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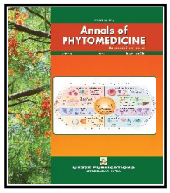

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Association mapping of physicochemical and antinutritional traits in Mango (*Mangifera indica* L.) cultivars of Telangana using SSR markers

B. Soujanya*◆, A. Kiran Kumar, S. Vanisri***, M. Sreedhar*** and A. Bhagwan****

** College of Horticulture, SKLTS Horticultural University, Rajendranaga-500030, Telangana, India*
*** SKLTS Horticultural University, Mulugu, Siddipet-502279, Telangana, India*
**** PJTS Agricultural University, Rajendranagar-500030, Telangana, India*

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Abstract

Mango (*Mangifera indica* L.) exhibits wide variation in fruit quality attributes, which are complex and quantitatively inherited, necessitating molecular tools for effective genetic improvement. The present investigation aimed to evaluate physicochemical traits, bioactive compounds and identify marker trait associations in fifty mango cultivars popularly grown in Telangana State, India using simple sequence repeat (SSR) markers. Twenty five post-harvest physicochemical and biochemical traits were assessed over two seasons, revealing significant genotypic variation. Fruit weight ranged from 131.16 to 770.64 g, pulp content from 47.20 to 94.20%, pulp-to-stone ratio from 1.30 to 7.32 and total soluble solids (TSS) from 12.75 to 21.10 °Brix. Considerable variation was also observed in nutritionally important bioactive compounds with total phenols ranging from 64.72 to 173.20 mg GAE/100 g, total flavonoids from 24.03 to 331.11 mg QE/100 g, β-carotene from 1.11 to 2.81 mg/100 g and total antioxidant activity from 91.74 to 326.38 µg/100 g. Crude fibre content varied between 3.10 and 7.01 g/100 g, indicating differences in dietary fibre and potential antinutritional effects. Molecular characterization using 60 SSR primers identified 42 polymorphic markers generating 109 alleles, of which 93 were polymorphic 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. Marker trait association analysis revealed significant associations for 18 traits involving 24 SSR markers explaining phenotypic variation (R^2) from 0.029 to 0.218. Markers LMMA 8, SSR 88, MiIIHR 33a, MiSHRS 36, MiIIHR 30a and MiSHRS 4 showed multi trait associations. These findings provide valuable molecular resources for marker assisted selection and mango quality improvement, subject to further validation in mapping populations.

1. Introduction

Mango is the most important and choicest fruit crop of tropical and subtropical world and known as “King of fruits” and “super fruit” belongs to the Anacardiaceae family and have the chromosome number 2n = 40 and n = 20. The genome size of mango is 4.39 × 108 bp in size (Arumuganathan and Earle, 1991). It is a delicious, juicy fruit and nutritionally rich with unique flavour, fragrances, taste and having health promoting qualities. Mangoes are rich in antioxidants, and their vitamin A precursors support vision, immunity, and reactive oxygen species scavenging according to Priyavadhana and Pandarinathan (2023). Mango is naturally rich in bioactive compounds like, fibre, antioxidants, vitamins A and C, and vitamin B6. The fruit also contains substances called triterpene and lupeol, which inhibit skin and colon cancer (Lemmens *et al.,* 2013; Rincon and Keer, 2010; Sogi and Ibrahim, 2012). Selvan (2006) investigated the physicochemical characteristics of hybrids and noted appreciable variation with respect to attributes like, fruit weight, fruit length, fruit width, peel thickness, TSS, acidity and TSS: acid ratio. The major phenolic compounds in mango pulp include mangiferin, quercetin, and ferulic acid. Mango is a rich source of polyphenols such as mangiferin, gallic acid, gallotannins, quercetin, isoquercetin, ellagic acid, and β-glucogallin, with gallic acid being the most abundant in the mesocarp (Singh *et al.*, 2022). These bioactive compounds provide multiple health benefits, including antioxidant, anti-inflammatory, anticarcinogenic, antidiabetic, immunomodulatory effects, and protection against cardiovascular diseases (Masibo and He, 2008; Hu *et al.*, 2021). Much research has examined the bioactive components of various mango cultivars; Muralidhara *et al.* (2019); Akhter *et al.* (2010); Hamdard *et al.* (2004) and Rajput and Pandey (1997) are only a few of these investigations.

The success of any crop improvement program depends mainly on nature and magnitude of genetic variability available in crop germplasm. In India, relatively few cultivars are traded internationally due to the highly specific requirements for cultivars with favorable colour, storage, and shipping traits and most of them being selections from naturally occurring open-pollinated seedlings (Iyer and Degani, 1997). Each of the main varieties of mango has a unique taste and flavor. Identification of mango cultivars generally based on morphological descriptors (IPGRI, 1989), but this type of identification is inaccurate due to the influence of the climatic conditions and the limiting number of discriminating traits. Thus, molecular characterization of cultivars has been widely used in detecting genetic diversity and relationship, identification and validation of varieties, association studies, phylogenetic analysis

Corresponding author: Dr. B. Soujanya
College of Horticulture, SKLTS Horticultural University, Rajendranaga-500030, Telangana, India
E-mail: bsoujanya129@gmail.com
Tel.: +91-9989431077

and DNA finger printing with different PCR based markers, among these microsatellites or simple sequence repeats (SSR's) gained much importance due to their multi allelic, co-dominant inheritance, good genome coverage and relative abundance.

In selection process for crop improvement, knowledge of association of various traits is the most important tool (Desai *et al*., 1994). The use of molecular markers supports the study of marker trait associations of biological and agronomic traits of interest on diverse genetic material (Khushboo *et al.,* 2018). Genome wide association mapping of 17 critical pomological traits in 60 mango cultivars by using 87 polymorphic SSR markers and they reported that a set of five genic-SSR markers (p<0.1) are significantly associated (r^2 = 19.92%) with six critical pomological traits (Lal *et al.,* 2017). In mango, information on genetic diversity and association of molecular markers with any morphological, agronomic and fruit quality traits is very meager (Padmakar *et al*., 2017). The present study was undertaken to assess genetic diversity and identification of marker trait associations for physicochemical traits in fifty mango cultivars grown in Telangana State

2. Materials and Methods

2.1 Collection of samples

The plant material used in the present investigation consisted of fifty mango cultivars collected from the Fruit Research Station, Sangareddy, Sri Konda Laxman Telangana State Horticultural University, Telangana. Mango fruits were harvested at full physiological maturity as determined by the °Brix values specific to each cultivar. The harvested fruits were washed, graded, weighed and packed in cartons and were immediately transported to the experimental laboratory for further analysis. Young, healthy leaves were collected from each cultivar for the isolation of total genomic DNA. The experiments were conducted at the College of Horticulture, Sri Konda Laxman Telangana State Horticultural University; the MFPI Quality Control Laboratory, Institute of Biotechnology, Professor Jayashankar Telangana State Agricultural University, Rajendranagar; and PRR Biotech Private Limited, Mehdipatnam, Hyderabad during the academic years 2018 to 2019, 2019 to 2020 and 2020 to 2021.

2.2 Estimation of physicochemical characters

Fifty mango cultivars were recorded for 25 physicochemical traits such as physiological loss in weight (PLW %), firmness (kg/cm^2), DA meter reading, fruit length (cm), fruit width (cm), fruit thickness (cm), fruit weight (g), peel per cent (%), pulp per cent (%), stone per cent (%), pulp to peel ratio, pulp to stone ratio, shelf-life (days), total soluble solids (°Brix), titratable acidity (%), brix-acid ratio, vitamin C (mg/100 g), reducing sugars (%), total sugars (%), non-reducing sugars (%), total phenols (mg GAE/100 g), total flavonoid content (mg quercetin equivalent/100 g), beta carotene (mg/100 g), total antioxidant activity (µg/100 g) and crude fibre (g/100 g) during two consecutive years 2018 to 2019 and 2019 to 2020. The mean of five randomly selected fruits in each variety was used for the analysis. Fresh pulp of each cultivar was weighed as required for different analyses.

