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Characterisation and heritability of physical and biochemical traits in mango (*Mangifera indica*)

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ABSTRACT

Characterising the quality of mango genotypes is a crucial step in selecting varieties with desirable traits that can expand the range of possibilities for creating new cultivars. The present study was carried out during 2020–2022 at ICAR-Central Institute for Subtropical Horticulture, Lucknow, Uttar Pradesh with the aim of characterisation and heritability of physical and biochemical traits in mango (*Mangifera indica* L.). The study involved 14 mango hybrids and their seven parents. The results revealed that high genotypic and phenotypic coefficient of variation were recorded for traits, viz. total flavonoid (49.37, 49.84), pulp weight (42.84, 23.04), fruit weight (31.72, 34.68), stone weight (28.87, 29.25), peel weight (23.81, 24.05) while moderate PCV and GCV were obtained for traits like stone thickness (17.76, 21.57) and stone length (17.07, 19.88). High broad-sense heritability estimates were obtained for most biochemical traits (e.g. total flavonoid: 98.1%, total phenol: 97.5%, total carotenoid: 96.9%, titratable acidity: 95.5%) and physical parameters (e.g. peel weight: 98.0%, stone weight: 97.4%), suggesting that environmental factors had little impact on phenotypic variation for these traits. Significant differences in physical and biochemical traits were recorded among mango hybrids and their parents. The first five principal components collectively accounted for 82.6% of the total variation in mango genotypes for different traits, viz. larger fruit size, higher pulp content, biochemical profiles, stone-related traits, levels of total soluble solids and nutraceutical contents.

Keywords: Heritability, Mango, Physical and biochemical, Principal component analysis

Mango (*Mangifera indica* L.) is one of the important and popular fruits of our country as well as world and referred to as the "King of Fruits" because to its broader adaptability, acceptability to consumers, incomparable taste, exotic flavour, high nutritious content, antioxidant richness, appeal to the general public and rich diversity. India, China, Pakistan, Mexico, Thailand, Indonesia, Brazil, Philippines, Nigeria, Vietnam, Bangladesh, and Pakistan are the world's major mango producing nations with India dominating in its production. They are an abundant source of vitamins including vitamin C, thiamine, riboflavin, niacin, and β-carotene (Murlidhara *et al.* 2019). Moreover, mangoes are packed with numerous phytonutrients as well as polyphenolic compounds that have been proven to be a powerful antioxidant (Almeida *et al.* 2011). It can be considered a great dietary supplement providing antioxidants such as ascorbic acid, carotenoids and phenolic compounds (Ribeiro *et al.* 2007). β-carotene is the most commonly found carotenoid in various genotypes of mango. During the ripening process, pigmentation is caused by carotenoid biosynthesis, alterations in carbohydrates or starch being converted into sugars, organic acids, phenolics and volatile compounds. Due to this reason, fruit ripens and soften to an optimal level of quality (Gill and Dhillon 2008). Additionally, even within the same area, varying environmental conditions over different years can modify ripeness and quality of the fruit (Devilliers 1998).

Assessing various promising mango hybrids/varieties for a particular ecosystem is essential for successful mango cultivation. There is great potential to improve its breeding, but several obstacles are in place such as: long juvenile phases, high clonal heterozygosity, single seed/fruit, recalcitrant seeds, polyembryony, early post-zygotic auto-incompatibility and needing a large area to evaluate hybrids (Pinto *et al.* 2011). Characterising the quality of mango genotypes is a crucial step in selecting varieties with desirable traits that can expand the range of possibilities for creating new cultivars. Through studying these fruits, we can ensure that each generation of mangoes is more flavourful and nutritious than the last (Pinto *et al.* 2005). Creating the perfect combination of traits in a single

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cultivar is an ambitious challenge for plant breeders. While it may be difficult, it is not impossible and can lead to the development of amazing new cultivars. Research on the genetic differences between individuals is important for understanding the amount of genetic variation that exists. The various hybrids are generated from germplasm by choosing them based on multiple characteristics such as the shape, colour, size, flavour, smell, taste, flowering time, ripening time, juice content, total soluble solids, and acidity (Singh *et al.* 2012). These characteristics are typically deemed to be the most relevant and pertinent properties for assessing which cultivars could be employed in selection processes while those that do not meet the criteria can be excluded in breeding endeavours (Meena and Bahadur 2015).

The first goal of every crop improvement strategy is to assess genetic variability and identify superior parents within a genotypically heterogeneous population (Gupta *et al.* 2016). Additionally, selection criteria are aided by the evaluation of genetic advancement and heredity. When evaluated in conjunction to correlation and route coefficient analysis, heritability is also useful in assessing the genetic gain of a crop (Munda *et al.* 2020, Begum *et al.* 2022). These new varieties offer exciting prospects for growers, as they can provide the consumer market with improved physical, chemical and sensory qualities. With these innovative cultivars, growers have a greater range of options to choose from when selecting produce for sale. This investigation was aimed for characterisation and heritability of physical and biochemical traits in mango hybrids and their parents.

MATERIALS AND METHODS

Study site: The present study was carried out during 2020–2022 at ICAR-Central Institute for Subtropical Horticulture, Lucknow (26°.92' N, 80°.72' E; at an elevation of 123 m amsl), Uttar Pradesh on 14 mango hybrids (Supplementary Fig. 1). It is situated in the northern region of India with an average annual rainfall of 1000 mm/year. The region is characterised by the subtropical climatic conditions with maximum and minimum temperatures of 35–45°C and 25–30°C, respectively during summers and 20–25°C and 5–7°C in winters, respectively.

