

STUDIES ON MAGNITUDE OF GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE FOR MORPHOLOGICAL AND BIOCHEMICAL CHARACTERS IN MANGO GERMPLASM

M. Sandhyarani^{1*}, Dr. R. Rajya Lakshmi², Dr. M. Madhavi³, Dr. B. Kanaka Mahalakshmi⁴, Dr. M. Paratpara Rao⁵, Dr. P. Vinaya Kumar Reddy⁶, V. Sekhar⁷

¹Ph.D. Scholar (Dept. of Fruit science), Dr. Y.S.R. Horticultural University, College of Horticulture, Venkatramannagudem, Andhra Pradesh, India

²Associate Dean, Dr. Y.S.R. Horticultural University, College of Horticulture, Parvathipuram, Andhra Pradesh, India

³Director of Research, Dr. Y.S.R. Horticultural University College of Horticulture, Venkataramannagudem, Andhra Pradesh, India

⁴Principal Scientist (Plant Pathology) and Head, Dr. Y.S.R. Horticultural University, Mango Research station, Eluru, Andhra Pradesh, India

⁵Associate Professor (Genetics and Plant Breeding), Dr. Y.S.R. Horticultural University, College of Horticulture, Venkataramannagudem, Andhra Pradesh, India

⁶Associate Professor (Fruit Science), Dr. Y.S.R. Horticultural University, College of Horticulture, Anantharajupeta, Andhra Pradesh, India

⁷Assistant Professor (Statistics), Dr. Y.S.R. Horticultural University, College of Horticulture, Venkataramannagudem, Andhra Pradesh, India

*Corresponding author: M. Sandhyarani, Mail Id: sandhyamaraboina12@gmail.com

ABSTRACT

The investigation entitled “studies on magnitude of genetic variability, heritability and genetic advance for morphological and biochemical characters in mango germplasm”. was carried out during the period 2021-2022 and 2022-23 at Mango Research Station, Nuzvid, Eluru District, Andhra Pradesh. The study included 36 genotypes and 4 checks viz., Banaganapalle, Chinnarasam, Jalal and Suvarnakha. In the study, High PCV and GCV values were recorded for trunk circumference (m), crown diameter E-W (m), crown diameter N-S (m), petiole length (cm), inflorescence width (cm), no. of hermaphrodite flowers in the inflorescence, fruit weight (g), pulp weight (g), peel weight (g), pulp to stone ratio, number of fruits/tree, fruit yield (kg/tree), stone length (cm), stone width (cm), stone weight (g), total soluble solids (^oBrix), titrable acidity (%), TSS: acid ratio, total sugars (%), reducing sugars (%), non reducing sugars (%), ascorbic acid (mg/100 g), total phenols content (mg of gallic acid/100 g) and β - carotene (μ g/100 g) and High heritability along with high genetic advance as per cent mean was observed for height of mature tree (m), trunk circumference (m), crown diameter E-W (m), crown diameter N-S (m), leaf blade length (cm), leaf blade width (cm), petiole length (cm), inflorescence length (cm), inflorescence width (cm), no. of hermaphrodite flowers in the inflorescence, fruit length (cm), fruit diameter (cm), fruit weight (g), pulp weight (g), peel weight (g), pulp to stone ratio, number of fruits/tree, fruit yield per tree (kg), stone length (cm), stone width (cm), stone weight (g), total soluble solids (^oBrix), titrable acidity (%), TSS: acid ratio, total sugars (%), reducing sugars (%), non reducing sugars (%), ascorbic acid (mg/100 g), total phenols content (mg of gallic acid/100 g) and β - carotene (μ g/100 g)

