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Genetic Diversity in Turmeric (*Curcuma longa* L.) Genotypes using Molecular Markers

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ABSTRACT: Turmeric being an economical crop hence it attracts to the farmers due to its versatile use in medicinal and spice industry. In the present study, genetic relatedness of 63 turmeric genotypes were assessed with using 37 SSR markers. A total of 90 amplicons were produced of which 61 amplicons were polymorphic accounting for 54.50 per cent and 29 amplicons were monomorphic. Among thirty seven primers pairs screened, CUMISAT 8 and CUMISAT 13 scored highest number of polymorphic alleles (5 amplicons). The cluster analysis of UPGMA reveals that all genotypes were grouped into six major clusters with four solitary clusters. The genotypes *viz*., TC-1, TC-2, TC-3, TC-4, TC-5, TC-8, TC-9 and TC-52 showed more similarity towards a commercially cultivated variety of Salem. Similarly, the genotypes *viz*., TC-59, TC-26, TC-33, TC-32 and TC-60-1 showed similarity towards released or improved variety Prathibha. The genotype TC-60-2, TC-61, TC-31 and Prabha seem to be very diverse compared to other genotypes. Hence, this molecular marker information will be a useful tool to identify the unique/diverse genotypes present in the collection. The study revealed genetic diversity and relatedness of turmeric genotypes collected by farmers with respect to the released varieties which can useful for selections in crop improvement.

Keywords: SSR, UPGMA, Amplicons, Cluster, Polymorphic and Monomorphic.

INTRODUCTION

Turmeric (*Curcuma longa* L.) is an important sacred and ancient spice of India popularly known as golden spice (Yadav and Tarun 2017). It is an herbaceous perennial, native to tropical South-East Asia, belonging to the family *Zingiberaceae*, under the order Scitaminae. It is a major rhizomatous spice produced and exported from India. Turmeric is a cross pollinated triploid species (2n = 3x = 63), which is being vegetatively propagated using its underground rhizomes (Sasikumar, 2005). It is widely used as a spice and condiment in the preparation of pickles and curries and as a colouring agent in textile, food and confectionery industries. It has attracted much attention due to its significant medicinal potential curcuma longa: a treasure of medicinal properties (Ansar *et al.,* 2020). Curcumin has proved to be a powerful antioxidant, anti-parasitic, antispasmodic and anti-inflammatory compounds that can also inhibit carcinogenesis and cancer growth (Wilson *et al*., 2005; Reanmongkol *et al*., 2006; Lin *et al*., 2010; Angel *et al*., 2014). It is also beneficial in treating gastrointestinal and respiratory disorders (Rajasekaran, 2011). Curcumin and curcuminoids (6 %) be one of the most promising compounds for Alzheimer's disease therapies (Shiyou *et al*., 2011).

Turmeric is grown in specific niche regions and it has crop duration of 8-9 months. It is grown both as sole and mixed crop especially with coconut. All over the regions there are custodian farmers who have a legacy of keeping the landraces of turmeric over decades and indeed the source of seed material to fellow farmers. They grow this crop as a matter of tradition in those regions. Many landraces are therefore existing all over the regions where this crop is being cultivated. The landraces are known by the names of the villages or sometimes by the family names of the custodian farmers. There is urgent need to establish the characters in the existing landraces

are delineating from the commercial varieties or share the commonality. Owing to the functional sterility, no sexually derived seeds are formed in this crop hence, rhizomes are the sole source of planting material. The rhizomes formed in clusters underground are separated and used as planting material. Over a period accumulated somatic mutations have contributed to the present day heterogeneity and heterozygous noticed among the landraces, rendering them to the population of genotypes. This is contributing to the unevenness in the crop and production.

In this paper we attempted to elucidated molecular diversity in native genetic resources and their similarity to commercially grown/ released varieties of turmeric in southern Karnataka.