Plant materials: The hybrids were maintained at 5 m × 2.5 m spacing and parent plants were maintained at 10 m × 10 m distance in randomised block design (RBD) with three replications. All the experimental trees were maintained under uniform cultural practices. The fruit samples of 14 mango hybrids and 07 parents were randomly harvested at physical maturity stage. Harvested fruit were washed under running tap water and then fruit surface was dried under running fan. After that fruits were kept in brown paper bags and then stored at room temperature for uniform ripening. The physico-chemical parameters were recorded after ripening of fruits. The fruit pulp was extracted and used for biochemical analysis.

Physical parameters: The physical parameters such as fruit weight, fruit length, fruit thickness, stone weight, stone length, stone width, pulp weight, peel weight and pulp per cent were measured using five fruits samples from different replications under each hybrid and fruit weight in grams was recorded using digital top pan balance of randomly selected fruit samples. The physical dimensions were measured using digital vernier callipers in millimetres and centimetres.

Biochemical parameters: A digital hand refractometer (0–53°B, Atago, Japan) was used to assess the total soluble solids of fruits at room temperature. The findings were represented in degrees Brix (°B). The total phenolic content (mg GAE/100 g FW) was estimated from the ripe pulp of mango hybrids using Folin-Ciocalteu reagents at 750 nm through UV-VIS spectrophotometers (Singleton *et al.* 1999). The total flavonoids content (mg QE/100 g FW) was estimated by spectrophotometric methods as defined by Dewanto *et al.* (2002). Total carotenoids (mg/100 g FW) were estimated with modified procedure of Ranganna (1997) using extraction solvents petroleum ether and acetone and read optical density at 452 nm using UV-VIS spectrophotometer (Model-1646, Deceibel, Delhi, India.). The total antioxidant content (mM Trolox/100 g FW) was measured through CUPRAC (cupric reducing antioxidant capacity) assay at 450 nm as advised by Apak *et al.* (2004).

Statistical analysis: The data have been analysed using R software version 4.3.1. The Pearson's correlation study with significance levels set at $*p<0.05$; $**p<0.01$; and $***p<0.001$. Results significance of various physical and biochemical parameters of mango was assessed by one-way analysis of variance and Principal component analysis (PCA) was carried out by using R software. Estimation of genetic parameters, viz. GCV, PCV and Heritability were also carried out using R software.

Genotype coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and heritability were calculated using formula:

$$PCV = (\sqrt{\sigma^2_p} \,/\, \text{General mean}) \times 100$$

$$GCV = (\sqrt{\sigma^2_g} \,/\, \text{General mean}) \times 100$$

Where σ^2p, Phenotypic variance; σ^2g, Genotypic variance. The values of PCV and GCV were classified as per Sivasubramaniam and Madhava Menon (1973): <10%, Low; 10 – 20%, Moderate; and >20%, High.

$$\text{Heritability} = (\text{Genotypic variance}/\text{Phenotypic variance}) \times 100$$

The values of heritability percent were classified as per Johnson *et al.* (1955):

0–30%, Low; 31 – 60%, Moderate; and >60%, High.

By using the formula given by Johnson *et al.* (1955), genetic advance was calculated:

$$GA = h^2\, k\, \sigma_p$$

Where GA, Genetic advance; h^2, Heritability in broad sense; k, Selection deferential which is equal to 2.06 at 5% intensity of selection (Lush 1940); and σp, Phenotypic standard deviation.

Genetic advance as percent mean = (GA/GM) × 100

Where GA, Genetic advance; GM, Genetic mean. The values of Genetic advance are classified as per the method of Johnson *et al.* (1955): <10%, Low; 10–20%, Moderate; and >20%, High.

RESULTS AND DISCUSSION

Estimation of variability in physical traits of mango genotypes: Mango genotypes exhibited notable variability in fruit weight, with values ranging from 178.53 g (H-4208) to 614.03 g (Mallika) (Table 1). Similarly, fruit length, width, and thickness vary across the varieties, reflecting diverse fruit shapes and sizes. For instance, Mallika mangoes displayed the longest fruit length (17.0 cm), while Neelum mangoes have the shortest (8.1 cm). These variations underscored the genetic diversity and phenotypic variability inherent in mango cultivars. The fruit related traits including pulp weight, peel weight, and fruit weight were the most diverse traits in the germplasm with a high coefficient of variation (CV> 40%) in natural populations of mango (Zhang *et al.* 2020). Variability in fruit length of mango with a range of 7–25.4 cm and fruit weight (136.4–840.1 g/fruit) was obtained by Jena *et al.* (2021). In addition to fruit size, the table presents data on peel weight, pulp weight, and stone characteristics. Peel weight varied among the genotypes H-4252 exhibiting thicker peels (98.67 g) than others. Pulp weight and percentage, which indicate the edible portion of the fruit, also vary significantly ranging from 95.77 g (Neelum) to 477.87 g (Mallika) and 57.51% (Neelum) to 77.57% (Mallika), respectively. Stone weight and dimensions provide insights into seed size and composition, with notable differences observed among the genotypes. Similar results were also achieved by Samal *et al.* (2012), Akin-Idowu *et al.* (2020) and Kumar *et al.* (2021). These parameters are critical for understanding fruit composition and potential applications in processing and seed propagation. Hybrid varieties like H-4252 and H-2047 demonstrated competitive fruit characteristics compared to common cultivars. For example, H-4252 exhibits the highest fruit weight (572.0 g) and pulp weight (395.67 g) among all genotypes, indicating its potential for high yield and market value. In contrast, cultivars like Mallika and Tommy Atkins displayed desirable traits such as large fruit size and high pulp percentage, making them popular choices among growers and consumers. Understanding the relationships between fruit characteristics is essential for growers, breeders, and stakeholders to make informed decisions regarding variety selection, cultivation practices, and market strategies.