Physiological loss in weight was calculated based on loss of weight in relation to the initial weight and expressed in percentage. Firmness was measured using a penetrometer, DA reading was taken using a DA meter, fruit length, width and thickness were measured using vernier callipers and fruit weight was recorded using an electronic balance. Peel, pulp and stone per cent were calculated based on their respective weights divided by fruit weight. Pulp to peel ratio and pulp to stone ratio were calculated by taking the total weight of pulp in relation to the weight of peel and stone, respectively. All varieties were scrutinized for any visible symptoms of spoilage, and the end of shelf-life was considered when 30 per cent of the fruits showed over-ripening or spoilage symptoms.

The biochemical traits such as total soluble solids (TSS) were measured using a refractometer, acidity was determined by IS 13844:2003 method and brix acid ratio was calculated by dividing the TSS with the acid value. Vitamin C was estimated by the AOAC (1997) method. Reducing sugars, total sugars and non-reducing sugars were determined by the procedure given by Lane and Eynon (1965). Total phenolic compounds were quantified using the Folin-Ciocalteu method given by Singleton and Rossi (1965). Total flavonoid content was determined by aluminium chloride colorimetric method described by Park *et al.* (2008) using quercetin as a standard. Beta carotene content was estimated using the method given by Srivastavaand Sanjeev Kumar (2002). Total antioxidant activity was determined according to the TBARS method as per the reference given by Ottolenghi (1959) and crude fibre content was estimated by the AOAC (1995) method.

2.3 Molecular characterization and marker trait associations

High quality genomic DNA was isolated from young leaves of all fifty cultivars using the CTAB (cetylhexadecyl-trimethyl ammonium bromide) method following the protocol of Doyle and Doyle (1990) with slight modifications in buffer composition and concentration. The isolated DNA was quantified using a Nanodrop as well as agarose gel electrophoresis and the final concentration was adjusted to 50 ng/µl for PCR reactions. The isolated DNA from fifty cultivars was subjected to molecular characterization using a set of 60 SSR primers based on previously reported studies (Ravishankar *et al.,* 2011; Begum *et al.,* 2012; Schnell *et al.,* 2005; Viruel *et al.,* 2005).

PCR amplification was performed in a gradient thermocycler with an initial denaturation step of 4 min, followed by 35 cycles each consisting of denaturation at 94°C for 1 min, annealing at 49°C-55°C for 1 min and extension at 72°C for 2 min. The final extension was carried out at 72°C for 7 min. The PCR products were then held at 4°C for 10 min. Amplification products were separated on 3 % agarose gel electrophoresis. A molecular weight marker, *i.e.,* a 50 bp DNA ladder was loaded alongside the SSR reactions. The SSR-PCR bands were visualized under an ultraviolet transilluminator and photographed using a gel documentation unit.

Allelic data generated from 42 polymorphic SSR markers along with 25 quantitative and qualitative traits were subjected to marker trait association analysis. The data thus generated were used for the identification of marker trait associations. Markers with a p value - ≤0.05 were considered significant for the respective traits.

2.4 Data analysis

All physicochemical characters were subjected to a completely randomized design with three replications and the level of significance was tested at 5% using the F test (Panse and Sukhatme, 1989) in WINDOWSTAT software version 9.2. The SSR bands were counted and scored as one for their presence or zero for their absence across

all genotypes. A total of 60 primers were used to generate binominal data, which were compiled using an Excel spread sheet. Parameters such as polymorphic information content, number of alleles, major allele frequency, and gene diversity were calculated using Power Marker v3.25.

The binary matrix data were analysed using NTSYS-pc (Numerical Taxonomy and Multivariate Analysis System) software version 2.02e (Rohlf, 1998). Jaccard's similarity coefficient was used and a dendrogram was constructed using the unweighted paired group method with arithmetic mean (UPGMA) to estimate genetic distances and phylogenetic relationships among individual genotypes. Marker trait associations for all characters were analysed using TASSEL (Trait Analysis by Association, Evaluation and Linkage) version 3.2 software (Bradbury *et al*., 2007).

3. Results

The results of the present study findings on evaluation of fifty mango genotypes for 25 post-harvest quantitative and qualitative traits, molecular characterization by using SSR primers and the combined analysis of phenotypic traits and polymorphic SSR allelic data enabled marker trait association studies, providing insights into the genetic basis of important post-harvest attributes.

3.1 Physicochemical characters

The evaluation of fifty mango genotypes for twenty-five post-harvest traits revealed significant differences among all the cultivars, indicating the presence of wide variability. The mean performance of physicochemical characters of the mango cultivars is presented in Table 1a, 1b, 1c, 1d. Among all the cultivars, Shajahan (4.21 %) recorded minimum physiological loss in weight, Mahamooda Uppal (2.55 kg/cm^2) exhibited the highest firmness, whereas maximum fruit length and fruit thickness were recorded in Ranitellakaya (13.24 cm and 12.14 cm, respectively), highest fruit width was recorded in Shajahan (11.66 cm). Whereas, Sora, Ranitellakaya, Shajahan and Nazeem Pas and significantly had maximum fruit weight (770.64 g, 638.45 g, 574.91 g and 506.80 g, respectively), Baneshan (9.20%) recorded minimum peel per cent. However, significantly minimum stone per cent was observed in Ranitellakaya (10.21%), Pulp per cent was observed maximum in Sora (94.26%). Baneshan (8.48) obtained highest pulp to peel ratio whereas, Vaddepalli Selection (7.32) recorded maximum pulp to stone ratio. Shelf-life was recorded maximum in Baneshan (7.50 days). Navaneetham (21.10 ºB) had the highest TSS, Allampur Baneshan (0.18%) recorded lowest titrable acidity. Zardalu (78.57) had the highest brix: acid ratio, Allampur Baneshan (31.97 mg/100 g) exhibited maximum vitamin C content, total sugars were obtained maximum in Pulihora (9.81%), reducing sugars were recorded maximum in Allampur Baneshan (4.90%), non-reducing sugars were found to be highest in Pulihora (5.80%), Mahamooda Vikarabad (173.20 mg GAE/100 g) recorded maximum total phenolics content, Yerra Mulgoa (331.11 mg QE/100 g) had maximum total flavonoid content, Beta carotene content was recorded maximum in Lalmuni (2.81 mg/100 g) and maximum total antioxidant activity obtained in Dashehari-35 (326.38 µg/100 g), crude fibre content was significantly recorded maximum in juicy cultivars, *viz*., NagulapalliIrsalu (7.01 g/100 g), YerraArati (6.65 g/100 g) and Yellow Arati (6.53 g/100 g). The present results were in agreement with the reports of Mamiro *et al*. (2007); Othman and Mbago (2009); Abdulrahm (2013) and Ubwa *et al*. (2014) in mango.

