

Molecular characterization and genetic diversity analysis of turmeric genotypes using RAPD, ISSR and SSR markers

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Abstract

Genetic diversity among fifteen turmeric (*Curcuma longa* L.) genotypes was assessed using three classes of molecular markers, namely Random Amplified Polymorphic DNA (RAPD), Inter-Simple Sequence Repeat (ISSR), and Simple Sequence Repeat (SSR) markers. A total of 242 scorable alleles were generated using 31 RAPD primers, of which 216 alleles (89.26%) were polymorphic across the genotypes. Nineteen ISSR primers amplified 91 scorable alleles, with 69 alleles (75.82%) exhibiting polymorphism. Similarly, 38 SSR primer pairs produced 113 scorable alleles, of which 97 alleles (85.84%) were polymorphic. Several markers generated genotype-specific alleles that enabled clear discrimination among accessions. Among RAPD markers, primer OPL-12 produced an unique allele at 600 bp in Acc. 849 and Narendra Haldi 98, while OPB-8 amplified a distinct allele at 850 bp in SLP 389/1. In ISSR analysis, primer ISSR-05 differentiated CO-2 from other genotypes at 450 and 700 bp, UBC-851 distinguished SLP 389/1 (530 bp) and Punjab Haldi-1 (900 bp), and UBC-857 uniquely identified Punjab Haldi-1 at 500 bp. Among SSR markers, CLEST-7 and CUMISAT-19 uniquely distinguished IISR Prathibha at 160 bp and 190 bp, respectively; CUMISAT-10 identified SLP 389/1 at 200 bp; CLEST-8 differentiated IISR Prathibha and Duggirala Red at 200 bp; and CUMISAT-33 distinguished Acc. 849 and Narendra Haldi 98 at 220 bp. The high level of polymorphism detected across marker systems indicates substantial genetic variability among the turmeric genotypes. The identified polymorphic and genotype-specific markers are valuable tools for precise germplasm characterization, avoidance of duplication in collections, population genetic and breeding studies in turmeric.

Keywords: Germplasm, ISSR, polymorphic, RAPD, SSR

Introduction

Turmeric “Golden Spice” is an important horticulture crop in terms of medicinal and nutraceutical values. India is the largest

producer and exporter of turmeric in the world, followed by China, Indonesia, Bangladesh and Thailand (Prasath *et al.*, 2019). India possesses a rich genetic diversity in turmeric, with numerous landraces, cultivars

and released varieties adapted to diverse agro-climatic regions, reflecting a broad spectrum of morphological and biochemical traits. So far, 51 turmeric varieties are released in India from different parts of the country. Off late, open pollinated seedling selection and hybridization programmes are effective in crop improvement programmes, apart from germplasm selection and to eventual sports arising during vegetative propagation. Identification of divergent type is necessary in pre breeding to select parents. Moreover, exploitation and utilization of plant genetic diversity using molecular tools is one of the techniques in molecular genetics studies to study the diversity. Molecular markers are used in varietal finger printing, hybridity test, genetic mapping, and to detect the mutant genes. Over the past decades, molecular markers have gained increasing importance for detecting polymorphisms at the DNA level. Unlike morphological and biochemical markers, which are often influenced by environmental conditions or developmental stages, DNA-based markers provide a more reliable means of assessing genetic variation (Tingey and Tufo, 1993). Among them, PCR-based molecular markers have been widely applied in numerous plant species for purposes such as identification, phylogenetic analysis, population studies, and genetic linkage mapping. Random Amplified Polymorphic DNA (RAPD) markers, in particular, are preferred due to their simplicity, cost-effectiveness, and efficiency in evaluating genetic relationships (Williams *et al.*, 1990). RAPD markers have proven useful in studying genetic variability within species or natural populations as well as in genotype identification. Inter Simple Sequence Repeat (ISSR) markers are easy to handle, highly informative and repeatable. SSR markers are more reproducible and useful in evaluating genetic diversity and cultivar identification (Lian *et al.*, 2006). Characterization of turmeric germplasm using molecular markers was reported using RAPD (Jan *et al.*, 2011), RAPD

and ISSR (Das *et al.*, 2011; Singh *et al.*, 2012, Verma *et al.*, 2015) and SSR markers (Sigrist *et al.*, 2010; Siju *et al.*, 2010; Hayakawa *et al.*, 2011). Identification of elite and unique genotypes with these markers may help to understand the distant and relationship within the species. The present study aims at screening of RAPD, ISSR and SSR primers across the turmeric genotypes to identify the polymorphic markers and to understand the diversity within the species.