Estimation of variability in biochemical traits of mango genotypes: The biochemical traits of mango genotypes were investigated to assess variability among different mango genotypes. Total Soluble Solid (TSS), Total Phenol Content (TP), Total Flavonoid Content (TF), Total Antioxidant Activity (TA), and Total Carotenoid Content (TC) were measured across a range of mango genotypes (Table 2). The TSS values of the mango genotypes exhibited considerable variability among genotypes, ranging from 12.87–22.50°Brix. TSS range of 14.33°Brix in St. Alexandria to 23.66°Brix in Amrapali was reported by Megha *et al.* (2022). Variability in TSS is indicative of differences in fruit sweetness, which is a key determinant of fruit quality and consumer preference. Mango varieties with higher TSS values are often preferred for their sweeter taste. The highest TSS values were observed in H-4208 (22.5°Brix) and H-4267 (22.1°Brix), suggested these genotypes offers exceptionally sweet and tasty fruits. Conversely, H-3803 (12.87°Brix) and Eldon (13.4°Brix) displayed the lowest TSS values, indicating comparatively lesser sweet fruit. Understanding the genetic and environmental factors influencing TSS variability is crucial for breeding programmes aimed at developing mango varieties with desirable fruit sweetness levels. Additionally, TSS values can guide post-harvest management practices and enlighten decisions regarding optimal harvest timing to ensure fruit quality and marketability (Zhao *et al.* 2021). The total phenol content varied significantly among the mango genotypes, ranging from 30.28–98.81 mg GAE/100 g FW. Among the parents, Neelum (98.81 mg GAE/100 g FW) exhibited the highest total phenol content, while Eldon showed the lowest (51.94 mg GAE/100 g FW). Mallika, Amrapali, and Neelum displayed relatively higher total phenol content compared to others, while Eldon had the lowest total phenol content among the parents. Relatively higher phenol content with a range of 96–123 mg GAE/100 g FW in mango genotypes of South West Nigeria was recorded by Akin-Idowu *et al.* (2020). A range of 297.50–560.60 µg/100 g FW variability in total phenol content of mango genotypes in the Himalayan plain region was observed by Saroj *et al.* (2023). The total flavonoid content also displayed considerable variation across the genotypes, ranging from 5.80–37.73 mg/100 g FW. Mallika had the highest total flavonoid content among the parents, while H-3669 had the highest total flavonoid content among the hybrids. Total flavonoid content in the range of 32.6–67.0 mg/100 g DW in six Thai mango cultivars was also testified by Rumainum *et al.* (2018). The observed variation in total phenol and total flavonoid content among hybrids and varieties could be attributed to genetic factors and environmental conditions during growth and ripening. These compounds are known for their antioxidant properties and potential health benefits (Jayarajan *et al.* 2019). The total antioxidant activity, as measured by total antioxidant, varied significantly among the genotypes ranged from 0.36–1.17 mM Trolox/100 g FW in Mallika. Among the hybrids, H-3669 (0.61 mM Trolox/100 g FW) showed the highest TA. Higher antioxidant activity indicates a higher potential for scavenging free radicals, thereby reducing oxidative stress (Saroj *et al.* 2023). Total carotenoid content varied from 1.53 mg/100 g FW to 8.29 mg/100 g FW. Amrapali had the highest TC content, while H-4015 had the lowest. Total carotenoid in the range of 0.48–7.50 mg/100 g FW was observed in mango genotypes (Muralidhara *et al.*

Table 1 Variability in the fruit physical traits of 14 mango hybrids along with their parents

