACAAGCAACTA	TTTAGAGCCAGTACAATTGTTACA	TTGGAAAATGGGAATAGGG	
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2	AATTGTTACA-1	TGGAAAATGGGAATAGGGT	rcA					• • • • • • • • • • • • • • • • • • • •
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6 7	AATTGTTACA-1	TGGAAAATGGGAATAGGGT						
8	AATTGTTACA-1	TGGAAAATGGGAATAGGGT	rc					
9	AATTOTTACA-1	TEGAAAATEGGAATAGGGT	CA					••••••
11	AATTGTTACA	TEGAAAATEGGGAATAGGGT	rc					
12	AATTGTTACA 1	TTGGAAAATGGGAATAGGGT	rca					
13	AATTGTTACA- 1	TGGAAAATGGGAATAGGGT	CATGT					
15	AATTGTTACA-1	TGGAAAATGGGAATAGGGT	rc					
16	AATT <mark>GTTAC</mark> A-1	TTGGAAAATGGGAA <mark>T</mark> AGGGT	rc					
17	AATTGTTACA-1	TGGAAAATGGGAATAGGGT						
19	AATTGTTACA- 1	TGGAAAATGGGAA <mark>T</mark> AGGGT	CA					
20	AATTGTTACA-1	TGGAAAATGGGAA <mark>T</mark> AGGGT	<u>c</u>					
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3 9 40	AATTGTTACA-1	TGGAAAATGGGAATAGGGT	rc					
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47	AATTGTTACATT	TGGAAAATGGGAATAGGGT	rc					
48	CCTTTTTGTT-1	TTGGAAAA <mark>TGGG</mark> AA <mark>TAGGG</mark> T	<mark>гс</mark> А					
49 50	AATTGTTACA-1	TGGAAAATGGGAATAGGGT						
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52 53	AATTGTTACA-1	TEGAAAATEGGAATAGGGT	ГС					
54	AATTGTTACA	TTGGAAAATGGGGAATAGGGT	rcA					
54 55	AATTGTTACA-1	TEGAAAATEGGAATAGGGT	TCA					· · · · · · · · · · · · · · · · · · ·
56	AATTGTTACA	TTGGAAAATGGGAATAGGGT	rcc					
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68 79	AATTGTTACA-1	TTGGAAAATGGGAATAGGGT						
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81	AATTGTTACA-1	TTGGAAAATGGGAATAGGGT	ГС <mark>А</mark>					
82	AATTOTTACA-1	TEGAAAATEGGAATAGGGT	TCA					
33 84	AATTGTTACA-1	TTGGAAAATGGGAATAGGGT	TCA					
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HOME PAGE





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.

NAVIGATION BAR









<i>Search By :</i> TE ID:	OR	Submit Reset	eg: dna7423
<i>Search By :</i> TE Type:	OR	Submit Reset	eg: Copia
<i>Search By :</i> Primer Type	OR	Submit Reset	eg: RJM
Search By : Chromosome:	OR	Submit Reset	eg: Fm03
Search By : Chromosome: Between: Start: Search By :	End:	Submit Reset	eg: Fm05, 10000 & 1000000
TE Family: Chromosome: Between: Start:	End:	Submit Reset	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 B	y:			
TI	EID: dna1039	Submit	Reset eg: dna7423	
Search By :	OK			
TE Type:				
		Transp	oson Details:	
Search By :	TE ID	dna7423	ТЕ Туре	DNA/CMC-EnSpm
Primer Type	Chromosome	Fm03	Start	50471905
	End Strand	- 504/2629	Score Physical Position	5 View
Search By :	Get	Primers		
Chromosome:		Submit Reset eg: Fm	03	
	OR			
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Between: Start:	End:	Submit Reset eg: Fm	05,10000&1000000	
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Between: Start:	End:	Submit Reset eg: Co	pia, Fm05, 890320, 13086892	