Materials and methods

Plant material and DNA extraction

The present study is based on 15 genotypes of turmeric (BSR-2, CO-2, Varna, Suvarna, IISR Prathibha, IISR Pragati, SLP 389/1, SC 61, Acc. 849, Rajapuri, Narendra Haldi-98, Duggirala Red, Rajendra Sonia, Punjab Haldi 1 and Megha Turmeric 1) representing from major turmeric grown areas and are conserved at turmeric national active germplasm site (NAGS) at ICAR Indian Institute of Spices Research, Kozhikode, Kerala. The genotypes were grown in green house and the fresh young leaf samples (2 g) were used for genomic DNA isolation. High quality genomic DNA was isolated from the fresh leaves of 15 turmeric genotypes following the protocol of Syamkumar *et al.*, (2003).

PCR analysis and gel electrophoresis

A set of 40 primers each of RAPD, ISSR and SSR were used among which 31 RAPD, 19 ISSR and 38 SSR markers amplified and were screened. The PCR reaction was carried out using 20 µl PCR mixture comprising of 10X reaction buffer with Template DNA (10 ng µl⁻¹), MgCl₂, dNTP mix (10 mM), primer (10 µM), *Taq* DNA polymerase (3 U µl⁻¹) and nuclease free water. The PCR reaction profile was used as follows: an initial hot start and denaturing step at 94°C for 5 min followed by 35 cycles at 94°C for 45 seconds, annealing temperature for 45 seconds, primer extension at 72°C for 1 min and final extension step at 72°C for 15 min were performed. Annealing

temperature was 37°C for RAPD and in case of ISSR and SSR primers specific annealing temperature was maintained. Primer details and annealing temperature details are given as (Supplementary table 1 to table 3). The PCR products were checked in 1.5% agarose gel for successful amplification of RAPD primers and ISSR primers, 3% agarose gel for SSR primers and stained with ethidium bromide.

Data analysis

Amplified fragments were scored manually for each marker system by recording the presence or absence of bands across the genotypes. The resulting data were transformed into a binary format, with band presence coded as '1' and absence as '0'. The informativeness of the primers in detecting polymorphism was quantified by calculating the polymorphism information content (PIC). PIC values were derived using the expression $PIC = 1 - \sum p_i^2$, where p_i corresponds to the relative frequency of the i^{th} allele (Smith *et al.*, 1997). Pairwise genetic relatedness among the genotypes was determined using Jaccard's similarity coefficient, which estimates similarity based on the proportion of shared amplified fragments (Jaccard, 1908). A similarity matrix was constructed employing the SIMQUAL routine in the NTSYS-pc software package (version 2.02; Rohlf, 2000). The similarity coefficients were subsequently subjected to hierarchical clustering using the Unweighted Pair Group Method with Arithmetic Mean (UPGMA), and the genetic relationships among the genotypes

were represented in the form of a dendrogram (Sneath and Sokal, 1973).

Results and discussion

In this investigation, the extent of genetic diversity in a set of 15 genotypes of turmeric was estimated using RAPD, ISSR and SSR markers. Polymorphism information content (PIC) value of each RAPD, ISSR and SSR primers is a measure of marker diversity. The PIC provides an estimate of discriminatory power of a locus by taking into account not only the number of alleles expressed, but also the relative frequency of those alleles. The detailed comparison between the markers (RAPD, ISSR, SSR) studied is given in Table 1.

Details of monomorphic/polymorphic markers produced by the 31 RAPD primers are furnished in Table 2. A total of 213 scorable alleles were generated by 31 RAPD primers, of which 190 were polymorphic among the genotypes. The amplification with the primers OPA 3 recorded the highest number of RAPD loci (14) followed by primers OPA 09 and OPD 18 which showed 13 loci. The primer OPH 8 (1) followed by OPK 7 (2), OPF 03 (3), OPW 11 (3) and OPD 20 (3) produced the least number of RAPD loci. The Polymorphic Information Content (PIC) value as a relative measure of polymorphism level among the polymorphic markers ranged between 0.23 (OPK 7) to 0.98 (OPG 11). The RAPD marker OPG 11 (0.98), OPA 10 (0.98) and OPW 11 (0.96) were found to be highly informative based on PIC.

