PLANT SCIENCE TODAY
Vol 12(2): 1-12
https://doi.org/10.14719/pst.7526

eISSN 2348-1900

RESEARCH ARTICLE

Evaluating correlation coefficients of mango (*Mangifera indica* L.) genotypes from western Uttar Pradesh

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Received: 30 January 2025; Accepted: 21 May 2025; Available online: Version 1.0: 27 May 2025; Version 2.0 : 10 June 2025

Cite this article: Amit K, Arvind K, Satya P, Vipin K, Atar S, Gaurav KA, Vibhu P, Saurabh KS, Kuldeep KS, Khursheed A, Ajay K. Evaluating correlation coefficients of mango (*Mangifera indica* L.) genotypes from western Uttar Pradesh . Plant Science Today. 2025; 12(2): 1-11. https://doi.org/10.14719/pst.7526

Abstract

The present investigation was carried out during 2021-22 and 2022-23 at Horticultural Research Centre, SVPUAT, Meerut, using twelve mango genotypes in a Randomized Block Design (RBD) with four replications. Phenotypic and genotypic correlation coefficients were computed using pooled data to determine interrelationships among morphological and biochemical traits of different genotypes in Mango. Phenotypically, fruit weight exhibited strong, positive and significant correlations with fruit pulp weight (0.915**), stone weight (0.783**), kernel weight (0.731**), fruit length (0.719**) and fruit width (0.674**), suggesting these traits can be considered for direct selection. Similarly, fruit pulp weight correlated positively with fruit length (0.732**), kernel weight (0.762**) and TSS (0.598**), while TSS showed strong association with fruit length (0.695**), pulp weight (0.582**) and kernel weight (0.412**). Total sugar was positively correlated with non-reducing sugar (0.812**), TSS (0.728**) and reducing sugar (0.395**), indicating a close biochemical interdependence in fruit quality. At the genotypic level, even stronger correlations were evident for many trait combinations. For instance, fruit weight with pulp weight (0.952**), kernel weight (0.749**) and fruit length (0.764**) were highly significant. Likewise, total sugar showed strong genotypic correlations with non-reducing sugar (0.870**) and TSS (0.776**). These results confirm that phenotypic correlations, complemented by genotypic values, serve as a practical guide for breeders. Traits such as fruit pulp weight, kernel weight, fruit length and TSS should be prioritized in selection programs to achieve simultaneous genetic improvement in both yield and fruit quality in mango.

Keywords: correlation coefficient; fruit yield; genotypes; mango; morphological traits; quality

Introduction

Mango (*Mangifera indica* L.) is the most popular fruit in tropical and subtropical regions of the world (1). Botanically, mango belongs to the dicotyledonous family Anacardiaceae. Its chromosome number is 2n = 40 and it is believed to have evolved through interspecific crossing and subsequent chromosome doubling (2). Mango is cross-pollinated and has a genome size of approximately 450 Mb. India is globally renowned for its vast diversity of mango varieties, each exhibiting unique flavor, texture and aroma (3). The fruit is believed to have originated in the Southeast Asia or Indo-Burma region (4, 5). Owing to its exceptional flavor, attractive color and richness in vitamins and minerals, mango is rightly regarded as the “King of Fruits” in tropical regions and is recognized as the “National Fruit of India” (6, 7). The total area under mango cultivation in India is 2.35 million hectares, with a production of 20.77 million tonnes (8). The major mango-growing states include Uttar Pradesh Andhra Pradesh, Karnataka, Bihar, Gujarat and Maharashtra.

The systematic evaluation of correlation coefficients among mango genotypes in Western Uttar Pradesh is vital for identifying key traits that influence fruit quality and yield (9). Understanding these relationships assists in the selection and breeding of superior cultivars, thereby enhancing agricultural productivity and the sustainability of the mango industry in the region (10). This study aims to provide insights into both genetic and phenotypic correlations, which are critical for effective breeding strategies and the development of mango varieties with improved agronomic performance and fruit quality. The evaluation of correlation coefficients among mango genotypes in Western Uttar Pradesh is therefore of significant importance in advancing regional mango breeding efforts. Mango, a major horticultural crop in India, holds immense economic and cultural value. However, the diverse agro-climatic conditions of Western Uttar Pradesh pose both opportunities and challenges for mango cultivation. Environmental variability in this region influences the phenotypic expression of traits, necessitating a thorough understanding of the genetic interrelationships among them (11).

Correlation analysis serves as a key tool for identifying the strength and direction of associations among morphological and quality traits in mango genotypes (12). By quantifying these relationships, breeders can prioritize traits that contribute most significantly to desired outcomes such as increased fruit size, sweetness and resistance to pests and diseases. Moreover, understanding these correlations helps mitigate the effects of undesirable trait linkages that may hinder breeding efforts (13). This study presents a comprehensive evaluation of genetic and phenotypic correlations among major traits in mango genotypes from Western Uttar Pradesh. The findings will support the selection of superior genotypes and inform breeding strategies tailored to the region's conditions. Ultimately, this research contributes to the development of mango varieties with enhanced yield, quality and adaptability, promoting the sustainability and profitability of mango production in the region.

Materials and Methods

The present experiment was conducted at Horticultural Research Centre of Sardar Vallabhbhai Patel University of Agriculture and Technology, Modipuram, Meerut, Uttar Pradesh, India, located at 29˚04' N latitude, 77˚42' E longitude and an altitude of 237.75 meters above mean sea level. The mango genotypes were replicated four times, resulting in a total of 48 trees. The experiment was conducted using a Randomized Block Design (RBD) featuring 12 mango genotypes and four replications which were selected from a 10-year-old orchard of mango located at University campus (Table 1).

Table 1. Mango (*Mangifera indica* L.) Genotypes evaluated for morphological and quality traits used in correlation analysis

Genotype Name	Source
Ambika	CISH, Lucknow
Pusa Arunima	IARI, New Delhi
Dashehari-51	CISH, Lucknow
Kesar	JAU, Junagadh (Gujarat)
Pusa Surya	IARI, New Delhi
Mallika	IARI, New Delhi
Amrapali	IARI, New Delhi
Burma Surakha	Saharanpur district
Neelum Chausa	Regional/local cultivar
Mithua Malda	Malda-type (selection)
Rataul	Baghpat district
Saurav	Saharanpur district

The trees were planted with a spacing of 6 meters by 6 meters. The region experiences a subtropical climate with considerable seasonal variation. During the study period, maximum summer temperatures reached 44.4 °C and 45.6 °C, while minimum winter temperatures dropped to 5.5 °C and 6.4 °C in 2021-22 and 2022-23, respectively. Frost is common from December to February. The southwest monsoon typically begins in the last week of June and withdraws by the end of September, with 80-90 % of the annual rainfall concentrated in July and August. The area also receives sporadic cyclonic rainfall during December–January and late spring. Annual rainfall totalled 1031 mm in 2021-22 and 960.5 mm in 2022-23, with highly uneven distribution. Standardized agronomic practices, including uniform nutrient and pest management, were adopted across treatments to ensure accurate and unbiased genetic assessment.

