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Research Article

SSR marker assisted assessment of genetic diversity among mango (*Mangifera indica* L.) genotypes

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Abstract
Mango (*Mangifera indica* L.) is one of the most economically important tropical fruit crops, valued for its nutritional quality, sensory attributes, and wide genetic variability. Assessment of genetic diversity among cultivated genotypes is essential for effective germplasm conservation and crop improvement. The present study was conducted to evaluate genetic diversity and relationships among 50 popular mango genotypes cultivated in Telangana, India, using simple sequence repeat (SSR) markers. A total of 60 SSR markers were screened, of which 42 produced clear and reproducible polymorphic amplification. These markers generated a total of 109 alleles. Allele size ranged from 100 bp (MiIIHR 06b) to 330 bp (MiIIHR 14b), with an average of 2.21 alleles per locus. Polymorphic information content (PIC) values ranged from 0.24 to 0.80, with a mean of 0.53, indicating moderate to high informativeness of the markers. Major allele frequency varied from 0.36 to 0.94, observed heterozygosity from 0.00 to 0.98, and gene diversity from 0.11 to 0.73, reflecting substantial genetic variation among the genotypes. Cluster analysis using Jaccard's similarity coefficient and UPGMA grouped the genotypes into three major clusters at a similarity coefficient of 0.62. The results demonstrate the effectiveness of SSR markers in discriminating mango genotypes and provide a valuable basis for selecting diverse parental material for mango breeding and improvement programmes.

Keywords: Mango, *Mangifera indica*, genetic diversity, SSR markers, molecular characterization, cluster analysis

INTRODUCTION

Mango (*Mangifera indica* L., 2n = 40) belongs to the family Anacardiaceae and is one of the most important tropical fruit crops cultivated in India, which harbours nearly 1000 cultivars and represents the world's largest mango germplasm resource (Mukherjee, 1950; Karihaloo *et al.,* 2003). Cultivated since prehistoric times, mango occupies approximately 2.29 million ha in India with a production of 20.44 million tonnes, and is widely grown across tropical and subtropical regions (Mitra, 2016; Yamanaka *et al.,* 2019). Major mango-producing countries include India, China, Thailand, Mexico and Pakistan, while within India, Uttar Pradesh, Andhra Pradesh, Odisha, Karnataka and Telangana are the principal mango-growing states (National Horticulture Database. 2023-24). India is recognized as the primary centre of origin and diversity, with domestication dating back nearly 4000 years and extending to the Malay Peninsula in Southeast Asia.

Mango fruits are rich in dietary fibre, antioxidant vitamins A and C, and vitamin B6, and contain bioactive compounds such as triterpenes and lupeol with anticancer properties. In addition, mango leaves are an important source of essential minerals and vitamins and are widely used in traditional medicine for the management of diabetes, asthma and renal disorders (Kumar *et al.,* 2021).

The mango genome size is estimated at 4.39 × 10^8 bp (Arumuganathan and Earle, 1991). Commercial mango cultivars exhibit high heterozygosity and region-specific adaptation, resulting in substantial genetic diversity. Although morphological descriptors have traditionally been used for diversity assessment (IPGRI, 2006), such traits are often environmentally influenced and may yield misleading inferences (Sankar *et al.,* 2011). DNA-based molecular markers provide a more precise

and reliable approach for genetic characterization (Varshney *et al.,* 2004). Among these, simple sequence repeat (SSR) markers are widely preferred due to their co-dominant inheritance, abundance and high reproducibility (Gupta and Varshney, 2000). Despite this, limited information is available on mango-specific SSR-based diversity studies. Telangana possesses rich mango germplasm conserved at the Fruit Research Station, Sangareddy, and the present study was undertaken to assess genetic diversity and relationships among popular mango cultivars of the region using SSR- markers.

MATERIALS AND METHODS

The experimental material used in the present study comprised of 50 (Table: 1-36 and 37-50 table and juicy cultivars, respectively) cultivars of mango were selected and taken from Fruit Research Station, Sangareddy, Telangana, India (**Table 1**). These cultivars represent widely grown and commercially important mango genotypes of the region.

DNA isolation and SSR analysis: Molecular characterization was carried out at the College of Horticulture, Sri Konda Laxman Telangana State Horticultural University, Rajendranagar; the Institute of Biotechnology, Professor Jayashankar Telangana State Agricultural University, Rajendranagar; and PRR Biotech Private Limited, Mehdipatnam, Hyderabad. Total genomic DNA was extracted from approximately 100 mg of fresh young leaf tissue using the cetyltrimethyl ammonium bromide (CTAB) method following Doyle and Doyle (1990). DNA quantity was measured using a biophotometer (Eppendorf, India), and quality was assessed by 1% agarose gel electrophoresis. DNA samples were diluted with TE buffer to a final concentration of 50 ng μl^{-1} and stored at −20°C until use.

