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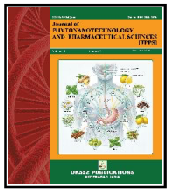

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Augmentation of pickling mango (*Mangifera indica* L.) genotypes and their biochemical profiling for genetic improvement

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Abstract

The current study comprises 36 pickling mango genotypes collected from different locations, namely; Sothuparai, Kumbakkarai, Adukkam, Manjalar, Marudhanadhi local, Bodinayakkanoor, Allinagaram (Theni), Kurangini, Velappar (Andipatti), Agamalai, Devadhanappatti, and existing genotypes at HC&RI, Periyakulam, and Central Farm. In each genotype, three trees were evaluated for their mean performance. Most of the genotypes came into bearing in Dec-Jan (early bearing), with high fruit setting (2.59%) and fruit retention (2.97%). As per the characterisation and evaluation, genotype MI-PM-01 exhibited the lowest total soluble solids and total sugars, high levels of ascorbic acid, and crude fibre. Hence, the MI-PM-01 genotype is most suitable for whole fruit pickle making due to its pickling quality and desirable traits, *viz*., high acidity, fibre content, and lower total soluble solids. So, genotype MI-PM-26 could be selected and used as a parent for the crossing program. For quality traits, high acidity, crude fibre, lowest TSS, and total sugars were observed in MI-PM-26 and MI-PM-01. Heritability and genetic advance as per cent of mean were found to be maximum acidity (3.32%) in MI-PM-01 and minimum acidity (0.27%) in MI-PM-35; ascorbic acid, crude fibre, and total sugars show an additive gene action, so selecting genotypes based on these traits will be effective.

1. Introduction

Mango (*Mangifera indica* L.) is one of Asia's pioneer fruits and is important worldwide. Mango is affectionately called the "king of fruits" with an excellent and delicious taste and fragrance (Singh *et al*., 2000). It combines sweetness and aroma with extraordinary nutritional values. A hundred grams (100 g) of fresh mango pulp provides 60-190 kcal, while 100 g of mango pulp weight represents 60 kcal on average (Lebaka *et al*., 2021). It is vibrant in large amounts of antioxidants, especially ascorbic acids or vitamin C (13.2-92.8 mg), Thiamine or vitamin B1 (0.01 - 0.04 mg), niacin or vitamin B3 (0.2-1.31 mg), vitamin B9 (0.12 mg), vitamin A (54 µg), α-tocopherol or vitamin E (0.79-1.02 mg), a mixture of sugar (16-18%), magnesium (8-19 mg), potassium (120-211 mg), phosphorus (10-18 mg), iron (0.09-0.41 mg), α-carotene, calcium (7-16 mg), carbohydrates (16.20-17.18 g), fibers (1.60 g), histidine (0-0.019), leucine (0-0.050), proteins (0.36-0.40 g), total lipid (0.4 g), carotenoids responsible for the bright yellow color, and phenolic compounds in 100 g of mango fruit (USDA, 2011). γ-octalactone, 1-octanol, 2,6-nonadienal and turpentine are volatile compounds that flavour mango (Sung *et al*., 2019). It possesses huge health advantages and prevents many chronic diseases due to the several nutrients it contains (Slavin and Lloyd, 2012). The antioxidants of these fruits are known to decrease the risk of cardiac disease, cancer, and viral infections (Jash and Brahmachari, 2015).

Mango is a highly cross-pollinated and heterozygous fruit crop, thus exhibiting wide genetic variability in seedling populations. In India, the Western Ghats have an enormous diversity of mango genotypes, including aromatic tiny pickle mangoes (Sherman *et al*., 2015). These undomesticated, small-sized fruit varieties are known as "Appemidi" and "Vadumangai" in Kannada and Tamil languages (Vasudeva *et al*., 2014). Pickle is one of the oldest preserved products, which is made from unripe mango. Mangoes have unique varieties that are only used for pickling and are rarely eaten as ripe fruit. The term pickle is derived from the Dutch word "Pekel", meaning brine (Rashmi, 2010). A pickle is an edible product preserved in common salt, vinegar and spices. Pickles are made from various fruits and vegetables like mango, lime, jackfruit, cauliflower, turnip, carrot and bamboo shoots. Among them, mango pickle ranks first and is mostly used throughout the country. Pickles are divided into four categories: vinegar pickles, citrus juice pickles, brine pickles and oil pickles. Besides the basic fruit or vegetable, vinegar, sugar, salt, oil and spices

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are commonly added to pickles. Mango pickles have a nutritional value of about 78 calories, protein 0.2 g, carbohydrates 18.5 g, fibre 0.3 g and fat 0.4 g per tablespoon. Mango pickle is loaded with vitamin C, which helps to boost the immune system and improve absorption of iron. All three genotypes of mango are roundish in shape, with pointed beaks; pulp colour is whitish and whitish yellow, the average weight of fruits is about 200-270 g, the pulp percentage is about 96.44 per cent and the peel thickness is about 13.2 mm (Gahane *et al*., 2019).

The pickling mango trees were mostly grown in forest lands, undulated terrain in mountainous tracts and river banks, etc., exhibit wide range of variability in desired horticultural traits like fruit shapes, size, consistency of juice, regularity of bearing, yields, high aroma and unique taste, flavor and tolerances to different biotic and abiotic stresses towards pickling mango, these genotypes effectively used for pickle (Jagtap *et al*., 2014). Aromatic pickle mango supports locals through dietary supplements, improved nutrition, and household income (Sherman *et al*., 2015). Moreover, meagre scientific studies and documentation of pickling mangoes were observed. The study is beneficial for further crop improvement programs and identifying promising pickling mango genotypes for pickle making. In this view, the present research is on characterising and evaluating pickling mango genotypes (*M. indica*) for quality and biochemical characteristics.

2. Materials and Methods

2.1 Material taken for the study

In this study, a total of 36 pickling mango genotypes were analysed, comprising 29 seedling-derived types and 7 grafted trees. The genotypes utilised in the experiment are detailed in Table 1. These accessions were assessed for various biochemical traits, including titratable acidity, firmness, total soluble solids (TSS), crude fibre content, total sugars, and ascorbic acid levels.