Table 1(a): Physicochemical characters of fifty mango cultivars popularly grown in Telangana State

S. No.	Cultivar	PLW (%)	Firmness (kg/cm^2)	DA reading	Fruit length (cm)	Fruit width (cm)	Fruit thickness (cm)	Fruit weight (g)	Peel (%)	Pulp (%)	Stone (%)	Pulp: Peel	Pulp: Stone	Shelf-life (Days)
1	Dasehari 35	7.90	1.08	0.53	9.02	5.60	5.03	160.2	20.84	57.92	24.07	3.48	2.89	5.67
2	Allampur Baneshan	5.72	1.56	0.91	11.55	8.56	9.01	354.63	10.15	47.34	15.22	5.04	2.98	5.83
3	Asif Us Samar	6.23	0.80	0.40	7.20	6.64	5.80	210.61	17.00	57.14	17.28	3.62	3.45	5.50
4	Azam Us Samar	6.20	0.99	0.54	9.94	5.99	5.91	209.71	22.90	62.53	23.55	5.22	3.50	5.50
5	Baneshan	7.47	0.91	0.54	9.94	7.45	6.56	280.94	9.20	72.86	13.30	8.48	5.23	7.50
6	Chinna Suvarnarekha	8.17	1.15	0.75	7.62	6.10	5.88	177.31	26.87	55.11	19.75	2.19	2.73	5.50
7	Dashehari	8.26	0.97	0.51	8.49	5.10	4.26	162.64	17.14	62.81	21.30	3.82	2.89	5.50
8	Dilpas and	6.80	2.32	0.84	10.17	6.36	6.62	282.24	14.97	70.59	12.99	6.02	5.77	5.50
9	Goa Bandar	8.21	1.18	0.91	6.54	6.53	6.33	169.77	20.37	65.29	18.95	3.36	3.49	6.50
10	Himayath	7.37	1.35	0.43	10.72	6.58	6.35	317.7	12.86	60.86	12.30	4.60	4.90	5.50
11	Jehangir	7.06	1.04	0.57	9.06	7.72	7.72	250.1	15.98	88.08	16.33	4.91	5.43	6.00
12	Kaju	7.23	2.06	0.43	8.52	8.69	9.03	176.4	14.34	47.20	19.85	3.38	2.47	6.50
13	Kalepahad	7.40	0.90	0.90	9.70	7.47	7.47	431.28	15.76	60.13	12.18	4.19	5.03	5.83
14	Kesar	5.55	1.13	0.44	9.24	5.81	5.67	180.8	17.52	58.53	20.60	3.52	2.65	6.67
15	Lalmuni	9.73	1.45	0.59	9.03	6.42	6.25	144.73	34.32	55.17	32.90	1.60	1.61	5.50
16	Latif Us Samar	6.66	1.11	0.48	7.49	6.50	6.42	214.42	34.21	62.09	31.00	1.81	1.99	5.83
17	Mahamooda Uppal	7.16	2.55	1.43	11.42	7.71	7.29	395.62	9.49	62.56	13.06	7.54	4.88	7.17
18	MahamoodaVikarabad	7.88	0.99	0.80	8.86	5.51	4.40	171.92	21.49	53.74	28.19	2.61	1.71	5.50

19	Manjeera	7.13	1.16	0.83	7.47	7.63	7.55	361.64	11.32	75.99	14.25	7.64	4.87	5.67
20	Mulgoa	6.25	1.18	0.52	9.14	7.77	6.43	262.13	11.47	65.44	22.57	6.15	2.78	5.67
21	Nazeem Pasand	7.82	2.34	1.62	12.49	11.58	12.10	506.8	22.23	49.76	14.18	2.23	3.40	7.17
22	Neeleshan	6.58	0.94	0.72	10.47	8.42	6.43	409.36	11.92	52.82	11.63	4.64	4.98	5.50
23	Neelum	7.07	1.00	0.59	8.13	5.76	5.39	170.18	20.82	61.78	18.01	3.12	3.63	5.50
24	Parasapalli Doodiya	9.21	0.92	0.90	8.22	6.46	5.12	141.21	14.15	57.57	21.72	4.43	2.62	5.00
25	Pulihora	4.90	0.92	0.88	7.61	5.69	5.46	208.87	23.00	56.94	21.67	2.64	2.64	5.83
26	Ranitellakaya	5.14	1.59	0.35	13.24	11.58	12.14	638.45	10.65	57.77	10.21	5.77	6.69	5.50

Table 1(b): Physicochemical characters of fifty mango cultivars popularly grown in Telangana State

S. No.	Cultivar	PLW (%)	Firmness (kg/cm²)	DA reading	Fruit length (cm)	Fruit width (cm)	Fruit thickness (cm)	Fruit weight (g)	Peel (%)	Pulp (%)	Stone (%)	Pulp: Peel	Pulp: Stone	Shelf-life (Days)
27	Rumani	6.80	0.94	0.89	6.56	7.86	7.70	311.34	16.57	69.45	19.00	4.37	3.63	5.33
28	Sannakulu	9.17	1.28	0.65	5.51	5.28	4.92	131.36	19.40	50.00	18.57	2.59	2.67	5.33
29	Shajahan	4.21	2.19	0.46	12.66	11.66	11.57	574.91	16.64	67.01	10.51	4.34	7.30	6.50
30	Shendriya	8.55	1.52	1.14	8.39	7.66	8.39	158.72	24.49	56.14	22.95	2.14	2.21	5.67
31	Sora	8.58	1.11	0.73	12.11	8.99	7.57	770.64	21.21	94.26	14.89	4.60	6.37	5.33
32	Suvarnarekha	7.42	1.01	0.44	9.86	5.51	5.07	212.56	20.95	58.37	21.03	2.92	2.76	6.50
33	Totapari	6.70	1.11	0.74	12.50	6.73	7.46	348.02	13.36	60.26	12.78	4.27	4.75	6.50
34	Vaddepalli Selection	7.26	1.04	0.73	10.56	8.87	6.56	450.9	10.62	69.87	10.46	7.11	7.32	7.00
35	Vanraj	6.12	1.34	0.72	8.18	7.57	7.61	349.41	12.17	59.66	13.52	5.14	4.08	7.33
36	Yerra Mulgoa	4.93	1.04	0.54	7.51	6.76	6.51	245.88	12.20	58.80	10.35	5.09	6.50	5.50
37	Aryavrtham Irsalu	7.13	1.27	1.04	11.03	8.14	8.51	236.95	23.17	42.35	21.15	1.88	1.81	5.00
38	Cherukurasam	9.16	1.06	0.95	10.03	6.50	5.95	289.5	18.84	54.75	18.60	3.05	2.91	5.17
39	Chinnarasam	6.41	0.96	0.82	10.13	6.08	5.03	261.29	20.93	52.47	15.30	2.55	3.49	5.17
40	Kothapalli Kobbari	7.43	1.09	1.00	9.22	6.44	6.56	270.44	16.22	53.18	17.16	3.54	3.05	5.33
41	Meetavari Peechumanu	7.60	1.24	1.81	10.11	7.73	8.47	214.86	15.56	31.72	23.80	1.91	1.30	5.33
42	Nagulapalli Irsalu	9.24	1.06	1.21	12.52	6.82	6.57	425.91	13.60	48.55	14.39	3.91	3.61	4.50
43	Navaneetham	9.16	1.02	1.30	8.60	6.65	5.42	244.33	19.97	67.62	24.07	3.38	2.63	4.67
44	Panakalu	7.19	1.54	1.92	8.65	7.40	7.57	148.29	22.44	52.48	24.41	2.26	2.08	6.17
45	Panchavarnam	8.81	1.21	0.74	7.21	6.68	5.57	215.67	24.78	73.89	28.56	2.88	2.70	5.17
46	Pandurivari Mamidi	6.04	1.21	1.82	8.22	6.45	5.89	214.13	23.27	55.93	28.93	2.42	1.83	4.83
47	Peddarasam	7.72	0.80	1.11	10.15	5.95	5.48	282.65	22.29	85.41	19.72	3.98	4.34	4.67
48	Yellow Arati	8.39	1.26	1.42	11.55	7.47	8.18	286.39	11.90	33.90	18.26	2.83	1.78	4.67
49	Yerra Arati	8.23	1.33	1.86	11.92	6.55	7.01	159.53	17.03	48.66	28.69	2.43	1.65	5.17
50	Zardalu	8.87	1.10	0.27	9.99	5.69	5.02	212.3	23.61	31.91	23.34	1.33	1.46	6.83
	Mean	7.320	1.250	0.850	9.490	7.140	6.820	280.110	18.040	59.090	18.950	3.860	3.550	5.740
	SEm±	0.030	0.020	0.018	0.032	0.028	0.026	1.002	0.539	0.530	0.426	0.027	0.033	0.221
	CD at 5%	0.084	0.057	0.050	0.089	0.078	0.074	2.793	1.503	1.479	1.188	0.075	0.092	0.617