Correlation coefficient

Correlation was estimated the association between various character-pairs. The correlations at genotypic and phenotypic levels were estimated from the analysis of variance and covariance as suggested (14). The analysis of variance and co-variance was used for estimation of correlation coefficient in the following manner.

Phenotypic correlation between character x and y

$$r_{xy}(p) = \frac{Cov_{xy}\,(p)}{\sqrt{Var_x\,(p) x\,Var_y\,(p)}}$$

Genotypic correlation between character x and y

$$r_{xy}(g) = \frac{Cov_{xy}\,(g)}{\sqrt{Var_x\,(g) x\,Var_y\,(g)}}$$

Where,

Cov_{xy} (p) = Phenotypic covariance between two characters x and y.

Cov_{xy} (g) = $\sqrt{Var_x\,(g)\ x\ Var_y\,(g)}$

Var_x (p) = Phenotypic variance for characters x

Var_x (g) = Genotypic variance for characters x

Var_y (p) = Phenotypic variance for characters y

Var_y (g) = Genotypic variance for characters y

Cov_{xy} (g) = Genotypic covariance between two characters x and y

The significance of correlation coefficient (r) was tested by comparing the observed value of correlation coefficient with the tabulated value for (n-2) degree of freedom. If the observed value is more than the table value, the correlation coefficient is said to be significant.

$$t = \frac{r}{\sqrt{1-r^2}} \times\sqrt{n-2}$$

Where,

r = correlation coefficient

n = number of genotypes

t = t calculated value

Results and Discussion

Genotypic correlation coefficient

A pooled genotypic correlation analysis conducted over two consecutive years (2021-22 and 2022-23) revealed key associations among fruit traits in mango (Table 2).

Fruit weight

Fruit weight showed negative and highly non-significant correlation with number of fruit yield per tree (-0.084). Fruit weight showed negative and non-significant correlation with number of fruits per tree. It may be noted here that genetic correlation is basically a correlation of phenotypic effect by different genotypic variants in mango (15, 16).

Fruit length

Fruit length showed positive and highly significant correlation with fruit weight (0.827**) whereas non-significant negative correlated with number of fruit yield per tree (-0.140). Fruit width showed positive and highly significant correlation with fruit weight (0.724*) followed by fruit length (0.649*) whereas non-significant positive correlated with number of fruit yield per tree (0.185). It may be worth noted here that two traits shared the proportion *ie*., positive and negative relation is due to the genetic influence among each other clearly stated the relationship with mango considering fruit length (17).

Fruit pulp weight

Fruit pulp weight showed positive and highly significant correlation with (fruit weight 0.975*) followed by fruit length (0.820*) and fruit width (0.649*) whereas non-significant positive correlated with number of fruit yield per tree (0.011). It may be noted here that more attention may be given to the traits having the greatest positive influence for any varietal improvement in mango (18-20).

Stone weight

Stone weight showed positive and highly significant correlation with fruit weight (0.839**) followed by fruit pulp weight (0.828**), fruit length (0.681**) and fruit width (0.666**) whereas non-significant negative correlated with number of fruit yield per tree (-0.102). The present results coincide previous results (21, 22).

Kernel length

Kernel length showed positive and highly significant correlation with stone weight (0.674**) followed by fruit width (0.616**), fruit length (0.543**), fruit pulp weight (0.497**) and fruit weight (0.489**) whereas non-significant positive correlated with number of fruit yield per tree (0.249). The correlation also confirmed in previous works in mango (23-25).

Kernel weight

Kernel weight showed positive and highly significant correlation with stone weight (0.854**) followed by fruit pulp weight (0.845**), fruit weight (0.815**), fruit width (0.800**), fruit length (0.765**) and stone length (0.689**) whereas non-significant positive correlated with number of fruit yield per tree (0.165). The correlation also confirmed in previous results (23-25).

Stone length

Stone length showed positive and highly significant correlation with fruit length (0.742**) followed byfruit weight (0.585**), stone length (0.541**), stone weight (0.536**), kernel weight (0.520**), fruit width (0.516**) and fruit pulp weight (0.479**) while non-significant negative correlated with number of fruit yield per tree (-0.487**). The positive and highly significant correlation provides an insight emphasizing their importance in yield improvement. The present results are in support with previous results (26, 27).

Kernel width

Kernel width showed positive and highly significant correlation with kernel weight (0.845**) followed by fruit pulp weight (0.714**), fruit weight (0.686**), fruit width (0.659**), fruit length (0.626**), stone weight (0.597**) and stone length (0.515**) whereas non-significant positive correlated with kernel length (0.324) and number of fruit yield per tree (0.315). Our results also agreed with those of (26, 28).

Total soluble solid

Total soluble solid showed positive and highly significant correlation with fruit length (0.828**) followed by fruit pulp weight (0.724**), fruit weight (0.661**), kernel width (0.497**), kernel weight (0.477**), fruit width (0.428**), stone length (0.366*) and stone weight (0.355*) whereas non-significant positive correlated with kernel length (0.298) and number of fruit yield per tree (0.188). The study assessed various traits in which Total soluble solid (TSS) showed positive and highly significant correlation with fruit characteristics. The higher genotypic correlation estimates the genes contributing to these traits are often co-inherited. The present research agrees with earlier reports of (28, 29).

Acidity

Acidity showed positive and highly significant correlation with total soluble solid (0.389*) followed by number of fruit yield per tree (0.345*), whereas non-significant positive correlated with stone length (0.146), fruit width (0.091) and fruit length (0.042) while non-significant negative correlated with kernel length (-0.142), fruit pulp weight (-0.144), fruit weight (-0.161), kernel weight (-0.235), stone weight (-0.307) and kernel width (-0.385*). Our study is well corroborated with the findings of (23,30,31). The present findings highlight the importance of sugar metabolism in determining fruit quality as suggested by previously studies (21, 32).