Table 1: Different genotypes of mango and their site of collection

S.No.	Genotypes	Location and site of collection	Latitude	Longitude
1.	MI-PM-01	Sothuparai local, Periyakulam, Theni	10° 07' 45.5"N	77° 27' 58.0"E
2.	MI-PM-02	Sothuparai local, Periyakulam, Theni	10° 07' 58.1"N	77° 27' 72.1"E
3.	MI-PM-03	Sothuparai local, Periyakulam, Theni	10° 07' 36.7"N	77° 27' 63.0"E
4.	MI-PM-04	Kumbakkarai forest areas, Periyakulam, Theni	10°10' 57.7"N	77° 31' 45.2"E
5.	MI-PM-05	Kumbakkarai forest areas, Periyakulam, Theni	10° 10' 53.7"N	77° 31' 46.9"E
6.	MI-PM-06	Kumbakkarai forest areas, Periyakulam, Theni	10° 10' 50.5"N	77° 31' 48.4"E
7.	MI-PM-07	Adukkam forest areas, Periyakulam, Theni	10° 11' 15.7"N	77° 32' 55.7"E
8.	MI-PM-08	Adukkam forest areas, Periyakulam, Theni	10° 10' 48.4"N	77° 45' 63.3"E
9.	MI-PM-09	Agamalai forest area, Theni	10° 09' 74.4"N	77° 31' 50.0"E
10.	MI-PM-10	Manjalar forest areas, Devadhanapatti, Dindigal	10° 10' 16.0"N	77° 39' 02.9"E
11.	MI-PM-11	Manjalar forest areas, Devadhanapatti, Dindigal	10° 10' 17.5"N	77° 39' 02.6"E
12.	MI-PM-12	Manjalar forest areas, Devadhanapatti, Dindigal	10° 10' 15.3"N	77° 39' 03.6"E
13.	MI-PM-13	Veerappa Ayyanar Kovil, Allinagaram, Theni	10° 10' 54.6"N	77° 26' 47.4"E
14.	MI-PM-14	Veerappa Ayyanar Kovil, Allinagaram, Theni	10° 10' 55.0"N	77° 26' 47.8"E
15.	MI-PM-15	Veerappa Ayyanar Kovil, Allinagaram, Theni	10° 10' 54.2"N	77° 26' 48.8"E
16.	MI-PM-16	Velappar areas, Andipatti, Theni	09°51'14.10"N	77° 35' 56.8"E
17.	MI-PM-17	Velappar areas, Andipatti, Theni	09° 51'10.3"N	77° 35' 55.6"E
18.	MI-PM-18	Velappar areas, Andipatti, Theni	09° 51' 09.3"N	77° 35' 53.9"E
19.	MI-PM-19	Kurangini foothills, Theni	10° 05' 04.5"N	77° 15' 00.5"E
20.	MI-PM-20	Kurangini foothills, Theni	10° 05' 59.5"N	77° 15' 03.3"E
21.	MI-PM-21	Kurangini foothills, Theni	10° 05' 01.6"N	77° 15' 02.1"E
22.	MI-PM-22	Marudhanadhi local	10° 14' 21.1"N	77° 40' 59.3"E
23.	MI-PM-23	Marudhanadhi local	10° 14' 25.7"N	77° 40' 51.7"E
24.	MI-PM-24	Devadhanappatti local, Dindigal	10° 10' 17.5"N	77° 39' 05.4"E
25.	MI-PM-25	Devadhanappatti local, Dindigal	10° 10' 18.4"N	77° 39' 04.3"E

26.	MI-PM-26	Munthal, Bodinayakkanoor local, Theni	10°2' 44.36"N	77°18'40.57"E
27.	MI-PM-27	Munthal, Bodinayakkanoor local, Theni	10° 2' 43.04"N	77°18'43.18"E
28.	MI-PM-28	Selayampatti local, Chinnamanoor, Theni	09° 52' 19.6"N	77° 23'01.2"E
29.	MI-PM-29	Selayampatti local, Chinnamanoor, Theni	09° 52' 20.1"N	77° 23'01.2"E
30.	MI-PM-30	Kottoor local, Cumbum, Theni	09° 52' 20.7"N	77° 23'01.6"E
31.	MI-PM-31	Kottoor local, Cumbum, Theni	09° 52' 19.1"N	77° 23'00.7"E
32.	MI-PM-32	Germplasm block of HC&RI, Periyakulam	10° 07' 19.2"N	77° 35'27.6"E
33.	MI-PM-33	Germplasm block of HC&RI, Periyakulam	10° 07' 19.2"N	77° 35'27.6"E
34.	MI-PM-34	Germplasm block of HC&RI, Periyakulam	10° 07' 19.2"N	77° 35'27.6"E
35.	MI-PM-35	Germplasm block of HC&RI, Periyakulam	10° 07' 19.2"N	77° 35'27.6"E
36.	MI-PM-36	Germplasm block of HC&RI, Periyakulam	10° 07' 19.2"N	77° 35'27.6"E

2.2 Observations recorded

In each location and mango germplasm accession, three similarly performing trees were selected for the evaluation. Identified trees were tagged, and observations were recorded as per the IPGRI (International Plant Genetic Resources Institute) descriptors. Based on the mean value, statistical analysis was carried out (Panse and Sukhatme, 1954).

2.2.1 Total soluble solids (°Brix)

A digital hand refractometer was used to measure the total soluble solids at the shoulder, middle and distal end of fifteen random fruits and mean values were expressed in degrees Brix (Ranganna, 1986).

2.2.2 Titratable acidity (%)

The titrable acidity of a particular fruit was measured in the sample with 0.1N NaOH using phenolphthalein as an indicator and expressed in percentage (%):

$$\text{Total tritable acidity (\%)} = \frac{1 \times \text{Equivalent weight of acid} \times \text{Normality of NaOH} \times \text{Titre value}}{10 \times \text{Weight of sample}} \times 100$$

2.2.3 Total sugars (%)

Total sugars of particular genotypes were measured using the Anthrone method:

$$\text{Total sugar (\%)} = \frac{\text{Factor} \times \text{Dilution}}{\text{Titter} \times \text{Weight of sample}} \times 100$$

2.2.4 Crude fibre content (%)

The crude fibre content of different pickling mango genotypes was estimated using the procedure given by Gould (1977).

$$\text{Crude fibre (\%)} = \frac{\text{Loss in weight}}{\text{Weight of sample taken}} \times 100$$

2.2.5 Ascorbic acid (mg g^{-1})

Ascorbic acid content in different accessions was measured using the analytical procedure of Cochran (1957):

Ascorbic acid (mg/g)

$$= \frac{\text{Titre value} \times \text{Dye factor} \times \text{volume made}}{\text{Aliquote taken Weight / Volume of sample}} \times 100$$

*Dye factor = 0.5/titre value

2.2.6 Firmness (kg/cm^2)

The firmness of fruits was measured using the penetrometer at the basal, middle and distal ends of the fruit and its average values were expressed in kg/cm^2.

2.3 Statistical analysis

Analysis of variance and components of genetic variability such as mean, range, genotypic and phenotypic coefficient of variance (GCV and PCV respectively,) heritability, and genetic advance as per cent mean (GAM) were estimated using standard statistical procedures.

2.3.1 Analysis of variance

To determine the significance of genotypic influence, the mean values of thirty-six pickling mango genotypes were subjected to an ANOVA estimate as proposed by Panse and Sukhatme (1954). The data for various characters were statistically examined using the model proposed by Yates (1964):

$$Y_{ij} = \mu + b_i + t_j + e_{ij}$$

where,

Y_{ij} = Performance of the j^{th} genotype in the i^{th} block

μ = general mean

b_i = true effect of the i^{th} block

t_j = true effect of the j^{th} genotype

e_{ij} = random error associated with the i^{th} block and j^{th} genotype

The ANOVA for all characters was worked out as listed below

Source of variation	Df	SS	MSS	F ratio
Replication	r – 1	RSS	RMSS	RMSS/EMSS
Treatments	t – 1	t_rSS	T_rMSS	T_rMSS/ EMSS
Error	(r – 1) (t – 1)	ESS	EMSS	
Total	(rt – 1)	TSS		

where,

r = No. of replications

t = Number of genotypes (or) treatments

df = Degrees of freedom

SS = Sum of squares

MSS = Mean sum of squares

RSS = Replication sum of squares

TrSS = Treatment sum of squares

ESS = Error sum of squares

TSS = Total sum of squares

RMSS = Replication mean sum of squares

T_rMSS= Treatment mean sum of squares

EMSS = Error mean sum of squares

Yates (1964) 'F' table values were used to perform the test of significance.

