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RESEARCH ARTICLE

# Assessment of genetic variability, heritability and genetic advance for yield and quality traits in mango (*Mangifera indica* L.) genotype under Western Uttar Pradesh conditions

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## Abstract

The present study was conducted at Horticultural Research Centre, Sardar Vallabhbhai Patel University of Agriculture and Technology, using pooled data from 2021 to 2023, to assess genetic variability, heritability and trait associations among twelve mango (*Mangifera indica* L.) genotypes. Significant genetic variation was observed across morphological and biochemical traits. High genotypic and phenotypic coefficients of variation (GCV and PCV) were recorded for total carotenoids, total antioxidants, fruit yield per tree, phenol content, fruit pulp weight, number of fruits per tree, fruit weight and ascorbic acid, suggesting substantial scope for genetic improvement through direct selection. All traits exhibited high heritability, indicating a strong genetic basis with limited environmental influence. Furthermore, high genetic advance as a percentage of the mean was recorded for most traits, while moderate values observed for total soluble solids and acidity indicate additive gene action. These findings highlight key traits for targeted selection in breeding programs aimed at enhancing fruit yield and quality in mango.

**Keywords :** fruit yield and quality; genetic advance; genetic variability; gcv & pcv; heritability; mango genotypes

## Introduction

Mango (*Mangifera indica* L.), a prominent member of the family Anacardiaceae, stands as one of the most important fruit crops in tropical and subtropical regions across the globe (1). With a chromosome number of 2n = 40, mango is believed to have evolved through interspecific hybridization and chromosome doubling (2, 3). Its delicious flavor, vibrant color, rich nutrient profile and wide consumer acceptance have earned it the title of “King of Fruits” and the honor of being India’s national fruit (4). Mango fruits are a rich source of vital nutrients, including carotenoids, vitamin C, phenolic compounds and flavonoids, contributing to their antioxidant and therapeutic properties (5).

India holds a dominant position in global mango production, with approximately 2.35 million hectares under cultivation and an annual production of about 20.77 million tonnes (6). The major mango-producing states include Uttar Pradesh, Andhra Pradesh, Karnataka, Bihar, Gujarat and Maharashtra. The vast agro-climatic diversity across these regions has given rise to a wide range of mango cultivars, each exhibiting distinct morphological and fruit quality traits. However, in spite of this diversity, systematic genetic characterization of mango germplasm in many regions, including Western Uttar Pradesh, remains limited.

Mango is a highly heterozygous and cross-pollinated crop, which results in considerable variability in both qualitative and quantitative traits. Understanding the extent of this variability is essential for crop improvement, particularly in identifying promising genotypes and parent lines for breeding programs. While some efforts have been made to assess variability at national and state levels, region-specific studies that capture the genetic potential of local cultivars are scarce. Such studies are crucial for enhancing yield, fruit quality and stress resilience through targeted breeding interventions (7).

To address these gaps, the present investigation focuses on evaluating the genetic variability of mango cultivars grown in Western Uttar Pradesh. The study aims to estimate key genetic parameters such as phenotypic and genotypic coefficients of variation, heritability and genetic advance for important morphological and fruit quality traits. These parameters are fundamental to understanding the nature of trait inheritance and the expected genetic gains through selection. Furthermore, identifying the traits that contribute most significantly to yield can inform breeding strategies and cultivar selection for the region.

Therefore, this study intends to provide a comprehensive understanding of trait variability among mango genotypes, aiding both breeders and growers in cultivar improvement and selection. By identifying superior genotypes and yield-contributing traits, the research contributes to ongoing efforts in enhancing mango productivity and quality in Western Uttar Pradesh, thereby supporting the development of region-specific, high-performing cultivars

## Materials and Methods

The experiment was conducted during 2021 to 2023 at Horticultural Research Centre, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, Uttar Pradesh. The study material comprised twelve diverse mango genotypes collected from various agro-climatic regions of India, representing a wide genetic base. These included ‘Ambika’ (Amrapali × Janardhan Pasand) and ‘Dashehari-51’ (a clonal selection of Dashehari) from CISH, Lucknow; ‘Pusa Arunima’ (Amrapali × Sensation), ‘Pusa Surya’ (a selection from Eldon), ‘Mallika’ (Neelum × Dashehari) and ‘Amrapali’ (Dashehari × Neelum) from IARI, New Delhi; ‘Burma Surakha’ and ‘Saurav’ from Saharanpur district; ‘Rataul’, an open-pollinated seedling selection from Baghpat district; and local varieties such as ‘Neelum Chausa’ and ‘Mithua Malda’ (a Malda type). ‘Kesar’, a widely recognized cultivar from the Gir region of Junagadh and Amreli districts in Gujarat, known for its GI (Geographical Indication) tag (GI No.185), was obtained from JAU, Junagadh.