Table 1. Level of polymorphism detected by RAPD, ISSR and SSR markers in turmeric

Parameter	RAPD	ISSR	SSR
Number of primers	31	19	38
Number of alleles	213	91	113
Range of alleles across primers	1-14	2-10	1-4
Number of polymorphic bands	190	69	97
Percent polymorphism	89.20	75.82	85.84
Mean polymorphic information content	0.75	0.72	0.5
Average marker index	4.5	2.71	1.13

Table 2. Polymorphism Information Content (PIC) of RAPD loci in turmeric

Primer	Total alleles	Monomorphic amplicons	Polymorphic amplicons	Total number of amplicons	Allele size range (bp)	PIC value
OPA 3	14	2	12	102	600-4000	0.89
OPA 9	13	1	12	80	600-2500	0.89
OPA 10	7	0	7	57	300-1900	0.98
OPA 15	9	1	8	83	350-1400	0.87
OPA 17	6	0	6	32	300-2000	0.76
OPB 5	4	0	4	21	250-1300	0.70
OPB 8	12	0	12	61	600-2500	0.88
OPB 20	6	2	4	51	500-1200	0.78
OPC 7	10	1	9	61	400-3000	0.86
OPC 20	7	0	7	52	1200-2500	0.83
OPD 3	5	2	3	51	600-1250	0.75
OPD 7	9	0	9	57	600-2500	0.84
OPD 10	11	0	11	76	875-2400	0.88
OPD 13	8	0	8	50	900-5000	0.86
OPD 14	6	0	6	44	800-2100	0.79
OPD 16	6	0	6	21	850-1200	0.68
OPD 18	13	1	12	101	650-3500	0.90
OPD 20	3	1	2	20	800-1200	0.405
OPE 2	6	1	5	32	900-1600	0.719
OPE 11	5	3	2	60	900-2900	0.764
OPF 3	3	0	3	17	1300-1750	0.443
OPF 9	8	1	7	73	400-1600	0.857
OPF 10	4	1	3	22	600-2000	0.500
OPG 11	6	0	6	58	300-3000	0.983
OPH 8	1	1	0	15	600	0.000
OPH 13	5	0	5	38	1300-3000	0.769
OPI 16	6	0	6	33	850-3000	0.774
OPK 7	2	0	2	15	2200-300	0.231
OPL 12	7	3	3	60	600-2000	0.786
OPM 15	8	1	7	57	500-3000	0.814
OPW 11	3	0	3	24	400-1000	0.958

Molecular profiles obtained using 19 ISSR primers are furnished in Table 3. A total of 91 scorable alleles were generated, of which 69 were polymorphic among the genotypes. Primers ISSR 14 & UBC 851 amplified the highest number of ISSR loci (10) followed by the primer ISSR 05 with 9 loci. The primer UBC 812 produced the least number of ISSR loci

(2). The polymorphism information content (PIC), reflecting the degree of informativeness among polymorphic markers, varied across the marker systems and ranged between 0.53 (UBC 282) to 0.87 (ISSR 14). The ISSR marker ISSR 14 (0.87), ISSR 12 (0.84), UBC 851 (0.83) and ISSR 05 (0.82) were found to be highly informative based on PIC.

Table 3. Polymorphism Information Content (PIC) of ISSR loci in turmeric

Primer	Total alleles	Monomorphic amplicons	Polymorphic amplicons	Total number of amplicons	Allele size range (bp)	PIC value
ISSR 01	6	0	6	41	500-1100	0.79
ISSR 03	5	2	3	56	300-1000	0.76
ISSR 05	9	3	6	70	400-1100	0.82
ISSR 09	3	0	3	21	500-700	0.61
ISSR 12	8	1	7	71	100-900	0.84
ISSR 14	10	4	6	102	250-1500	0.87
ISSR 15	4	4	0	60	300-1000	0.75
UBC 282	3	2	1	31	200-1000	0.53
UBC 812	2	1	1	25	500-510	0.48
UBC 820	5	0	5	32	250-1100	0.71
UBC 821	4	2	2	51	500-1000	0.74
UBC 834	7	1	6	55	250-1100	0.79
UBC 841	4	1	3	36	250-490	0.65
UBC 842	7	0	7	41	250-1500	0.76
UBC 851	10	0	10	47	300-1300	0.83
UBC 857	4	1	3	24	250-1500	0.54

Of the 38 pairs of SSR primers analysed in the 15 turmeric genotypes, total of 113 scorable alleles was generated, of which 97 were polymorphic. Primers CUMISAT 22, CUMISAT 28, CUMISAT 36 and CLEST 7 recorded the highest number of alleles (5). The primers CUMISAT 31, CLEST 3 and CLEST 4 were monomorphic with PIC value 0. The PIC values, used to quantify the extent of polymorphism among the markers, showed considerable variation and ranged between 0.13 (CUMISAT 34) to 0.78 (CUMISAT 28). Among SSR marker CUMISAT 28 (0.78), CUMISAT 8 (0.75), CUMISAT 36 (0.74) and CLEST 13 (0.71) were found to be highly informative based on PIC (Table 4). The markers with high PIC can be used for turmeric DNA profile system.