MATERIAL AND METHODS

The experimental material comprised of 63 genotypes with check varieties-Prabha, Prathibha and Salemas checks and they were collected from potentially turmeric growing areas of southern districts of Karnataka *viz*., Chamarajanagar, Mysore, Mandya and Shivamogga of the farmer's field (Table 1). The collected landraces/genotypes were serially numbered by prefixing the caption COH/TC (COHB-College of Horticulture Bengaluru; TC-Turmeric). The experiment was laid out in Augmented Block Design (Federer, 1956). About 30-40g weight healthy mother rhizome of different genotypes were line planted during May 2018-19 and 2019-20 during *kharif* season with a spacing of 30 × 30 cm between row to row and plant to plant were maintained. All the agronomic package of practices was adapted to grow a healthy crop (Anon., 2017). Observations were recorded for plant height, number of leaves, leaf area, leaf area index, petiole length, number of tillers, fresh weight of aerial parts and rhizomes, dry weight of aerial parts and rhizomes, dry matter production, number of mother rhizomes and fingers, fresh and dry weight of mother rhizomes and fingers, length and girth of mother rhizomes and fingers, crop duration, fresh yield of rhizomes, cured rhizome yield, curcumin and oleoresin content. The analysis of variance was carried out as per the method suggested by Panse and Sukhatm (1967).

Plant materials. Fresh leaf samples were collected from all genotypes which were planted at PSMA block COH, Bengaluru.

DNA extraction. Total DNA was extracted from fresh leaves by the modified Cetyl Tri-methyl Ammonium Bromide (CTAB) method (Saiki *et al.,* 1988). The DNA was spooled out, washed twice with 70 per cent ethanol and dissolved in TE buffer (10 mM Tris, 0.1 mM EDTA, pH 8.0). DNA was checked for its quality and quantity by 0.8 per cent agarose gel electrophoresis and UV Spectrometer.

Molecular markers. In this study, SSR (Simple Sequence Repeat) markers were chosen based on polymorphic value in turmeric of previous studies (Table 4) and used to assess polymorphism between the genotypes.

PCR analysis and gel electrophoresis. The PCR reactions were carried out using 10 µl reaction mixture containing 3µl of master mix (dNTPs, Taq polymerase and Taq buffers are included), 5µl of nucleus free water, 0.5µl of forward and reverse primers each and 1µl diluted genomic DNA. The PCR reaction was started with initial denaturing step with94°C for 5min followed by 35 cycles of denaturation at 94°C for 1 min, annealing at 56°C for 1 min and primer elongation at 72°C for 1 min; and ended with final extension step at 72ºC. The SSR-PCR products were analyzed on 3 per cent agarose gel, visualized by staining with ethidium bromide and transillumination under short-wave UV light. DNA ladder used in the electrophoresis was of 100 bp.

Data analysis

Scoring. Amplified DNA fragments detected after electrophoresis separation in each genotype was scored for the presence (1) or absence (0) of clear and unambiguous bands. The number of different bands observed in these population consider as individual allele. Diversity analysis of scored data for 63 genotypes with check varieties were analyzed by using Darwin software. Pair-wise genetic similarities among genotypes were computed using genetic similarity coefficients and corresponding dendrograms of genetic relatedness was constructed by apply Unweighted Pair Group Method with Arithmetic mean (UPGMA) clustering algorithm.

RESULTS AND DISCUSSION

Genetic diversity study based on SSR marker in turmeric genotypes

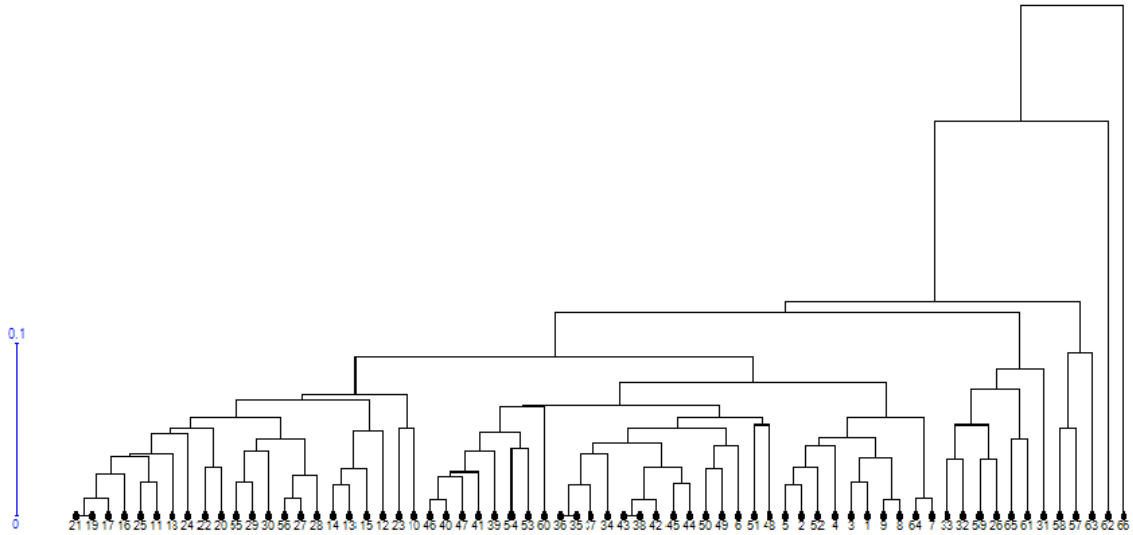
Primer selection for SSR analysis. After screening 56 SSR primers, thirty-seven primers showing clear amplification were selected for molecular characterization and the number of bands varied from 1-5 with an average of 1.64 bands per primer and the size of the amplicon ranged from 100 to 1000 bp. The only bands which are more than 100 bp were selected for scoring.