Table 1(c): Physicochemical characters of fifty mango cultivars popularly grown in Telangana State

S. No.	Cultivar	TSS (°Brix)	Acidity (%)	Vitamin C	Brix: acid	TS (%)	RS (%)	NRS (%)	TPC	TFC	BC	TAA	Fibre Content
1	Dasehari 35	17.83	0.26	26.51	51.08	8.56	4.23	4.77	136.70	175.56	2.63	326.38	5.55
2	Allampur Baneshan	16.68	0.18	31.39	66.50	8.81	4.90	3.89	142.46	107.61	1.89	251.58	4.08
3	Asif Us Samar	17.70	0.59	26.22	31.46	8.66	3.97	4.66	142.02	147.05	1.77	216.03	4.33
4	Azam Us Samar	18.72	0.36	25.58	45.11	8.63	4.07	4.26	131.17	123.27	2.19	91.74	4.44
5	Baneshan	17.22	0.27	29.90	62.28	8.19	4.90	3.41	149.61	135.16	2.32	274.3	3.81
6	Chinna Suvarnarekha	16.12	0.54	26.92	31.92	7.98	4.07	3.84	87.68	87.00	2.35	191.44	4.16
7	Dashehari	17.89	0.40	23.35	44.88	8.85	4.03	4.90	147.69	196.23	2.47	232.22	5.17
8	Dilpasand	17.22	0.24	27.68	71.22	8.85	4.08	4.78	67.71	83.79	2.17	209.82	4.62
9	Goa Bandar	19.65	0.51	30.97	40.49	8.66	3.70	4.97	146.93	180.30	2.16	199.49	3.10
10	Himayath	17.73	0.49	26.99	37.20	8.64	4.01	4.69	88.64	99.95	1.79	290.9	3.18
11	Jehangir	18.42	0.54	25.27	35.86	9.29	3.73	5.69	120.99	134.21	1.22	192.5	4.33
12	Kaju	16.96	0.25	19.74	65.00	8.98	4.79	4.19	80.03	64.54	1.85	191.66	3.22
13	Kalepahad	18.00	0.42	26.76	43.80	8.89	4.05	4.89	88.13	24.03	2.13	191.76	4.76
14	Kesar	19.71	0.40	27.52	49.37	8.61	4.00	4.63	67.22	60.99	2.44	243.66	4.77
15	Lalmuni	17.72	0.55	28.52	34.77	9.39	4.08	5.44	81.98	136.22	2.81	182.18	3.59
16	Latif Us Samar	18.68	0.61	25.39	33.43	9.27	4.24	5.03	86.46	147.92	1.50	249.76	4.85
17	Mahamooda Uppal	16.61	0.24	25.15	70.79	9.60	4.41	5.15	82.02	98.66	1.52	193.35	4.26
18	Mahamooda Vikarabad	19.83	0.56	20.86	38.31	9.48	4.35	5.18	173.20	153.21	1.57	218.52	4.87
19	Manjeera	18.43	0.53	27.63	36.64	9.74	4.78	5.02	86.77	106.21	1.32	230.64	4.89
20	Mulgoa	19.40	0.65	27.84	31.16	8.85	4.14	4.61	121.41	163.42	1.77	150.25	4.21
21	Nazeem Pasand	16.88	0.24	22.74	72.05	9.76	4.77	5.07	70.85	50.92	1.11	228.8	6.16
22	Neeleshan	17.35	0.52	25.70	34.86	8.75	4.86	4.01	73.23	110.68	1.86	276.07	3.88
23	Neelum	19.47	0.46	25.39	44.40	9.54	4.08	5.47	143.35	160.05	2.13	187.02	3.71
24	Parasapalli Doodiya	20.22	0.39	26.14	53.60	9.39	4.16	5.30	91.80	103.87	1.54	218.04	4.20
25	Pulihora	19.91	0.42	25.93	47.01	9.81	4.08	5.80	140.91	263.02	2.08	216.44	4.37
26	Ranitellakaya	17.79	0.24	24.45	74.24	9.35	4.88	4.54	66.91	69.21	1.15	179.01	4.50

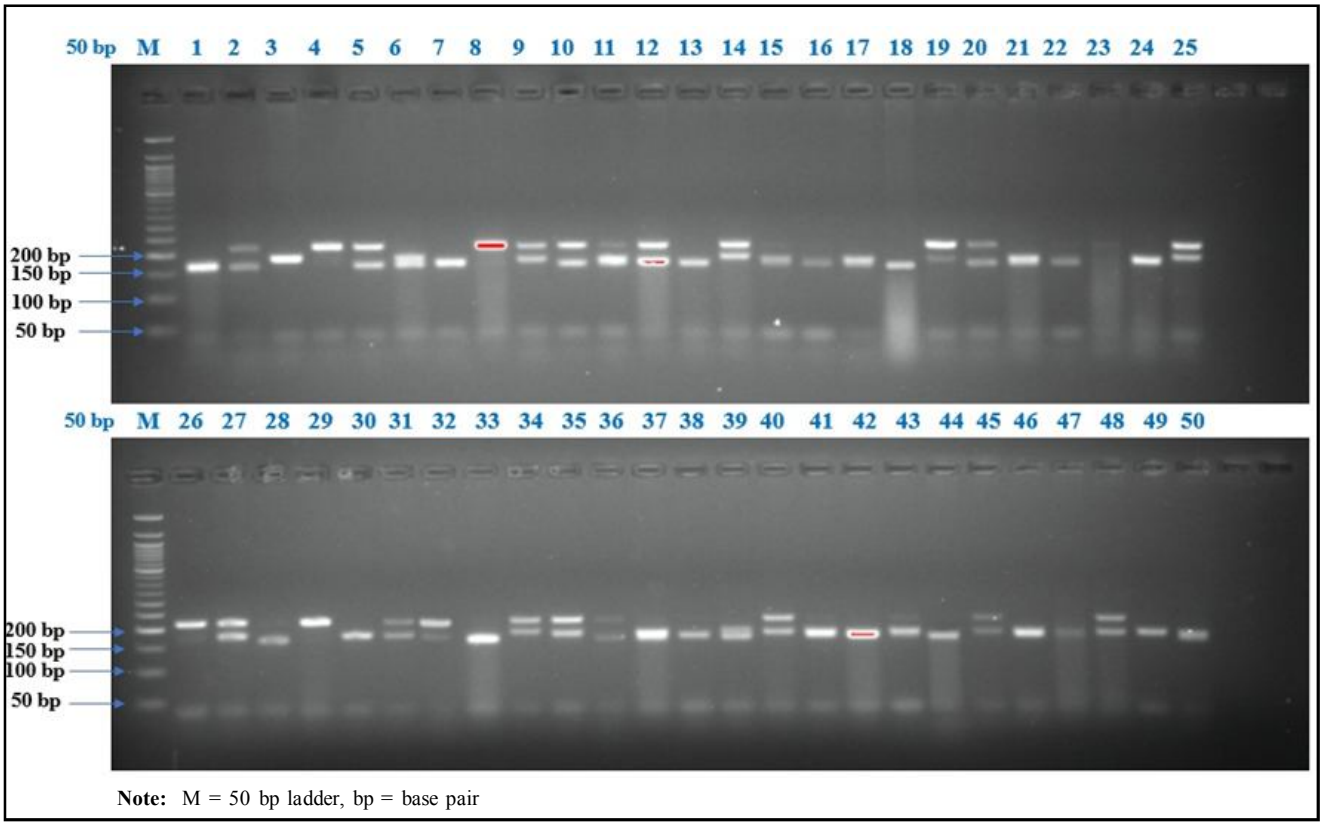
Table 1(d): Physicochemical characters of fifty mango cultivars popularly grown in Telangana State