KEYWORDS: Genetic variability, heritability, genetic advance, mango germplasm

INTRODUCTION

Mango (*Mangifera indica* L.) is the most nutritive and delicious fruit crop belonging to the Anacardiaceae family and originated in Indo-Burma region. Due to its popularity and importance, mango is often named ‘King of fruits’ for its luscious flavour and taste. It is recognized as the pride fruit of India, being the richest source of vitamin A (4800 I.U.), vitamin C, minerals and other nutrients (Bhamini et al., 2018). In India, mango is cultivated in an area of 2325 thousand hectares with production of 208.99 lakh tonnes and 9.0 MT/ha productivity. The major mango-growing states in India encompass Uttar Pradesh, Karnataka, Andhra Pradesh, Telangana, Bihar, West Bengal and Gujarat etc. Notably, in Andhra Pradesh it is cultivated in an area of 378.94 thousand ha, yielding a production of 4926.22 MT and productivity of 13 MT/ha (NHB Data base, 2020-21).

The extent of variability present in a population is crucial because it serves as the foundation for efficient selection. Since the observed variability in a population is the total of variation caused by genotypic and environmental variables, understanding the nature and extent of genetic variation that contributes to gain under selection is critical. The success of character improvement through selection is determined by heritability and genetic advance. Once the population's relative amount of variability has been determined, the overall variability must be partitioned into heritable and non-heritable components. The effectiveness with which genotypes can be selected based on phenotypic performance is measured by the magnitude of heritability. A high heritability number shows that the phenotype of the trait strongly reflects the genotype, implying that genotypic constitution has a significant role in the development of the character. From a breeding perspective, such attributes are regarded as reliable.

MATERIALS AND METHODS

The experiment was conducted to “study the magnitude of genetic variability, heritability and genetic advance for morphological and biochemical characters in mango germplasm”. The experiment was laid out in an Augmented Block Design consisting of 36 genotypes and 4 checks viz., Banaganapalle, Chinnarasam, Jalal and Suvarnarekha. The details of genotypes are furnished in Table 1. Genotypes are named as per the names of the blocks i.e. B, C, D, E, F, G, H and I.

Table 1. List of 36 genotypes and 4 checks used in the study.

S.No.	Genotype	S.No.	Genotype
1	B-6	21	F-16
2	B-9	22	G-7
3	B-10	23	G-19
4	B-17	24	G-28
5	B-20	25	G-30
6	C-1	26	H-5
7	C-6	27	H-7
8	C-13	28	H-16
9	C-24	29	H-17
10	D-7	30	H-32
11	D-12	31	H-49
12	D-13	32	H-58
13	E-2	33	I-1
14	E-3	34	I-2
15	E-6	35	I-3
16	E-8	36	I-4
17	E-11	37	Banaganapalle (Table variety)
18	F-4	38	Chinnarasam (Juicy variety)
19	F-10	39	Jalal (Pickle variety)
20	F-12	40	Suvarnarekha (Coloured variety)

Estimation of genetic parameters

In order to assess and quantify the genetic variability among the genotypes for the characters under study, the following parameters were estimated.

Genotypic and phenotypic variances

The genotypic and phenotypic variances were computed based on the expected mean sum of squares as follows:

$$\sigma^2_g = \frac{M_2 - M_3}{r}$$

$$\sigma^2_p = \sigma^2_g + \sigma^2_e \text{ or } \frac{M_2 - M_3}{r} + \frac{M_3}{r}$$

Where,

σ^2_g = Genotypic variance (GV)

σ^2_p = Phenotypic variance (PV)

σ^2_e = Environmental variance (EV)

M_2 = Treatment Mean Square

M_3 = Error Mean Square

Coefficient of variation

Genotypic and phenotypic coefficients of variation were computed according to Burton (1952) based on the estimates of genotypic and phenotypic variance as follows:

a)

$$GCV = \frac{\sqrt{GV}}{\bar{X}} \times 100$$

Genotypic coefficient of variation (GCV)

b) **Phenotypic coefficient of variation (PCV)**

$$PCV = \frac{\sqrt{PV}}{\bar{X}} \times 100$$

Where,

GCV = Genotypic coefficient of variation

PCV = Phenotypic coefficient of variation

GV = Genotypic variance

PV = Phenotypic variance

$\bar{X}$ = General mean of character

The GCV and PCV values were classified as described by Sivasubramanian and Madhavamenon (1973).