2.3.2 Components of variance

Genotypic variance (Vg) = Genotype MSS " Error MSS / r

Environmental variance (Ve) = ErSS

Phenotypic variance (Vp) = Vg + Ve

The importance of treatments MSS was calculated using F-table values at the 1% and 5% probability levels. Furthermore, the calculation was only performed when the treatment effects were significant. To compare the means of different entries, CD was computed using the following formulae:

Critical difference (CD) = S.E (d) × t

$$\text{S.E (d)} = \sqrt{2 \times \frac{EMSS}{r}}$$

where,

t = Table value at 5 (%) or 1 (%) probability level, respectively

r = No. of replications

2.3.3 Phenotypic and genotypic variance

The proposed method for estimating the variability parameters uses the variance table's mean square values (Johnson *et al*., 1955).

$$\text{Genotypic variance } (s^2g) = \frac{M_g - M_e}{r}$$

Phenotypic variance (s^2p) = $s^2g + s^2e$

where,

r = Number of replications

M_g = Mean sum of squares for genotypes

M_e = Mean sum of squares for error

s^2e = Mean sum of squares for error

2.3.4 Phenotypic and genotypic coefficient of variation

The coefficients of variation for phenotypic and genotypic traits were computed using (Burton, 1974):

$$PCV = \sqrt{\frac{\text{Phenotypic variance}}{\text{Mean}}} \times 100$$

$$GCV = \sqrt{\frac{\text{Genotypic variance}}{\text{Mean}}} \times 100$$

The following PCV and GCV values were categorised as low, moderate and high based on the Sivasubramaniam and Madhava Menon (1973) approach:

0-10%	Low
10-20%	Moderate
More than 20%	High

2.3.5 Heritability (%)

According to Lush (1940), heritability in a broad sense was calculated and expressed as a percentage:

$$h^2 \text{ in a broad sense} = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Johnson *et al*. (1955), the heritability range was classified as,

Less than 30%	Low
30-60%	Moderate
More than 60%	High

The genetic advance was estimated by the method suggested by Johnson *et al*. (1955):

$$\text{Genetic advance} = \frac{\sigma^2 g}{\sigma^2 p} \times k \times \sqrt{\sigma^2_p}$$

where,

k = Selection differential (at 5 % selection intensity, k = 2.06)

σ^2_g = genetic variance

σ^2_p = phenotypic standard deviation

The genetic advance was also noted as a per cent of the mean:

$$\text{Genetic advance as per cent of mean} = \frac{\text{Genetic advance}}{\text{Grand mean}} \times 100$$

The genetic advance was classified as:

Low	0-10%
Moderate	10 -20%
High	More than 20%

3. Results

The analysis of variance revealed highly significant differences between genotypes for the biochemical parameters under this study.

3.1 Firmness (kg/cm²)

The data recorded showed significant variation in firmness shown in Table 2 and it ranged from 11.62 kg/cm² to 18.92 kg/cm² with a mean value of 14.72 kg/cm² obsereved in firmness, among the thirty-six genotypes, MI-PM-25 (19.92) recorded the maximum firmness followed by MI-PM-08 (18.92 kg/cm²) and MI-PM-11(17.62 kg/cm²), while the minimum firmness was recorded in MI-PM-13 (11.62 kg/cm²) followed by MI-PM-32 (11.68 kg/cm²) and MI-PM-06 (11.86 kg/cm²).

3.2 Total soluble solids (°Brix)

The total soluble solids content in the pickling mango genotypes differed from 9.46° brix to 17.28° Brix with a mean value of 13.11°brix shown in Table 2. Among the thirty-six genotypes, MI-PM-06 recorded the lowest total soluble solid content of 9.46 °brix, followed by MI-PM-05 (10.08 °brix) and MI-PM-23 (10.90 °brix), whereas the maximum total soluble solid content was present in MI-PM-35 (17.28 °brix), followed by MI-PM-33 (16.25 °brix) and MI-PM-26 (15.18 °brix).

3.3 Acidity (%)

Data recorded showed a significant variation in acidity, as shown in Table 2, and it ranged from 0.27% to 3.32%. Among the thirty-six genotypes, MI-PM-04 (3.32%) registered the highest acidity, followed by MI-PM-01 (3.22%) and MI-PM-18 (3.07%), while the lowest value of 0.27% was recorded in MI-PM-35, followed by MI-PM-33 (0.33%) and MI-PM-26 (0.38%), with a general mean of 1.83%.

3.4 Ascorbic acid content (mg g^{-1})

Ascorbic acid content had significant variation among the different genotypes, as shown in Table 2, and it ranged from 12.56 mg g^{-1} to 52.98 mg g^{-1} with a general mean value of 29.55 mg g^{-1}. Among thirty-six genotypes, MI-PM-02 (52.98 mg g^{-1}) recorded maximum ascorbic acid content, followed by MI-PM-23 (51.40 mg g^{-1}) and MI-PM-16 (47.34 mg g^{-1}), whereas the minimum ascorbic acid content was recorded in MI-PM-30 (12.56 mg g^{-1}), followed by MI-PM-27 (14.62 mg g^{-1}) and MI-PM-29 (15.94 mg g^{-1}). Ascorbic acid and total sugars in most of the evaluated strains ranged between 12.8 mg g^{-1} (Halasage) and 137.67 mg g^{-1} (Dashehari); similarly, total sugar content was higher in Banganapalli (16.47 mg g^{-1}) and lower in Kalakai (1.19 mg g^{-1}).

3.5 Crude fibre content (%)

The data given in Table (9.2) showed significant differences in crude fibre content, which ranged from 0.56% to 2.76%. Among the genotypes, MI-PM-07 (2.76%) recorded the maximum crude fibre content, followed by MI-PM-18 (2.68%) and MI-PM-23 (2.19%). The minimum percentage of crude fibre was recorded in MI-PM-35 (0.58%) and MI-PM-29 (0.63%), with a mean value of 1.28%.

3.6 Total sugar (mg g^{-1})

Total sugar content ranged from 3.97 to 12.82 mg g^{-1}, with a mean value of 7.94 mg g^{-1}, as shown in Table 2. Among the evaluated picking mango genotypes, MI-PM-16 recorded minimum total sugar content of 2.92 mg g^{-1}, followed by MI-PM-17 (3.36 mg g^{-1}) and MI-PM-06 (3.38 mg g^{-1}), while the highest number of total sugars recorded in MI-PM-36 (12.82 mg g^{-1}), followed by MI-PM-34 (12.80 mg g^{-1}) and MI-PM-33 (12.34 mg g^{-1}).