SSR profile analysis. The SSR fingerprint for sixty three genotypes along with check varieties (Prabha, Salem and Prathibha) of turmeric using thirty seven primers revealed a total of 90 scorable well defined, consistent, unambiguous, readable and reproducible polymorphic bands were used to estimate genetic diversity (Table 2).

A total of 90 bands and 6,202 data points were observed among which 61 were polymorphic alleles with an average of 1.64 polymorphic alleles per primer. Among thirty seven primers screened, CUMISAT 8 and CUMISAT 13 scored highest number of polymorphic alleles (5 bands) followed by seven primer showing three alleles per marker CUMISAT 2, CUMISAT 3, CUMISAT 7, CUMISAT 22 (Plate 1), CUMISAT 23(Plate 2), CUMISAT 30 and CUMISAT 37) and

Clone (4, 6 and 9) respectively. Minimum number of polymorphic alleles (1 bands) per marker was noticed in CUMISAT 19, CUMISAT 20 and CUMISAT 25. The primers CUMISAT (3, 5, 7, 9, 10, 13, 16, 17, 18, 23 and 35) and Clone 2 produced highest polymorphism of 100 per cent followed by CUMISAT (2, 22, 27 and 37) and clone 4, Clone 6 and Clone 9 produced 75.00per cent polymorphism. The main cause for a high level of polymorphism could be intra-specific variation were reported by Singh *et al*. (2015); Nayak *et al.* (2006) who demonstrated that high number of polymorphic loci revealed profound intra-specific variation among turmeric cultivars. Whereas primer CUMISAT (19, 20, and 25) produced least polymorphism of 50.00 per cent and CUMISAT (1, 6, 11, 14, 26, 28, 29 and 33) and Clone (1, 3 and 8) showed no polymorphism. This indicated that, these primers are useful to determine the genetic differences among *Curcuma longa* genotypes and to study phylogenetic relationship.

Similarity vs Dissimilarity Analysis. Based on UPGMA analysis of molecular data generating through genotyping of SSR markers, studied turmeric genotypes were grouped into six major clusters and four solitary clusters (Table 3) and depicted the same in dendrogram (Fig.1). This clustering analysis revels that, the cluster IV was occupies maximum number of genotypes (22), followed by cluster VI (14), cluster III (9) and cluster II (5) and cluster V and I (2), while three genotypes and check variety Prabha formed with solitary cluster. Therefore, the genotype TC-60-2, TC-61 and TC-31 seems to be very diverse compared to other genotypes. The cluster III showed nine genotypes and showing more similarity to Salem. Similarly, the cluster II covering five genotypes had shown more similarity with Prathibha. This molecular analysis clearly showed that, even though morphologically genotypes showing similar phenotypes and they are genotypically different. This similarity may be due to the collected genotypes were mixed together and placed into several groups by farmers when they used as source of propagation materiel. Hence, their results from cluster analysis did not show any distinct relationship with their region. Solitary clusters have TC-31, TC-60-2 and TC-61 were found dissimilar from other genotypes which may due to accumulation of spontaneous or natural mutation and subsequent adaptation to prevailed agro ecological conditions which in turn may also be responsible for such variations. The results were compatible with Syamkumar and Sasikumar (2007); Singh *et al.* (2012).