Hybrids/Parents	Fruit weight (g)	Fruit length (cm)	Fruit width (cm)	Fruit thickness (cm)	Peel weight (g)	Pulp weight (g)	Pulp percent (%)	Stone weight (g)	Stone length (cm)	Stone width (cm)	Stone thickness (cm)
H-1042	291.87 ± 21.75^{bcd}	11.07 ± 0.74^{cdef}	6.87 ± 0.21^{abc}	5.97 ± 0.14^{abc}	65.17 ± 0.83^{efg}	193.37 ± 22.31^{cde}	65.69 ± 2.54^{abc}	33.33 ± 0.72^{hij}	8.97 ± 0.58^{cdef}	2.87 ± 0.05^{b}	1.57 ± 0.03
H-1723	284.93 ± 7.15^{bcd}	9.93 ± 0.24^{ef}	6.67 ± 0.26^{abc}	6.23 ± 0.10^{abc}	65.67 ± 1.19^{ef}	181.6 ± 7.41^{cde}	63.66 ± 1.02^{abc}	37.67 ± 0.98^{fghi}	7.2 ± 0.05^{ef}	3.5 ± 0.12^{ab}	2.13 ± 0.05
H-2047	367.17 ± 9.62^{b}	13.03 ± 0.41^{bcde}	7.0 ± 0.16^{abc}	6.3 ± 0.42^{abc}	73.67 ± 0.54^{cd}	251.83 ± 10.59^{bcde}	68.51 ± 1.06^{abc}	41.67 ± 0.72^{defg}	10.83 ± 0.26^{abc}	4.3 ± 0.09^{a}	1.73 ± 0.05
H-2709	265.17 ± 15.92^{bcd}	10.37 ± 0.07^{def}	6.53 ± 0.30^{abc}	6.53 ± 0.30^{abc}	50.33 ± 1.91^{j}	171.17 ± 17.86^{cde}	64.02 ± 2.98^{abc}	43.67 ± 0.98^{cde}	6.6 ± 1.34^{f}	3.73 ± 0.11^{ab}	8.23 ± 5.21
H-3669	259.71 ± 33.93^{bcd}	10.3 ± 0.12^{ef}	6.7 ± 0.05^{abc}	6.7 ± 0.24^{abc}	40.67 ± 1.52^{k}	194.37 ± 33.85^{cde}	73.64 ± 3.15^{ab}	24.67 ± 0.72^{l}	7.3 ± 0.45^{def}	3.5 ± 0.12^{ab}	1.63 ± 0.18
H-3803	360.1 ± 17.43^{b}	12.63 ± 0.68^{bcde}	6.87 ± 0.31^{abc}	6.23 ± 0.24^{abc}	70.67 ± 1.96^{cde}	243.1 ± 15.02^{bcde}	67.37 ± 0.96^{abc}	46.33 ± 0.72^{cd}	9.63 ± 0.47^{cde}	3.5 ± 0.17^{ab}	1.8 ± 0.05
H-3842	379.1 ± 4.91^{b}	14.73 ± 0.28^{ab}	8.23 ± 0.18^{a}	6.67 ± 0.24^{abc}	65.33 ± 1.19^{ef}	274.77 ± 4.83^{bc}	72.47 ± 0.34^{ab}	39 ± 1.41^{efgh}	10.73 ± 0.14^{abc}	3.27 ± 0.52^{ab}	1.63 ± 0.03
H-4015	348.4 ± 21.01b	11.1 ± 0.26^{bcdef}	7.7 ± 0.17^{a}	6.4 ± 0.09^{abc}	68.33 ± 1.78^{def}	240.4 ± 19.42^{bcde}	68.73 ± 1.51^{abc}	39.67 ± 0.27^{efg}	9.47 ± 0.36^{cdef}	4.27 ± 0.42^{a}	1.6 ± 0.08
H-4061	282.43 ± 4.73^{bcd}	12.23 ± 0.93^{bcde}	7.87 ± 0.58^{a}	7.37 ± 0.58^{ab}	63.67 ± 0.72^{fgh}	172.87 ± 7.64^{cde}	64.46 ± 0.36^{abc}	36.67 ± 0.72^{ghi}	8.93 ± 0.40^{cdef}	3.67 ± 0.07^{ab}	1.67 ± 0.03
H-4189	289.4 ± 15.69^{bcd}	10.47 ± 0.07^{def}	6.73 ± 0.03^{abc}	6.1 ± 0.05^{abc}	58.67 ± 1.52^{gh}	198.73 ± 16.77^{cde}	68.35 ± 1.97^{abc}	32 ± 0.47^{ijk}	8.77 ± 0.18^{cdef}	3.4 ± 0.08^{ab}	1.33 ± 0.07
H-4208	178.53 ± 5.50^{cd}	10.03 ± 0.19^{ef}	5.53 ± 0.22^{c}	5.27 ± 0.21^{c}	39.77 ± 1.25^{k}	111.33 ± 5.18^{de}	62.27 ± 0.96^{bc}	27.33 ± 1.44^{kl}	8.23 ± 0.33^{cdef}	3.23 ± 0.10^{ab}	1.7 ± 0.08
H-4252	572.0 ± 34.84^{a}	14 ± 1.55^{abcd}	8.23 ± 0.57^{a}	7.83 ± 0.48^{a}	98.67 ± 1.9^{6}a	395.67 ± 34.65^{ab}	68.83 ± 1.96^{abc}	77.67 ± 1.19^{a}	10.83 ± 0.64^{abc}	3.8 ± 0.33^{ab}	1.77 ± 0.12
H-4267	249.97 ± 19.78^{bcd}	10.27 ± 0.19^{ef}	6.7 ± 0.31^{abc}	6.17 ± 0.24^{abc}	48.67 ± 2.42^{j}	176.63 ± 18.83^{cde}	70.23 ± 1.85^{abc}	24.67 ± 1.19^{l}	8.83 ± 0.36^{cdef}	3.6 ± 0.21^{ab}	1.87 ± 0.10
H-4352	365.1 ± 28.55^{b}	10.8 ± 0.62^{cdef}	7.4 ± 0.31^{abc}	6.97 ± 0.28^{abc}	70.33 ± 1.78^{cde}	256.77 ± 29.50^{bcd}	69.77 ± 2.39^{abc}	38.0 ± 0.94^{efgh}	8.83 ± 0.31^{cdef}	3.73 ± 0.14^{ab}	1.7 ± 0.14
Mallika	614.03 ± 39.27^{a}	17.0 ± 0.65^{a}	7.97 ± 0.71^{a}	6.1 ± 0.59^{abc}	81.83 ± 1.21^{b}	477.87 ± 37.98^{a}	77.57 ± 1.31^{a}	54.33 ± 0.27^{b}	12.63 ± 0.24^{ab}	4.47 ± 0.26^{a}	1.17 ± 0.15
Neelum	165.77 ± 5.76^{d}	8.1 ± 0.09^{f}	5.63 ± 0.12^{bc}	5.13 ± 0.07^{c}	39.67 ± 1.44^{k}	95.77 ± 7.36^{e}	57.51 ± 2.54^{c}	30.33 ± 0.54^{jkl}	6.97 ± 0.05^{ef}	3.53 ± 0.07^{ab}	1.63 ± 0.05
Tommy Atkins	337.2 ± 27.85^{b}	10.77 ± 0.18^{cdef}	8.0 ± 0.24^{a}	7.37 ± 0.24^{ab}	48.33 ± 2.42^{j}	240.2 ± 28.38^{bcde}	70.6 ± 2.54^{abc}	48.67 ± 1.91^{bc}	8.57 ± 0.28^{cdef}	4.43 ± 0.15^{a}	1.77 ± 0.07
Ambika	317.33 ± 17.03^{bc}	11.67 ± 0.15^{bcdef}	7.67 ± 0.14^{ab}	6.63 ± 0.23^{abc}	75.67 ± 1.19^{bc}	198 ± 17.00^{cde}	62.08 ± 1.98^{bc}	43.67 ± 2.13^{cde}	10.23 ± 0.14^{abcd}	3.73 ± 0.10^{ab}	2.07 ± 0.07
Amrapali	252.77 ± 5.70^{bcd}	12.23 ± 0.18^{bcde}	6.33 ± 0.11^{abc}	5.33 ± 0.14^{c}	51.67 ± 1.44^{ij}	167.43 ± 6.68^{cde}	66.16 ± 1.13^{abc}	33.67 ± 0.72^{hij}	10.63 ± 0.24^{abc}	3.4 ± 0.00^{ab}	1.73 ± 0.07
Dashehari	290.67 ± 36.04^{bcd}	14.23 ± 0.59^{abc}	6.83 ± 0.05^{abc}	5.8 ± 0.05^{bc}	66.33 ± 2.84^{ef}	183.o ± 36.71^{cde}	60.79 ± 5.92^{bc}	41.33 ± 1.44^{defg}	12.87 ± 0.05^{a}	3.27 ± 0.03^{ab}	1.57 ± 0.03
Eldon	378.3 ± 2.16^{b}	12.23 ± 0.48^{bcde}	7.93 ± 0.31^{a}	6.6 ± 0.37^{abc}	58 ± 0.29h^{i}	220.23 ± 48.64^{cde}	74.07 ± 0.47^{ab}	42.7 ± 0.29^{def}	9.87 ± 0.48^{bcde}	4.1 ± 0.05^{ab}	1.93 ± 0.07