Table 2: Different genotypes of mango with their biochemical observations

S.No.	Genotypes	Firmness (kg/cm²)	TSS (° Brix)	Acidity (%)	Ascorbic acid (mg g^{-1})	Crude fibre (%)	Total sugars (mg g^{-1})
1	MI-PM-01	12.78	9.46	3.32	52.98	2.76	2.92
2	MI-PM-02	13.02	12.68	2.03	44.56	1.435	5.87
3	MI-PM-03	14.41	14.4	2.48	24.96	1.14	8.91
4	MI-PM-04	12.93	11.05	3.22	51.395	2.68	3.36
5	MI-PM-05	15.95	10.08	2.95	28.9	1.29	5.64
6	MI-PM-06	11.86	11.62	2.86	34.42	1.08	3.38
7	MI-PM-07	16.64	12.92	2.78	45.97	1.96	6.19
8	MI-PM-08	18.92	13.32	3.02	31.42	2.12	5.66
9	MI-PM-09	15.67	12.6	1.18	22.69	1.62	9.34

10	MI-PM-10	17.62	12.44	2.86	26.6	1.18	9.82
11	MI-PM-11	16.14	13.36	1.6	24.92	0.96	8.44
12	MI-PM-12	14.46	11.5	2.22	34.62	1.42	3.97
13	MI-PM-13	11.62	12.66	2.68	26.62	1.51	4.44
14	MI-PM-14	14.33	13.32	2.26	28.98	1.18	5.96
15	MI-PM-15	15.68	12.98	1.75	39.96	1.19	8.77
16	MI-PM-16	16.24	11.5	3.02	47.34	1.35	4.94
17	MI-PM-17	13.13	11.18	2.68	26.08	1.47	3.36
18	MI-PM-18	12.58	12.52	3.07	32.85	1.91	5.12
19	MI-PM-19	17.51	14.68	1.13	18.99	0.56	8.44
20	MI-PM-20	13.69	11.33	2.46	38.67	2.145	6.06
21	MI-PM-21	14.07	11.15	2.92	29.9	1.945	7.42
22	MI-PM-22	15.63	12.6	2.96	45.68	2.08	5.28
23	MI-PM-23	16.96	13.32	2.72	31.46	2.19	4.47
24	MI-PM-24	14.42	12.62	1.42	30.12	0.62	8.82
25	MI-PM-25	19.92*	14.48	0.6	25.64	0.86	11.845
26	MI-PM-26	12.65	15.18	0.9	19.59	0.955	9.22
27	MI-PM-27	12.95	14.22	0.45	14.62	0.85	10.98
28	MI-PM-28	17.58	13.82	0.83	15.94	0.68	9.92
29	MI-PM-29	16.52	15.18	0.37	12.56	0.625	9.94
30	MI-PM-30	13.32	14.75	0.52	18.84	0.71	10.82
31	MI-PM-31	14.42	14.47	0.77	22.64	0.84	11.02
32	MI-PM-32	11.68	15.18	0.54	16.92	0.79	11.18
33	MI-PM-33	13.34	16.25	0.33	22.52	0.62	12.34
34	MI-PM-34	14.47	14.6	0.39	20.48	0.92	12.80
35	MI-PM-35	14.16	17.28	0.27	25.48	0.58	11.06
36	MI-PM-36	12.68	14.08	0.44	28.62	0.77	12.82
	Minimum	11.62	9.46	0.27	12.56	0.58	2.92
	Maximum	19.92	17.28	3.32	52.98	2.76	12.82
	Mean	14.72	13.11	1.83	29.55	1.28	7.95
	CD at 5%	4.52	2.68	0.87	9.63	0.69	2.77
	SE(d)	2.23	1.32	0.43	4.74	0.34	1.36

3.7 Pearson correlation coefficients

The Pearson correlation coefficients indicate the strength and direction of the relationships among the six variables (P1-P6). The diagonal values are 1.00, representing the perfect correlation of each variable with itself. Variable P1 exhibited very weak correlations with all other variables, ranging from – 0.09 to 0.04, indicating that it is largely independent of the remaining traits. In contrast, the other variables showed moderate to strong relationships. P2 had a strong negative correlation with P3 (r = –0.80), P4 (r = –0.65), and P5 (r = –0.69), while it showed a strong positive correlation with P6 (r = 0.76). Similarly, P3 was strongly and positively associated with P4 (r = 0.72) and P5 (r = 0.80), but exhibited a very strong negative correlation with P6 (r = –0.88). Variable P4 also showed a strong positive relationship with P5 (r = 0.75) and a moderately strong negative relationship with P6 (r = –0.68). Likewise, P5 was strongly negatively correlated with P6 (r = –0.74). The correlogram visually represents these relationships using ellipses and colour intensity.

Dark teal, narrow ellipses indicate strong positive correlations, whereas dark brown, narrow ellipses represent strong negative correlations. Nearly circular, light-colored shapes indicate weak or negligible correlations. Overall, the analysis suggests that P2, P3, P4, P5, and P6 are highly interrelated, exhibiting both positive and negative associations, while P1 remains largely uncorrelated with the other variables. The strongest positive association was observed between P3 and P5 (r = 0.80), whereas the strongest negative association occurred between P3 and P6 (r = –0.88). These findings indicate that changes in P3 are closely accompanied by changes in P5 in the same direction, while increases in P3 are associated with substantial decreases in P6. Such information is valuable for identifying variables that are closely associated and for understanding the underlying relationships among the measured traits.

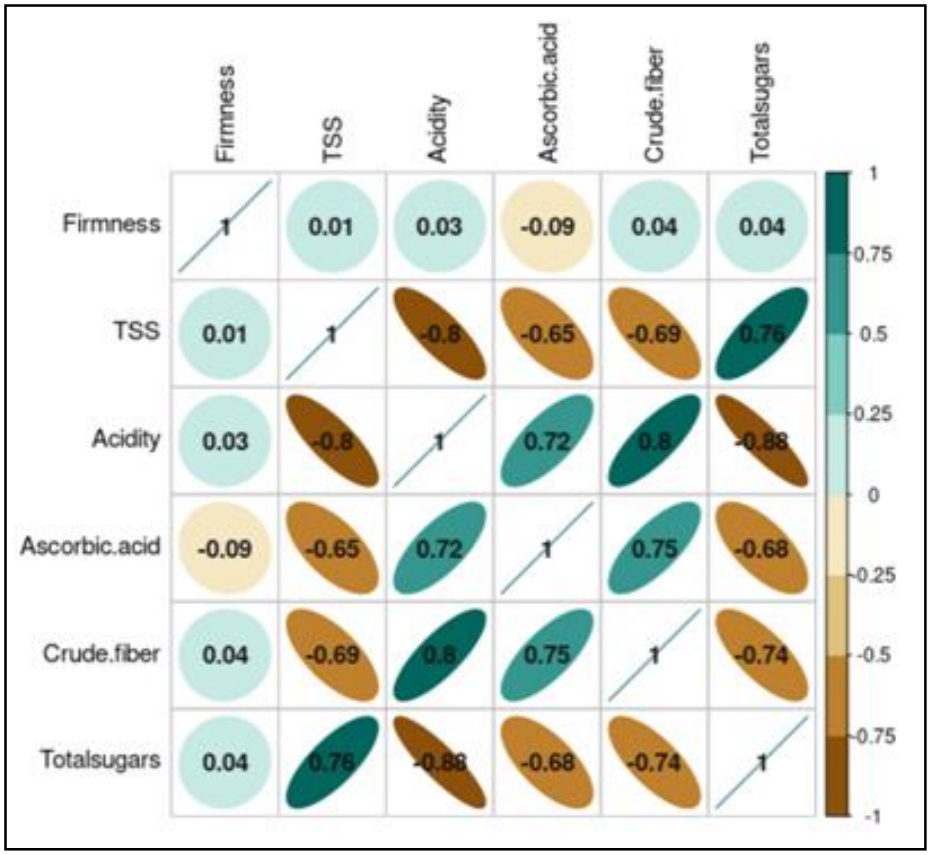

Figure 1: Correlogram represents the correlation among mango fruit quality parameters.