Reducing sugar

Reducing sugar showed positive and highly significant correlation with fruit length (0.348*) whereas non-significant positive correlated with kernel weight (0.298) followed by fruit width (0.274), total soluble solid (0.266), stone weight (0.263), fruit pulp weight (0.236), acidity (0.198), fruit weight (0.187), stone length (0.117), kernel length (0.102) and kernel width (0.089) while non-significant negative correlated with number of fruit yield per tree (-0.264).

Non-reducing sugar

Non-reducing sugar showed positive and highly significant correlation with total soluble solid (0.965**) followed by fruit length (0.631**), kernel width (0.597**), fruit pulp weight (0.583**), fruit weight (0.457**), kernel weight (0.434**) and number of fruit yield per tree (0.404*) whereas non-significant positive correlated with fruit width (0.279), acidity (0.247), stone length (0.207), stone weight (0.168), reducing sugar (0.132) and kernel length (0.061).

Table 2. Genotypic correlation coefficient among different characters in mango based on pool data of 2021-22 and 2022-23

CTR	NF	FWT	FL	FW	FPW	SWT	SL	KWT	KL	KW	TSS	Acidity	RS	NRS	TS	TC	AA	PC	TA	FY
NF	1.000	-0.084	-0.140	0.185	0.011	-0.102	0.249	0.165	-0.487**	0.315	0.188	0.345*	-0.264	0.404*	0.279	0.215	0.185	0.409*	0.395*	0.621**
FWT			0.827**	0.724**	0.975**	0.839**	0.489**	0.815**	0.585**	0.686**	0.661**	-0.161	0.187	0.457**	0.470**	0.093	0.682**	0.293	0.509**	0.708**
FL				0.649**	0.820**	0.681**	0.543**	0.765**	0.742**	0.626**	0.828**	0.042	0.348*	0.631**	0.724**	0.002	0.729**	0.423*	0.576**	0.593**
FW					0.649**	0.666**	0.616**	0.800**	0.516**	0.659**	0.428**	0.091	0.274	0.279	0.320	-0.270	0.778**	0.129	0.309	0.668**
FPW						0.828**	0.497**	0.845**	0.479**	0.714**	0.724**	-0.144	0.236	0.583**	0.603**	0.252	0.729**	0.344*	0.618**	0.777**
SWT							0.674**	0.854**	0.536**	0.597**	0.355*	-0.307	0.263	0.168	0.253	-0.166	0.697**	0.089	0.213	0.573**
SL								0.689**	0.541**	0.515**	0.366*	0.146	0.117	0.207	0.230	-0.224	0.503**	0.385*	0.322	0.599**
KWT									0.520**	0.845**	0.477**	-0.235	0.298	0.434**	0.506**	-0.036	0.877**	0.140	0.411*	0.751**
KL										0.324	0.298	-0.142	0.102	0.061	0.089	-0.417*	0.309	0.239	0.161	0.167
KW											0.497**	-0.385*	0.089	0.597**	0.547**	-0.113	0.613**	0.143	0.533**	0.702**
TSS												0.389*	0.266	0.965**	0.980**	0.438**	0.530**	0.663**	0.887**	0.695**
Acidity													0.198	0.247	0.276	0.251	0.057	0.573**	0.354*	0.199
RS														0.132	0.471**	-0.029	0.655**	-0.191	0.146	-0.034
NRS															0.974**	0.451**	0.446**	0.601**	0.899**	0.693**
TS																0.396*	0.616**	0.480**	0.863**	0.608**
TC																	-0.034	0.258	0.409*	0.325
AA																		0.145	0.435**	0.655**
PC																			0.789**	0.575**
TA																				0.724**
FY																				1.000

*, ** significant at 5% and 1% level, respectively

[Where, CTR: Characters; NF: Number of Fruits per Tree; FWT: Fruit Weight; FL:Fruit Length; FW: Fruit Width; FPW: Fruit Pulp Weight; SW: Stone Weight; SL: Stone Length; KWT: Kernel Weight; KL: Kernel Length; KW: Kernel Width; TSS: Total Soluble Sugar; Acidity: Acidity; RS: Reducing Sugar; NRS: Non-Reducing Sugar; TS: Total Sugar; TC: Total Carotenoids; AA: Ascorbic Acid; PC: Phenol Content; TA: Total Antioxidants; FY: Fruit Yield per Tree]

Total sugar

Total sugar showed positive and highly significant correlation with total soluble solid (0.980**) followed by non-reducing sugar (0.974**), fruit length (0.724**), fruit pulp weight (0.603**), kernel width (0.547**), kernel weight (0.506**), reducing sugar (0.471**) and fruit weight (0.470**) whereas non-significant positive correlated with fruit width (0.320), number of fruit yield per tree (0.279), acidity (0.276), stone weight (0.253) and stone length (0.230) and kernel length (0.089). The accumulation of sugar is one of the main features in ripening. Previous works also showed similar and significant results (33, 34).

Total carotenoid

Carotenoids were positively and significantly associated with non-reducing sugar (0.451**), TSS (0.438**) and total sugar (0.396*). indicating that sweeter fruits may also exhibit higher pigment accumulation. However, many correlations with other traits were non-significant or negative, including reducing sugar and kernel traits. This indicates a more independent expression, suggesting for targeted selection without impacting yield directly. These results agree with previous studies (34, 35).

Ascorbic acid

Ascorbic acid showed positive and highly significant correlation with kernel weight (0.877**) followed by fruit width (0.778**), fruit length(0.729**), fruit pulp weight (0.729**), stone weight(0.697**), fruit weight (0.682**), reducing sugar (0.655**), total sugar (0.616**), kernel width (0.613**), kernel width (0.530**), stone length (0.503**) and non-reducing sugar (0.446**) whereas non-significant positive correlated with kernel length (0.309), number of fruit yield per tree (0.185) and acidity (0.057) while non-significant negative correlated with total carotenoid (-0.034). Similar findings were reported in previous works in mango (36).