PCR amplification was performed using 60 SSR markers (**Table 2**) following the protocol described by Sambrook and Russel (2012). The SSR primers were selected based on previously published reports (Ravishankar *et al.,* 2011; Begum *et al.,* 2012; Schnell *et al.,* 2005; Viruel *et al.,* 2005). Amplified products were resolved on 3% agarose gels prepared in 1× TBE buffer at 80 V using a horizontal gel electrophoresis unit, stained with ethidium bromide, and documented using a gel Bio-Rad gel documentation system.

*Data analysis:*Clear and reproducible SSR bands were scored as presence (1) or absence (0) to generate binary data. Genetic parameters, including polymorphic information content (PIC), number of alleles, major allele frequency and gene diversity, were calculated using PowerMarker v3.25. Cluster analysis and similarity matrix construction were performed using NTSYS-pc software version 2.02e (Rohlf, 1998) based on Jaccard's similarity coefficient, and a dendrogram was generated using the Unweighted Pair Group Method with Arithmetic Mean (UPGMA) to visualize genetic relationships among the genotypes.

RESULTS AND DISCUSSION

Genetic diversity among 50 mango genotypes was assessed using 60 SSR markers, of which 42 primers produced clear and reproducible polymorphic amplification (**Table 3**). These markers generated a total of 109 alleles, indicating a high level of allelic variation. Similar level of polymorphism was reported earlier by Wahdan *et al.* (2011), who observed polymorphic amplification in 36 of 42 SSR primers among Egyptian mango strains. Allele sizes ranged from 100 bp (MiIIHR 06b) to 330 bp (MiIIHR 14b), which is comparable with previously reported ranges of 90–370 bp (Begum *et al.,* 2012) and 100–400 bp (Anshuman Singh *et al.,* 2012) in mango.

The number of alleles per locus varied from two to four, with an average of 2.21 alleles per SSR marker. These results are consistent with earlier reports in mango by Schnell *et al.* (2006), Singh and Bhat (2009), Anshuman *et al.* (2012), Kumar *et al.* (2013) and Malathi *et al.* (2013), who reported allele numbers ranging from moderate to high across different germplasm sets. The polymorphic information content (PIC) values ranged from 0.24 to 0.80, with a mean of 0.53, indicating moderate to high discriminatory power of the SSR markers employed. Markers such as MiIIHR 19a, MiIIHR 02c, SSR-39, MiSHRS-32, MiIIHR 26a and MiIIHR 32a exhibited higher PIC values, demonstrating their effectiveness in distinguishing mango genotypes. Comparable PIC ranges have been reported by Begum *et al.* (2016) and Ravishankar *et al.* (2011) in mango, further validating the robustness of the marker system used in this study.

Major allele frequency ranged from 0.36 to 0.94, with a mean value of 0.65, corroborating earlier findings by Malathi *et al.* (2013). Observed heterozygosity varied widely from 0.00 to 0.98, with an average of 0.41, reflecting the highly heterozygous nature of mango. Similar heterozygosity trends have been reported in mango by Anju Bajpai *et al.* (2008), Malathi *et al.* (2013) and May Sandar Kyaing *et al.* (2019). Gene diversity values ranged from 0.11 to 0.73, with a mean of 0.45, consistent with previous studies in mango by Anju *et al.* (2008) and Lokesh *et al.* (2018), indicating substantial genetic variation among the evaluated genotypes. The gel images of SSR markers and banding pattern generated in all mango cultivars are given in **Fig 1-4.**

Cluster analysis based on Jaccard's similarity coefficient and UPGMA grouped the 50 mango genotypes into three major clusters at a similarity coefficient of 0.62 (**Table 4; Fig. 5**), revealing considerable genetic divergence could be attributed to the cross-pollinated nature of mango crop. Similarity coefficients ranged from 0.61 to 0.88, with the highest similarity observed between Mahamooda Vikarabad and Manjeera, followed by Ranitellakaya and Shajahan, and Baneshan and Vaddepalli Selection. Cluster I was the largest, comprising 43 genotypes further subdivided into three sub-clusters. Sub-cluster IA with 0.66 similarity comprised 21 cultivars, primarily table