All experimental trees were maintained at a uniform spacing of 6 × 6 meters and were 8 to 10 years old at the time of observation, representing the bearing stage suitable for reliable yield and quality assessment. The trial was laid out in a Randomized Block Design (RBD) with four replications, comprising a total of 48 trees. Each genotype was represented by four plants per replication. Standard agronomic practices including nutrient and pest management were uniformly followed across all treatments to ensure accurate genetic evaluation. Twenty morphological and quality traits were recorded to assess genetic variability, inter-trait associations and direct and indirect effects through correlation and path coefficient analysis. The traits under study included number of fruits per tree, fruit yield (kg/tree), fruit weight, fruit length, fruit width, pulp weight, stone weight, stone length, kernel weight, kernel length, kernel width, acidity (%), total soluble solids (° Brix), reducing sugar (%), non-reducing sugar (%), total sugar (%), total carotenoids (mg/100 g), ascorbic acid (mg/100 g), phenol content (mg GAE/100 g) and total antioxidants (µmol Trolox/100 g). This comprehensive evaluation aimed to capture the extent of genetic diversity and identify potential genotypes and traits for targeted mango improvement programs.

The morphological characterization was done adopting standard mango descriptors developed by IPGRI (8). The number of fruits per tree was counted for each mango genotype. The yield per tree was recorded over the study period. Fruit weight and pulp weight, stone weight and kernel weight were measured by weighing balance. The digital Vernier calipers was used to measure the fruit length, fruit width, stone length, kernel length and kernel width.

The chemical analysis conducted by following standard protocols. Total soluble solids (TSS) were measured by using hand refractometer. Titratable acidity, reducing and non-reducing sugar was determined by method described in AOAC (9). Total sugars were estimated as suggested by Ranganna (10). The total carotenoid was determined through the ranganna method (10). The titration method was followed for the estimation of ascorbic acid in mango juice (11). Total phenol estimation was carried out with the Folin-Ciocalteau reagent (12). The antioxidant (AOX) activity in the mango fruits was assessed using the CUPRAC (Cupric Reducing Antioxidant Capacity) method, as described by (13).

The broad sense heritability was calculated for combined analysis by using the formula suggested by (14, 15). The genotypic and phenotypic co- efficient of variations were computed by the formula suggested by (16). The expected genetic advance under selection for different characters was estimated as suggested by (14, 15). Genetic advance as a percent of the mean for each character was calculated following (14).

### Statistical analysis

The acquired observations were statistically analyzed using the recommended standard approach (17). This analysis ensured the accuracy and reliability of the results, with statistical C.D. at 5 % validation performed to determine the significance of differences among treatments.

## Results and Discussion

The results pertaining to genetic variability, heritability and genetic advance for twenty morphological and quality traits of mango genotypes are summarized in Table 1. The estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) revealed that PCV values were consistently higher than their corresponding GCV values for all characters evaluated in the pooled data, indicating the influence of environmental factors on trait expression.

In the pooled analysis, high genotypic variability (GCV >25 %) was observed for total carotenoids (49.95 %), total antioxidants (36.58 %), fruit yield per tree (34.11 %), phenol content (31.82 %) and fruit pulp weight (30.48 %). Traits exhibiting moderate genotypic variation (10–25 %) included number of fruits per tree (24.30 %), fruit weight (23.43 %), ascorbic acid content (23.10 %), non-reducing sugars (18.40 %), stone weight (14.90 %), reducing sugars (14.77 %), total sugars (13.85 %), kernel weight (13.24 %), fruit length (12.88 %), kernel length (12.54 %), stone length (12.32 %), fruit width (11.41 %), kernel width (10.88 %) and acidity (10.04 %). Total soluble solids (7.14 %) exhibited low genotypic variability (GCV <10 %).