'SEARCH BY TE ID'



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Search By : Chromosome: Betweep: Primer Type J ISBP	unction 938 DNA tr	Pr <u>TE Typ</u> ansposon-TIR-C Pr	rimers Details ne ACTA, Unknown imers Details	s: Part-I TE I TE Source trep_complete : Part-II TE	D: dna1039 Orientation FORWARD D: dna1039	Primer Start	Prime	er Len 0	Tm ⁰ C 59.93	GC% 50
Search By : Chromosome: Between Primer Type J ISBP	unction 938 DNA tr	Pr <u>TE Typ</u> ansposon-TIR-C Pr panning_lod	rimers Details e ACTA, Unknown imers Details Insertion_type	s: Part-I TE I TE Source trep_complete :: Part-II TE Product_size	D: dna1039 Orientation FORWARD D: dna1039 Primer_type	Primer Start	<u>Ргіте</u> 2 Гуре ТІ	er Len	Tm ⁰ C 59.93	GC% 50
Search By : Chromosome: Betweep: Primer Type J ISBP J GAGAAACCTTGGTATGG	Unction 938 DNA tr	PI <u>TE Typ</u> ansposon-TIR-C Pr panning_loc	rimers Details e ACTA, Unknown imers Details Insertion_type Fragment	s: Part-I TE I TE Source trep_complete : Part-II TE Product_size 317	D: dna1039 Orientation FORWARD D: dna1039 Primer_type	Primer Start 899 Junction TE_ 938 TIR-C Unkt	E Prime 2 Type TI VA Noson- ACTA, tre	er Len 0 E_sourc	Tm ⁰ C 59.93 e Orier te RE	GC% 50
Search By : Chromosome: Betweep Primer Type J ISBP	Unction 938 DNA to 938 DNA to Junctiona_s	Pr <u>TE Typ</u> ransposon-TIR-C Pr panning_loc	rimers Details e ACTA, Unknown imers Details Insertion_type Fragment imers Details	s: Part-I TE I TE Source trep_complete : Part-II TE Product_size 317 : Part-III TE	D: dna1039 Orientation FORWARD D: dna1039 Primer_type ISBP	Primer Start 899 Junction TE_ 938 TIR-C Unkr	E Prime 2 Type TI NA Doson- ACTA, Iown tre	er Len	Tm ⁰ C 59.93 e Orier te RE	GC% 50
Search By : Chromosome: Between Primer Type J ISBP J GAGAAACCTTGGTATGC	Unction 938 DNA to 938 DNA to Junctiona_s CCCA C	Pri TE Typ ansposon-TIR-C Pr panning_loc Pri Tm ^o C GC	rimers Details ACTA, Unknown imers Details Insertion_type Fragment imers Details % Prir	s: Part-I TE I TE Source trep_complete : Part-II TE Product_size 317 : Part-III TE part-III TE ner_Seq	D: dna1039 Orientation FORWARD D: dna1039 Primer_type ISBP	Primer Start 899 Junction TE_ 938 Transp 71R-C Unkr	E Prime 2 Fype TI NA ACTA, NOWN tre Joc2	er Len	Tm ⁰ C 59.93 e Oriel te RE	GC% 50 htation /ERSE

'SEARCH BY TE ID'



- Mag + 1-42,100,000 bp





Search By :						
TE ID:		Submit R	eset eg: dna7423			
	OR					
Search By :						
TE Type: Copia		Submit R	eset eg: Copia			
	OR					
Search Bv :				ТЕ Тур	oe:Copia Total TEs toun	d:1038
Defense Turne			ТЕ Туре	TE ID	Get	
Primer Type		Submit	Copia	copia235	More Details	
	OR		Copia	copia236	More Details	
Search Rv.			Copia	copia237	More Details	
Scarch by .			Copia	copia250	More Details	-
Chromosome:		Submit	Copia	copia252	More Details	
	OR		Copia	copia253	More Details	1
Carach Deve			Copia	copia254	More Details]
Search By :			Copia	copia255	More Details	
Chromosome:			Copia	copia256	More Details	
Determine Charle	E a de		Соріа	copia257	More Details	
Between: Start:	End:	Submit	eset eg: Fm05, 10000	& 1000000		
	OR					
Search By :						
TE Family:						
ci						
Chromosome:						
Between: Start:	End:	Submit R	eset eg: Copia, Fm05,	890320,13086892		