{Numbers (1-60) serial represent as each genotype and TC-60-1 (61), TC-60-2 (62), TC-61 (63), Selam (64), Prathibha (65) and Prabha (66) respectively}

Fig. 1. UPGMA dendrogram based on SSR analysis in turmeric genotypes.

Fig. 2. General view of the collected genotypes/landraces.

Fig. 3. Morphological variation in the collected genotypes.

Table 1: Genotypes collected from major turmeric growing districts of Karnataka.

District	Taluk	Villages	No. Sample	No. of genotype
Chamarajanagar	Chamarajanagar	Thamadahalli	6	20
		Udigala	3	
		K KUndi	1	
		ShivapuraYelle	1	
		Chandikote	1	
		Karinanjupura	2	
		Haradanahalli	2	
		Ramasamudra	1	
		Somavarpet	1	
		COHB, Haradanahalli	2	
	Gundlupet	Lakkur	2	14
		Angala	1	
		Raghavapura	2	
		Terkanambi	2	
		Vijayapura	3	
		Begur	1	
		Hebbur	1	
		Malahalli	1	
		Patterahalli	1	
Mysuru	Nanjanagud	Devanur	2	12
		ChikkaKowlande	1	
		DoddaKowlande	4	
		Konanur	2	
		KonapuradaYelle	2	
		ChunchanaHalliYalle	1	
Mandya	Malavalli	Doddaboovalli	2	8
		Mallinathapura	4	
		Purigali	2	
Shimoga	Shikaripura	Kotta	2	8
		Nimbegondi	2	
		Issur	1	
		Gama	1	
		Haragoppa	1	
		Haragoppa Thanda	1	
	Thirthahalli	Uthalli	1	1
Total			**63**	
Known varieties from SAUs	COH(S)	Prabha	1	3
	UAHS, KVK	Prathibha	1	
	Hort. Farm Yellapura	Salem	1	

Table 2: Marker wise information on number observed alleles, number of polymorphic alleles, number of monomorphic alleles and polymorphic percentage.

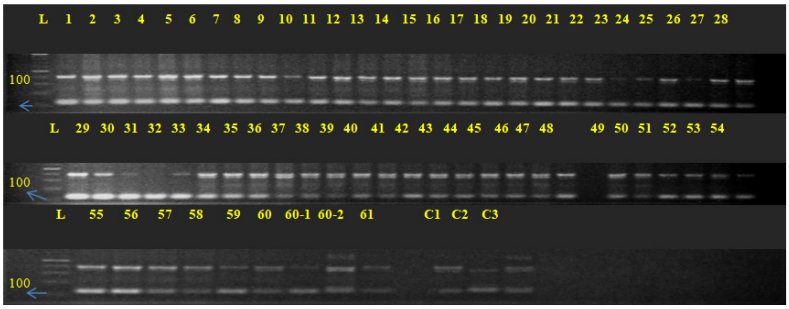
Sr. No.	Primer Name	Number of alleles observed	Number of polymorphic alleles	Number of monomorphic alleles	Polymorphic percentage (%)
1.	CUMISAT 1	01	00	01	00.00
2.	CUMISAT 2	04	03	01	75.00
3.	CUMISAT 3	03	03	00	100.00
4.	CUMISAT 5	02	02	00	100.00
5.	CUMISAT 6	01	00	01	00.00
6.	CUMISAT 7	03	03	00	100.00
7.	CUMISAT 8	06	05	01	66.67
8.	CUMISAT 9	02	02	00	100.00
9.	CUMISAT 10	02	02	00	100.00
10.	CUMISAT 11	01	00	01	00.00
11.	CUMISAT 12	01	00	01	00.00
12.	CUMISAT 13	05	05	00	100.00
13.	CUMISAT 14	02	00	02	00.00
14.	CUMISAT 16	02	02	00	100.00
15.	CUMISAT 17	02	02	00	100.00
16.	CUMISAT 18	02	02	00	100.00
17.	CUMISAT 19	02	01	01	50.50
18.	CUMISAT 20	02	01	01	50.50
19.	CUMISAT 21	01	00	01	00.00
20.	CUMISAT 22	04	03	01	75.00
21.	CUMISAT 23	03	03	00	100.00
22.	CUMISAT 24	03	02	01	66.66
23.	CUMISAT 25	02	01	01	50.00
24.	CUMISAT 26	01	00	01	00.00
25.	CUMISAT 28	02	00	02	00.00
26.	CUMISAT 29	01	00	01	00.00
27.	CUMISAT 30	04	03	01	75.00
28.	CUMISAT 33	01	00	01	00.00
29.	CUMISAT 35	02	02	00	100.00
30.	CUMISAT 37	04	03	01	75.00
31.	Clone 1	02	00	02	00.00
32.	Clone 2	02	02	00	100.00
33.	Clone 3	01	00	01	00.00
34.	Clone 4	04	03	01	75.00
35.	Clone 6	04	03	01	75.00
36.	Clone 8	02	00	02	00.00
37.	Clone 9	04	03	01	75.00
Total		**90**	**61**	**29**	**54.30**