Phenol content

Phenol content showed positive and highly significant correlation with total soluble solid (0.663**) followed by non-reducing sugar(0.601**), acidity (0.573**), total sugar (0.480**), fruit length (0.423*), number of fruit yield per tree (0.409*), stone length (0.385*) and fruit pulp weight (0.344*) whereas non-significant positive correlated with fruit weight (0.293), total carotenoid (0.258), kernel length (0.239), ascorbic acid (0.145), kernel width (0.143), kernel weight (0.140), fruit width (0.129) and stone weight (0.089) while non-significant negative correlated with reducing sugar (-0.191). The present results coincide with those of previous works (37, 38).

Total antioxidants

Total antioxidants showed positive and highly significant correlation with non-reducing sugar (0.899**) followed by total soluble solid (0.887**), total sugar (0.863**), phenol content (0.789**), fruit pulp weight (0.618**), fruit length (0.576**), kernel width (0.533**), fruit weight (0.509**), ascorbic acid (0.435**), kernel width (0.411*), total carotenoid (0.409*), number of fruit yield per tree (0.395*) and acidity (0.354*) whereas non-significant positive correlated with stone length (0.322), fruit width (0.309), stone weight (0.213), kernel length (0.161) and reducing sugar(0.146). It is clear from the data that positive and highly significant correlation with non-reducing sugar which states that traits can be improved as genetic correlation quantifies the genetic influences on one trait and those on other (39, 40).

Fruit yield per tree

Fruit yield per tree had highly significant correlations with fruit pulp weight (0.777**), kernel weight (0.751**), fruit weight (0.708**) and TSS (0.695**), showing that yield is strongly influenced by both internal and external fruit characteristics. Traits such as ascorbic acid, non-reducing sugar and total sugar also showed strong positive associations. This confirms that higher-yielding genotypes can also possess superior quality, allowing breeders to improve both simultaneously. These findings emphasize the importance of focusing on traits with positive genetic influences for targeted breeding programs. In agreement to the present study previous findings have been done (41-43).

Phenotypic correlation coefficient

Fruit weight

Fruit weight revealed genotypic correlation coefficient in Table 3, non-significant negative correlated with number of fruit yield per tree (-0.096). Fruit length showed positive and highly significant correlation with fruit weight (0.764**) while non-significant negative correlated with number of fruit yield per tree (-0.125).

Fruit width

Fruit width showed positive and highly significant correlation with fruit weight (0.687**) and fruit length (0.556**) whereas non-significant positive correlated with number of fruit yield per tree (0.181). The present study is very well documented from earlier findings (15-16).

Fruit pulp weight

Fruit pulp weight showed positive and highly significant correlation with fruit weight (0.952**), fruit length (0.775**) and fruit width (0.596**) whereas non-significant positive correlated with number of fruit yield per tree (0.008).

Stone weight

Stone weight showed positive and highly significant correlation with fruit weight (0.800**), fruit pulp weight (0.779**), fruit length (0.626**) and fruit width (0.588**) while non-significant negative correlated with number of fruit yield per tree (-0.093). Significant genetic or phenotypic correlation coefficient between two traits does not always predict interdependence in ber (44, 45), in peach (46), in avocado (47).

Kernel length

Kernel length showed positive and highly significant correlation with stone weight (0.622**), fruit width (0.565**), fruit weight (0.477**), fruit length (0.470**) and fruit pulp weight (0.451**) whereas non-significant positive correlated with number of fruit yield per tree (0.219). It may be noted here that correlation coefficient analysis measures the magnitude of any relationship between fruit and fruit yield characters in mango (48).

Table 3. Phenotypic correlation coefficient among different characters in mango based on pool data of 2021-22 and 2022-23

CTR	NF	FWT	FL	FW	FPW	SWT	SL	KWT	KL	KW	TSS	Acidity	RS	NRS	TS	TC	AA	PC	TA	FY
NF	1.000	-0.096	-0.125	0.181	0.008	-0.093	0.219	0.138	-0.446**	0.290	0.149	0.337*	-0.268	0.392*	0.252	0.206	0.185	0.390*	0.396*	0.594**
FWT			0.764**	0.687**	0.952**	0.800**	0.477**	0.749**	0.544**	0.657**	0.555**	-0.150	0.185	0.430**	0.451**	0.089	0.662**	0.293	0.494**	0.702**
FL				0.556**	0.775**	0.626**	0.470**	0.731**	0.650**	0.514**	0.735**	-0.002	0.323	0.637**	0.623**	0.003	0.664**	0.388*	0.567**	0.555**
FW					0.596**	0.588**	0.565**	0.666**	0.507**	0.612**	0.272	0.141	0.203	0.235	0.340*	-0.263	0.734**	0.114	0.291	0.632**
FPW						0.779**	0.451**	0.820**	0.433**	0.667**	0.636**	-0.167	0.250	0.546**	0.573**	0.252	0.705**	0.331*	0.600**	0.771**
SWT							0.622**	0.768**	0.515**	0.491**	0.326	-0.253	0.220	0.186	0.216	-0.165	0.678**	0.086	0.194	0.546**
SL								0.628**	0.507**	0.474**	0.255	0.159	0.119	0.192	0.241	-0.222	0.471**	0.383*	0.305	0.566**
KWT									0.443**	0.728**	0.427**	-0.291	0.321	0.408*	0.467**	-0.027	0.806**	0.123	0.386*	0.717**
KL										0.301	0.205	-0.086	0.030	0.066	0.092	-0.393*	0.303	0.232	0.144	0.149
KW											0.388*	-0.315	0.081	0.497**	0.516**	-0.101	0.579**	0.141	0.504**	0.657**
TSS												0.305	0.228	0.823**	0.776**	0.392*	0.473**	0.586**	0.771**	0.624**
Acidity													0.112	0.200	0.258	0.204	0.079	0.521**	0.327	0.164
RS														0.105	0.436**	-0.027	0.603**	-0.183	0.137	-0.026
NRS															0.870**	0.436**	0.412*	0.577**	0.874**	0.656**
TS																0.365*	0.606**	0.447**	0.818**	0.587**
TC																	-0.045	0.261	0.396*	0.325
AA																		0.132	0.428**	0.638**
PC																			0.767**	0.570**
TA																				0.703**
FY																				1.000

*, ** significant at 5% and 1% level, respectively

[Where, CTR: Characters; NF: Number of Fruits per Tree; FWT: Fruit Weight; FL:Fruit Length; FW: Fruit Width; FPW: Fruit Pulp Weight; SW: Stone Weight; SL: Stone Length; KWT: Kernel Weight; KL: Kernel Length; KW: Kernel Width; TSS: Total Soluble Sugar; Acidity: Acidity; RS: Reducing Sugar; NRS: Non-Reducing Sugar; TS: Total Sugar; TC: Total Carotenoids; AA: Ascorbic Acid; PC: Phenol Content; TA: Total Antioxidants; FY:Fruit Yield per Tree]

Kernel weight

Kernel weight showed positive and highly significant correlation with fruit pulp weight (0.820**), stone weight (0.768**), fruit weight (0.749**), fruit length (0.731**), fruit width (0.666**) and stone length (0.628**) whereas non-significant positive correlated with number of fruit yield per tree (0.138). Similar observations were stated in previous results (26, 29).