Table 1. List of mango cultivars and collection site

S.No.	Genotypes	Sampling Unit	Collection Site
1	Dashehari 35	Mother Block FRS	Sangareddy, Telangana
2	Allampur Baneshan	Mother Block FRS	Sangareddy, Telangana
3	Asif Us Samar	Mother Block FRS	Sangareddy, Telangana
4	Azam Us samar	Mother Block FRS	Sangareddy, Telangana
5	Baneshan	Mother Block FRS	Sangareddy, Telangana
6	Chinna Suvarnarekha	Mother Block FRS	Sangareddy, Telangana
7	Dashehari	Mother Block FRS	Sangareddy, Telangana
8	Dilpasand	Mother Block FRS	Sangareddy, Telangana
9	Goa Bandar	Mother Block FRS	Sangareddy, Telangana
10	Himayath	Mother Block FRS	Sangareddy, Telangana
11	Jehangir	Mother Block FRS	Sangareddy, Telangana
12	Kaju	Mother Block FRS	Sangareddy, Telangana
13	Kalepahad	Mother Block FRS	Sangareddy, Telangana
14	Kesar	Mother Block FRS	Sangareddy, Telangana
15	Lalmuni	Mother Block FRS	Sangareddy, Telangana
16	Latif Us Samar	Mother Block FRS	Sangareddy, Telangana
17	Mahamooda Uppal	Mother Block FRS	Sangareddy, Telangana
18	Mahamooda Vikarabad	Mother Block FRS	Sangareddy, Telangana
19	Manjeera	Mother Block FRS	Sangareddy, Telangana
20	Mulgoa	Mother Block FRS	Sangareddy, Telangana
21	Nazeem Pasand	Mother Block FRS	Sangareddy, Telangana
22	Neeleshan	Mother Block FRS	Sangareddy, Telangana
23	Neelum	Mother Block FRS	Sangareddy, Telangana
24	Parasapalli Doodiya	Mother Block FRS	Sangareddy, Telangana
25	Pulihora	Mother Block FRS	Sangareddy, Telangana
26	Ranitellakaya	Mother Block FRS	Sangareddy, Telangana
27	Rumani	Mother Block FRS	Sangareddy, Telangana
28	Sannakulu	Mother Block FRS	Sangareddy, Telangana
29	Shajahan	Mother Block FRS	Sangareddy, Telangana
30	Shendriya	Mother Block FRS	Sangareddy, Telangana
31	Sora	Mother Block FRS	Sangareddy, Telangana
32	Suvarnarekha	Mother Block FRS	Sangareddy, Telangana
33	Totapari	Mother Block FRS	Sangareddy, Telangana
34	Vaddepalli Selection	Mother Block FRS	Sangareddy, Telangana
35	Vanraj	Mother Block FRS	Sangareddy, Telangana
36	Yerra Mulgoa	Mother Block FRS	Sangareddy, Telangana
37	Aryavrtham Irsalu	Mother Block FRS	Sangareddy, Telangana
38	Cherukurasam	Mother Block FRS	Sangareddy, Telangana
39	Chinnarasam	Mother Block FRS	Sangareddy, Telangana
40	Kothapalli Kobbari	Mother Block FRS	Sangareddy, Telangana
41	Meetavari Peechumanu	Mother Block FRS	Sangareddy, Telangana
42	Nagulapalli Irsalu	Mother Block FRS	Sangareddy, Telangana
43	Navaneetham	Mother Block FRS	Sangareddy, Telangana
44	Panakalu	Mother Block FRS	Sangareddy, Telangana
45	Panchavarnam	Mother Block FRS	Sangareddy, Telangana
46	Pandurivari Mamidi	Mother Block FRS	Sangareddy, Telangana
47	Peddarasam	Mother Block FRS	Sangareddy, Telangana
48	Yellow Arati	Mother Block FRS	Sangareddy, Telangana
49	Yerra Arati	Mother Block FRS	Sangareddy, Telangana
50	Zardalu	Mother Block FRS	Sangareddy, Telangana