Table 3: Clustering of turmeric genotypes based on SSR marker.

Cluster name	Genotypes	Genotypes
Solitary Clusters	04	TC-60-2, TC-61, TC-31 and Prabha
Cluster- 1	02	TC-57 and TC-58
Cluster- 2	06	TC-59, TC-26, TC-33, TC-32, TC-60-1 and Prathibha
Cluster- 3	10	TC-8, TC-9, TC-3, TC-1, TC-4, TC-52, TC-2, TC-6 and TC-7 Salem
Cluster- 4	22	TC-43, TC-38, TC-42, TC-44, TC-35, TC-36, TC-34, TC-37, TC-45, TC-50, TC-49, TC-6, TC-48, TC-51, TC-46, TC-40, TC-47, TC-41, TC-39, TC-53, TC-54 and TC-60
Cluster- 5	02	TC-23 and TC-10
Cluster- 6	20	TC-19, TC-21, TC-17, TC-16, TC-25, TC-11, TC-18, TC-24, TC-22, TC-20, TC-55, TC-29, TC-30, TC-56, TC-27, TC-28, TC-14, TC-13, TC-15 and TC-12

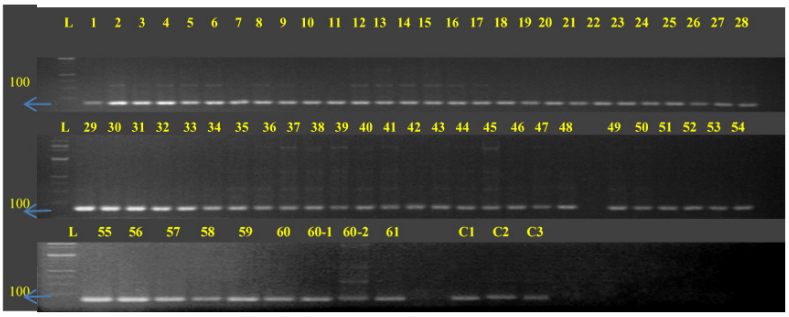
Table 4: List of SSR markers used in the genetic diversity study and their forward, reverse primer sequence.