Stone length

Stone length showed positive and highly significant correlation with fruit length (0.650**), fruit weight (0.544**), stone weight (0.515**), fruit width (0.507**), stone length (0.507**), kernel weight (0.443**) and fruit pulp weight (0.433**) while non-significant negative correlated with number of fruit yield per tree (-0.446**). Significant observations were quoted in previous research (16, 48, 49).

Kernel width

Kernel width showed positive and highly significant correlation with kernel weight (0.728**), fruit pulp weight (0.667**), fruit weight (0.657**), fruit width (0.612**), fruit length (0.514**), stone weight (0.491**) and stone length (0.474**) whereas non-significant positive correlated with kernel length (0.301) and number of fruit yield per tree (0.290). It may be noted here that this study identifies yield-related attributes that can be used to improve mango fruit production in mango (50, 51).

Total Soluble Solid (TSS)

TSS exhibited strong positive and highly significant correlations with fruit length (0.735**), fruit pulp weight (0.636**), fruit weight (0.555**), kernel weight (0.427**) and kernel width (0.388*). These associations suggest that sweeter mango genotypes often possess larger fruits and denser pulp, offering better consumer appeal and processing value. Although correlations with yield (0.149) and stone traits were positive but non-significant, the path coefficient analysis underscores TSS as a key indirect contributor to yield. These findings align with earlier reports (28, 29).

Acidity

Acidity showed non-significant positive correlated with number of fruit yield per tree (0.337), total soluble solid (0.305), stone length (0.159) and fruit width (0.141) while non-significant negative correlated with fruit length (-0.002), kernel length (-0.086), fruit weight (-0.150), fruit pulp weight (-0.167), stone weight (-0.253), kernel weight (-0.291) and kernel width (-0.315). Our research findings showed that and emphasized the importance of selecting desired characteristics for increased production. The current study is well corroborated with early findings (23, 30, 31).

Reducing sugar

Reducing sugar showed non-significant positive correlated with fruit length (0.323), kernel weight (0.321), fruit pulp weight (0.250), total soluble solid (0.228), stone weight (0.220), fruit width (0.203), fruit weight (0.185), stone length (0.119), acidity (0.112), kernel width (0.081) and kernel length (0.030) while non-significant negative correlated with number of fruit yield per tree (-0.268).

Non-reducing sugar

Non-reducing sugar showed positive and highly significant correlation with total soluble solid (0.823**), fruit length (0.637**), fruit pulp weight (0.546**), kernel width (0.497**), fruit weight (0.430**), kernel weight (0.408*) and number of fruit yield per tree (0.392*) whereas non-significant positive correlated with fruit width (0.235), acidity (0.200), stone length (0.192), stone weight (0.186), reducing sugar (0.105) and kernel length (0.066). Previous works showed similar and significant results (33, 34).

Total sugar

Total sugar showed positive and highly significant correlation with non-reducing sugar (0.870**), total soluble solid (0.776**), fruit length (0.623**), fruit pulp weight (0.573**), kernel width (0.516**), kernel weight (0.467**), fruit weight (0.451**), reducing sugar (0.436**) and fruit width (0.340*) whereas non-significant positive correlated with acidity (0.258), number of fruit yield per tree (0.252), stone length (0.241), stone weight (0.216) and kernel length (0.092). The present experiment headlines the significant positive and negative effects of direct and indirect components on several qualities. Similar observations were observed in previous works in mango (52, 53) and in Tamarind (54).

Total carotenoid

Carotenoids showed highly significant positive correlations with non-reducing sugar (0.436**), TSS (0.392*) and total sugar (0.365*), establishing its linkage with fruit maturity and pigmentation. While negatively correlated with kernel and stone traits, these findings suggest carotenoid content is more responsive to sugar accumulation than fruit size. This trait is vital for improving nutritional value and visual appeal (34, 35). The present experiment it may be noted here that carotenoid exhibited positive and highly significant correlation with different quality traits which states the increase in total carotenoid content (34, 35).

Ascorbic acid

Ascorbic acid displayed strong positive and highly significant correlations with kernel weight (0.806**), fruit width (0.734**), pulp weight (0.705**) and other size-related traits. This implies that larger fruits tend to accumulate more vitamin C, enhancing their nutritional profile. Weak correlations with yield and acidity highlight its utility in quality-focused breeding rather than yield-specific selection. Previous studies also similar with the present findings in mango (55-57).

Phenol content

Phenol content showed positive and highly significant correlation with non-reducing sugar followed by acidity, TSS, total sugar, number of fruit per tree, fruit length, stone length, fruit pulp weight, whereas non-significant positive correlated with followed by fruit weight, total carotenoid, kernel length, kernel width, fruit width, ascorbic acid, kernel weight, stone weight, while whereas non-significant negative correlated with reducing sugar (57, 58).