Search By :				
TE ID:	Submit Reset	eg: dna7423		
OR] 0		
Search By :				
TE Type: Copia	Submit Reset	eg: Copia		
OR				
Search Bv :			TE	Type: Copia Total TEs tound: 1038
Drimor Tuno	Qubmit	ТЕ Туре	TE ID	Get
Primer Type	Submit	Copia	copia235	More Details
OR		Copia	copia236	More Details
Sparch Rv ·		Copia	copia23/	More Details
Search by ,		Copia	copia250	More Details
Chromosome:	Submit	Copia	copia251	More Details
OR		Copia	copia253	More Details
- / -		Copia	copia254	More Details
Search By :		Copia	copia255	More Details
Chromosomer		Copia	copia256	More Details
chroniosonie.		Copia	copia257	More Details
Between: Start: End:	Submit Reset	eg Em05 to		
OR				
Sea	60	nia Dotaile:		
	CU	pia Detaits.		
Ch TE ID	copia256	Chromosome	e	Fm03
Start	16160283	End		16166976
Bet Strand	+	Score		6694
Physical Position	<u>View</u>	LTR Region	Similarity	6
5`-LTR Start	2147483647	5`-LTR End		16160283
5 ⁻ LTR Length	16160720	3 ⁻ LTR Star	t	438
3 ⁻ LTR Length	16166525	3°-LTR Leng	ith	16166976
Get	Primers			



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± 88 ₹

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± ≜ 22 ₹

- Mag + 1-50,640,000 bp

Copia Details:						
TE ID	copia256	Chromosome	Emo			
Start	16160283	End				
Strand	+	Score				
Physical Position	View			· · · · · · · · · · · · · · · · · · ·		
5`-LTR Start	2147483647	5 -				
5°-LTR Length	16160720	3 ⁻ LTR				
3`-LTR Length	16166525	3°-LTR Leng				
Get	Primers			EA		
				■ ‡ 3		
				±≢ =		



Primers Details: Part-I TE ID: copia256																
Primer No	Primer	r Туре	Junction TE T		Туре	TE Source		Orient	ation Primer Start		Prime	r Len	Tm ⁰	C GC	%	
1	ISE	BP	2688					FORW	/ARD		2297	2	0	59.7	8 5	0
P :	Primers Details: Part-II TE ID: copia256															
Primer S	eq	Junction	a_spannir	ig_loc	Insert	ion_type	PLOQ	uct_size	Primer_	_type	Junction	TE_Type	TE_SOL	irce c	rientat	ion
GAAGCCAATGGAT	CTTGAGC		0		Fra	gment		470	ISB	P	2688				REVERS	E
Primers Details: Part-III TE ID: copia256																
Start_prime	r Pri	mer_Len	Tm ⁰ C	GC%		Primer	_Seq		Jur	Junctiona_spanning_loc2		I	iserti	on_type	e	
2766		20	59.88	40	Π	GCAACATGA	ACAG	TGCA			0			Erad	ment	