Polymorphism in a given population is often due to the existence of genetic variants represented by the number of alleles at a locus and their frequency of distribution in a population. Variability using molecular markers has been examined in turmeric by different researchers (Nayak *et al.*, 2006; Syamkumar and Sasikumar, 2007; Sigrist *et al.*, 2010; Siju *et al.*, 2010; Khan *et al.*, 2013; Senan *et al.*, 2013; Singh *et al.*, 2015; Prashanth *et al.*,

2016; Sahoo *et al.*, 2017). Moreover, current diversity studies increasingly integrate molecular markers with morpho-biochemical traits to identify elite genotypes. Lavudya *et al.*, 2024 characterized 24 turmeric genotypes using agronomic, biochemical, and SSR marker data revealed broad genetic variability and grouped the genotypes into four major clusters, supporting the use of molecular markers alongside phenotypic traits for selection and breeding.

Similarity index

The similarity coefficients based on RAPD, ISSR and SSR markers ranged from 0.37 to 0.83. The low values of similarity index indicate that the genotypes were most diverse. The total diversity obtained was also high which is evident from the wide range of similarity index values. The genotypes Acc. 849 and Narendra Haldi 98, which are similar in morphological and rhizome characters, had maximum similarity (0.83). Low similarity of 0.37 was observed between Duggirala Red, a long duration variety and IISR Pragati, a short duration variety (Table 5).

Table 4. Polymorphism Information Content (PIC) of SSR loci in turmeric

Primer	Total alleles	Monomorphic amplicons	Polymorphic amplicons	Total number of amplicons	Allele size range (bp)	PIC value
CUMISAT 1	2	1	1	24	220-250	0.47
CUMISAT 2	3	0	3	17	170-190	0.49
CUMISAT 3	3	0	3	20	190-500	0.63
CUMISAT 5	3	0	3	24	170-200	0.52
CUMISAT 6	3	0	3	19	200-220	0.52
CUMISAT 7	3	0	3	21	150-210	0.58
CUMISAT 8	4	0	4	31	150-400	0.75
CUMISAT 10	3	0	3	19	185-210	0.46
CUMISAT 13	3	1	2	32	250-300	0.64
CUMISAT 16	4	0	4	24	175-210	0.67
CUMISAT 19	3	0	1	19	180-210	0.55
CUMISAT 20	3	1	2	21	160-200	0.44
CUMISAT 21	3	0	3	22	160-200	0.53
CUMISAT 22	5	0	5	34	130-180	0.74
CUMISAT 23	3	1	2	21	150-200	0.43
CUMISAT 24	3	0	3	25	130-160	0.60
CUMISAT 25	2	1	1	18	150-200	0.28
CUMISAT 26	3	0	3	23	180-210	0.67
CUMISAT 28	5	0	5	37	140-230	0.78
CUMISAT 29	2	1	1	24	150-180	0.47
CUMISAT 30	2	0	2	20	170-180	0.42
CUMISAT 31	1	1	0	15	180	0.00
CUMISAT 32	4	0	4	16	130-150	0.69
CUMISAT 33	3	0	3	17	180-220	0.69
CUMISAT 34	2	0	2	14	120-140	0.13
CUMISAT 36	5	0	5	32	180-300	0.74
CUMISAT 37	2	1	1	21	210-200	0.41
CLEST 2	2	1	1	22	190-200	0.4
CLEST 3	1	1	0	15	200	0.00
CLEST 4	1	1	0	15	200	0.00
CLEST 7	5	1	4	29	120-180	0.61
CLEST8	4	0	4	28	150-180	0.67
CLEST 9	4	0	4	29	180-240	0.63
CLEST 13	4	0	4	30	150-190	0.71
CLEST 14	2	1	1	20	180-200	0.38
CLEST 15	2	1	1	17	190-200	0.21
CLEST 16	2	0	2	21	180-200	0.45
CLEST 17	4	0	4	22	180-210	0.64