Total antioxidant

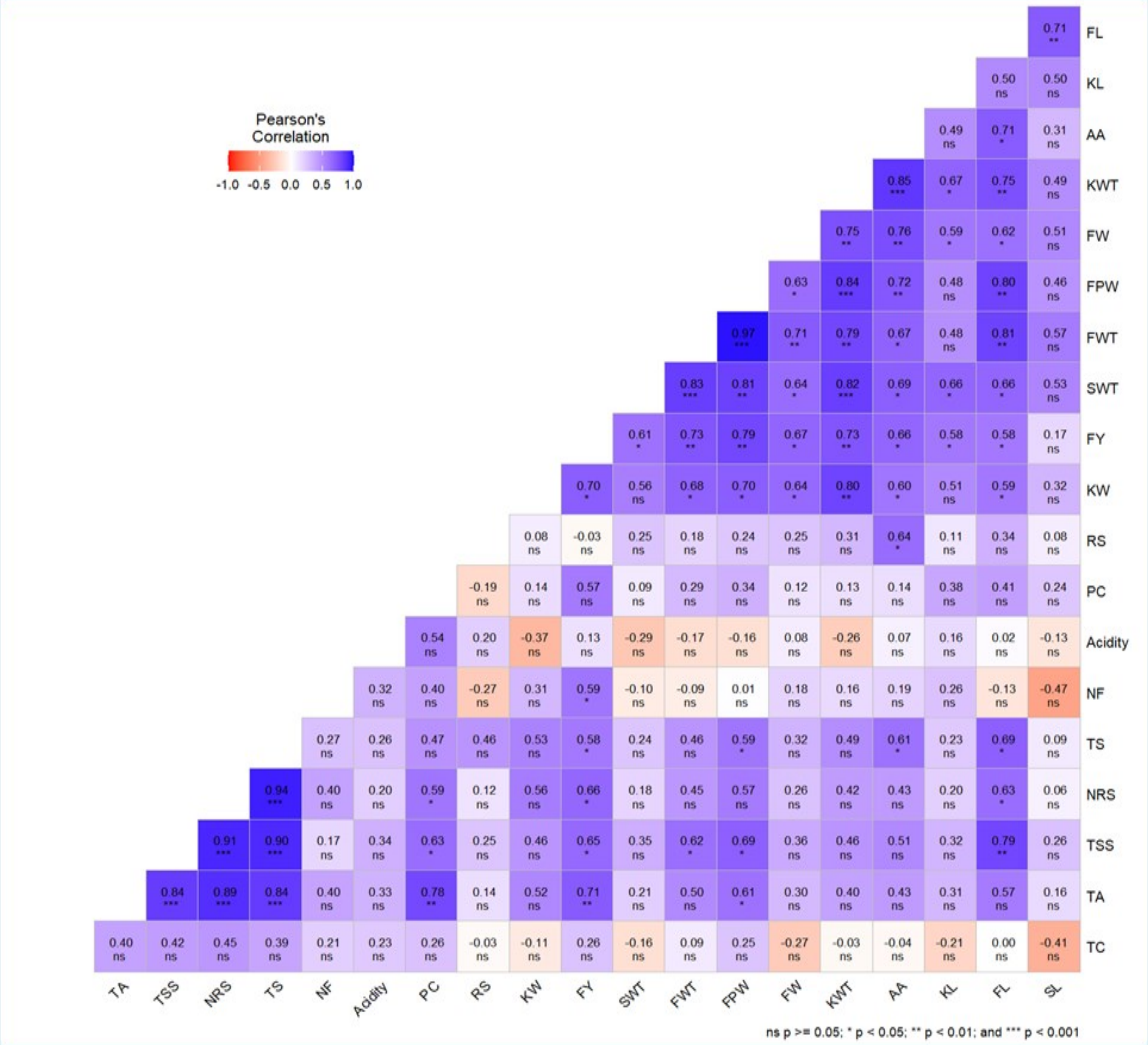
Total antioxidant also reveals from the data that positive and highly significant correlation with non-reducing sugar which states that traits can be improved as genetic correlation quantifies the genetic influences which modifies the phenotypic appearances (39, 40, 55, 59).

Fruit yield per tree

Phenotypic correlations with component traits revealed both positive and negative, mostly non-significant, associations, highlighting the complex nature of yield (Fig. 1). Traits such as non-reducing sugar, pulp weight and TSS showed moderate positive correlations, indicating potential for indirect selection. The data supports the concept that while traits may be heritable, they are not always genetically identical, emphasizing the need for integrated selection indices (42, 52).

Pearson's correlation coefficient analysis of traits associated between morphological and qualitative variable of mango genotypes

Phenotypic correlation among yield and yield-attributing traits plays a crucial role in determining an effective selection strategy for yield improvement (14, 20). It provides insights into the correlated genetic responses to directional selection, aiding in the formulation of selection indices a key tool for plant breeders and researchers. Positive correlations between desirable traits are particularly beneficial, as they facilitate simultaneous improvement of multiple attributes (12, 44). Yield, being a complex and multifaceted trait, is significantly influenced by its component traits. Understanding the correlations between these traits and their relationship with yield can simplify the selection process, enabling targeted improvements. The correlation values, derived from variance and covariance analyses, offer a statistical foundation for evaluating the associations among all possible trait combinations, thereby enhancing the efficiency of breeding



TA	TSS	NRS	TS	NF	Acidity	PC	RS	KW	FY	SWT	FWT	FPW	FW	KWT	AA	KL	FL	SL	
																		0.71 **	FL
																	0.50 ns	0.50 ns	KL
																0.49 ns	0.71 *	0.31 ns	AA
															0.85 ***	0.67 *	0.75 **	0.49 ns	KWT
														0.75 **	0.76 **	0.59 *	0.62 *	0.51 ns	FW
													0.63 *	0.84 ***	0.72 **	0.48 ns	0.80 **	0.46 ns	FPW
												0.97 ***	0.71 **	0.79 **	0.67 *	0.48 ns	0.81 **	0.57 ns	FWT
											0.83 ***	0.81 **	0.64 *	0.82 ***	0.69 *	0.66 *	0.66 *	0.53 ns	SWT
										0.61 *	0.73 **	0.79 **	0.67 *	0.73 **	0.66 *	0.58 *	0.58 *	0.17 ns	FY
									0.70 *	0.56 ns	0.68 *	0.70 *	0.64 *	0.80 **	0.60 *	0.51 ns	0.59 *	0.32 ns	KW
								0.08 ns	-0.03 ns	0.25 ns	0.18 ns	0.24 ns	0.25 ns	0.31 ns	0.64 *	0.11 ns	0.34 ns	0.08 ns	RS
							-0.19 ns	0.14 ns	0.57 ns	0.09 ns	0.29 ns	0.34 ns	0.12 ns	0.13 ns	0.14 ns	0.38 ns	0.41 ns	0.24 ns	PC
						0.54 ns	0.20 ns	-0.37 ns	0.13 ns	-0.29 ns	-0.17 ns	-0.16 ns	0.08 ns	-0.26 ns	0.07 ns	0.16 ns	0.02 ns	-0.13 ns	Acidity
					0.32 ns	0.40 ns	-0.27 ns	0.31 ns	0.59 *	-0.10 ns	-0.09 ns	0.01 ns	0.18 ns	0.16 ns	0.19 ns	0.26 ns	-0.13 ns	-0.47 ns	NF
				0.27 ns	0.26 ns	0.47 ns	0.46 ns	0.53 ns	0.58 *	0.24 ns	0.46 ns	0.59 *	0.32 ns	0.49 ns	0.61 *	0.23 ns	0.69 *	0.09 ns	TS
			0.94 ***	0.40 ns	0.20 ns	0.59 *	0.12 ns	0.56 ns	0.66 *	0.18 ns	0.45 ns	0.57 ns	0.26 ns	0.42 ns	0.43 ns	0.20 ns	0.63 *	0.06 ns	NRS
		0.91 ***	0.90 ***	0.17 ns	0.34 ns	0.63 *	0.25 ns	0.46 ns	0.65 *	0.35 ns	0.62 *	0.69 *	0.36 ns	0.46 ns	0.51 ns	0.32 ns	0.79 **	0.26 ns	TSS
	0.84 ***	0.89 ***	0.84 ***	0.40 ns	0.33 ns	0.78 **	0.14 ns	0.52 ns	0.71 **	0.21 ns	0.50 ns	0.61 *	0.30 ns	0.40 ns	0.43 ns	0.31 ns	0.57 ns	0.16 ns	TA
0.40 ns	0.42 ns	0.45 ns	0.39 ns	0.21 ns	0.23 ns	0.26 ns	-0.03 ns	-0.11 ns	0.26 ns	-0.16 ns	0.09 ns	0.25 ns	-0.27 ns	-0.03 ns	-0.04 ns	-0.21 ns	0.00 ns	-0.41 ns	TC