Note: 1-36 and 37-50 table and juicy cultivars, respectively

Table 2. SSR markers used for DNA amplification in 50 mango genotypes

S. No.	Marker	Forward	Reverse
1	MiIlHR 01a	GGATGCACAACAACAAGCAC	TCAGCAAGCAATCCCTTCTT
2	MiIlHR 02c	CCCCAACATTTCATAAACACA	CCTCCTTACATGCCTCCTTG
3	MiIlHR 03a	GTCGATGCCTGGAATGAAGT	AAGCATCGAACAGCTCCAAT
4	MiIlHR 04c	CGTTTTTGACCCTCTTGAGC	CCGCATACTTCCCTTCACAT
5	MiIlHR 05c	CTCTCCCTCACTTGCTCCAC	AGACCACCGACAACGAAAAC
6	MiIlHR 06 b	CGCCGAGCCTATAACCTCTA	ATCATGCCCTAAACGACGAC
7	MiIlHR 08 b	TGCTCTCTACTGCCCCGTAT	GTCACACCAATCGGGAATCT
8	MiIlHR 11a	CAGTGAAACCACCAGGTCAA	TGGCCAGCTGATACCTTCTT
9	MiIlHR 12a	GCCCCATCAATACGATTGTC	ATTTCCCACCATTGTCGTTG
10	MiIlHR 13	CCCAGTTCCAACATCATCAG	TTCCTCTGGAAGAGGGAAGA
11	MiIlHR 14 b	CCGAAACAACTCTTCCTCCA	TGCTCTCTGGCCTCTTCTTC
12	MiIlHR 15b	CTAACCATTCGGCATCCTCT	TCTGTGATAGAATGGCAAAAGAA
13	MiIlHR 16a	TTTCACTTGGTTCTGGATTGC	ATTTCCCACCATTGTCGTTG
14	MiIlHR 17 b	GCTTGCTTCCAACTGAGACC	GCAAAATGCTCGGAGAAGAC
15	MiIlHR 18 b	TCTGACGTCACCTCCTTTCA	ATACTCGTGCCTCGTCCTGT
16	MiIlHR 19a	TGATATTTTCAGGGCCCAAG	AAATGGCACAAGTGGGAAAG
17	MiIlHR 22a	TGGCCGAACTAGCAAACTCT	CCCCATTTCGAGAAAATTCC
18	MiIlHR 23a	TCTGACCCAACAAAGAACCA	TCCTCCTCGTCCTCATCATC
19	MiIlHR 24 b	GCTCAACGAACCCAACTGAT	TCCAGCATTCAATGAAGAAGTT
20	MiIlHR 25a	TGTGAGTCTCCGTTTGTGCT	CCCTCTCATTTTCCCAGTCA
21	MiIlHR 26a	GCGAAAGAGGAGAGTGCAAG	TCTATAAGTGCCCCCTCACG
22	MiIlHR 28c	GCGGTCGCAGACAAATTCTATA	ACAACTCGAGATTGTCACATCTTT
23	MiIlHR 29a	CGATGAGGATGGTTGGTTTT	CATCAACAGTCGCCATCAAT
24	MiIlHR 30a	AGCTATCGCCACAGCAAATC	GTCTTCTTCTGGCTGCCAAC
25	MiIlHR 31 b	TTCTGTTAGTGGCGGTGTTG	CACCTCCTCCTCCTCCTCTT
26	MiIlHR 32a	TGGTGGTGTTTGTTTGCAGT	ACCACCCGCAGTATTGAAAG
27	MiIlHR 33a	GAAGCACTTGTCTCCCTTGC	CCTCACACTCCTCCACCTGT
28	MiIlHR 34 b	CTGAGTTTGGCAAGGGAGAG	TTGATCCTTCACCACCATCA
29	MiIlHR 35a	TGGTGAAGCTTGTTGTCTGC	TGGCTTGACTGTTTTTCAGC
30	MiIlHR 36 b	TCTATAAGTGCCCCCTCACG	ACTGCCACCGTGGAAAGTAG
31	SSR-15	TTTACCAAGCTAGGGTCA	CACTCTTAAACTATTCAACCA
32	SSR-18	CGTCATCCTTTACAGCGAACT	CATCTTTGATCATCCGAAAC
33	SSR-20	CGCTCTGTGAGAATCAAATGGT	GGACTCTTATTAGCCAATGGGATG
34	SSR-36	CCTCAATCTCACTCAACA	ACCCCACAATCAAACTAC
35	SSR-39	TGTCTACCATCAAGTTCG	GCTGTTGTTGCTTTACTG
36	SSR-46	TCATTGCTGTCCCTTTTC	ATCGCTCAAACAATCC
37	SSR-52	AAAAACCTTACATAAGTGAATC	CAGTTAACCTGTTACCTTTTT
38	SSR-55	ATATCTCACGGCTTCGAATGA	TATTAATTTTCACAGACTATGTTCA
39	SSR-57	CATGGAGTTGTGATACCTAC	CAGAGTTAGCCATATAGAGTG
40	SSR-60	ATTATTTACCCTACAGAGTGC	GTATTATCGGTAATGTCTTCAT
41	SSR-61	AAAGATAGCATTTAATTAAGGA	GTAAGTATCGCTGCTGTTTGTTATT
42	SSR-65	ATAGATTCATATCTTCTTGCAT	TATAAATTATCATCTTCACTGC
43	SSR-82	TCTGACCCAACAAAGAACCA	TCCTCCTCGTCCTCATCATC
44	SSR-83	AGCTATCGCCACAGCAAATC	GTCTTCTTCTGGCTGCCAAC
45	SSR-84	TCTATAAGTGCCCCCTCACG	ACTGCCACCGTGGAAAGTAG
46	SSR-88	CTGAGTTTGGCAAGGGAGAG	TTGATCCTTCACCACCATCA
47	MiSHRS-1	TAACAGCTTTGCTTGCCTCC	TCCGCCGATAAACATCAGAC
48	MiSHRS-4	CCACGAATATCAACTGCTGCC	TCTGACACTGCTCTTCCACC
49	MiSHRS-32	TTGATGCAACTTTCTGCC	ATGTGATTGTTAGAATGAACTT
50	MiSHRS-36	GTTTTCATTCTCAAAATGTGTG	CTTTCATGTTCATAGATGCAA
51	MiSHRS-44	AACCCATCTAGCCAACCC	TTGACAGTTACCAAACCAGAC
52	MiSHRS-48	TTTACCAAGCTAGGGTCA	CACTCTTAAACTATTCAACCA
53	LMMA-1	ATGGAGACTAGAATGTACAGAG	ATTAAATCTCGTCCACAAGT
54	LMMA-2	AAATAAGATGAAGCAACTAAAG	TTAGTGATTTTGTATGTTCTTG
55	LMMA-4	AAAAACCTTACATAAGTGAATC	CAGTTAACCTGTTACCTTTTT
56	LMMA-6	ATATCTCAGGCTTCGAATGA	TATTAATTTTCACAGACTATGTTCA
57	LMMA-7	ATTTAACTCTTCAACTTTCAAC	AGATTTAGTTTTGATTATGGAG
58	LMMA-8	CATGGAGTTGTGATACCTAC	CAGAGTTAGCCATATAGAGTG
59	LMMA-9	TTGCAACTGATAACAAATATAG	TTCACATGACAGATATACACTT
60	MngSSR-14	TCATTAAGCTGTGGCAACCA	CATTGCATAGATGTGGTCATT