Table 5. Jaccard's coefficient of similarity derived from RAPD, ISSR and SSR data in turmeric

Genotype	G1	G2	G3	G4	G5	G6	G7	G8	G9	G10	G11	G12	G13	G14	G15
G1	1.00														
G2	0.68	1.00													
G3	0.46	0.43	1.00												
G4	0.74	0.62	0.46	1.00											
G5	0.69	0.61	0.48	0.80	1.00										
G6	0.64	0.54	0.43	0.62	0.61	1.00									
G7	0.58	0.50	0.44	0.54	0.55	0.52	1.00								
G8	0.49	0.46	0.49	0.50	0.48	0.52	0.47	1.00							
G9	0.46	0.45	0.45	0.44	0.45	0.44	0.64	0.49	1.00						
G10	0.43	0.40	0.83	0.41	0.41	0.43	0.42	0.48	0.45	1.00					
G11	0.54	0.51	0.53	0.54	0.52	0.52	0.47	0.73	0.49	0.51	1.00				
G12	0.63	0.56	0.44	0.71	0.68	0.56	0.51	0.49	0.41	0.42	0.52	1.00			
G13	0.50	0.47	0.51	0.50	0.51	0.54	0.46	0.74	0.49	0.50	0.81	0.52	1.00		
G14	0.44	0.44	0.39	0.37	0.40	0.41	0.54	0.45	0.62	0.42	0.48	0.39	0.48	1.00	
G15	0.58	0.51	0.46	0.59	0.57	0.67	0.50	0.53	0.45	0.45	0.56	0.61	0.56	0.42	1.00

G1: Punjab Haldi 1

G2: SLP 389/1

G3: NarendraHaldi 98

G4: IISR Pragati

G5: CO 2

G6: SC 61

G7: BSR 2

G8: Suvarna

G9: IISR Prathiba

G10: Acc. 849

G11: Varna

G12: Rajendra Sonia

G13: Megha Turmeric 1

G14: Duggirala Red

G15: Rajapuri

Clustering

A dendrogram was constructed for 15 genotypes using Jaccard's similarity index values using the NTSYS-pc Version 2.02. In Sequential Agglomerative Hierarchical Non overlapping (SAHN), UPGMA was used to generate dendrogram.

Based on the dendrogram, the 15 genotypes formed seven clusters at similarity coefficient of 0.64 (Fig 1). Similarly Siju *et al.*, (2010) reported the average discriminating power of microsatellite markers (0.62) using SSR in turmeric.

Cluster I : Narendra Haldi 98, Acc. 849

Cluster II : Duggirala Red

Cluster III : BSR 2, IISR Prathibha

Cluster IV : Suvarna, Megha Turmeric 1, Varna

Cluster V : SC 61, Rajapuri

Cluster VI : SLP 389/1

Cluster VII : Punjab Haldi 1, IISR Pragati, CO 2, Rajendra Sonia

Cluster I (Narendra Haldi 98 and Acc. 849) formed the separate cluster from other. Both the genotypes possessed similar phenotype and chemo type. Cluster II and Cluster III comprised of genotypes with long duration and bold rhizomes. Cluster IV comprised of genotypes with slender rhizome. Cluster V comprised of genotypes which are grouped based on similarity of rhizome character and rhizome colour (yellow colour rhizome) apart from molecular similarity. Cluster VI grouped with one genotype, which possessed unique pigmentation in the pseudostem sprouts (Aarthi *et al.*, 2018). Cluster VII comprised of genotypes with short plant height, bold rhizomes and short duration. Cluster VI and Cluster VII had a morphological similarity which was clustered in a separate sub-cluster. The cluster IV was having four genotypes; the genotypes are morphologically characterized as slender rhizomes with high recovery (Aarthi *et al.*, 2018). ACC 849 and Narendra Haldi 98 clustered separately, which has morphologically bigger mother rhizome (Aarthi *et al.*, 2018).