3.8 Genetic variability, heritability and GAM for different traits

3.8.1 Biochemical traits

Firmness exhibited moderate estimates for the phenotypic coefficient of variation of 17.71%, and lower estimates for the genotypic coefficient of variation (9.23%) and heritability percentage (27.15%), coupled with low genetic advance as a percentage of the mean (9.91%). (Sankaran *et al*., 2021) conducted a study to evaluate 400 mango genotypes, and the results indicate that almost all the characters of every genotype had significant differences due to their heterozygous nature. PCV values were high in fruit weight, followed by fruit diameter and fruit length. All the parameters used to assess the variability estimates, namely phenotypic coefficient of variation (14.60%), genotypic coefficient of variation (10.56%), heritability (52.36%) and genetic advance as a per cent of the mean (15.74%), were found to be moderate for total soluble solids. They also state that heritability and genetic advance were maximum for fruit length, fruit weight, fruit thickness, fruit diameter, TSS and pulp recovery. Bhoyar and Kumar (2020) evaluated seedling-originated mango trees present in the Kangra district of Himachal. They reported that a wide range of variability has been observed for quantitative and qualitative characters. All the parameters used to assess the variability were found to be high for TSS. The estimated value for the phenotypic coefficient of variation, genotypic coefficient of variation, heritability and genetic advance as a per cent of mean was 60.89%, 56.26%, 85.35 % and 107.06%, respectively. Higher estimates of genotypic and phenotypic coefficient of variation of 33.73% and 37.35% were observed. High heritability percentage of 81.54% along with high genetic advance as per cent of the mean (62.74%) was found in ascorbic acid content. Sapota genotypes were reported to have most of the characters with higher PCV than GCV, indicating most of the characters had a wide range of variability among selected genotypes. They also revealed that characters like seed width, pulp percentage, ascorbic acid, phenols, TSS and total sugars were recorded in the lowest range of GCV and PCV (Vikram *et al*., 2014). Assess the genetic variability for nine genotypes of Guava. The GCV and PCV range of other characters are categorised as high acidity. The highest and lowest heritability estimates were found for fruit TSS (61.99%) (Gupta *et al*., 2018).

All the variability parameters: namely, phenotypic coefficient of variation, genotypic coefficient of variation, heritability and genetic advance as per cent of mean, were found to be high for crude fibre. The estimates for the phenotypic coefficient of variation, genotypic coefficient of variation, heritability and genetic advance as per cent of mean were 43.28%, 50.78%, 72.62% and 75.97%, respectively.

Total sugar exhibited higher estimates of the phenotypic coefficient of variation (39.07%), genotypic coefficient of variation (35.10%) and high heritability percentage (80.69%), along with high genetic advance as a per cent of the mean (64.95%).

The estimates for phenotypic coefficient of variation, genotypic coefficient of variation, heritability and genetic advance as per cent of mean were 65.02%, 63.89 %, 96.55% and 129.32%, respectively. They also state that high heritability with high genetic advance as a percentage of the mean has been noticed for the traits of TSS. Arivazhagan *et al.* (2019) experimented to evaluate eight Sapota cultivars to assess variability and correlation among fruit characters. The results showed that most of the characters had higher PCV values than GCV, while the lowest GCV and PCV values were found for total soluble solids. Sridhar *et al.* (2018) characterised sixteen mango cultivars, and the results revealed that narrow differences were noticed between GCV and PCV; this simply indicates these traits are less affected by environmental influence. Reducing and non-reducing sugars, titratable acidity, ascorbic acid, and TSS acid ratio are those traits that register a higher magnitude of PCV and GCV. Among various traits of reducing and non-reducing sugars, ascorbic acid, and TSS acid ratio had a higher range of PCV, GCV, and GA as per cent mean along with a higher magnitude of heritability. Based on a study conducted by Galal *et al.* (2017) in mango, the magnitude of PCV was higher than GCV, but close estimates were noticed for most of the traits. In the case of heritability, TSS and acidity are those traits that had the highest range of heritability. Patel *et al.* (2021) characterised 20 mango varieties; they noticed the broad range of variability for most of the traits. Traits included in this study had higher estimates of PCV and GCV. Most of the traits included in this present investigation had a higher magnitude of PCV and GCV along with high heritability, except canopy spread. They also state that fruit yield per tree had a positive and significant correlation with the number of fruits per tree, both at the genotypic and phenotypic levels.

Table 3: Genotypic and phenotypic coefficient variation with heritability and genetic advances mean different traits of pickling mango

S.No.	Traits	Mean	Min	Max	PCV	GCV	h^2 (%)	GAM
1.	Firmness (kg/cm^2)	17.72	11.62	18.92	17.71	9.23	27.15	9.91
2.	TSS (^{o}Brix)	13.11	9.46	17.28	14.60	10.56	52.36	15.74
3.	Acidity (%)	1.83	0.27	3.32	60.89	56.26	85.35	107.06
4.	Ascorbic acid (mg/100 g)	29.55	12.56	52.98	37.35	33.73	81.54	62.74
5.	Crude fibre (%)	1.28	0.56	2.76	50.78	43.28	72.62	75.97
6.	Total sugars (mg g^{-1})	7.94	2.92	12.82	39.07	35.10	80.69	64.95

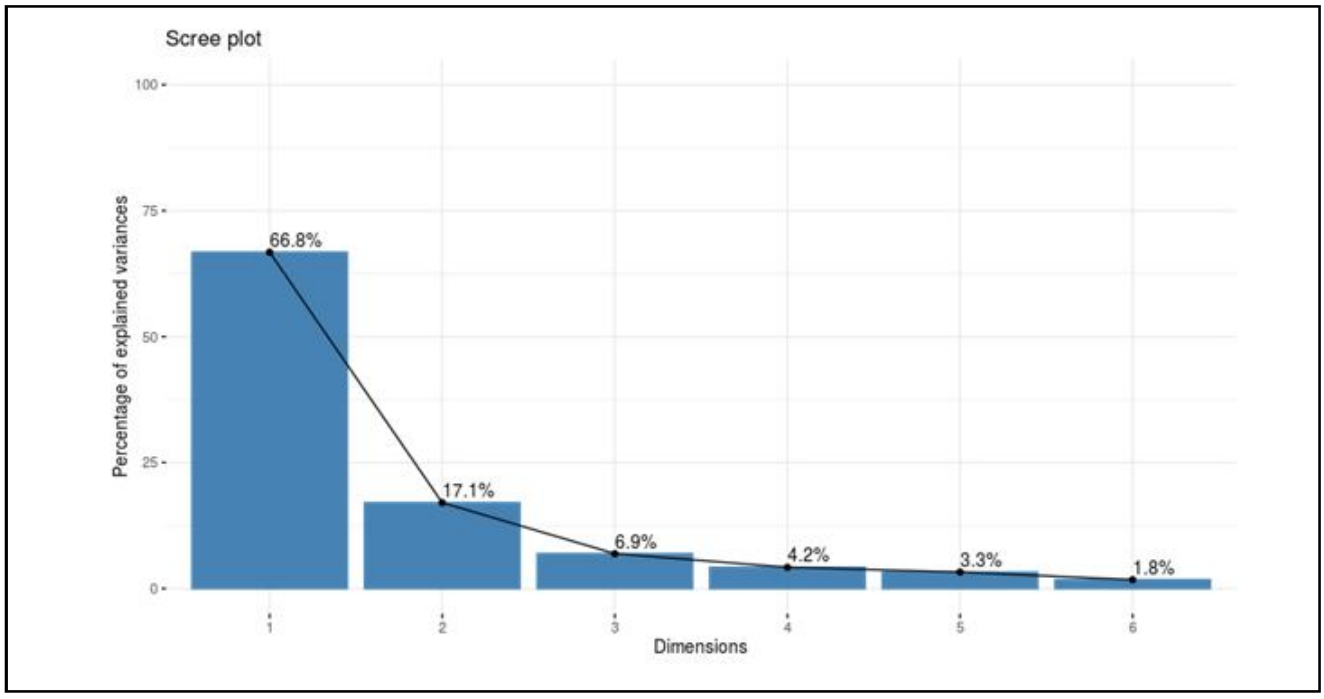

Figure 2: Scree plot showing the percentage of variance explained by the principal components (PCs).