S. No.	Cultivar	TSS (°Brix)	Acidity (%)	Vitamin C	Brix: acid	TS (%)	RS (%)	NRS (%)	TPC	TFC	BC	TAA	Fibre Content
27	Rumani	19.84	0.42	20.16	48.74	8.69	4.24	4.55	78.36	90.47	1.89	222.74	4.72
28	Sannakulu	19.70	0.55	27.57	36.72	8.48	4.87	3.64	160.00	153.05	1.68	187.76	4.73
29	Shajahan	16.88	0.24	25.56	69.41	9.65	4.85	4.86	64.72	123.54	1.28	173.02	4.49
30	Shendriya	19.92	0.55	29.52	35.46	9.82	4.64	5.19	164.73	101.27	2.41	232.13	5.79
31	Sora	16.03	0.61	27.16	25.65	9.39	4.32	5.14	80.80	47.32	1.54	181.73	4.12
32	Suvarnarekha	16.78	0.55	20.96	31.96	8.71	4.28	4.43	75.10	138.32	2.62	218.28	4.29
33	Totapari	16.54	0.62	28.12	28.31	9.77	4.72	5.04	83.24	81.83	2.45	251.77	4.82
34	Vaddepalli Selection	17.37	0.24	27.49	74.49	9.69	4.80	4.83	86.51	113.04	1.56	211.67	4.67
35	Vanraj	12.75	0.36	27.28	36.97	9.68	4.60	5.25	89.49	50.56	2.58	216.31	3.41

36	Yerra Mulgoa	19.27	0.44	24.85	44.10	9.45	4.15	5.37	128.31	331.11	2.60	227.59	4.30
37	Aryavrtham Irsalu	16.76	0.24	25.34	60.70	9.58	4.20	5.45	87.85	88.35	1.79	221.58	5.78
38	Cherukurasam	18.16	0.32	25.44	53.85	8.64	4.29	4.36	87.08	161.56	1.59	220.81	6.45
39	Chinnarasam	19.97	0.50	20.76	40.43	9.32	4.10	5.27	83.91	118.70	1.56	257.89	5.38
40	Kothapalli Kobbari	19.97	0.49	27.37	43.52	8.91	4.07	4.94	88.07	144.51	1.86	285.41	6.27
41	Meetavari Peechumanu	13.19	0.45	23.45	31.62	8.56	4.08	4.54	74.38	58.85	1.48	278.19	5.98
42	Nagulapalli Irsalu	18.39	0.48	29.09	40.78	8.98	4.09	4.90	98.83	84.31	1.38	221.42	7.01
43	Navaneetham	21.10	0.46	24.98	48.26	8.11	4.26	3.82	69.95	58.29	1.70	275.08	6.12
44	Panakalu	17.09	0.40	21.04	44.90	9.30	4.29	4.98	83.21	70.59	1.43	285.01	6.40
45	Panchavarnam	17.74	0.53	24.08	34.44	9.39	4.32	5.04	86.02	145.15	1.18	219.96	6.23
46	Pandurivari Mamidi	18.23	0.53	19.07	36.75	9.43	4.07	5.42	86.85	121.97	1.42	173.3	5.24
47	Peddarasam	20.02	0.53	29.14	38.59	8.92	4.42	4.56	72.50	48.06	1.68	232.3	5.92
48	Yellow Arati	14.01	0.56	26.76	25.57	9.68	4.48	5.26	127.86	97.42	1.95	239.02	6.53
49	Yerra Arati	15.99	0.21	25.40	78.06	9.71	4.46	5.22	128.04	102.87	1.77	168.98	6.65
50	Zardalu	19.41	0.25	20.51	78.57	8.14	4.08	4.08	156.94	176.53	2.74	217.82	5.86
	Mean	17.940	0.426	25.630	46.710	9.090	4.320	4.810	103.170	117.810	1.880	221.070	4.880
	SEm ±	0.101	0.026	0.470	0.849	0.044	0.026	0.044	0.697	1.640	0.020	1.283	0.037
	CD at 5%	0.283	0.073	1.310	2.368	0.123	0.072	0.123	1.945	4.573	0.057	3.579	0.103

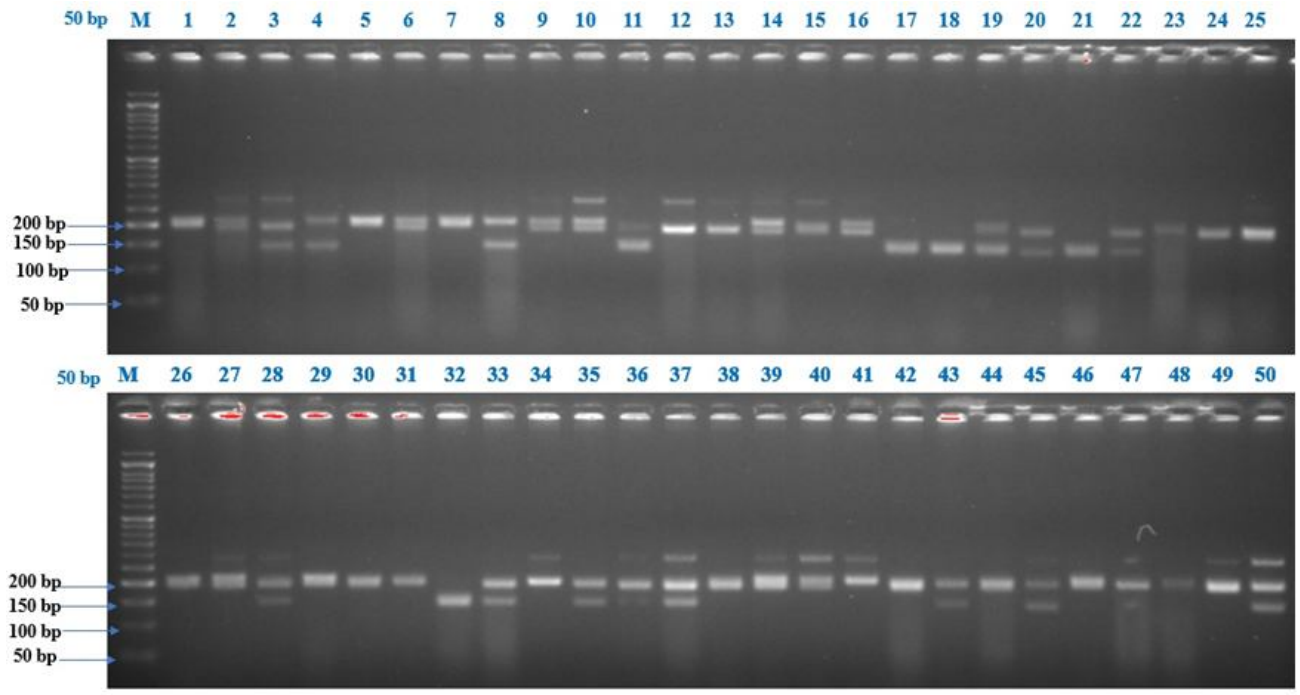
Note: TS: Total sugars (%); RS: reducing sugars (%); NRS: Non-reducing sugars (%); TPC: Total phenolic content (mg of gallic acid/100 g); TFC: Total flavonoid content (mg QE/100 g); BC: Beta carotene (mg/100 g); TAA: Total Antioxidant activity (µg/100 g) Fibre Content (g/100 g).