Table 3. Polymorphic SSR markers used for characterization of 50 mango genotypes

S. No.	Marker	Product size in bp	Number of alleles	PIC values	Major allele frequency	Heterozygosity	Gene diversity
1	MiIIHR 01a	240-250	2	0.45	0.84	0.32	0.27
2	MiIIHR 02c	190-220	3	0.76	0.38	0.40	0.66
3	MiIIHR 04c	160-180	2	0.38	0.76	0.48	0.36
4	MiIIHR 05c	190-210	2	0.36	0.74	0.52	0.38
5	MiIIHR 06 b	100-120	2	0.46	0.86	0.28	0.24
6	MiIIHR 12a	170-180	2	0.38	0.76	0.48	0.36
7	MiIIHR 13	170-190	2	0.53	0.71	0.30	0.41
8	MiIIHR 14 b	320-330	2	0.24	0.64	0.72	0.46
9	MiIIHR 15b	130-160	3	0.69	0.71	0.38	0.45
10	MiIIHR 16a	210-220	2	0.47	0.65	0.54	0.46
11	MiIIHR 17 b	220-240	2	0.44	0.67	0.46	0.44
12	MiIIHR 18 b	170-185	2	0.56	0.94	0.00	0.11
13	MiIIHR 19a	170-210	4	0.80	0.36	0.69	0.73
14	MiIIHR 23a	130-155	3	0.50	0.48	0.98	0.62
15	MiIIHR 24 b	240-250	2	0.31	0.64	0.64	0.46
16	MiIIHR 25a	145-150	2	0.54	0.65	0.34	0.46
17	MiIIHR 26a	140-160	3	0.71	0.49	0.56	0.63
18	MiIIHR 28c	120-130	2	0.57	0.59	0.30	0.48
19	MiIIHR 30a	190-200	2	0.61	0.59	0.26	0.48
20	MiIIHR 31 b	250-265	2	0.52	0.73	0.30	0.39
21	MiIIHR 32a	200-210	2	0.71	0.60	0.08	0.48
22	MiIIHR 33a	160-170	2	0.52	0.53	0.38	0.50
23	MiIIHR 36 b	220-230	2	0.52	0.70	0.32	0.42
24	SSR-20	300-310	2	0.39	0.74	0.48	0.38
25	SSR-36	230-240	2	0.62	0.55	0.30	0.50
26	SSR-39	170-190	3	0.75	0.52	0.40	0.57
27	SSR-46	190-200	2	0.56	0.68	0.28	0.44
28	SSR-52	120-210	2	0.48	0.58	0.44	0.49
29	SSR-55	120-130	2	0.42	0.77	0.42	0.35
30	SSR-57	260-270	2	0.38	0.65	0.62	0.46
31	SSR-65	240-260	3	0.56	0.54	0.86	0.60
32	SSR-82	120-140	3	0.56	0.56	0.82	0.58
33	SSR-83	190-200	2	0.50	0.60	0.40	0.48
34	SSR-88	180-200	2	0.47	0.83	0.30	0.28
35	MiSHRS-1	190-200	2	0.67	0.75	0.06	0.38
36	MiSHRS-4	150-160	2	0.60	0.70	0.20	0.42
37	MiSHRS-32	190-200	2	0.74	0.52	0.04	0.51
38	MiSHRS-36	180-190	2	0.59	0.69	0.24	0.43
39	MiSHRS-48	210-220	2	0.65	0.57	0.18	0.49
40	LMMA-6	110-120	2	0.51	0.78	0.28	0.34
41	LMMA-8	250-260	2	0.25	0.58	0.72	0.49
42	MngSSR-14	170-180	2	0.63	0.51	0.22	0.50
	Total/Mean	**-**	**109**	**0.53**	**0.65**	**0.41**	**0.45**

purpose varieties. Notably, the highest genetic similarity within this group was observed between Ranitellakaya and Shajahan (86%), followed by Baneshan and Vaddepalli Selection (83%). The inclusion of the new clone Dashehari-35 alongside Dashehari (0.73 similarity) validates its genetic identity for cultivation in Telangana. Sub-cluster IB at 0.67 similarity a heterogeneous group of 20 table and juicy cultivars. Mahamooda Vikarabad and Manjeera exhibited the highest similarity (88%), indicating identical allelic profiles. Sub-cluster IC with 0.70 similarity contained two prominent juicy cultivars, chinna rasam and Navaneetham. While Cluster II included four genotypes and Cluster III comprised three genotypes.