Sr. No.	Primer Name	Forward primer 5'→3'	Reverse primer 5'→3'
1.	CuMiSat-01	AAA CCG CAA GAA AAC TGA AG	CTC TTC CCT GAA CGA TTC C
2.	CuMiSat-02	TAT GTG ATG GTT GGG ACG	GTA GTG GAG GAA GAC GCC
3.	CuMiSat-03	GCA CTA CTT CCT TCT CGT TCA A	CGT CGT AAA GAT TAG CGT GTG
4.	CuMiSat-04	TCA GGT TTC AGG GTG TAG AAG	CCC AGC AAG ATT TTA CCA AG
5.	CuMiSat-05	AGC AGT GCG TCT TTC ATC	CTC TTG TCA CGG AAC CTC
6.	CuMiSat-06	AAG AAA CTC CAA CCA CAA TCC	CTT GTC TTC CTC CTC CAT TG
7.	CuMiSat-07	AGC ATG TGT CTA GCT CTT TGC	AAG CAG TCG TTC CTC TAC TGA C
8.	CuMiSat-08	CAT TGC GTG CCC ACT TCC	CCT CCC TGT CGC TCT CCT C
9.	CuMiSat-09	AGT TGT GAA AGG GAT AGA GTA GTT G	AAG AAA GCA AAT GCC AAG G
10.	CuMiSat-10	CAC CCT ATG AGT GCT AAC TGA AG	ACC TGC ACC ACG ATC AAC
11.	CuMiSat-11	ACA GTC CCC TTC CCA CTC	TCT TGT TCC TAT GCT CTA CGC
12.	CuMiSat-12	AAG GTT GCT GCT TGT TGA GAA	GCA TAT TGC CTT ACA TGC CTA A
13.	CuMiSat-13	CCC GAA GCC ATT TCT CAG	TCG TCT CTC CTC TGC CAA C
14.	CuMiSat-14	GCT GAC TGT GGC AAA AGA GTC	GCT GCG CTT CTTCTT AAT GAC
15.	CuMiSat-15	GCA GAA CTC ACC AAG TAA TGG C	TTG AAC AAC CAA CAC CCT AAC TG
16.	CuMiSat-16	CAT TTG TTC TGC TCG CTT CTA C	CTG CTC CGC TGT CTC TCA C
17.	CuMiSat-17	ATG TGG TTG AGG AAT GAT GAG AC	CTA TTT CCC ATA GCC CTT GTA GC
18.	CuMiSat-18	GTT CAC AGC TTT AGC AGG GAC AA	CTC CTC TCC ATA TTC TCC ATC TCG
19.	CuMiSat-19	CAT GCA AAT GGA AAT TGA CAC	TGA TAA ATT GAC ACA TGG CAG TC
20.	CuMiSat-20	CAT GCA AAT GGA AAT TGA CAC	TGA TAA ATT GAC ACA TGG CAG TC
21.	CuMiSat-21	TCA TTC AAA GTC CGA TGG AA	TTC GAG TGC AGA AGG AGA ATT A
22.	CuMiSat-22	AAT TTA TTA GCC CGG ACC AC	AAG AAA GTG AGT AGA AAC CAA AGC
23.	CuMiSat-23	CGT GGA AGG TGA GTT TGA C	CAG AAG GGA ACT GAG ATG G
24.	CuMiSat-24	AGG TAT TCT ACT CGA CCA AG	AAA TTC ATA TAG CCC CAT C
25.	CuMiSat-25	TAC ATG AGA AAC AAC AAA GCC C	AGT TAG CCA AGT CCC AAT TTA GC
26.	CuMiSat-26	CAT TCC GAT GAA TTG TAT G	GCA GTT GTT TTG CTT CAG
27.	CuMiSat-27	TAT AGA TAG CCA TGC TGA AG	CCA TTT TAG TTC ATT ACG TG
28.	CuMiSat-28	TTC AAC TTC TCC TCG CTC AG	GCA AGG TCT GCA TCT ATT TCT C
29.	CuMiSat-29	GTG GTA TCC CCA TGA AGA GC	ATG ACC AAG CCC TTT CAC C
30.	CuMiSat-30	CTC TAA TGT CGC CTC TCA CG	GCA TCT CCC GTT CTT CTC C
31.	CuMiSat-31	GGA GGAGGA GAA GCA GAA G	GAC AGG CGA AGG AAG AAA C
32.	CuMiSat-32	TGT TGT AGG TAG AAG CAA ATG AC	TTG GTG TCC TAA TTC TTT CAA C
33.	CuMiSat-33	ATG GAT GGA TAC AAC AACAAC	TAT AAA CAC ACT CCC TCT TGG
34.	CuMiSat-34	AAG TTG GTG AAG GAT TAG AGC TAC	CAC CTA GTG GGA TAA ATC TTG G
35.	CuMiSat-35	GGT TCG TCG CTG GAA AGT AAT	GCA TCT CAA CAG GGG CTG
36.	CuMiSat-36	TGG GCT CAA TGG TTG ATA CG	CTC CTC ATC GCT ATC CGA GG
37.	CuMiSat-37	CCA TTG GCG AGG ATG AAG C	CCT GCC AAG CAA AGC CAA G
38	CuMiSat-38	TCA TCA TAA ACA CTC CTG	GAA GAA GAG GCT AAG TTC
39	CuMiSat-39	TAT CCC CTG AAA ACT AAT CC	AAA ATG TCA CGA ACT ATT GC
40	Clon-01	ACT GGA CTG TCC GAG AGC AT	TCG TTT AGC GAC AAC GGA TT
41	Clon-02	CTA TTA AGC GCA GTC CCC AG	AGT CTC TCG TGC GTT CCA GT
42	Clon-03	CTC TCA CGA CGT CTC CAT CA	AGA CTC GCG TGT ACA GAG CA
43	Clon-04	TAA ATT TGC GAA GGC AAT CC	CCG CAG AGG AAT TTG AAG AG
44	Clon-05	CTC GCG CTC AAG ACA TTA GA	TCG AGT CAT GCA GGA CGT AT
45	Clon-06	TTG CCA GTG TGC TTG TTC TC	TTG AAG GGA ACA CTG AAG GG
46	Clon-07	TAC GCG TGG ACT AGC TGA TG	CCT TGC TTT GGT GGC TAG AG
47	Clon-08	CCG GTG AGG GTG ATA TCT TG	AAG CTC AAG CTC AAG CCA AT
48	Clon-09	GGA GGA GGC AGT TGA TTT GT	GCT TTG GTG GCT AGA GAT GC
49	Clon-10	GTG GGA ATT GGA TTG CTC TC	GAG AAC TCC CCA TGC TTC AG
50	Clon-11	GGG CTT TGT TTA GTT GTC GTG	CAG GAA TGA AGT CGG CAA C
51	Clon-12	GAT TGG ATC ACA TGG TGT GC	TGG GTT GAT GGT TTC TCT GTT
52	Clon-13	CCC ATT TGG CAC ATA GTT TTC	GCT TGT TGG TGT TGA ATG CT
53	Clon-14	TCA GTC GAG GGG TTC CTA CT	GAG AGC TGA TCG CAA AAA C
54	Clon-15	GTC GCC CGA TCT ATT GTA GC	GAT CCA TCC TCC CCT AAA GC
55	Clon-16	TTG TGC CAA GTG AGG ATT TG	ACT CGC TTC TGC TCA TCC AT
56	Clon-17	TTC TTC ACG CAC CTT CCT G	GGG TGA ATC AGA GGA CAA TCA