3.2 Molecular analysis



Note: M = 50 bp ladder, bp = base pair

Figure 1: SSR profile of fifty mango cultivars generated by the primer MiIIHR 02c.



Note: M = 50 bp ladder:bp = base pair

Figure 2: SSR profile of fifty mango cultivars generated by the primer MiIIHR 19a.

Table 2: Details of polymorphic SSR primers used for characterization of 50 mango genotypes

S. No.	Marker	Product size in bp	No. 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	0.4	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	0.3	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	0.11
13	MiIIHR 19a	170-210	4	0.8	0.36	0.69	0.73
14	MiIIHR 23a	130-155	3	0.5	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	0.3	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	0.3	0.39
21	MiIIHR 32a	200-210	2	0.71	0.6	0.08	0.48
22	MiIIHR 33a	160-170	2	0.52	0.53	0.38	0.5
23	MiIIHR 36 b	220-230	2	0.52	0.7	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	0.3	0.5
26	SSR-39	170-190	3	0.75	0.52	0.4	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	0.6
32	SSR-82	120-140	3	0.56	0.56	0.82	0.58
33	SSR-83	190-200	2	0.5	0.6	0.4	0.48
34	SSR-88	180-200	2	0.47	0.83	0.3	0.28
35	MiSHRS-1	190-200	2	0.67	0.75	0.06	0.38
36	MiSHRS-4	150-160	2	0.6	0.7	0.2	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	0.5
	Mean				**0.65**	**0.4**	**0.45**

A total of 60 SSR primers were employed to assess the extent of genetic diversity among fifty table and juicy mango cultivars. Out of the 60 primers screened, 42 primers exhibited polymorphism, revealing a total of 109 alleles, of which 93 alleles were polymorphic. The amplified allele sizes ranged from 100 bp (MiIIHR 06 b) to 330 bp (MiIIHR 14 b), indicating considerable variability across the SSR loci. The average number of alleles per SSR primer was 2.21 with individual loci producing between 2 and 4 alleles.

The polymorphic information content (PIC) values varied from 0.24 to 0.80 with a moderate mean value of 0.53 across all SSR loci indicating a moderate level of discriminatory power among the primers used (Table 2). The major allele frequency ranged from 0.357 (MiIIHR 19a) to 0.940 (MiIIHR 18b) with a mean value of 0.646. Observed heterozygosity values ranged from 0.000 (MiIIHR 18b) to 0.980 (MiIIHR 23a) with an average heterozygosity of 0.41, reflecting variation in allelic expression among the genotypes. Gene diversity values ranged from 0.11 (MiIIHR 18b) to 0.73 (MiIIHR 19a) with an overall mean of 0.45, further confirming the presence of substantial genetic variability among the mango cultivars studied. Representative gel images showing highly polymorphic SSR markers and the banding patterns generated across all mango cultivars are presented in Figures 1 and 2.

The UPGMA dendrogram constructed based on Jaccard's similarity coefficients for the assessment of genetic divergence revealed a significant level of diversity among the mango genotypes. The similarity coefficients ranged from 0.61 to 0.88, indicating the presence of fairly adequate genetic variability within the studied material. The highest genetic similarity was observed between Mahamooda Vikarabad and Manjeera with a similarity coefficient of 0.88 (88%), followed by Ranitellakaya and Shajahan with a similarity of 0.86 (86%), and Baneshan and Vaddepalli Selection with a similarity coefficient of 0.83 (83%). Based on the cluster analysis, the fifty mango cultivars were broadly grouped into three major clusters at a similarity coefficient of 0.62, designated as Cluster I, Cluster II, and Cluster III, along with further sub-grouping within each cluster according to their genetic relationships, as illustrated in Figure 3. Cluster I was the largest, comprising 43 genotypes. Within this cluster, table and juicy cultivars were interspersed and showed grouping only at the subgroup level rather than at the major cluster level. Cluster II consisted predominantly of 4 juicy cultivars, whereas Cluster III was composed of 3 table cultivars.

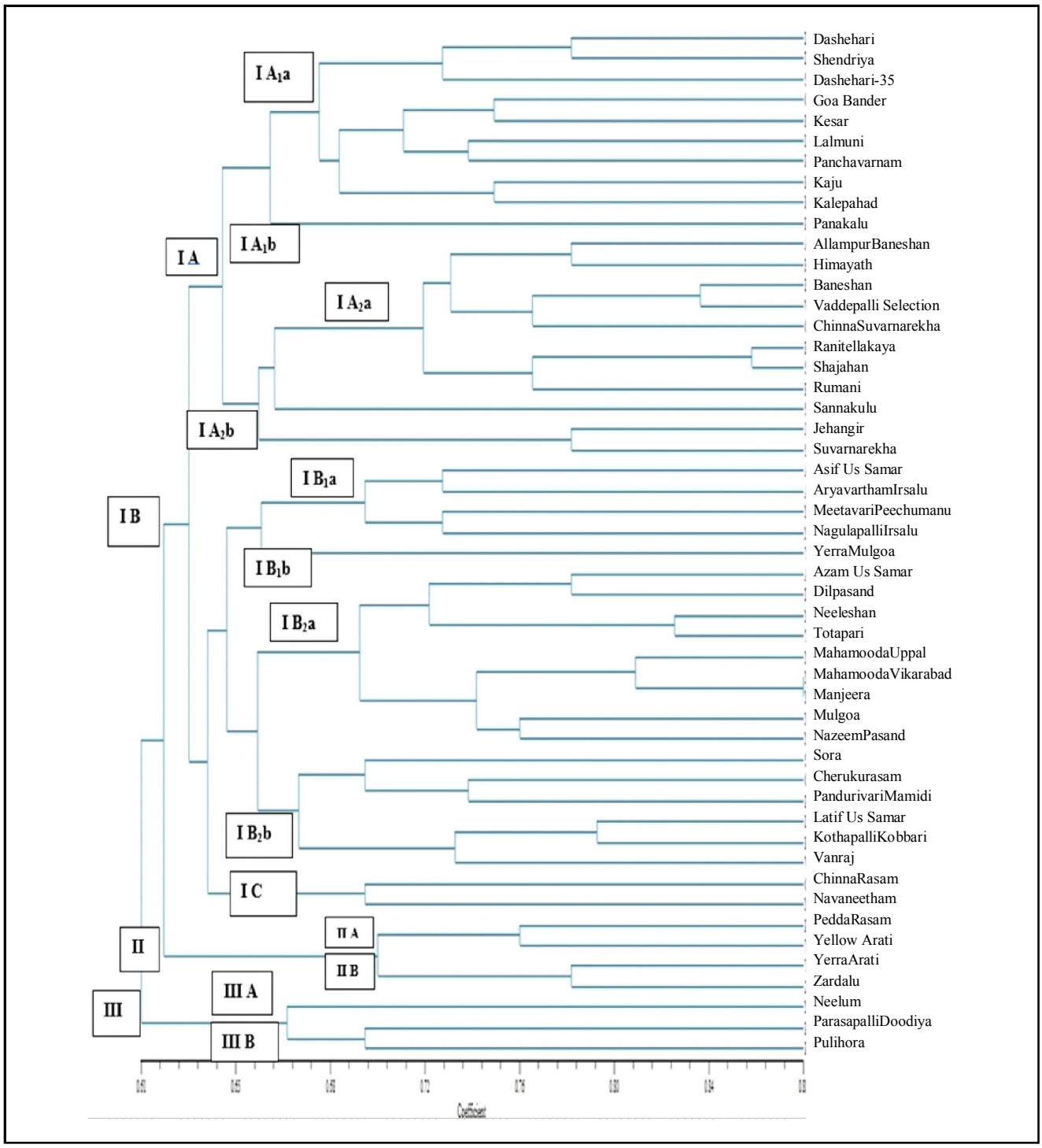


Figure 3: Dendrogram of 50 genotypes constructed by using jaccard'ssimilarity coefficient based UPGMA.