**Table 1** Genetic parameters for different character in mango (Pooled data 2021-22 and 2022-23)

| Characters | Mean | Range (Min) | Range (Max) | GCV (%) | PCV (%) | Heritability (%) | GA (% mean) |
|---|---|---|---|---|---|---|---|
| Number of fruits per tree | 248.56 | 137.63 | 351.19 | 24.30 | 24.68 | 96.96 | 49.30 |
| Fruit yield (kg) per tree | 62.86 | 31.60 | 108.82 | 34.11 | 34.34 | 98.63 | 69.78 |
| Fruit weight (g) | 250.62 | 144.52 | 331.33 | 23.43 | 23.73 | 97.45 | 47.64 |
| Fruit length (cm) | 11.04 | 8.24 | 12.90 | 12.88 | 13.49 | 91.19 | 25.34 |
| Fruit width (cm) | 6.62 | 5.24 | 7.69 | 11.41 | 12.07 | 89.45 | 22.23 |
| Fruit pulp weight (g) | 167.35 | 74.98 | 248.46 | 30.48 | 30.81 | 97.89 | 62.12 |
| Stone weight (g) | 32.66 | 21.95 | 38.60 | 14.90 | 15.47 | 92.80 | 29.57 |
| Stone length (cm) | 9.99 | 7.21 | 11.96 | 12.54 | 13.07 | 91.98 | 24.77 |
| Kernel weight (g) | 17.74 | 13.84 | 22.63 | 13.24 | 13.87 | 91.12 | 26.04 |
| Kernel length (cm) | 6.30 | 4.81 | 7.38 | 12.32 | 12.79 | 92.75 | 24.44 |
| Kernel width (cm) | 2.79 | 2.36 | 3.40 | 10.88 | 11.55 | 88.73 | 21.12 |
| TSS (Brix) | 18.89 | 17.06 | 22.03 | 7.14 | 8.15 | 76.84 | 12.89 |
| Acidity (%) | 0.24 | 0.20 | 0.28 | 10.04 | 11.14 | 81.25 | 18.65 |
| Reducing Sugar (%) | 5.26 | 4.23 | 6.61 | 14.77 | 15.35 | 92.59 | 29.27 |
| Non-reducing sugar (%) | 10.27 | 7.50 | 14.62 | 18.40 | 18.95 | 94.30 | 36.81 |
| Total sugar (%) | 16.08 | 12.83 | 20.31 | 13.85 | 14.42 | 92.20 | 27.39 |
| Total carotenoid (mg/100g) | 4.83 | 1.39 | 8.94 | 49.95 | 50.21 | 98.97 | 102.37 |
| Ascorbic acid (mg/100 g) | 31.58 | 20.58 | 45.31 | 23.10 | 23.51 | 96.52 | 46.75 |
| Phenol content (mg GAE/100 g) | 64.48 | 41.29 | 119.73 | 31.82 | 32.08 | 98.42 | 65.04 |
| Totalantioxidants (µmol Trolox 100g) | 0.66 | 0.42 | 1.28 | 36.58 | 36.92 | 98.15 | 74.66 |

Similarly, at the phenotypic level, traits such as total carotenoids (50.21 %), total antioxidants (36.92 %), fruit yield per tree (34.34 %), phenol content (32.08 %) and fruit pulp weight (30.81 %) showed high phenotypic variability (PCV >25 %). Moderate phenotypic variation (10–25 %) was recorded for number of fruits per tree (24.68 %), fruit weight (23.73 %), ascorbic acid (23.51 %), non-reducing sugars (18.95 %), stone weight (15.47 %), reducing sugars (15.35 %), total sugars (14.42 %), kernel weight (13.87 %), fruit length (13.49 %), kernel length (13.07 %), stone length (12.79 %), fruit width (12.07 %), kernel width (11.55 %) and acidity (11.14 %). As with GCV, the lowest phenotypic variation was recorded for total soluble solids (8.15 %).

The marked differences between PCV and GCV in most characters indicate a substantial environmental effect on their expression. This variation among genotypes underscores the genetic diversity present within the studied material. Such findings are in agreement with the earlier reports of (18-21) in mango.

Traits exhibiting high GCV and PCV values suggest a predominance of genetic variance and imply strong potential for improvement through direct selection. In contrast, traits with low GCV and PCV indicate limited genetic variability, making genetic advancement through selection more challenging. These observations corroborate the findings of (22, 23), further validating the results obtained in the present investigation.