The selection and hybridization programmes in mango can be affected based on the clustering. The clustering pattern revealed that genotypes did not segregate strictly according to their utility (table or juicy types) at

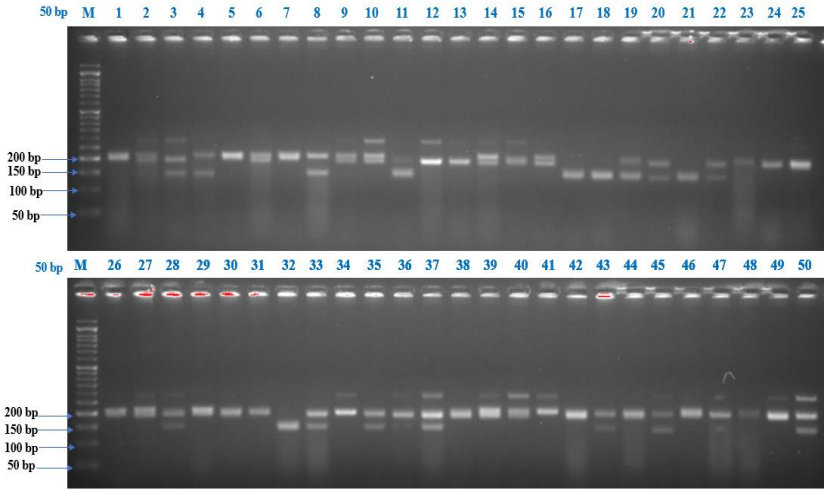

Fig. 1. SSR amplification profile of 50 mango genotypes generated using primer MillHR 19a

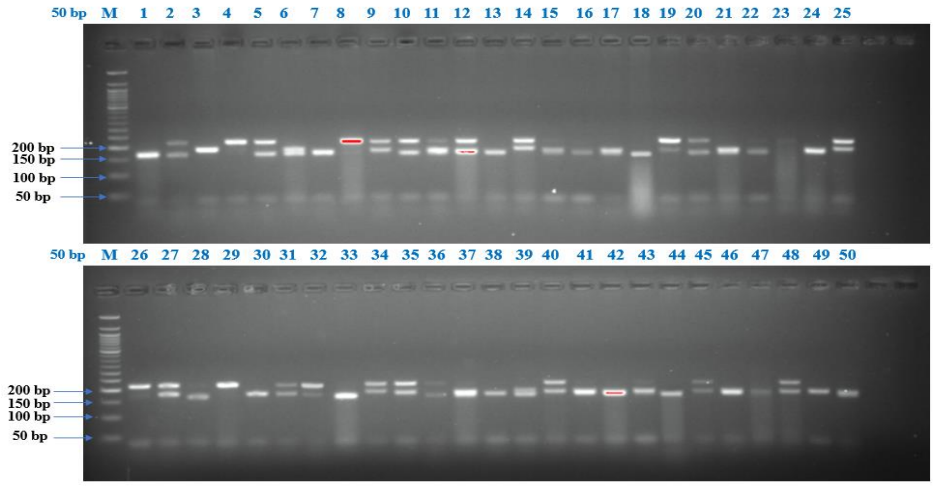

Fig. 2. SSR amplification profile of 50 mango genotypes generated using primer MillHR 02c

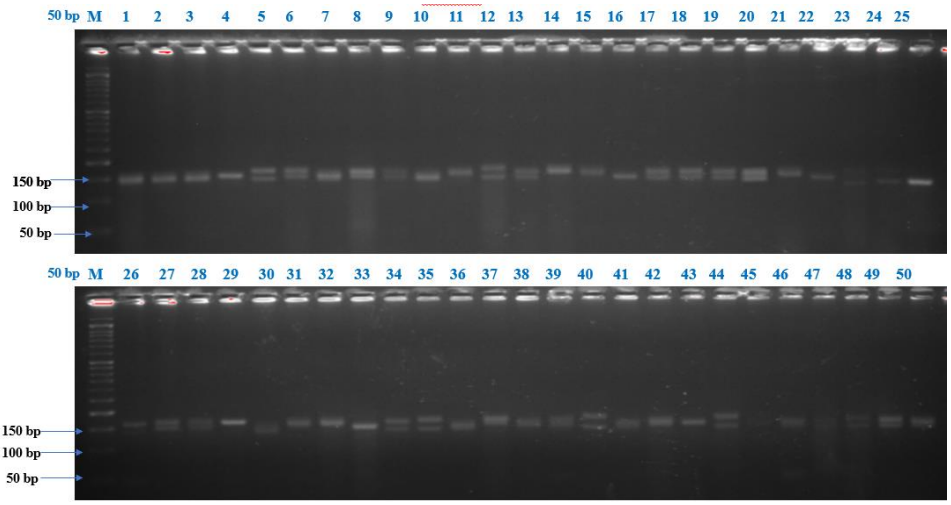

Fig. 3. SSR amplification profile of 50 mango genotypes generated using primer MillHR 26a