ns p >= 0.05; * p < 0.05; ** p < 0.01; and *** p < 0.001

Fig. 1. Pearson's correlation coefficient matrix revealing the relationship between morphological and qualitative variable of mango genotypes.

[Where, Total Carotenoids: TC; Total Antioxidants: TA; Total Soluble Sugar: TSS; Non-Reducing Sugar: NRS; Total Sugar: TS; Number of Fruits per Tree: NF; Acidity: Acidity; Phenol Content: PC; Reducing Sugar: RS; Kernel Width: KW; Fruit Yield per Tree: FY; Stone Weight: SW; Fruit Weight: FWT; Fruit Pulp Weight: FPW; Fruit Width: FW; Kernel Weight: KWT; Ascorbic Acid: AA; Kernel Length: KL; Fruit Length: FL; Stone Length: SL] programs focused on yield enhancement (20, 60, 61).

Principal Component Analysis (PCA) of morphological and qualitative variable of mango genotypes

The structure of a data set is studied using Principal Components Analysis (PCA), a statistical method for multivariate analysis, to identify the processes influencing the scores of the variables present in the data. Several linear combinations of observable variables are created using PCA and these linear combinations are referred to as components or factors. The variation pattern of vegetative and qualitative traits of mango was studied using principal components. The factors serve to condense the correlations present in the observed correlation matrix and possessed the capacity to precisely duplicate the observed matrix (62). Out of eight PCs observed in the study, only five were reported significant due to Eigen values more than 1 which contributed 89.36 % to total variations. Rest of the three PCs Eigen values found less than 1 and non-significant for the study (Table 4). Twenty traits were scattered throughout a range of ordinates and the length of the vectors revealed contribution of primary component of characters and quality of depiction.

From PCA biplot analysis, traits were divided into main and subgroups based on homogeneity and dissimilarity. Five sets of traits were reported which were considered into PC1 and PC2. Most of the traits *viz*., Fruit pulp weight, stone length, stone weight, reducing sugar, karnel weight, fruit grith, fruit weight, kernel length, ascorbic acid, fruit length, kernel width, fruit pulp weight, were clustered under group I and non-reducing sugar, Total antioxidant, Total sugar, TSS, Fruit yield per tress came under cluster II. However Total carotenoids, acidity, phenol content, number of fruits per tree categorized under group III. The almost traits come under I, II and III respectively. Notably, the PCA biplot expressed that group II, II and III which significantly contributed to PC1 was highly involved with Pusa Surya and Arka Aruna genotype mango. Parameters of group I, II, III, VI and V seems to be free from each other for qualities based on angles between vectors derived from the middle point of biplot (Fig. 2).

Conclusion

The investigation revealed that genotypic and phenotypic correlation coefficients are powerful analytical tools for deciphering complex trait relationships in mango. By identifying key trait associations, the findings provide a strategic framework for breeders to enhance fruit quality and yield simultaneously. Especially, strong positive correlations were observed between fruit yield per tree and crucial morphological and biochemical traits, including fruit weight, pulp weight, fruit length, width, kernel weight, TSS, non-reducing sugar, total sugar and ascorbic acid. These traits emerged as reliable selection indices for yield improvement and quality enhancement. The integration of biochemical traits like sugars, carotenoids, phenolics and antioxidants into selection criteria offers added value, aligning mango breeding with consumer health trends and industry demands. These traits, being significantly correlated with yield and quality parameters, underscore the need for a holistic breeding approach that balances productivity and nutritional value.

Future research should aim to validate key trait associations through QTL mapping and marker-assisted

Table 4. Extracted eigenvalues and correlation values for morphological and qualitative parameters with the first five principal components

Variables	**Principal components**				
	PC1	**PC2**	**PC3**	**PC4**	**PC5**
Extracted eigenvalues	9.582	3.652	1.766	1.518	1.358
Explained variance (%)	47.91	18.26	8.831	7.592	6.789
Cumulative variance (%)	47.91	66.17	75.001	82.593	89.36
Morphological and qualitative characters of mango genotypes					
NF	0.232	0.544	-0.705	-0.203	0.309
FY	0.863	0.221	-0.401	-0.081	0.006
FWT	0.863	-0.284	0.048	0.001	-0.245
FL	0.881	-0.161	0.29	0.185	-0.12
FW	0.732	-0.36	-0.203	0.078	0.328
FPW	0.909	-0.153	0.066	-0.122	-0.244
SWT	0.716	-0.545	-0.072	-0.026	-0.051
SL	0.478	-0.539	0.165	0.588	-0.203
KWT	0.861	-0.377	-0.14	-0.209	0.036
KL	0.634	-0.259	-0.35	0.349	0.233
KW	0.764	-0.197	-0.294	-0.306	-0.122
TSS	0.816	0.425	0.282	0.09	-0.116
ACD	0.131	0.615	0.122	0.488	0.511
RS	0.302	-0.162	0.664	-0.234	0.579
NRS	0.74	0.558	0.106	-0.123	-0.15
TS	0.77	0.442	0.321	-0.184	0.073
TC	0.149	0.665	0.173	-0.317	-0.28
AA	0.813	-0.22	0.107	-0.231	0.415
PC	0.504	0.569	-0.151	0.549	-0.104
TA	0.761	0.553	0.043	0.078	-0.086