3.3 Marker trait association studies

In the present study, the allelic data of 42 polymorphic markers with 25 quantitative and qualitative traits were subjected to marker trait association (Table 3). Significant associations were observed for 24 markers with at least one of the traits studied. The markers with *p*-value of $p \leq 0.05$ were identified as significantly associated with the respective traits and explained considerable amount of phenotypic variation by exhibiting substantial R^2 values ranging from 0.029 (fruit length) to 0.218 (TSS). Significant marker trait associations were observed for 18 traits only. The number of markers associated with individual traits ranging from 1 (fruit length, total sugars, antioxidant activity and fibre content) to 6 (pulp: stone ratio).

Table 3: Significant markers-trait associations from 42 polymorphic SSR markers in 50 mango genotypes

S. No.	Trait	Marker associated	$p<0.05$	R^2 value
1	Fruit length (cm)	SSR 83	0.0394	0.0298
2	Fruit width (cm)	MiIIHR 16 a	0.0111	0.0732
		MngSSR 14	0.0181	0.0556
3	Fruit thickness (cm)	SSR 39	0.0423	0.0934
		MngSSR 14	0.0172	0.0641
4	Fruit weight (g)	MISHRS 32	0.0127	0.0859
		MiIIHR 33 a	0.0230	0.0773
		SSR 83	0.0443	0.0661
5	Pulp per cent	LMMA 8	0.0013	0.1524
		MISHRS 36	0.0031	0.1434
		SSR 57	0.0130	0.1211
		SSR 88	0.0178	0.1151
		SSR 36	0.0433	0.0942
6	Pulp: stone ratio	SSR 57	0.0116	0.1108
		LMMA 8	0.0128	0.1092
		MISHRS 36	0.0178	0.1033
		SSR 36	0.0358	0.0890
		SSR 88	0.0366	0.0886
		MiIIHR 33 a	0.0411	0.0859
7	Firmness (kg/cm^2)	MiIIHR 28 c	0.0231	0.0476
		MiIIHR 5c	0.0379	0.0424
8	DA reading	MiIIHR 24 b	0.0181	0.0797
		SSR 55	0.0188	0.0792
		SSR 20	0.0442	0.0651
		MiIIHR 33 a	0.0471	0.0640
9	TSS (^oBrix)	SSR 65	0.0173	0.2181
		MiIIHR 30 a	0.0023	0.1959
		MISHRS 4	0.0373	0.1310
10	Brix:acid ratio	SSR 88	0.0441	0.1064
		MISHRS 36	0.0482	0.1037
11	Vitamin C (mg/100g)	SSR 88	0.0099	0.0420
		MISHRS 4	0.0203	0.0373
		LMMA 8	0.0212	0.0370
12	Total sugars (%)	MiIIHR 32 a	0.0195	0.0567
13	Reducing sugars (%)	MiIIHR 30 a	0.0091	0.0567
		LMMA 6	0.0357	0.0441
14	Non reducing sugars (%)	MiIIHR 32 a	0.0264	0.0808
		MiIIHR 17 b	0.0328	0.0768
		MiIIHR 28 c	0.0397	0.0732
15	Total flavonoid content	MiIIHR 30 a	0.0047	0.0904
	(mg qurcetin equivalent/100 g)	LMMA 6	0.0404	0.0631
16	Beta carotene (mg/100 g)	MISHRS 4	0.0071	0.0621
		LMMA 8	0.0178	0.0542
17	Antioxidant activity (µg/100 g)	MiIIHR 23 a	0.0299	0.1715
18	Fibre content (g/100 g)	SSR 82	0.0234	0.0303

Of the18 associated traits pulp: stone ratio showed significant association with six SSR markers, *viz.,* SSR 57, LMMA 8, MISHRS 36, SSR 36, SSR 88, MiIIHR 33a followed by pulp per cent with five SSR markers, *viz.,* LMMA 8, MISHRS 36, SSR 57, SSR 88, SSR 36. DA reading exhibited significant association with four SSR markers, *viz.,* MiIIHR 24 b, SSR 55, SSR 20 and MiIIHR 33a. Three SSR markers, *i.e.,* MISHRS 32, MiIIHR 33a and SSR 83 showed significant association with fruit weight; markers SSR 65, MiIIHR 30a and MISHRS 4 showed significant association with TSS; markers SSR 88, MISHRS 4 and LMMA 8 were found to be associated with vitamin C and markers MiIIHR 32a, MiIIHR 17b and MiIIHR 28c were associated with non reducing sugars. Two SSR markers MiIIHR 16a and MngSSR 14 associated with fruit width; SSR 39 and MngSSR 14 were associated with fruit thickness; markers MiIIHR 28c and MiIIHR 5c associated with firmness; SSR 88 and MISHRS 36 associated with brix: acid ratio; MiIIHR 30a and LMMA 6 associated with reducing sugars; MISHRS 4 and LMMA 8 associated with beta carotene content and markers MiIIHR 30a and LMMA 6 showed significant association with total phenolics content. The traits, *viz.,* fruit length, total sugars, total antioxidant activity and fibre content recorded significant association with one SSR marker each, *viz.,* SSR 83, MiIIHR 32a, MiIIHR 23a and SSR 82, respectively.

4. Discussion

4.1 Physicochemical characters

All physicochemical characters of mango cultivars were given in Table 1. The present study indicated that, wide variation was noticed among all the table and juicy cultivars, most of the cultivars significantly superior in both quantitative and qualitative traits studied. Ranitellakaya, Baneshan, Shajahan, Allampur Baneshan, Pulihora, Vaddepalli Selection, Mahamooda Vikarabad, Mahamooda Uppal, Nazeem Pasand, Yerra Mulgoa, Navaneetham, Zardalu, Panakalu were significantly superior in different quantitative as well as qualitative trait

Hence, these varieties can be used as one of the parents in hybridization programme for improvement of quality and develop new varieties in mango. Selection of these varieties can be based on the requirement of traits, even though they were not commercial. The above results are in agreement with the findings of Anila and Radha (2003); Karihaloo *et al*. (2003); Mannan *et al*. (2003); Noferini *et al.* (2008); Lakshminarayana (1980); Subedi *et al*. (2009); Yadav *et al.* (2010); Begum *et al.* (2016); Himabindu *et al.* (2017); Lokesh Bora *et al.* (2017); Soujanya *et al.* (2017); Padmakar *et al.* (2017); Rezwan Molla *et al.* (2019) in mango, Tayebe Basaki *et al.* (2011) in pomegranate.