3.9 PCA analysis

Principal component analysis (PCA) was performed to evaluate the relationships among the physicochemical traits of the samples and to reduce the dimensionality of the dataset while preserving the maximum amount of variation. The scree plot (Figure 1) indicated that the first principal component (PC1) explained approximately 68% of the total variation, followed by PC2 (17%), PC3 (7%), PC4 (4%), PC5 (3%), and PC6 (2%). The cumulative variance explained by the first two principal components was approximately 85%, suggesting that these components effectively summarised the variability present in the dataset. Since the first two principal components accounted for the majority of the total variation, they were considered adequate for interpreting the relationships among the measured variables and the distribution of the samples.

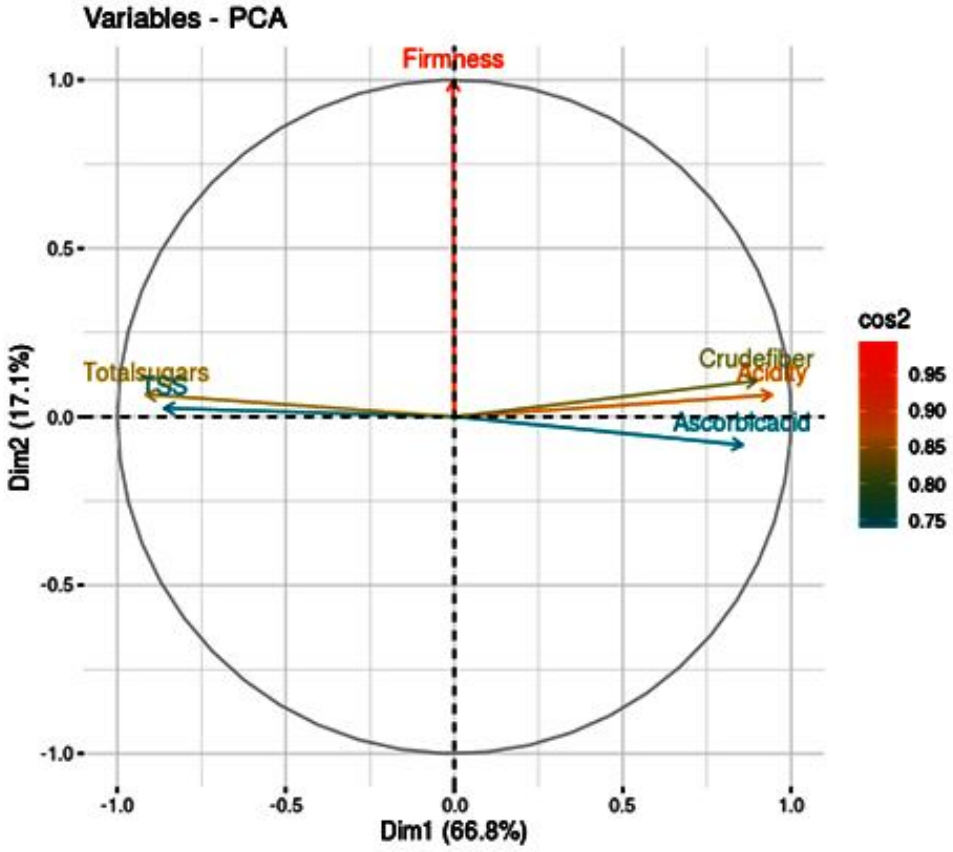

Figure 3: PCA variable correlation circle illustrating the relationships among the fruit quality traits.

3.9.1 PCA variable correlation circle

The variable correlation circle (Figure 3) illustrates the contribution and association of the measured quality traits with the first two principal components. Crude fibre and acidity were positioned close to each other on the positive side of PC1, indicating a strong positive association between these variables. Ascorbic acid also showed a positive association with PC1 but was oriented slightly downward, suggesting a moderate relationship with acidity and crude fibre. In contrast, total sugars (TSS) were located on the negative side of PC1, indicating a strong negative association with acidity, crude fibre, and ascorbic acid. Firmness was aligned almost entirely along the positive direction of PC2, indicating that it contributed predominantly to the second principal component and was largely independent of the variables associated with PC1. The long vector lengths and their proximity to the unit circle indicate that these variables were well represented by the first two principal components.

3.9.2 PCA score plot

The PCA score plot (Figure 4) revealed considerable variation among the experimental samples based on their physicochemical characteristics. Samples were distributed across all four quadrants, indicating substantial diversity in their quality attributes. Samples P1 and P4 were located on the extreme positive side of PC1, suggesting that they were characterised by relatively higher acidity, crude fibre, and ascorbic acid contents. Conversely, samples P26, P29, P30, P32, P33, P34, P35, and P36 were positioned on the negative side of PC1, indicating their association with higher total sugar content. Samples such as P8 and P10 exhibited high positive PC2 scores, reflecting greater firmness. Samples located near the origin, including P3, P9, P11, and P15, showed average values for most of the measured traits and contributed less to the discrimination among treatments. Overall, the score plot demonstrated clear variability among the samples based on their physicochemical composition.