Search By : TEID:	OR	Submit Reset e	g: dna7423			
Search By : TE Type:	OR	Submit Reset e	g: Copia			
Search By: Primer Type RJM		Submit Reset eg	: RJM			
Search By	OR	Primers Type Detail:	s: RJM Total Found:7	/12		
TETI		Primer Tyne	TE Type		Get	
Sel copia1	000	RJM	Copia		More Details	
cr copia1	004	RJM	Copia	<u>e Details</u>		
Ret copia1	008	RJM			<u>De</u>	tails
copia1	000					tails
CODIDI		Copia Detai	ls:		NAMES IN	
TE ID	conia	1000 Chrom	IOSOMA		Fm00	le
Start	3274	0008 End		32	748171	
Strand	-	+ Score		52	8164	
Physical Position	ical Position View		egion Similarity		6	1
5`-LTR Start	-LTR Start 2147483647		R End	32	740008	
5`-LTR Length	5`-LTR Length 32741408		R Start		1401	
3`-LTR Length	3274	6771 <u>3`-LT</u>	R Length	32	748171	
Get	Prin	ners				



	Cop	ia Details:	Fm09 [4755]
TE ID	copia1000	Chromosome	<u>210</u> F.N. ₹_
Start	32740008	End	
Strand	the second the second	Score	
Physical Position	<u>View</u>		
5`-LTR Start	2147483647	EB 52-	· · · · · · · · · · · · · · · · · · ·
5°-LTR Length	32741408	31-LTK	
3`-LTR Length	32746771	31-LTR Le.	· · · · · · · · · · · · · · · · · · ·
Get	Primers		
			Ξcopia1000







	Primers Details: Part-F TE ID: copia1000								
Primer	Primer	Junction	TE Tuno	TE Courco	Orientation	Primer	Primer	T 0c	CCOL
No	Туре	Junction	тстуре	TE Source	Unentation	Start	Len	Imec	GC%0
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:			Submit	Reset	eg: dna7423				
	OR								
Search By :									
TE Type:		5	Submit	Reset	eg: Copia				
	OR								
Search By :									
Primer Type		5	Submit	Reset	eg: RJM				
	OR								
Search By:									
Chromosome: Fm03		9	Submit F	Reset	eg: Fm03				
	OR								
Search By :						(Chromosome: F	m03 Total TEs four	nd:4089
Chromosomo									
					ТЕ Туре	TE ID		Get	
chi oniosonie.					TE Type Copia	TE ID copia235		Get More Details	
Between: Start:	End:		Submit		TE Type Copia Copia	TE ID copia235 copia236		Get More Details More Details	
Between: Start:	End: OR		Submit		TE Type Copia Copia Copia Copia	TE ID copia235 copia236 copia237 copia250		Get More Details More Details More Details	
Between: Start:	End: OR		Submit		TE Type Copia Copia Copia Copia Copia	TE ID copia235 copia236 copia237 copia250 copia251		Get More Details More Details More Details More Details More Details	
Between: Start:	End: OR		Submit		TE Type Copia Copia Copia Copia Copia Copia	TE ID copia235 copia236 copia237 copia250 copia251 copia252		Get More Details More Details More Details More Details More Details More Details	
Between: Start:	End: OR		Submit		TE Type Copia Copia Copia Copia Copia Copia Copia	TE IDcopia235copia236copia237copia250copia251copia252copia253		Get More Details	
Between: Start: Search By : TE Family:	End: OR		Submit		TE Type Copia Copia Copia Copia Copia Copia Copia Copia	TE IDCopia235Copia236Copia237Copia250Copia251Copia252Copia253Copia253		Get More Details	
Between: Start: Search By : TE Family: Chromosome:	End: OR		Submit		TE Type Copia Copia Copia Copia Copia Copia Copia Copia Copia	TE IDCopia235Copia236Copia237Copia250Copia251Copia251Copia252Copia253Copia254Copia255		Get More Details More Details More Details More Details More Details More Details More Details More Details More Details More Details	
Between: Start: Search By : TE Family: Chromosome: Between: Start:	End: OR		Submit		TE Type Copia Copia Copia Copia Copia Copia Copia Copia Copia Copia	TE ID Copia235 Copia236 Copia237 Copia250 Copia251 Copia252 Copia253 Copia254 Copia255 Copia255		Get More Details More Details	