4.2 Molecular analysis

Figures 2 and 3 illustrate the gel images of highly polymorphic SSR markers and the corresponding banding patterns observed across all fifty mango cultivars. Of the 60 SSR primers screened, 42 primers exhibited polymorphism, generating a total of 109 alleles of which 93 were polymorphic. The amplified fragment sizes ranged from 100 bp (MiIIHR 06 b) to 330 bp (MiIIHR 14 b), demonstrating substantial allelic variation among the cultivars. The average number of alleles per SSR locus was 2.21 with individual loci producing between 2 and 4 alleles.The polymorphic information content (PIC) values of the SSR markers varied from 0.24 to 0.80, with a moderate mean value of 0.53, indicating a moderate discriminatory power for distinguishing among the mango genotypes. Markers showing the highest PIC values included MiIIHR 19a (0.80), MiIIHR 02c (0.76), SSR-39 (0.75), MiSHRS-32 (0.74) and MiIIHR 26a and 32a (0.71), suggesting that these loci are highly informative for genetic diversity studies. The major allele frequencies, observed heterozygosity and gene diversity values also showed considerable variation, reflecting the underlying genetic differences among the cultivars.

The allelic range and PIC values observed in this study are consistent with earlier reports. Begum *et al.* (2012) documented polymorphic bands ranging from 90 bp to 370 bp in mango cultivars, while Anshuman Singh *et al.* (2012) reported allelic sizes between 100 and 400 bp. Similarly, Molla *et al.* (2010, 2019) and Ravishankar*et al.* (2011) noted that high PIC values are often associated with dinucleotide repeats and genotypic differences among cultivars. The present results corroborate these findings, demonstrating the effectiveness of SSR markers in detecting genetic variability in mango germplasm.However, in agreement with Ravishankar *et al.* (2011, 2016), SSR-anchored primers were not able to categorize the cultivars strictly based on fruit type (ripe versus unripe), suggesting that the genetic variation detected by these markers is independent of post-harvest fruit characteristics. Overall, the SSR analysis highlights the presence of substantial genetic diversity among the fifty mango cultivars, providing a foundation for future breeding and conservation programs.

The dendrogram revealed that, genotypes are derivatives of genetically similar type clustered more together and the clustering of genotypes according to their utility purpose was only at subgroup level, and not along the major group level. The varieties could not be grouped based on usage, *viz*., table or juicy cultivars. These findings are in agreement with Eiadthong *et al.* (2000), where in SSR-anchored primers could not separate the cultivars according to the types eaten as ripened fruit or unripe fruits.

4.3 Marker trait association studies

In mango, information on genetic diversity and the association of molecular markers with morphological, agronomic, and fruit quality traits is still limited (Padmakar *et al.,* 2017). The application of molecular markers facilitates the study of marker-trait associations for biologically and agronomically important traits across diverse genetic material (Khushboo *et al.,* 2018). Based on the present data, several SSR markers were found to be associated with more than one trait, which is of particular interest for breeding programs. This observation may be attributed to the pleiotropic effects of linked quantitative trait loci (QTLs) influencing multiple traits.

Among the markers analysed, LMMA 8 was associated with several key traits, including pulp per cent, pulp-to-peel ratio, vitamin C and beta-carotene content. Similarly, SSR 88 was linked to pulp per cent, pulp-to-stone ratio, brix:acid ratio and vitamin C. Comparable marker trait associations have been reported in other crops: TayebeBasaki *et al*. (2011) identified associations between 30 microsatellite markers and morphological traits in 202 pomegranate genotypes; Khadivi-Khub (2013) reported that 38 SSR alleles and 135 RAPD markers were associated with 14 fruit traits in cherries using multiple regression analysis (MRA) and Ipek *et al.* (2015) observed similar associations in olive.

In the present study, SSR markers LMMA 8, SSR 88, MiIIHR 33a, MiSHRS 36, MiIIHR 30a and MiSHRS 4 exhibited significant

associations with the majority of the traits evaluated. These markers can be considered multi-trait associated markers and may be utilized for trait identification, selection of suitable parents for hybridization and the development of mapping populations to accelerate mango improvement programs. Nevertheless, the association of these markers requires validation in mapping populations for confirmation before practical breeding application.

5. Conclusion

The present investigation unequivocally demonstrated substantial genetic and biochemical diversity among the fifty mango cultivars evaluated from Telangana State. Significant variation was recorded for all the 25 post-harvest physicochemical traits studied, indicating the presence of wide exploitable variability for mango improvement programmes. Fruit weight ranged from 131.16 to 770.64 g, pulp content from 47.20 to 94.20%, pulp tostone ratio from 1.30 to 7.32 and total soluble solids (TSS) from 12.75 to 21.10 °Brix, reflecting considerable differences in edible quality, processing suitability and consumer preference among the cultivars.The biochemical profiling revealed wide variation in nutritionally important bioactive compounds. Total phenolic content ranged from 64.72 to 173.20 mg GAE/100 g, total flavonoid content from 24.03 to 331.11 mg QE/ 100 g, β-carotene from 1.11 to 2.81 mg/100 g and total antioxidant activity from 91.74 to 326.38 µg/100 g. These results confirm mango as a rich source of antioxidant phytochemicals with potential health-promoting properties. However, variation was also observed for crude fibre content (3.10 to 7.01 g/100 g) and phenolic compounds, which at higher concentrations may act as antinutritional factors by reducing protein digestibility and mineral bioavailability. The observed genotypic differences therefore provide scope for selecting cultivars with an optimal balance between high bioactive compound content and minimal antinutritional effects, particularly for fresh consumption and processing purposes. Molecular characterization using 60 SSR primers identified 42 polymorphic markers, generating 109 alleles of which 93 were polymorphic 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 SSR markers. Markers such as MiIIHR 19a (PIC=0.80), MiIIHR 02c (0.76), SSR-39 (0.75), MiSHRS-32 (0.74), MiIIHR 26a (0.71) and MiIIHR 32a (0.71) exhibited high discriminatory power and are particularly useful for mango diversity analysis and germplasm characterization. Cluster analysis grouped the fifty cultivars into three major clusters at a similarity coefficient of 0.62, confirming substantial genetic divergence among the genotypes. Marker trait association analysis revealed significant associations for 18 out of 25 traits with 24 SSR markers showing association with at least one trait. The proportion of phenotypic variation explained (R^2) ranged from 0.029 (fruit length) to 0.218 (TSS). Notably, pulp-to-stone ratio showed association with six SSR markers (SSR 57, LMMA 8, MiSHRS 36, SSR 36, SSR 88 and MiIIHR 33a), while pulp per cent was associated with five markers (LMMA 8, MiSHRS 36, SSR 57, SSR 88 and SSR 36). Key nutritional and bioactive traits such as vitamin C, â-carotene, flavonoids, antioxidant activity and fibre content were also significantly associated with specific SSR markers. Markers LMMA 8, SSR 88, MiIIHR 33a, MiSHRS 36, MiIIHR 30a and MiSHRS 4 exhibited multi trait associations, indicating their linkage with genomic regions controlling multiple quality, nutritional and bioactive traits.In conclusion, the combined evaluation of physicochemical traits, bioactive compounds, antinutritional components and SSR based molecular markers provides a comprehensive understanding of mango fruit quality and its genetic control. The identified superior genotypes and multi trait associated markers can be effectively utilized for parent selection, development of mapping populations and marker assisted selection aimed at improving fruit quality, nutritional value and post-harvest performance. Nevertheless, validation of these marker trait associations in structured mapping populations is essential to ensure their reliability before large scale application in mango breeding programmes.

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Conflict of interest

The authors declare no conflicts of interest relevant to this article.

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