Classification	GCV and PCV
Low	Less than 10%
Moderate	10-20%
High	More than 20%

Heritability

Heritability in broad sense was computed as the ratio of genetic variance to the total phenotypic variance. It has been estimated as per the formula given by Hanson et al. (1956).

$$\text{Heritability in broad sense } (h^2_{bs}) = \frac{\text{Genotypic variance } (\sigma_g^2)}{\text{Phenotypic variance } (\sigma_p^2)} \times 100$$

Heritability in broad sense was categorized as per the classification given by Johnson et al. (1955).

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

Genetic advance

Genetic advance was calculated based on formula given by Johnson et al. (1955).

Expected genetic advance (GA) = $K \times \sigma_p \times h^2$

Where,

K = Selection differential at 5% selection intensity (2.06)

σ_p = Phenotypic standard deviation

h^2 = Heritability in broad sense

Genetic advance as per cent of mean (GAM)

$$\text{GAM} = \frac{\text{GA}}{\bar{X}} \times 100$$

Where,

GA = Genetic advance

$\bar{X}$ = Grand mean of the character

The range of genetic advance as per cent of mean was classified as suggested by Johnson et al. (1955).

Classification	Genetic advance
Low	Less than 10%
Moderate	10-20%
High	More than 20%

RESULTS AND DISCUSSION

Genetic variability, heritability and genetic advance

The genetic parameters viz., phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in broad sense and genetic advance as per cent mean for 30 characters were studied among 36 genotypes and 4 checks viz., Banaganapalle, Chinnarasam, Jalal and Suvarnarekha are presented in (Table 2), (Figure 1 and Figure 2). The evaluated genotypes and checks exhibited a wide range of variability for all the characters.

Tree characters

1. Height of mature tree (m)

The GCV (18.1) and PCV (18.16) were found to be moderate, heritability (99.39%) and genetic advance as per cent of mean (37.18%) were found to be high. Moderate estimates of GCV and PCV indicates the influence of both additive and non-additive gene action as a result of which it can be expected that selection has scope to improve this trait. However, high heritability and genetic advance as per cent of mean indicates the presence of additive gene action in inheritance of this trait, hence selection would be effective for later generations. Similar results were obtained in mango by Majumder et al. (2012) and Sridhar et al. (2018) with respect to high heritability coupled with high genetic advance for height of mature tree.

2. Trunk circumference (m)

The GCV (27.72), PCV(27.88), heritability (98.91%) and genetic advance as per cent of mean (56.80%) were found to be high. High estimates of GCV and PCV recorded for this trait indicated the presence of additive gene action. So, improvement can be done by selection. However, high heritability accompanied with high genetic advance as per cent of mean indicated that the heritability is due to additive gene effects and thus simple selection based on phenotypic performance of this trait was effective. Similarly high GCV, PCV and heritability were reported by Elaiyaraja et al. (2021) for trunk circumference in mango.

3. Crown diameter E-W (m)

The GCV (20.59), PCV (20.69), heritability (99.01%) and genetic advance as per cent of mean (42.20%) were found to be high, indicated the presence of additive gene action in inheritance of this trait and simple selection will be highly rewarding for improving this character.

4. Crown diameter N-S (m)

The GCV (21.58), PCV (21.64), heritability (99.42%) and genetic advance as per cent of mean (44.32%) were found to be high for this trait which indicated the presence of additive gene action.

Leaf characters

1. Leaf blade length (cm)

The GCV (15.42) and PCV (15.53) were found to be moderate, while heritability (98.57%) and genetic advance as per cent of mean (31.53%) were found to be high for this character, which indicated the presence of both additive and non-additive gene action. Similar findings were reported by Sridhar et al. (2018) and Sathappan and Dhanasekaran (2020) in mango with respect to high heritability coupled with high genetic advance for leaf blade length.