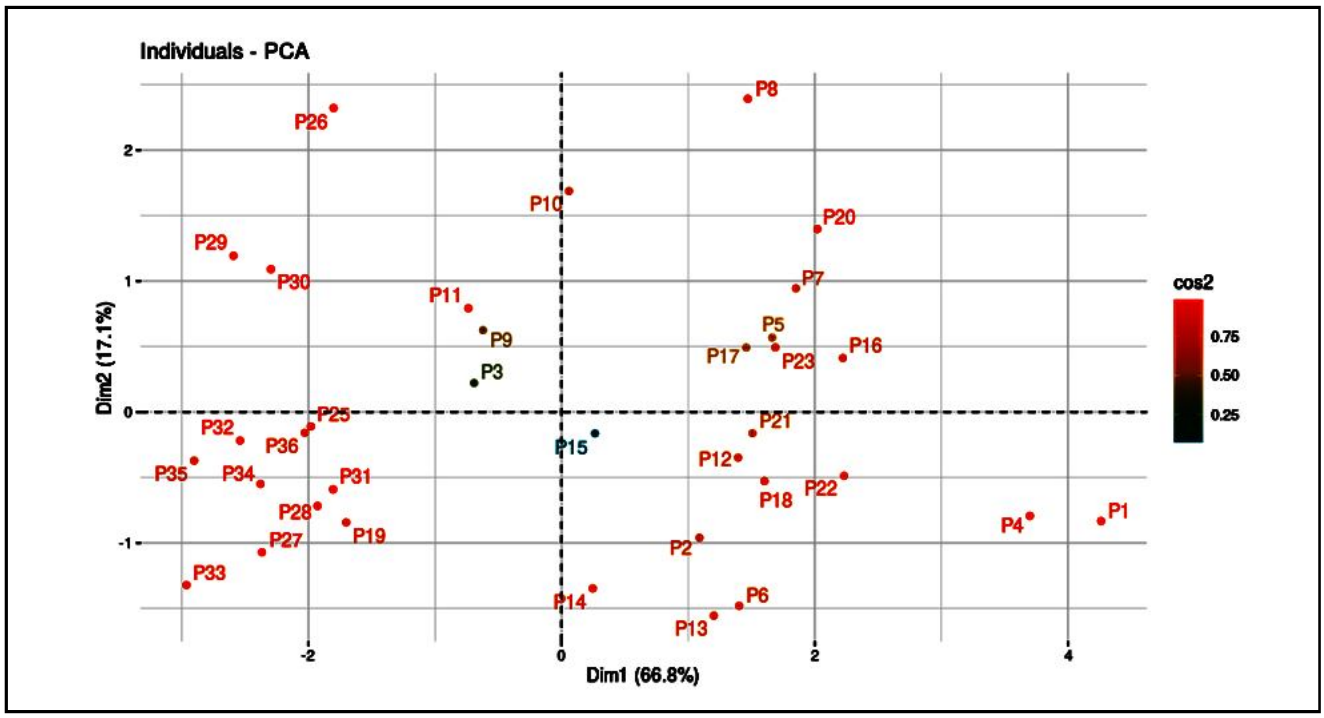

Figure 4: PCA score plot showing the distribution of mango genotypes based on fruit quality traits.

3.9.3 PCA biplot

The PCA biplot (Figure 5) simultaneously illustrates the distribution of the samples and the contribution of the measured variables. Samples located in the direction of a particular variable vector were positively associated with that characteristic. Samples P1, P4, P7, P8, P16, P17, and P20 were positioned close to the vectors representing acidity, crude fibre, and ascorbic acid, indicating that these samples possessed comparatively higher values for these quality parameters. On the other hand, samples P26, P29, P30, P32, P33, P34, P35, and P36 were associated with the total sugars (TSS) vector, indicating relatively higher sugar content. Sample P10 was located near the firmness vector, suggesting that it exhibited greater fruit firmness than most of the other samples. The opposite orientation of the total sugars vector relative to acidity and crude fibre confirms the negative relationship among these variables, whereas the proximity of acidity, crude fibre, and ascorbic acid vectors indicates strong positive correlations among these quality attributes.

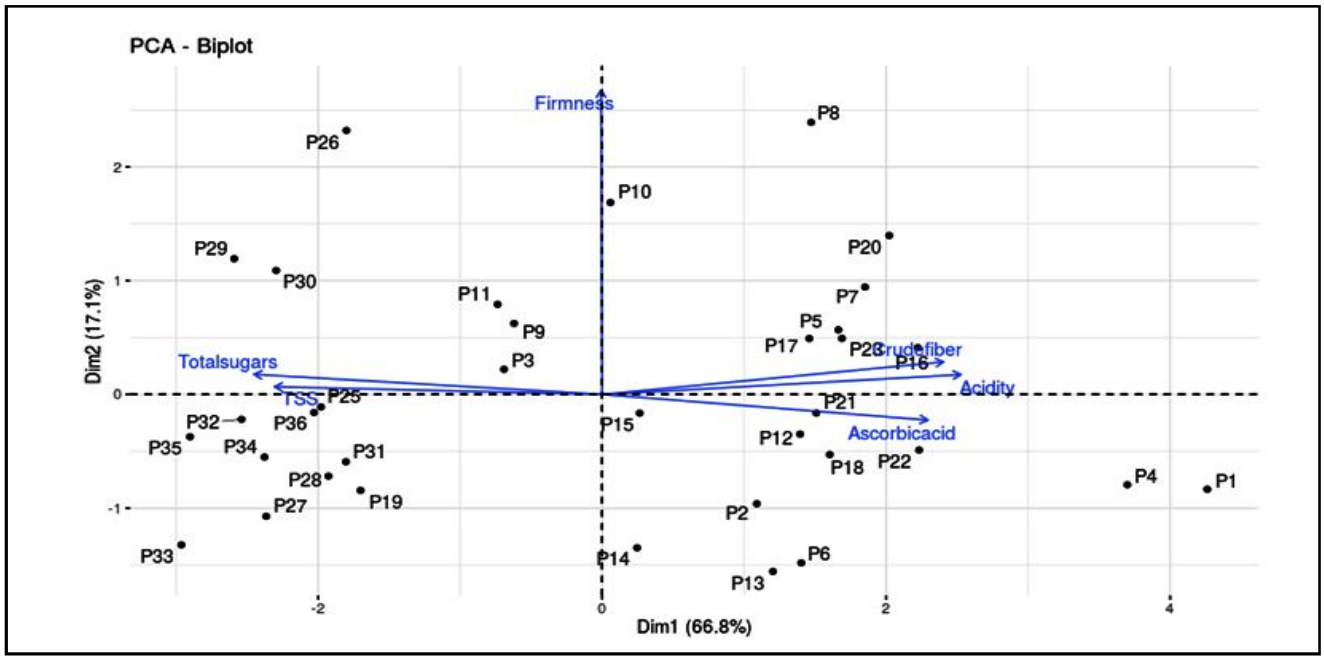

Figure 5: PCA biplot represents the association between mango genotypes and fruit quality traits.

3.9.4 Correlation of variables with principal components

The correlation plot (Figure 6) shows the contribution of each variable to the six principal components. PC1 exhibited strong positive correlations with acidity, ascorbic acid, and crude fibre, while showing strong negative correlations with total sugars (TSS). This indicates that PC1 primarily represents the contrast between sugar accumulation and the other quality attributes. PC2 was dominated almost exclusively by firmness, indicating that fruit firmness varied independently of the remaining physicochemical traits. The subsequent principal components (PC3-PC6) explained relatively small proportions of the total variation and showed weaker correlations with the measured variables. Therefore, the first two principal components were sufficient to describe the major variation present in the dataset and effectively summarised the relationships among the physicochemical characteristics of the samples.