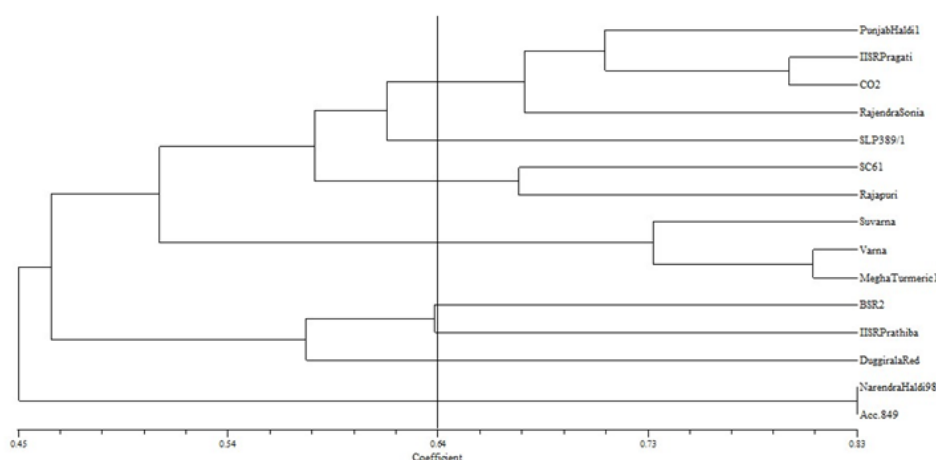


Fig. 1. Dendrogram based on UPGMA analysis of genetic similarities estimated among the 15 genotypes of turmeric using RAPD, ISSR and SSR primers

Variability using ISSR markers has been examined in turmeric by different researchers. This shows the potentiality of RAPD, ISSR and SSR markers for the characterization of genotypes. The diverse genotypes could also be utilized as parents in hybridization.

Markers specific to genotypes

Several molecular markers in this study generated genotype-specific alleles that effectively distinguished individual turmeric genotypes. For RAPD markers, primer OPL-12 amplified a unique allele at ~600 bp in Acc. 849 and Narendra Haldi-98, while OPB-8 produced a distinctive ~850 bp fragment in SLP 389/1 (Fig. 2). In the ISSR analysis, primer ISSR-05 revealed unique bands at ~450 and 700 bp that separated CO-2 from the other genotypes, UBC-851 distinguished SLP 389/1 and Punjab Haldi-1 with alleles at ~530 bp and ~900 bp, respectively, and UBC-857 generated a specific band at ~500 bp for Punjab Haldi-1 (Fig. 3). Among SSR markers, CLEST-7 and CUMISAT-19 uniquely identified IISR Prathibha at ~160 bp and ~190 bp, CUMISAT-10 distinguished SLP 389/1 at ~200 bp, CLEST-8 separated IISR Prathibha and Duggirala Red at ~200 bp, and CUMISAT-33 produced a diagnostic ~220 bp band in Acc. 849 and Narendra Haldi-98 (Fig. 4).

These genotype-specific markers provide clear evidence of genetic differentiation among the accessions and reinforce the effectiveness of molecular markers in diversity studies. Similar multi-marker approaches combining RAPD, ISSR, and other marker systems have successfully resolved genetic variation in turmeric, demonstrating broad polymorphism and distinguishing cultivars for germplasm characterization and breeding applications (e.g., RAPD and ISSR markers showing high polymorphism and utility in cultivar discrimination) (Porandla *et al.*, 2025). Furthermore, SSR markers have been shown to produce high polymorphic information content and robust clustering patterns that reflect genetic relationships among turmeric germplasm, making them valuable for conservation and crop improvement efforts (Burman *et al.*, 2025).

The identification of diagnostic alleles in specific genotypes has practical implications for germplasm management, allowing precise identification and avoidance of redundancy in gene banks. In addition to supporting genetic diversity assessments, such markers can be employed in marker-assisted selection to track desirable alleles in breeding programs. These findings align with recent studies highlighting the combined use of diverse molecular markers to capture comprehensive genetic variation in