2. Leaf blade width (cm)

The GCV (15.51) and PCV (15.64) were found to be moderate, while heritability (98.38%) and genetic advance as per cent of mean (31.69%) were found to be high for this character, which indicated the influence of both additive and non-additive gene action. These results were in agreement with the findings of Sridhar et al. (2018) and Sathappan and Dhanasekaran (2020) they reported that high heritability coupled with high genetic advance with respect to leaf blade width in mango.

3. Petiole length (cm)

The GCV (33.16), PCV (33.24), heritability (99.53%) and genetic advance as per cent of mean (68.14%) were found to be high for this trait, which indicated the presence of additive gene action in the inheritance of this trait and simple selection will be highly rewarding for improvement of this character.

Inflorescence characters

1. Inflorescence length (cm)

The GCV (17.00) and PCV (17.13) were found to be moderate, while heritability (98.50%) and genetic advance as per cent of mean (34.76%) were found to be high for this trait, which indicated the influence of both additive and non-additive gene action. Similar findings were reported by Abdul et al. (2022) with respect to moderate PCV for inflorescence length in mango.

2. Inflorescence width (cm)

High GCV (29.87), PCV (29.94), heritability (99.57%) and genetic advance as per cent of mean (61.41%) were found, which indicated the presence of additive gene action in the inheritance of this trait and simple selection will be highly rewarding for improvement of this character. Similarly high GCV and PCV with respect to inflorescence width were reported by Sridhar et al. (2018) and Kumar et al. (2023) in mango.

3. No. of hermaphrodite flowers in the inflorescence

The GCV (41.89), PCV (41.97), heritability (99.60%) and genetic advance as per cent of mean (86.11%) were found to be high, which indicated the additive gene action and improvement could be done for this trait by simple direct selection.

Fruit characters

1. Fruit length (cm)

Moderate values of GCV (18.22) and PCV (18.26) were found, while heritability (99.49%) and genetic advance as per cent of mean (37.43%) were found to be high, which indicated the influence of both additive and non-additive gene action. Similar findings were reported by Nayak et al. (2013) and Sankaran et al. (2020) with respect to high heritability accompanied with greater genetic advance as per cent of mean for fruit length in mango.

2. Fruit diameter (cm)

The GCV (12.43) and PCV (12.67) were found to be moderate, while heritability (96.33%) and genetic advance as per cent of mean (25.14%) were found to be high for this trait, which indicated the influence of both additive and non-additive gene action. Similar findings were reported by Sankaran et al. (2020) in mango with respect to high heritability accompanied with greater genetic advance as per cent of mean for fruit diameter.

3. Fruit weight (g)

High values of GCV (38.10), PCV (38.14), heritability (99.79%) and genetic advance as per cent of mean (78.41%) were found for this trait, which indicated the presence of additive gene action in the inheritance of this trait and simple selection will be highly rewarding for improvement of this character. Similarly high heritability

and genetic advance as per cent of mean were reported by Nayak et al. (2013) and Kumar et al. (2023) in mango.

4. Pulp weight (g)

The GCV (37.81), PCV (37.90), heritability (99.53%) and genetic advance as per cent of mean (77.70%) were found to be high for this trait, which indicated the presence of additive gene action. Similar findings of high variability were reported by Karibasappa et al. (1999) and Rathor (2005) for pulp weight in mango.

5. Peel weight (g)

The GCV (35.92), PCV (35.95), heritability (99.86%) and genetic advance as per cent of mean (73.95%) were found to be high, which indicated the additive gene action and improvement could be done for this trait by simple direct selection. Similarly high PCV and GCV were reported by Simi (2006) and Rajan et al. (2009) for peel weight in mango.

6. Pulp to stone ratio

The GCV (35.63), PCV (35.83), heritability (98.88%) and genetic advance as per cent of mean (72.99%) were found to be high for this trait, which indicated the presence of additive gene action in the inheritance of this trait and simple selection will be highly rewarding for improvement of this character. Similar results of high variability were reported in mango by Kokadwar et al. (1992) and Rajan et al. (2009) for pulp to stone ratio.