*Results are means of three determinations ± standard deviations. Mean values in a column with same alphabetic letter(s) are not significantly different as per Duncan's Multiple Range test.

2019). Carotenoids are essential for human health, with potential roles in eye health and immune function. The higher TC content in certain hybrids/varieties suggests a higher nutritional value in terms of carotenoid intake.

Assessment of variability in genetic parameters: The effectiveness of crop breeding programmes relies significantly on the presence of genetic variation and the heritability of traits under consideration. Assessing genetic variation aids breeders in determining the most appropriate strategies and selection criteria for enhancing target traits. In the present study, genetic components like genotypic variance, phenotypic variance, genotypic coefficient of variation, phenotypic coefficient of variation, heritability, genetic advance and genetic advance as percentage of mean were evaluated for 16 physical and biochemical traits (Table 3) in the studied mango genotypes. Wide variation was observed in fruit weight (165.77–614.03 g), followed by pulp weight (95.77–477.87 g), stone weight (24.67–77.67 g), peel weight (39.67–98.67 g), and total phenol (30.28–98.81 mg GAE/100 g FW). The wide range of variation observed in traits such as fruit weight, pulp weight, stone weight, peel weight, and total phenol indicates significant diversity among the mango genotypes studied (Akin-Idowu *et al.* 2020). Greater variations in fruit weight (145.70–870.60 g) were also reported in some selected mango cultivars by Jena *et al.* (2021).

The results suggested that phenotypic coefficient variances (PCV) were slightly greater than genotypic coefficient variances (GCV) for all traits. The slightly greater PCV compared to GCV for most traits suggest that environmental factors had a relatively minor influence on trait expression, indicating a predominantly genetic control over these traits (Rajan *et al.* 2009, Das *et al.* 2021). High genotypic and phenotypic coefficient of variation were recorded for traits such as total flavonoid (49.375, 49.84), pulp weight (42.84, 23.04), fruit weight (31.72, 34.68), stone weight (28.87, 29.25), peel weight (23.81, 24.05) while moderate PCV and GCV were obtained for traits like stone thickness (17.76, 21.57) and stone length (17.07, 19.88). Similar results on these traits were also obtained by Himabindu and Srihari (2016) and Indian *et al.* (2022). Conversely, low PCV and GCV were observed in traits such as pulp percent (6.01, 9.21). Moderate to low PCV and GCV in the traits indicated that the trait more influenced by environment (Terfa and Gurmu 2020). The difference between PCV and GCV was narrow for most biochemical parameters like total carotenoid, total phenol content, and total flavonoid content, as well as physical parameters like peel weight and stone weight, indicating minimal influence of the environment on these traits and such traits can be

Table 2 Variability in the fruit biochemical traits of 14 mango hybrids along with their parents