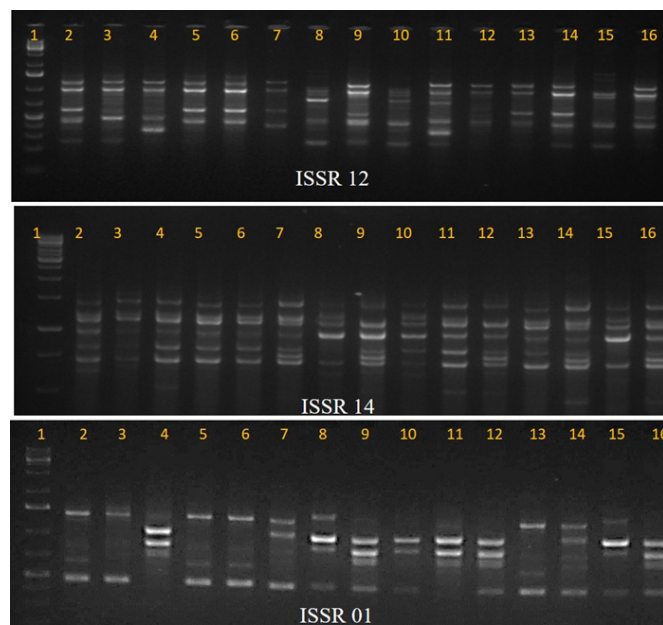


Fig. 2. RAPD banding pattern of 15 genotypes: OPF 9, OPA 3 and OPA 9 (1. 1Kb ladder, 2. Punjab Haldi 1, 3. SLP 389/1, 4. Narendra Haldi 98, 5. IISR Pragati, 6. CO 2, 7. SC 61, 8. BSR 2, 9. Suvarna, 10. IISR Prathiba, 11. Acc. 849, 12. Varna, 13. Rajendra Sonia, 14. Mega Turmeric 1, 15. Duggirala Red, 16. Rajapuri)

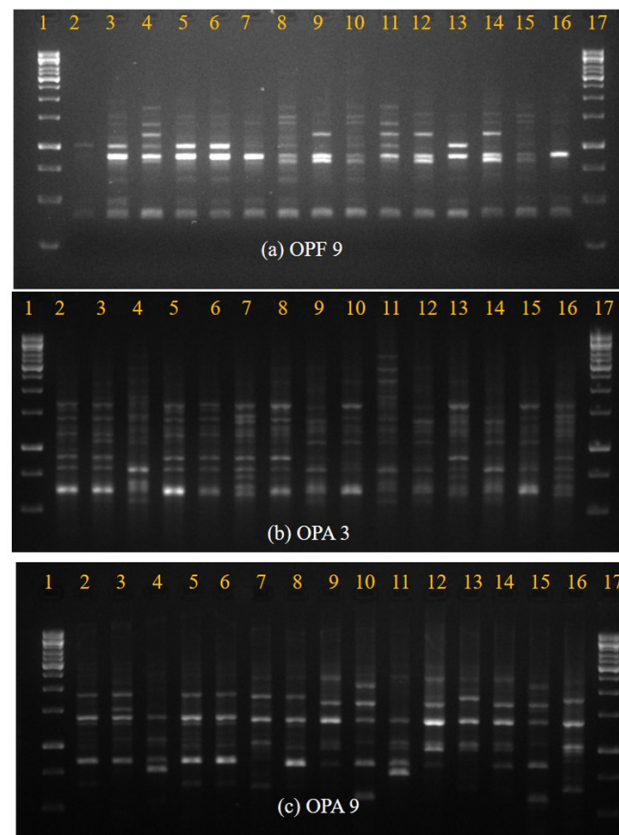


Fig. 3. ISSR banding pattern of 15 genotypes ; ISSR 12, ISSR 14, ISSR 01 (1. 1Kb ladder, 2. Punjab Haldi 1, 3. SLP 389/1, 4. Narendra Haldi 98, 5. IISR Pragati, 6. CO 2, 7. SC 61, 8. BSR 2, 9. Suvarna, 10. IISR Prathiba, 11. Acc. 849, 12. Varna, 13. Rajendra Sonia, 14. Mega Turmeric 1, 15. Duggirala Red, 16. Rajapuri)