7. Number of fruits/tree

High GCV (83.55), PCV (83.62), heritability (99.84%) and genetic advance as per cent of mean (171.99%) were found for this trait, which indicated the presence of additive gene action. Similar findings were reported by Abdul et al. (2022) in mango with respect to high heritability accompanied with greater genetic advance as per cent of mean for number of fruits/tree.

8. Fruit yield (kg/tree)

The GCV (50.39), PCV (50.60), heritability (99.18%) and genetic advance as per cent of mean (103.38%) were found to be high, which indicated the additive gene action and improvement could be done for this trait by simple direct selection. Similarly high heritability accompanied with greater genetic advance as per cent of mean were reported by Sridhar et al. (2018) and Abdul et al. (2022) in mango.

Stone characters

1. Stone length (cm)

The GCV (27.62), PCV (27.70), heritability (99.45%) and genetic advance as per cent of mean (56.75%) were found to be high, which indicated the additive gene action and improvement could be done for this trait by simple direct selection. Similar results of high variability were obtained for stone length in mango by Rajan et al. (2009).

2. Stone width (cm)

The GCV (21.89), PCV (21.94), heritability (99.54%) and genetic advance as per cent of mean (44.98%) were found to be high, which indicated the presence of additive gene action in the inheritance of this trait and simple selection will be highly rewarding for improvement of this character.

3. Stone weight (g)

The GCV (38.40), PCV (38.45), heritability (99.76%) and genetic advance as per cent of mean (79.01%) were found to be high for this trait, which indicated the presence of additive gene action. Similar findings were reported by Rathor (2005) and Rajan et al. (2009) in mango with respect to high GCV and heritability accompanied with greater genetic advance as per cent of mean for stone weight.

Biochemical characters

1. Total soluble solids (°Brix)

The GCV (38.45), PCV (38.55), heritability (99.50%) and genetic advance as per cent of mean (79.01%) were found to be high, which indicated the additive gene action and improvement could be done for this trait by simple direct selection. Similar findings were reported by Sankaran et al. (2020) in mango with respect to high heritability accompanied with greater genetic advance as per cent of mean for TSS.

2. Titrable acidity (%)

High GCV (43.75), PCV (43.75), heritability (100.00%) and genetic advance as per cent of mean (90.12%) were found, which indicated the presence of additive gene action in the inheritance of this trait and simple selection will be highly rewarding for improvement of this character. Similarly high heritability and genetic advance as per cent of mean were reported by Sridhar et al. (2018) for this trait in mango.

3. TSS: acid ratio

The GCV (97.24), PCV (97.28), heritability (99.92%) and genetic advance as per cent of mean (200.23%) were found to be high, which indicated the presence of additive gene action. Similarly high GCV, PCV, heritability and genetic advance as per cent of mean were reported by Sridhar et al. (2018) in mango for TSS: acid ratio.

4. Total sugars (%)

The GCV (61.01), PCV (61.07), heritability (99.79%) and genetic advance as per cent of mean (125.55%) were found to be more, which indicated the presence of additive gene action in the inheritance of this trait and simple selection will be highly rewarding for improvement of this character. The findings were in accordance with Attri et al. (1999) with respect to heritability and Karibasappa et al. (1999) with respect to PCV and GCV in mango.

5. Reducing sugars (%)

High GCV (59.41), PCV (59.46), heritability (99.83%) and genetic advance as per cent of mean (122.29%) were found, which indicated the additive gene action and improvement could be done for this trait by simple direct selection. Higher estimates of variability for reducing sugars were reported by Simi (2006) and Rathod (2007) in mango.

6. Non reducing sugars (%)

The GCV (70.04), PCV (70.20), heritability (99.55%) and genetic advance as per cent of mean (143.96%) were found to be high, which indicated the presence of additive gene action. Similarly high GCV, PCV, heritability and genetic advance as per cent of mean for non reducing sugars were reported by Sridhar et al. (2018) in mango.