'SEARCH BY CHROMOSOME'

<i>Search By :</i> TEID:	OR	Submit	Reset eg: dna7423			
Search By : TE Type:	OR	Submit	Reset eg: Copia			
Search By : Primer Type	OR	Submit	Reset eg: RJM			
Search By : Chromosome: Fm03	OP	Submit	Reset eg: Fm03			
Sparch Rv.	OR				Chromosome: Fm03	Total TEs found: 4089
Search by .			TE Type	TE ID	Ge	t
Chromosome:			Copia	copia235	More D	etails
Between: Start:	End:	Submit	Copia	copia236	More D	etails
between our d	0.0	0.00000	Copia	copia237	More D	etails
	OR		Copia	copia250	More D	etails
Search Bv :			Copia	copia251	More D	etalls
			Copia	copia252	More D	etails
TE Family:			Copia	copia255	More D	etails
Chromosome:			Copia	copia255	More D	etails
Retween: Start:	End	Submit	Copia	copia256	More D	<u>etails</u>
between. start.	LITON	Cabinit	Copia	contra 5	Mara D	etail <u>s</u>
				Copia	Details:	
			TE ID	copia256	Chromosome	Fm03
			Start	16160283	End	16166976
			Strand	+	Score	6694
			Physical Position	View	LTR Region Similarity	6

-LTR Start

-LTR Length

-LTR Length

2147483647

16160720

16166525

Primers

5`-LTR End

3`-LTR Start

3°-LTR Length

16160283

438

16166976

'SEARCH BY CHROMOSOME'







	Primers Details: Part-I TE ID: copia1000								
Primer No	Primer Type	Junction	ТЕ Туре	TE Source	Orientation	Primer Start	Primer Len	Tm ⁰ 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









HOW TO VIEW THE DETAILS





HOW TO VIEW THE DETAILS



Name:	copia1000		
View:	on Map		
View:	More Details		

0000

VIEWING THE DETAILS



Name:	copia1000
View:	on Map
View:	More Details

	Сор	pia Details:	Fm09 [4755]
TE ID	copia1000	Chromosome	
Start	32740008	End	
Strand	+	Score	
Physical Position	<u>View</u>		
5`-LTR Start	2147483647	5 -	
5`-LTR Length	32741408	3°-LTK	
3`-LTR Length	32746771	3°-LTR Le	± 23
Get	Primers		
			Copia1000
			≍ <u>₹</u>
			÷
			- nag + 1-58,900,000 bp

Primers Details: Part-I TE ID: copia1000									
Primer No	Primer Type	Junction	ТЕ Туре	TE Source	Orientation	Primer Start	Primer Len	Tm ⁰ 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

Chromosome-wise Map





Comparative map





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



Comparative map



Comparative Maps (Right Side) Add Map Set	Comparative Maps (Right Side)	Comparative Maps (Right Side)	
No Map Set Selected	Add Map Set	== A 1 ==	
	Sequence : Brachypodium - BdTEMap [3]	Os1 [3,3]	Select
	Sequence : Rice - OsTEMap [12]	Os3 [7,7]	The chir.
Min. Correspondences: 0	Min. Correspondences. 0	Min. Correspondences: 0	
Stack 1	Stack 1	Stack 1 🗌	Interest
Refresh Menu Add Maps	Refresh Menu Add Maps	Refresh Menu Add Maps	& CIICK
Format: Name ITotal correspondences to slot	Format:	Format: Name ITotal correspondences to slot	Add
Max correspondences to single map]	Name [Total correspondences to slot, Max correspondences to single map]	Max correspondences to single map]	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					
Copia	Download	Download					
Gypsy	<u>Download</u>	<u>Download</u>					
LINE	<u>Download</u>	No Primers					
SINE	<u>Download</u>	No Primers					
Transposon	<u>Download</u>	<u>Download</u>					