L-Ladder, 1st Row TC-1 to TC-28, 2nd Row TC-29 to TC-56 and 3rd Row TC-57 to TC-61., C1 (Prabha) and C2 (Prathibha) and C3 (Salem)

Plate 1: PCR amplicons with SSR marker (CUMISAT-22) in turmeric genotypes.



L-Ladder, 1st Row TC-1 to TC-28, 2nd Row TC-29 to TC-56 and 3rd Row TC-57 to TC-61., C1 (Prabha) and C2 (Prathibha) and C3 (Salem)

Plate 2: PCR amplicons with SSR marker (CUMISAT-23) in turmeric genotypes.

CONCLUSIONS

A comparison of these values of allelic diversity among the genotypes, clearly emphasize the scope for introgression of genes through hybridization among the cultivars for increasing genetic diversity in the cultivated turmeric pool. This also reiterates the need for genetic diversity evaluation among the principal genotype classes and cataloguing them for the benefit of the future. Molecular investigation of 63 genotypes with SSR markers showed that, the genotypes *viz*., TC-1, TC-2, TC-3, TC-4, TC-5, TC-8, TC-9 and TC-52 showed more similarity towards commercial cultivated variety of Salem. Similarly, the genotypes *viz*., TC-59, TC-26, TC-33, TC-32 and TC-60-1 showed similarity towards released or improved variety Prathibha. The genotype TC-31, TC-60-2 and TC-61 were more diverse among the collected genotypes. Hence, this molecular marker information will be useful tool to identify the unique/diverse genotypes present in a collection.

FUTURE SCOPE

Among 63 collected genotypes TC-31, TC-60-2 and TC-61 were more diverse. Hence, these genotypes can be further study by other markers and utilized in crop improvement programme. SSR marker CUMISAT 8 and CUMISAT 13 producing high polymorphic alleles (>4) can be used for molecular diversity studies in turmeric.

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Conflict of Interest. None.

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