7. Ascorbic acid (mg/100 g)

High GCV (30.66), PCV (30.77), heritability (99.29%) and genetic advance as per cent of mean (62.93%) were found, which indicated the additive gene action and improvement could be done for this trait by simple direct selection. The higher estimates of variability for this trait were earlier reported by Singh (2005) and Rathod (2007) in mango.

8. Total phenols content (mg of gallic acid /100 g)

The GCV (46.20), PCV (46.27), heritability (99.70%) and genetic advance as per cent of mean (95.03%) were found to be high, which indicated the presence of additive gene action.

9. β - Carotene ($\mu\text{g}/100\text{ g}$)

High GCV (39.48), PCV (39.55), heritability (99.62%) and genetic advance as per cent of mean (81.17%) were found, which indicated the presence of additive gene action in the inheritance of this trait and simple selection will be highly rewarding for improvement of the character. Similar results of high values of heritability for β -carotene were reported in mango by Attri et al. (1999) and Rathor (2005).

The extent of variability present in a population is crucial because it serves as the foundation for efficient selection. Since the observed variability in a population is the total of variation caused by genotypic and environmental variables, understanding the nature and extent of genetic variation that contributes to gain under selection is critical.

In the present investigation, phenotypic coefficient of variation was higher than corresponding genotypic coefficient of variation indicating the influence of environmental factors in the expression of these characters.

High PCV and GCV values were recorded for trunk circumference (m), crown diameter E-W (m), crown diameter N-S (m), petiole length (cm), inflorescence width (cm), no. of hermaphrodite flowers in the inflorescence, fruit weight (g), pulp weight (g), peel weight (g), pulp to stone ratio, number of fruits/tree, fruit yield(kg/tree), stone length (cm), stone width (cm), stone weight (g), total soluble solids ($^{\circ}\text{Brix}$), titrable acidity (%), TSS: acid ratio, total sugars (%), reducing sugars (%), non reducing sugars (%), ascorbic acid (mg/100 g), total phenols content (mg of gallic acid/100 g) and β - carotene ($\mu\text{g}/100\text{ g}$) which suggested the existence of genetic variability among these characters. So, improvement of these characters can be done by selection.

Moderate PCV and GCV values were recorded for height of mature tree (m), leaf blade length (cm), leaf blade width (cm), inflorescence length (cm), fruit length (cm) and fruit diameter (cm) indicated the presence of considerable genetic variability as a result of which it can be expected that selection has scope to improve these traits.

The success of character improvement through selection is determined by heritability and genetic advance. Once the population's relative amount of variability has been determined, the overall variability must be partitioned into heritable and non-heritable components. The effectiveness with which genotypes can be selected based on phenotypic performance is measured by the magnitude of heritability. A high heritability number shows that the phenotype of the trait strongly reflects the genotype, implying that genotypic constitution has a significant role in the development of the character. From a breeding perspective, such attributes are regarded as reliable.

High heritability along with high genetic advance as per cent mean was observed for height of mature tree (m), trunk circumference (m), crown diameter E-W (m), crown diameter N-S (m), leaf blade length (cm), leaf blade width (cm), petiole length (cm), inflorescence length (cm), inflorescence width (cm), no. of hermaphrodite flowers in the inflorescence, fruit length (cm), fruit diameter (cm), fruit weight (g), pulp weight (g), peel weight (g), pulp to stone ratio, number of fruits/tree, fruit yield per tree (kg), stone length (cm), stone width (cm), stone weight (g), total soluble solids ($^{\circ}\text{Brix}$), titrable acidity (%), TSS: acid ratio, total sugars (%), reducing sugars (%), non reducing sugars (%), ascorbic acid (mg/100 g), total phenols content (mg of gallic acid/100 g) and β -carotene ($\mu\text{g}/100\text{ g}$) indicated that the heritability is most likely due to additive gene effects and thus simple selection based on phenotypic performance of these characters may be effective.

Table 2. Estimates of genetic variability, heritability and genetic advance for morphological and biochemical characters in mango genotypes.