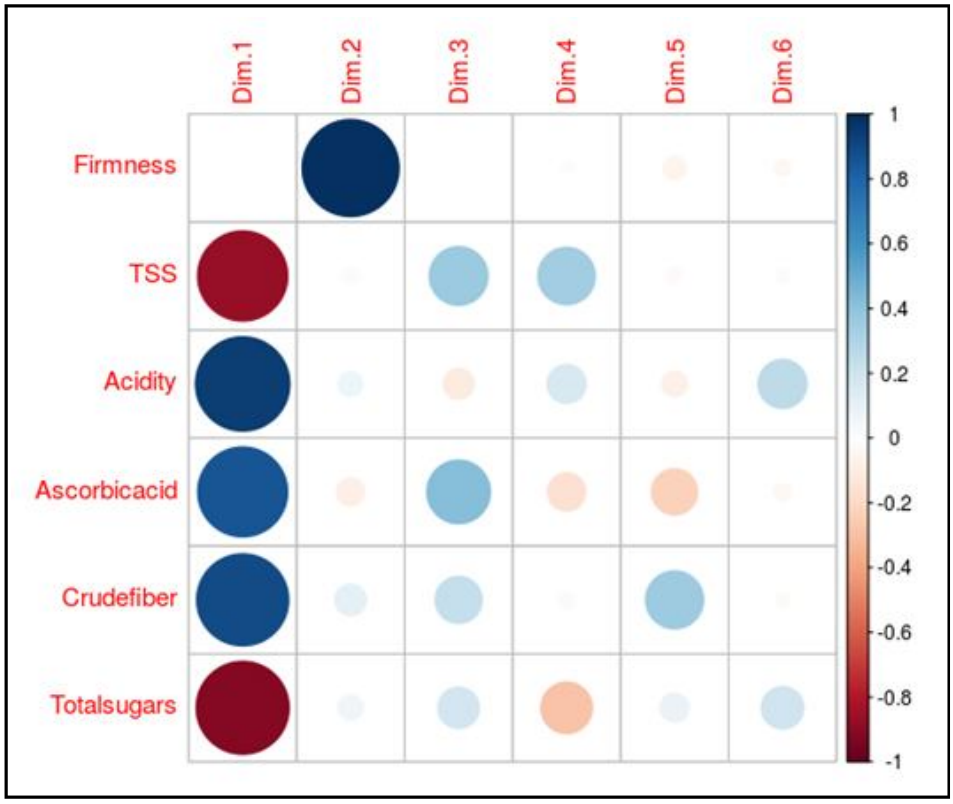

Figure 6: Correlation of fruit quality traits with principal components (PC1-PC6).

4. Discussion

Vasugi *et al.* (2012) evaluated the biochemical parameters of 43 different pickling mango accessions, collected from different parts of Karnataka. The total soluble solid content was high (25.2^0 Brix) in Kovesara and lower in Kalakai (7.5^0 Brix). They also state that acidity levels in pickling mango genotypes range between 0.11% to 7.48%, cultivar Himsagar had the lowest value and genotype Aruna Gowda Apple had the highest. In general mango cultivar had TSS of 0.7 to 23.5^0 Brix, reducing and non-reducing sugars of 1.67 to 5.81 mg g^{-1} and 6.07 to 14.9 mg g^{-1}, ascorbic acid from 60 to 170.8 mg g^{-1}, whereas, total sugars/acid ratio was ranged from 15.3 to 73.4 mg g^{-1}, according to Barholia and Yadav (2014) who studied about commercial varieties and landraces of mango genotypes. According to Musyimi (2016), Kent and Apple mangoes recovered the most juice, while Sabine mangoes recovered the least juice at 53 per cent. They also stated that Apple and Ngowe mango varieties had the highest total sugar content of 17.0 to 23.9 mg g^{-1}, while the Sabine cultivar had the lowest. Samar, Aman Dusahri, Bahisht Chaunsa and Anwar Ratual these mango cultivars had values of 5.40, 5.47, and 5.33 for juice pH. Titratable acid and ascorbic acid declined with the fruit's maturation time. Anwar Ratual, Samar Bahisht Chaunsa, and Langra, on the other hand, showed notable increases in total sugar content of 20.7 mg g^{-1}, 20.4 mg g^{-1} and 20.3 mg g^{-1} (Naz *et al.*, 2014). Sellamuthu *et al.* (2013) evaluated bio-active compounds and quality parameters of six mango cultivars namely Tommy Atkins, Sabre, Rosa, Zill, Peach and Phiva. They revealed that the cultivar sabre had the highest amount of ascorbic acid content of 69.71 mg/100 g, they also had higher antioxidant activity. Simi and Rajmohan (2013) experimented to evaluate the fifty traditional mango genotypes/varieties located in different districts of Kerala. Based on these findings they classified 50 types into three different groups, *i.e.*, pickling, table and dual purposes. Among the pickling mango genotypes should have a higher amount of Ascorbic acid (119.05 mg g^{-1}), titratable acidity (4.02%), crude fiber (2.80%) and lower the amount of total soluble solids, total sugars compared to the table and dual-purpose, that makes them these genotypes are ideal for pickle making purpose. Based on the findings of (Singh *et al.*, 2013) triable acidity, crude fibre, the ascorbic acid level in a particular genotype is the most important traits for pickle making. The acidity level in that evaluated pickling mango genotype ranges between 1.92% to 3.34%, out of 33 unique

wild pickling mango accessions Balekoppada Appe had the highest and Dannalli Appe had the lowest. Similarly, ascorbic acid levels in certain pickling mango accessions are more than 100 mg g^{-1} of fruit pulp. Local accessions Kashmiri had the highest Ascorbic acid content of 114.1 mg g^{-1}. In this study, the NA-7 cultivar was rated the highest for yielding top-quality pickles among all the tested varieties. Conversely, research by Singh *et al*. (2013) indicated that the NA-6 and NA-9 aonla cultivars contain lower fiber content. Recent findings indicate a gradual increase in pickle browning over the storage period. This is likely due to non-enzymatic reactions, such as the oxidation of phenols or the interaction between ascorbic acid and sugar, which result in the formation of brown pigments. Similar observations have been reported in studies on aonla pickle, supporting these findings (Gupta *et al*., 2018; Shinde *et al*., 2004; Supasin *et al*., 2022).

5. Conclusion

The study concludes that the quality attributes of biochemical traits like titrable acidity (3.32%), ascorbic acid (52.98 mg g^{-1}) and crude fiber (2.76%) were maximum in genotype MI-PM-01. PCV and GCV estimates were maximum for traits like acidity percentage, ascorbic acid, crude fiber and total sugars. High heritability coupled with high GAM was noticed for firmness (%). The genotype MI-PM-26 is suitable for sliced fruit pickle making because of its moderate level of acidity, ascorbic acid and crude fibre, while MI-PM-01 is suited for whole fruit pickle making due to its high acidity, ascorbic acid, crude fibre and lower TSS and total sugars. The identification of genotypes MI-PM-26, MI-PM-28, and MI-PM-01 exhibiting desirable traits presents promising opportunities for future breeding and cultivation programs. These selected genotypes, with their favourable characteristics, can be further evaluated under diverse agro-climatic conditions to confirm their stability and performance. The collected scion shoots, already multiplied, will serve as valuable planting material for establishing experimental orchards, enabling large-scale field trials and potential commercial propagation. Continued research on their adaptability, yield potential, and resistance to biotic and abiotic stresses will contribute to developing superior cultivars tailored to regional needs.

Availability of data and material

All data are provided within the manuscript.

Authorship contribution statement

R.V. Sundarrajan and P. Vinitha : Supervision, academic oversight and overall monitoring of the research work; **M. Kabilan and P. Sudheer Kumar Reddy:** Conceptualization, supervision, critical review and overall guidance of the manuscript; **R. Naveen and M. Amaravel:** Software handling, reference management, data organization and visualization of the review content; **C. Aadhithyan:** Literature survey, data curation and critical analysis of published studies; **Adnan A. Khan:** Critical review, validation of scientific content and final approval of the manuscript.

Consent for publication

All authors gave their full consent for publication and submission to this journal.

Conflict of interest

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

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Ethics approval

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