Hybrid/Variety	Total soluble solid (°B)	Total phenol (mg GAE/100 g)	Total flavonoid (mg QE/100 g)	Total antioxidant (mM Trolox/100 g)	Total carotenoids (mg/100 g)
H-1042	$20.33^{abc} \pm 0.20$	$61.8^{ef} \pm 1.72$	$30.47^{b} \pm 1.05$	$0.77^{def} \pm 0.02$	$3.89^{ef} \pm 0.03$
H-1723	$21.67^{ab} \pm 1.46$	$64.31^{def} \pm 0.60$	$11.93^{h} \pm 1.21$	$0.94^{bc} \pm 0.01$	$3.88^{a} \pm 0.02$
H-2047	$21.27^{ab} \pm 0.39$	$44.17^{ij} \pm 1.57$	$25.47^{c} \pm 1.33$	$0.63^{gh} \pm 0.02$	$5.39^{bc} \pm 0.09$
H-2709	$20.87^{abc} \pm 0.36$	$94.17^{a} \pm 0.71$	$19.33^{de} \pm 0.98$	$0.86^{cd} \pm 0.04$	$6.25^{f} \pm 0.02$
H-3669	$19.93^{abc} \pm 0.43$	$90.83^{a} \pm 1.56$	$37.73^{a} \pm 0.49$	$0.61^{gh} \pm 0.01$	$5.9^{ef} \pm 0.00$
H-3803	$12.87^{e} \pm 1.44$	$75.84^{bc} \pm 0.90$	$18.67^{def} \pm 0.96$	$0.61^{gh} \pm 0.03$	$5.64^{ef} \pm 0.00$
H-3842	$21.67^{ab} \pm 0.30$	$80.0^{b} \pm 0.90$	$5.87^{i} \pm 0.22$	$0.61^{gh} \pm 0.04$	$5.81^{cd} \pm 0.18$
H-4015	$19.47^{abcd} \pm 0.36$	$55.83^{fgh} \pm 1.87$	$5.8^{i} \pm 0.26$	$0.62^{gh} \pm 0.02$	$1.53^{bc} \pm 0.12$
H-4061	$21.8^{ab} \pm 0.16$	$30.28^{k} \pm 0.30$	$12.6^{h} \pm 0.36$	$0.57^{ghi} \pm 0.01$	$2.13^{c} \pm 0.21$
H-4189	$21.73^{ab} \pm 0.99$	$60.42^{fg} \pm 1.04$	$28.53^{bc} \pm 0.51$	$0.59^{gh} \pm 0.03$	$3.84^{c} \pm 0.02$
H-4208	$22.5^{a} \pm 0.41$	$71.81^{bcd} \pm 0.60$	$15.27^{fgh} \pm 0.36$	$0.65^{fgh} \pm 0.02$	$5.59^{c} \pm 0.02$
H-4252	$19.5^{abcd} \pm 0.31$	$64.31^{def} \pm 2.06$	$6.47^{i} \pm 0.16$	$0.67^{efg} \pm 0.02$	$6.35^{g} \pm 0.19$
H-4267	$22.1^{ab} \pm 0.54$	$56.8^{fgh} \pm 1.20$	$12.4^{h} \pm 0.49$	$0.52^{hij} \pm 0.00$	$5.92^{g} \pm 0.02$
H-4352	$17.2^{bcde} \pm 0.50$	$50.56^{hi}j \pm 0.82$	$7.8^{i} \pm 0.30$	$0.38^{jk} \pm 0.02$	$7.02^{ef} \pm 0.25$
Mallika	$21.5^{ab} \pm 1.03$	$89.91^{a} \pm 3.37$	$28.13^{bc} \pm 0.43$	$1.17^{a} \pm 0.02$	$7.08^{c} \pm 0.00$
Neelum	$13.57^{e} \pm 0.75$	$98.81^{a} \pm 0.68$	$14.81^{gh} \pm 0.19$	$1.03^{b} \pm 0.01$	$4.53^{bc} \pm 0.05$
Tommy Atkins	$14.67^{de} \pm 0.88$	$42.45^{j} \pm 0.36$	$26.33^{c} \pm 0.43$	$0.36^{k} \pm 0.01$	$2.39^{c} \pm 0.01$
Ambika	$15.83^{cde} \pm 0.59$	$56.25^{fgh} \pm 0.39$	$13.33^{h} \pm 0.05$	$0.79^{de} \pm 0.01$	$4.07^{b} \pm 0.50$
Amrapali	$21.4^{ab} \pm 1.27$	$70.69^{cde} \pm 0.30$	$20.13^{d} \pm 0.14$	$0.85^{cd} \pm 0.00$	$8.29^{b} \pm 0.04$
Dashehari	$20.33^{abc} \pm 0.85$	$57.64^{fgh} \pm 0.60$	$18.27^{defg} \pm 0.22$	$0.54^{ghi} \pm 0.00$	$6.23^{de} \pm 0.02$
Eldon	$13.4^{e} \pm 0.08$	$51.94^{ghi} \pm 2.47$	$15.67^{efgh} \pm 0.24$	$0.43^{ijk} \pm 0.00$	$3.48^{g} \pm 0.12$

*Results are means of three determinations ± standard deviations. Mean values in a column with same alphabetic letter(s) are not significantly different as per Duncan's Multiple Range test. GAE, Gallic acid equivalent; QE, Quercetin equivalent.

Table 3 Genetic components of sixteen traits of mango genotypes

Traits	Mean	Range		σ^2g	σ^2p	H^2b (%)	GCV (%)	PCV (%)	GA (%)	GAM
		Minimum	Maximum							
Fruit weight (g)	323.58	165.77	614.03	10709.55	12798.89	83.70	31.73	34.68	195.01	59.78
Fruit length (mm)	11.75	8.10	17.00	3.59	4.97	72.20	16.10	18.94	3.32	28.18
Fruit width (mm)	7.07	5.53	8.23	0.48	0.92	52.60	9.76	13.45	1.04	14.57
Fruit thickness (mm)	6.36	5.13	7.83	0.34	0.74	45.60	9.09	13.46	0.81	12.65
Pulp weight (g)	221.71	95.77	477.87	6418.34	9016.09	71.20	36.22	42.84	139.25	62.83
Pulp percent (%)	67.14	57.51	77.57	16.45	38.65	42.60	6.01	9.22	5.45	8.08
Peel weight (g)	62.16	39.67	98.67	217.72	222.19	98.00	23.82	24.06	30.09	48.56
Stone weight (g)	39.72	24.67	77.67	132.41	135.99	97.40	28.87	29.25	23.39	58.68
Stone length (mm)	9.35	6.60	12.87	2.56	3.48	73.80	17.07	19.88	2.83	30.21
Stone width (mm)	3.66	2.87	4.47	0.13	0.29	43.80	9.65	14.57	0.48	13.16
Stone thickness (mm)	2.02	1.17	8.23	0.13	5.98	2.10	17.76	21.58	0.11	5.35
TSS (°B)	19.51	12.87	22.50	9.44	12.08	78.10	15.99	18.09	5.60	29.11
Total antioxidant (mg/100 g)	0.69	0.36	1.17	0.04	0.04	95.50	30.31	31.04	0.41	61.10
Total carotenoid (mg/100 g)	5.09	1.53	8.29	3.05	3.15	96.90	34.89	35.43	3.54	70.74
Total phenol (mg/100 g)	65.84	30.28	98.81	324.41	332.67	97.50	27.63	27.98	36.64	56.21
Total flavonoid (mg/100 g)	17.97	5.80	37.73	77.74	79.22	98.10	49.38	49.84	17.99	100.76

σ^2g, Genotypic variance; σ^2p, Phenotypic variance; GCV, Genotypic coefficient of variance; PCV, Phenotypic coefficient of variance; H^2b, Broad sense heritability; GA, Genetic advance; GAM, Genetic advance as percentage of mean.

used for direct selection.