[Where, Total Carotenoids: TC; Total Antioxidants: TA; Total Soluble Sugar: TSS; Non-Reducing Sugar: NRS; Total Sugar: TS; Number of Fruits per Tree: NF; Acidity: Acidity; Phenol Content: PC; Reducing Sugar: RS; Kernel Width: KW; Fruit Yield per Tree: FY; Stone Weight:SW; Fruit Weight: FWT; Fruit Pulp Weight: FPW; Fruit Width: FW; Kernel Weight: KWT; Ascorbic Acid: AA; Kernel Length: KL; Fruit Length: FL; Stone Length: SL]

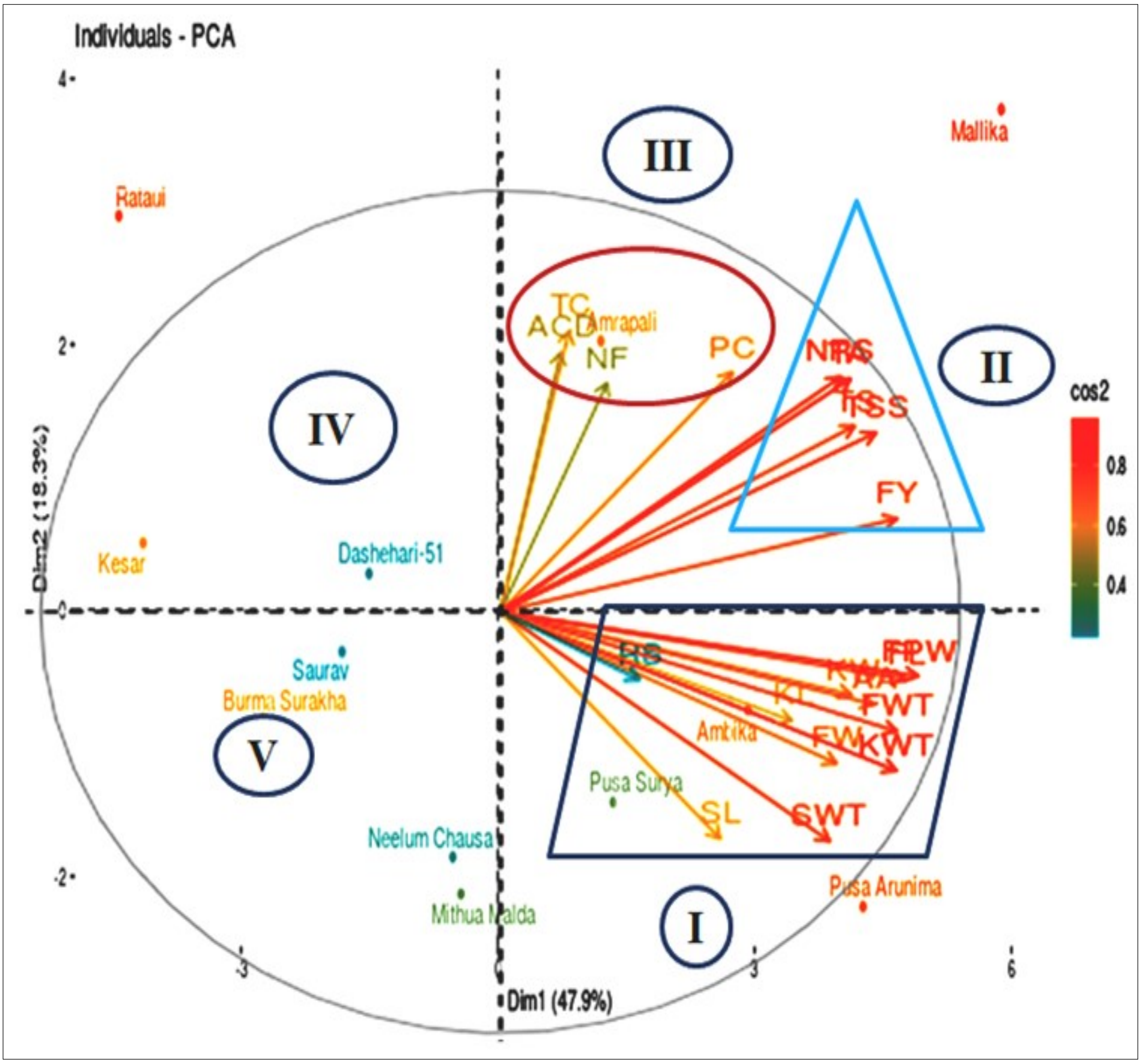


Fig. 2. Principal Components Analysis (PCA) of morphological and qualitative traits of mango genotypes

selection to expedite elite genotype development. Conducting multi-location and seasonal trials will help determine the environmental stability of these correlations. As well, genomic and transcriptomic analyses can clarify the genetic mechanisms underlying sugar accumulation, antioxidant production and yield traits. Breeding efforts should also prioritize climate-resilient genotypes by integrating these trait correlations, ultimately guiding the creation of high-yielding, nutritionally rich and commercially viable mango cultivars.

Acknowledgements

The authors acknowledge the support rendered by Department of Fruit Science, College of Horticulture, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, Uttar Pradesh, India for providing necessary facilities to carry out the research work.

Authors' contributions

AK[1] conducted the experiment and wrote the main manuscript text. AK[2] provided substantial guidance and facilitated the research by offering necessary laboratory facilities. SP assisted with data analysis. VK and AS provided experimental guidance and contributed to the manuscript draft preparation. GKA, VP, SKS, KKS, KA and AK[3] reviewed and approved the manuscript. This collaborative effort demonstrates the authors' commitment to producing a high-quality manuscript that accurately represents the research findings and contributes to the scientific community.

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Compliance with ethical standards

Conflict of interest: The authors declare no competing interests.

Ethical issues: None

Declaration of generative AI and AI-assisted technologies in the writing process: No

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