In the pooled data analysis, broad-sense heritability estimates revealed a high magnitude (> 60 %) for all twenty traits under investigation. The highest heritability was observed for total carotenoids (98.97 %), followed closely by fruit yield per tree (98.63 %), phenol content (98.42 %), total antioxidants (98.15 %), fruit pulp weight (97.89 %), fruit weight (97.45 %), number of fruits per tree (96.96 %) and ascorbic acid (96.52 %). Other traits such as non-reducing sugars (94.30 %), stone weight (92.80 %), stone length (92.75 %), reducing sugars (92.59 %), total sugars (92.20 %), kernel length (91.98 %), fruit length (91.19 %), kernel weight (91.12 %), fruit width (89.45 %), kernel width (88.73 %), acidity (81.25 %) and total soluble solids (76.84 %) also exhibited high heritability.

The consistently high heritability across all traits suggests that genetic variance is the predominant contributor to phenotypic variation, with minimal influence from environmental factors. This indicates a strong genetic control over these traits, implying that they are likely to be stably inherited and can respond well to selection. In particular, traits showing such high heritability are more likely to resemble their parental genotypes, making them ideal candidates for improvement through conventional breeding.

However, heritability in the broad sense encompasses both additive and non-additive genetic effects. Therefore, while high heritability provides an indication of genetic determination, it must be interpreted with caution especially in the presence of dominant or epistatic interactions. Thus, heritability is most meaningful when assessed in conjunction with genetic advance as a percentage of mean, which provides an estimate of the expected gain from selection and reflects the additive genetic component more accurately.

The integration of heritability and genetic advance offers a robust framework for predicting genetic improvement and hence, is vital for developing effective selection strategies. Traits with high heritability coupled with high genetic advance suggest additive gene action and are amenable to improvement through selection. Conversely, high heritability with low genetic advance may indicate non-additive gene action, requiring alternative breeding approaches.

The findings of the present investigation align well with earlier reports who also observed high heritability estimates in mango for several morphological and biochemical traits (18, 23 -27).

The pooled data analysis revealed substantial genetic advance as a percentage of mean (GA %) for the majority of traits, suggesting significant potential for genetic improvement through selection. Traits such as total carotenoids (102.37 %), total antioxidants (74.66 %), fruit yield per tree (69.78%), phenol content (65.04 %), fruit pulp weight (62.12 %), number of fruits per tree (49.30 %), fruit weight (47.64 %), ascorbic acid (46.75 %), non-reducing sugars (36.81 %), stone weight (29.57 %), reducing sugars (29.27 %), total sugars (27.39 %), kernel weight (26.04 %), fruit length (25.34 %), kernel length (24.77 %), stone length (24.44 %), fruit width (22.23 %) and kernel width (21.12 %) exhibited high GA % (> 20 %), indicating the dominance of additive gene action in their expression while, moderate GA % (10–20 %) was recorded for acidity (18.65 %) and total soluble solids (12.89 %). Despite being moderate, these values still hold breeding significance, especially when accompanied by high heritability and moderate to high GCV.

These findings underline that high heritability estimates, when interpreted in isolation, may not always reflect true genetic gain unless supported by high GA %. The concurrent expression of high heritability, elevated GCV and substantial GA % observed in many traits suggests the predominance of additive genetic variance. This genetic architecture favors effective selection strategies and facilitates the identification and propagation of superior genotypes in mango.

Furthermore, the integration of these parameters affirms that genetic improvement through simple recurrent selection methods is not only feasible but also potentially efficient for traits governed largely by additive effects. This holistic approach to trait selection is consistent with the observations reported in mango (23, 28-32).

The pooled data analysis revealed substantial variability in the percent contribution of individual traits toward overall genetic divergence among mango genotypes, with values ranging from 1.86 % to 7.71 % (Fig. 1). Among the twenty morphological and quality traits evaluated, kernel length exhibited the maximum contribution (7.71 %), followed by stone length (7.29 %), kernel width (7.22 %), stone weight (6.62 %), acidity (6.10 %), fruit width (6.00 %), fruit length (5.80 %) and fruit weight (5.66 %). Other notable contributors included reducing sugar (5.45 %), total sugar (5.31 %), non-reducing sugar (5.14 %), kernel weight (5.13 %), number of fruits per tree (5.04 %) and total soluble solids (4.94 %). Traits with moderate contributions included fruit pulp weight (3.92 %), phenol content (3.32 %), total carotenoids (3.10 %), ascorbic acid (2.40 %) and fruit yield per tree (1.98 %). The lowest contribution toward genetic divergence was recorded for total antioxidants (1.86 %). Significant genetic variability was observed among mango genotypes for both morphological and quality traits, as supported by (28, 33). High variation in biochemical traits like ascorbic acid and phenol content confirms genotypic influence, as noted by (34, 35). These findings align with earlier reports indicating strong breeding potential (31, 36, 37).