Heritability is a measure of degree of transmission of characters from parents to progeny. Estimates of heritability helps effective selection of superior genotype from diverse population. High broad-sense heritability estimates were obtained for most biochemical traits (e.g. total flavonoid: 98.1%, total phenol: 97.5%, total carotenoid: 96.9%, total antioxidant: 95.5%) and physical parameters (e.g. peel weight: 98.0%, stone weight: 97.4%), suggesting that environmental factors had little impact on phenotypic variation for these traits. Similar results were also achieved by Sankaran *et al.* (2020) and Elaiyaraja *et al.* (2021). Traits with high heritability and genetic advance, such as total flavonoid content, total carotenoid content, total phenol content, titratable acidity, and weight of fruit (pulp, peel, and stone), are likely to be additive and can be inherited through selection (Rajan *et al.* 2009). Conversely, traits like pulp per cent, fruit thickness, and fruit width, with high heritability and low genetic advance, indicate a non-additive nature, suggesting that hybridisation may be necessary for character transfer to the next generation. The findings provided valuable insights that traits with high heritability and genetic advance such as fruit weight and pulp weight are likely to be additive and can be inherited through selections. In physical parameters, high heritability (98%) and high GA (30.09%) was found in peel weight followed by stone weight with heritability (97.40%) and GA (23.39%). Among the biochemical parameters high heritability (97.50%) and high GA (36.64%) were found in total phenols followed by total flavonoid content with heritability (98.10%) and high GA (17.99%). Mallika and Amrapali having maximum desirable combinations (TSS + Antioxidants + Pulp percentage) could be used as parents in mango breeding programme while hybrids, viz. H-3669 and H-2709 possessed maximum desirable combinations (TSS + Antioxidants + Pulp percentage) and identified as potential genetic stocks.

Exploring genetic components and variability in mango genotypes through principal component analysis: The first five principal components with Eigenvalue >1 collectively accounted for 82.6% of the total variation in mango genotypes (Table 4). Each principal component captured distinct aspects of fruit morphology, biochemical composition, and stone-related traits. PC1 predominantly represented traits related to fruit size and weight, with significant contributions include fruit weight (14.57), pulp weight (13,67), fruit width (12.066), peel weight (11.036). Genotypes with larger fruit size and higher pulp content contributed more to PC1. PC2 focused on the biochemical composition of mango fruits, with notable contributions from total carotenoid (21.24), total phenol (20.37), total antioxidant (20.25). This component highlighted variations in the biochemical profiles among

Table 4 Contribution of traits to different PCs

Trait	FWt	FL	FWd	FTh	PlW	PlpWt	PlpP	SWt	SL	SWd	STh	TSS	TP	TF	TA	TC
PC1	14.57	10.63	12.07	6.31	11.04	13.67	6.14	10.32	7.65	5.09	0.80	0.02	1.12	0.38	0.15	0.07
PC2	1.35	5.48	4.42	10.79	0.28	2.47	0.02	0.11	3.23	2.02	0.49	4.90	20.37	2.58	20.26	21.25
PC3	0.81	3.98	0.11	5.10	0.06	0.53	0.07	7.81	16.05	7.37	33.14	7.53	11.48	0.22	5.53	0.22
PC4	0.15	0.10	0.07	0.04	10.94	1.36	31.22	6.06	1.49	6.93	0.92	0.04	1.19	38.00	1.44	0.04
PC5	0.18	0.17	0.59	10.51	0.07	0.01	2.70	0.76	2.04	4.68	19.36	46.70	1.14	0.50	5.77	4.84

FWt, Fruit weight; FL, Fruit length; FWd, Fruit width; FTh, Fruit thickness; PlW, Peel weight; PlpWt, Pulp weight; PlpP, Pulp percent; SWt, Stone weight; SL, Stone length; SWd, Stone width; STh, Stone thickness; TSS, Total soluble solids; TP, Total phenol; TF, Total flavonoid; TA, Total antioxidant; TC, Total carotenoids.

different mango genotypes. PC3 primarily captured stone-related traits such as stone thickness (33.14), stone length (16.05), stone weight (7.81), stone width (7.36), this suggested that genotypes with larger or thicker stones make a greater contribution to PC3, as evidenced by the variation in stone characteristics among them. PC4 exhibits significant contributions from total flavonoid (38.0), pulp percentage (31.21), pulp weight (10.94), stone width (6.93), and stone weight (6.05). These traits likely pertain to the characteristics of the pulp and stone. The features that have made substantial contributions in PC5 are TSS (46.70), stone thickness (19.35), fruit thickness (10.94), and total antioxidant (5.76). PC5 appeared to encompass a blend of characteristics related to the quality of fruit and its biochemical composition. This suggests that genotypes with elevated levels of soluble solids, flavonoid content, and wider fruit contribute more significantly to PC5.