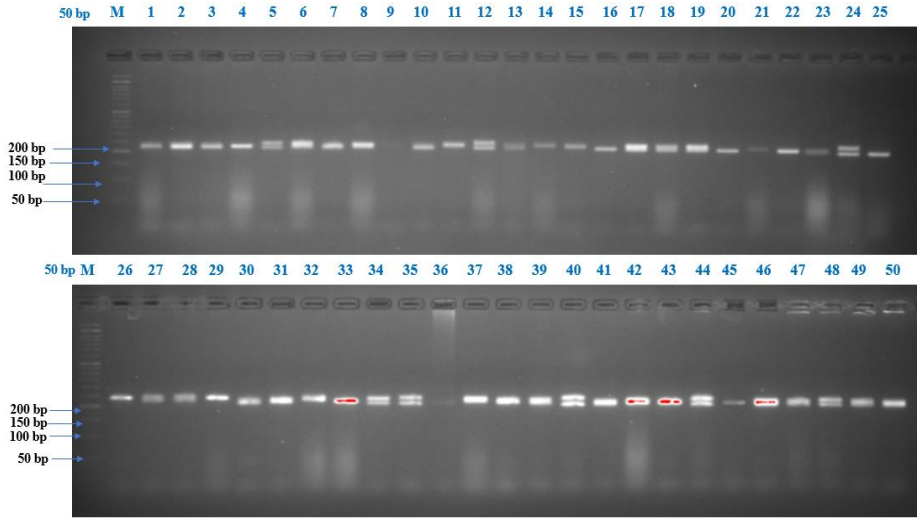

Fig. 4. SSR amplification profile of 50 mango genotypes generated using primer SSR-36. (Refer Table 1 for name of the genotypes)