## Conclusion

The present investigation revealed substantial genetic variability among the twelve mango genotypes, underscoring significant opportunities for targeted genetic improvement. The predominance of high GCV, PCV, heritability and genetic advance in key traits such as fruit yield, carotenoids and antioxidants highlights the strong genetic influence and potential for effective selection. Traits with moderate variability, including TSS and acidity, indicate the need for attention in long-term breeding programs due to their additive genetic effects. The marked divergence among genotypes, particularly the high percent contribution of kernel length, identifies critical traits for future selection strategies. The consistent pattern of PCV exceeding GCV reflects environmental influence, although the overall genetic potential remains promising. These findings advocate for the strategic deployment of selection and hybridization approaches to enhance mango productivity and quality.

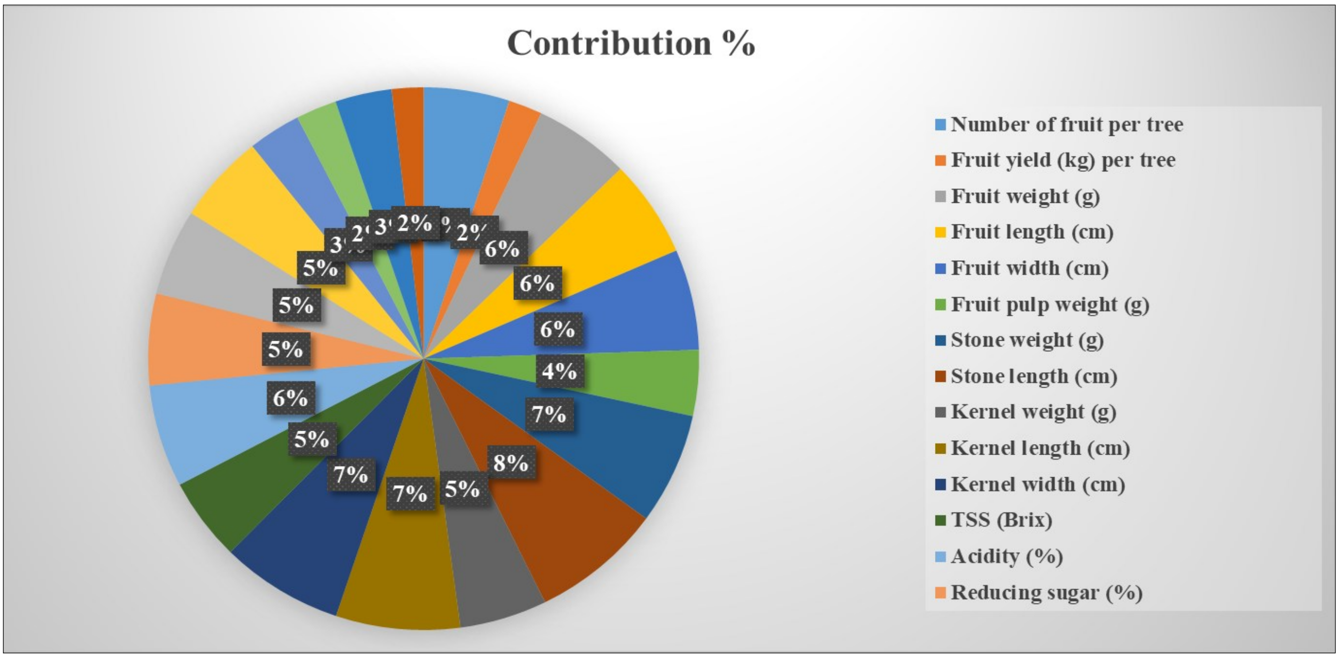

**Fig. 1:** Contribution (%) of different character in mango (Pooled data 2021-23)

## Authors' contributions

AK1 conducted the experiment and wrote the main manuscript text. AK2 also provided substantial guidance and facilitated the research by offering access to essential laboratory facilities. SP assisted with data analysis. AS and HK provided experimental guidance and contributed to the preparation of manuscript draft. SKS, KKS, SS, GKA and VP reviewed and approved the final version of the manuscript. This collaborative effort demonstrates the authors' commitment to producing a high-quality work 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 do not have any conflict of interest to declare.

**Ethical issues:** None

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