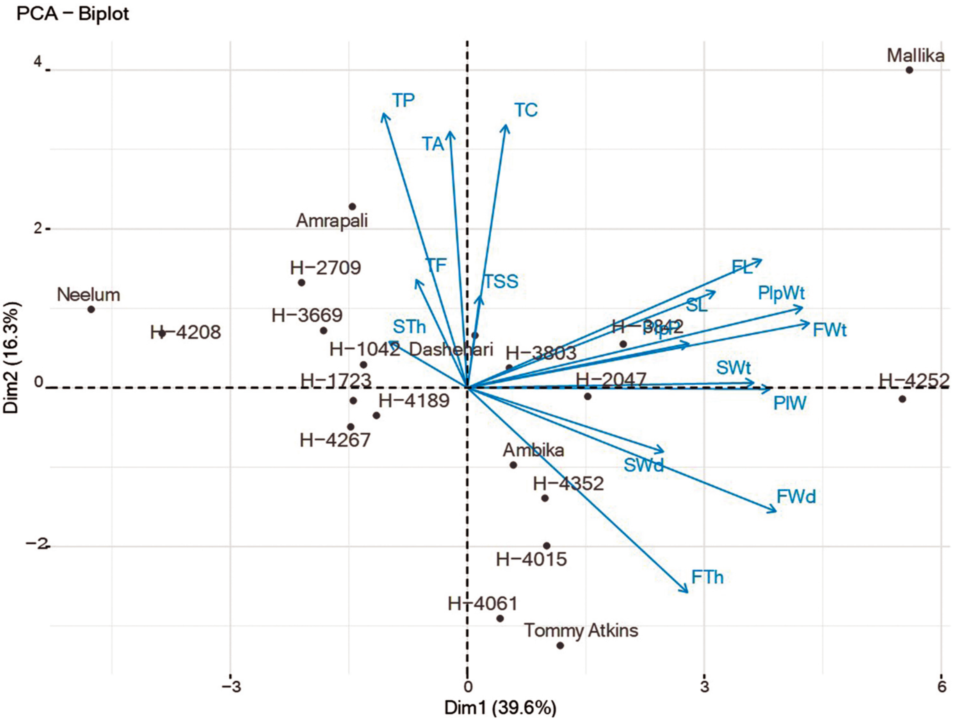

Fig. 1 PCA biplot displaying the relationship between mango genotypes for sixteen traits. FWt, Fruit weight; FL, Fruit length; FWd, Fruit width; FTh, Fruit thickness; PlW, Peel weight; PlpWt, Pulp weight; PlpP, Pulp percent; SWt, Stone weight; SL, Stone length; SWd, Stone width; STh, Stone thickness; TSS, Total soluble solids; TP, Total phenol; TF, Total flavonoid; TA, Total antioxidant; TC, Total carotenoids.

The PCA biplot (Fig. 1 and 2) illustrated the intricate relationships between mango genotypes concerning 16 key traits. Notably, the biplot revealed distinct clusters formed by specific mango genotypes and traits, offering insights into their trait profiles. For instance, Amrapali, H-2709, H-3669, and H-1042 are clustered together, indicating similarity in their trait profiles. Similarly, H-1723, H-4189, and H-4267 form another cluster, suggesting shared characteristics among these genotypes. Moreover, the orientation similarity of total phenol (TP) and total carotenoid (TC) vectors suggests a positive correlation between TP and TC content across mango genotypes. Similarly, the close positioning of

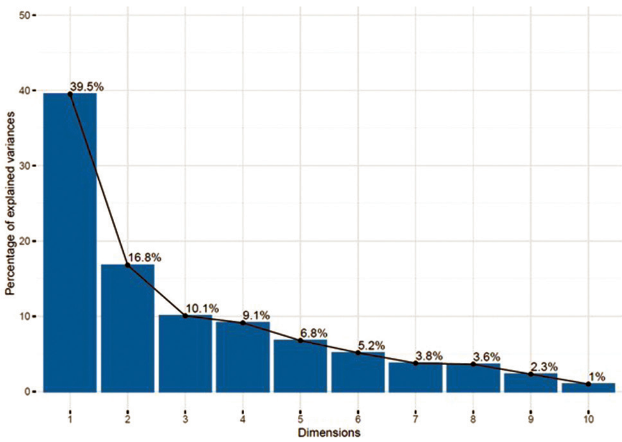

Fig. 2 Scree plot from PCA analysis.

TSS and total flavonoid (TF) vectors indicates a potential association between fruit sweetness (TSS) and flavonoid content (TF). Furthermore, Fruit weight and Pulp weight are closely positioned, indicating a correlation between these traits. Conversely, genotypes like H-4252, H-4061, Mallika, and Neelam are distant from the main clusters, possibly indicating outliers. These outliers could offer valuable insights for further investigation into the factors contributing to their unique trait profiles.

Relationship between variables of mango genotypes: The Pearson's correlation matrix provided in the correlogram (Supplementary Fig. 2) that depicts the strength and direction of linear relationships between pairs of variables within mango genotypes. Through correlation analysis, significant insights emerge regarding the interplay of biochemical traits among these genotypes, laying groundwork for enhanced fruit quality and nutritional value. Based on the correlation analysis, it can be inferred that certain biochemical traits of mango genotypes are positively or negatively associated with each other. For instance, traits such as fruit weight and fruit length display robust positive correlations, indicating a tendency for these traits to co-vary positively among mango genotypes. Conversely, negative correlations are observed between traits like total phenol, total flavonoid, and stone thickness that may be environment-dependent. Significant negative correlations between TPC, TFC, total carotenoid obtained in selected BARI cultivars and commercial cultivars of Langra (Sabuz *et al.* 2024). By discerning the associations between various traits, breeders and researchers can strategically select for desired trait combinations, optimize breeding programmes.

The comprehensive study on physical and biochemical traits of mango genotypes and their parents revealed significant variability, underscoring the genetic diversity inherent in mango cultivars. Fruit weight, length, width, thickness, peel weight, pulp weight, pulp percentage, stone weight, and dimensions varied significantly among the genotypes, offering insights into fruit composition critical for processing and propagation. Hybrid varieties exhibited competitive fruit characteristics, suggesting potential for high yield and market value. Biochemical traits like total soluble solids, total phenol, total flavonoid, total antioxidant, and total carotenoid varied widely among genotypes, indicative of diverse nutritional profiles and antioxidant capacities. Heritability estimates indicated predominantly genetic control over most traits, offering opportunities for targeted breeding efforts to improve fruit quality and nutritional content.

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