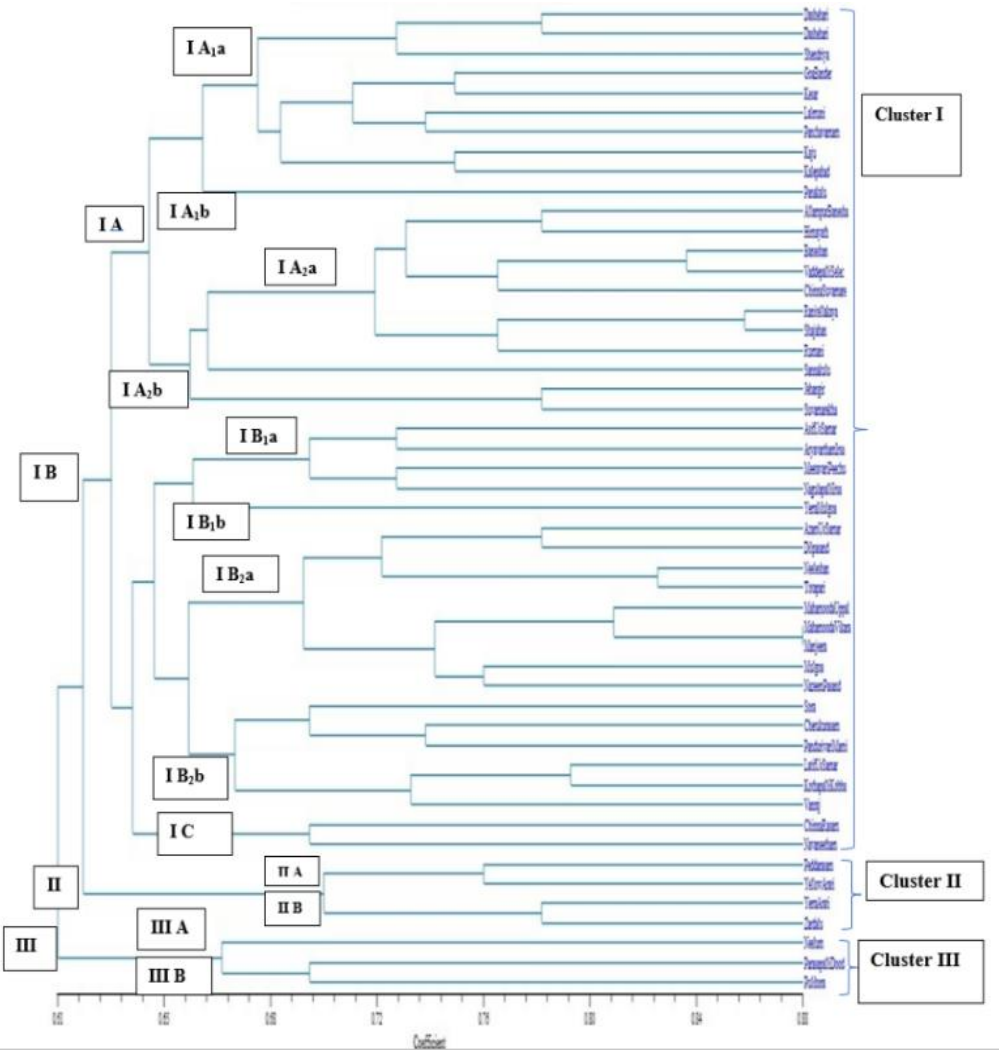

Fig. 5. Dendrogram constructed using Jaccard's similarity coefficient based on UPGMA

Table 4. Cluster-wise grouping of mango genotypes

Cluster		Genotypes	Number of genotypes
Cluster IA (21 genotypes)	Cluster IA_1a	Dashehari-35, Dashehari, Goa Bander, Kaju, Kalepahad, Kesar, Lalmuni, Panchavarnam, Shendriya	9
	Cluster IA_1b	Panakalu	1
	Cluster IA_2a	Allampur Baneshan, Baneshan, Chinna Suvarnarekha, Himayath, Ranitellakaya, Rumani, Vaddepalli Selection, Shajahan	8
	Cluster IA_2b	Jehangir, Sannakulu, Suvarnarekha	3
Cluster IB (20 genotypes)	Cluster IB_1a	Aryavartham Irsalu, Asif Us Samar, Meetavari Peechumanu, Nagulapalli Irsalu	4
	Cluster IB_1b	Yerra Mulgoa	1
	Cluster IB_2a	Azam Us Samar, Dilpasand, Mahamooda Uppal, Mahamooda Vikarabad, Manjeera, Mulgoa Nazeem Pasand, Neeleshan, Totapari,	9
	Cluster IB_2b	Cherukurasam, Kothapalli Kobbari, Latif Us Samar, , Pandurivari Mamidi, Sora, Vanraj	6
Cluster IC (2 genotypes)		Chinna Rasam, Navaneetham	2
Cluster II (4 genotypes)	Cluster II A_1	Pedda Rasam, Yellow Arati	2
	Cluster IIA_2	Yerra Arati, Zardalu	2
Cluster III (3 genotypes)	Cluster $IIIA_1$	Neelum	1
	Cluster $IIIA_2$	Parasapalli Doodiya, Pulihora	2

the major cluster level, but rather at sub-cluster levels. Understanding the genetic diversity among the varieties is important in mango production, improvement and breeding, knowledge on this field can supply useful information for further scientific progress in developing new genotypes (Rajwana *et al*., 2010). Hybrids such as Manjeera and Neeleshan grouped closely with one of their parental lines, while the other parent was positioned in a different cluster, indicating considerable parental divergence. Similar observations were reported by Shareefa (2008) and Malathi *et al.* (2018). Genotypes originating from the same geographical region were distributed into different sub-clusters. This pattern indicates that the clustering of cultivars was largely independent of geographical boundaries, demonstrating that geographic isolation alone is not the sole determinant of genetic diversity. These findings are in agreement with Eiadthong *et al.* (2000). The inability to distinctly separate table and juicy cultivars corroborates earlier reports by Rahman *et al.* (2007); Anju *et al.* (2008); Kumar *et al.* (2013); Ariffin *et al.* (2015); Begum *et al.* (2016) and Lokesh *et al.* (2018) in mango.

Overall, the SSR-based clustering and diversity parameters highlight substantial genetic variability among mango genotypes of Telangana, underscoring the effectiveness of SSR markers in resolving genetic relationships and identifying diverse parental material for mango improvement programmes.

The present study demonstrates that SSR markers are highly effective in resolving genetic diversity and relationships among mango genotypes cultivated in Telangana. The moderate to high polymorphism detected, particularly with markers such as MiIIHR 19a, MiIIHR 02c, SSR-39, MiSHRS-32, MiIIHR 26a and MiIIHR 32a, highlights their utility for molecular characterization and germplasm management. UPGMA-based clustering revealed substantial genetic divergence among genotypes, with grouping patterns independent of fruit usage type and geographical origin. The use of a larger number of SSR markers with broader genome coverage could enable a more accurate assessment of genetic diversity. Overall, the findings confirm the robustness of SSR-based diversity analysis and provide a reliable foundation for the selection of genetically diverse parental material, conservation of mango germplasm, and future applications in mango breeding, genetic purity assessment and marker-assisted improvement programmes.

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