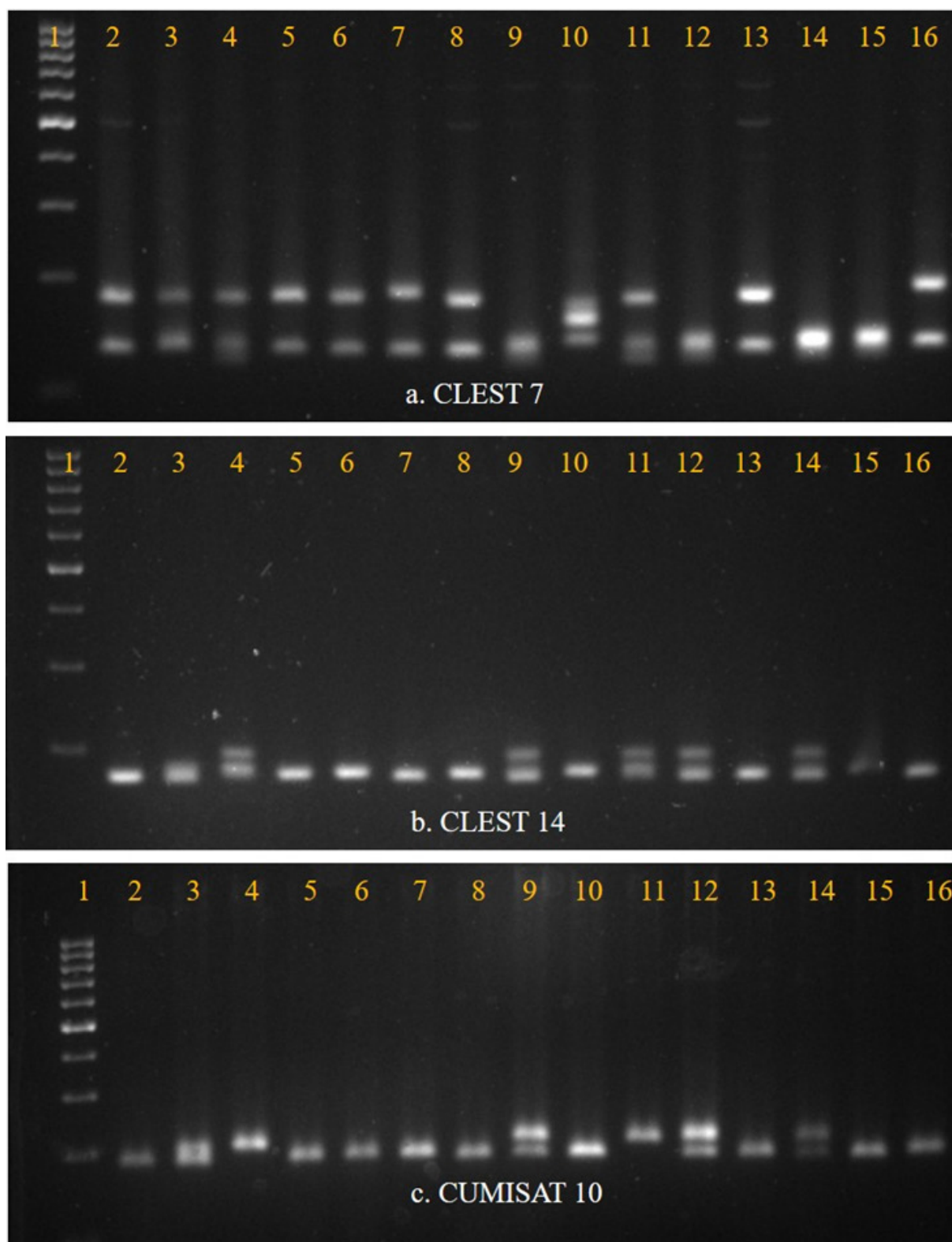


Fig. 4. SSR banding pattern of 15 genotypes: CLEST 7, CLEST 14 and CUMISAT 10 (1. 100bp ladder, 2. Punjab Haldi 1, 3. SLP 389/1, 4. Narendra Haldi 98, 5. IISR Pragati, 6. CO 2, 7. SC 61, 8. BSR 2, 9. Suvarna, 10. IISR Prathiba, 11. Acc. 849, 12. Varna, 13. Rajendra Sonia, 14. Mega Turmeric 1, 15. Duggirala Red, 16. Rajapuri)

Curcuma longa and guide effective utilization of turmeric genetic resources in breeding and conservation strategies.

Conclusion

The present study demonstrates the effectiveness of integrating RAPD, ISSR, and SSR marker systems to comprehensively assess genetic diversity among vegetative propagated turmeric genotypes. The combined use of dominant and co-dominant markers enabled the detection of a high level of polymorphism and facilitated the generation of genotype-specific molecular fingerprints, thereby overcoming the limitations associated with phenotypic characterization in clonally propagated crops. A key novelty of this investigation lies in the identification of diagnostic alleles capable of uniquely distinguishing several turmeric genotypes, including elite cultivars and accessions with close morphological resemblance.

Importantly, the outcomes of this study highlight the relevance of molecular fingerprinting in distinctness, uniformity, and stability (DUS) testing, varietal registration, and plant variety protection (PVP). By revealing genetic variation at the DNA level, the study strengthens the scientific basis for cultivar identification and legal protection in turmeric. Overall, the findings underscore the significance of deploying molecular tools alongside morphological and pedigree information to gain deeper insights into genetic diversity, thereby supporting the sustainable conservation, utilization, and genetic improvement of turmeric genetic resources.

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