S.No.	Characters	Mean	Range		Coefficient of variation		Heritability (broad sense) (%)	Genetic advance as per cent mean at 5%
			Min	Max	Genotypic	Phenotypic		
1.	Height of mature tree (m)	9.46	6.33	13.58	18.10	18.16	99.39	37.18
2.	Trunk circumference (m)	1.62	0.53	2.63	27.72	27.88	98.91	56.80
3.	Crown diameter E-W (m)	10.49	5.54	13.43	20.59	20.69	99.01	42.20
4.	Crown diameter N-S (m)	10.56	6.61	15.73	21.58	21.64	99.42	44.32
5.	Leaf blade length (cm)	20.49	15.34	26.96	15.42	15.53	98.57	31.53
6.	Leaf blade width (cm)	5.09	3.52	6.49	15.51	15.64	98.38	31.69
7.	Petiole length (cm)	2.69	1.41	5.36	33.16	33.24	99.53	68.14
8.	Inflorescence length (cm)	25.50	15.12	34.61	17.00	17.13	98.50	34.76
9.	Inflorescence width (cm)	13.66	8.08	26.06	29.87	29.94	99.57	61.41
10.	No. of hermaphrodite flowers in the inflorescence	99.77	27.54	175.44	41.89	41.97	99.60	86.11
11.	Fruit length (cm)	13.95	9.74	21.35	18.22	18.26	99.49	37.43
12.	Fruit diameter (cm)	22.46	17.25	27.79	12.43	12.67	96.33	25.14
13.	Fruit weight (g)	279.11	135.03	605.35	38.10	38.14	99.79	78.41
14.	Pulp weight (g)	122.51	40.27	270.31	37.81	37.90	99.53	77.70

Note: PCV, GCV and Genetic advance as per cent mean: Low = 0-10%; Medium = 10-20% and High = 20% above.

Heritability: Low = Less than 30%; Medium = 30-60% and High = More than 60%.

S.No.	Characters	Mean	Range		Coefficient of variation		Heritability (broad sense) (%)	Genetic advance as per cent mean at 5%
			Min	Max	Genotypic	Phenotypic		
15.	Peel weight (g)	50.55	21.22	93.21	35.92	35.95	99.86	73.95
16.	Pulp to stone ratio	3.70	1.60	6.60	35.63	35.83	98.88	72.99
17.	Number of fruits/tree	206.16	30.11	989.49	83.55	83.62	99.84	171.99
18.	Fruit yield (kg/tree)	53.16	6.97	184.44	50.39	50.60	99.18	103.38
19.	Stone length (cm)	9.66	3.39	14.42	27.62	27.70	99.45	56.75
20.	Stone width (cm)	4.28	2.48	6.11	21.89	21.94	99.54	44.98
21.	Stone weight (g)	35.08	11.07	73.82	38.40	38.45	99.76	79.01
22.	Total soluble solids (°Brix)	13.48	7.88	20.93	38.45	38.55	99.50	79.01
23.	Titrate Acidity (%)	0.32	0.14	0.47	43.75	43.75	100.00	90.12
24.	TSS: acid ratio	48.00	16.59	149.46	97.24	97.28	99.92	200.23
25.	Total sugars (%)	9.10	4.75	17.48	61.01	61.07	99.79	125.55
26.	Reducing sugars (%)	3.64	1.40	6.82	59.41	59.46	99.83	122.29
27.	Non reducing sugars (%)	5.46	2.36	10.66	70.04	70.20	99.55	143.96
28.	Ascorbic acid (mg/100 g)	36.32	21.73	52.01	30.66	30.77	99.29	62.93
29.	Total phenols content (mg of gallic acid/100 g)	91.38	53.22	134.52	46.20	46.27	99.70	95.03
30.	β- Carotene (µg/100 g)	1289.79	685.50	1942.11	39.48	39.55	99.62	81.17

Note: PCV, GCV and Genetic advance as per cent mean: Low = 0-10%; Medium = 10-20% and High = 20% above.

Heritability: Low = Less than 30%; Medium = 30-60% and High = More than 60%.

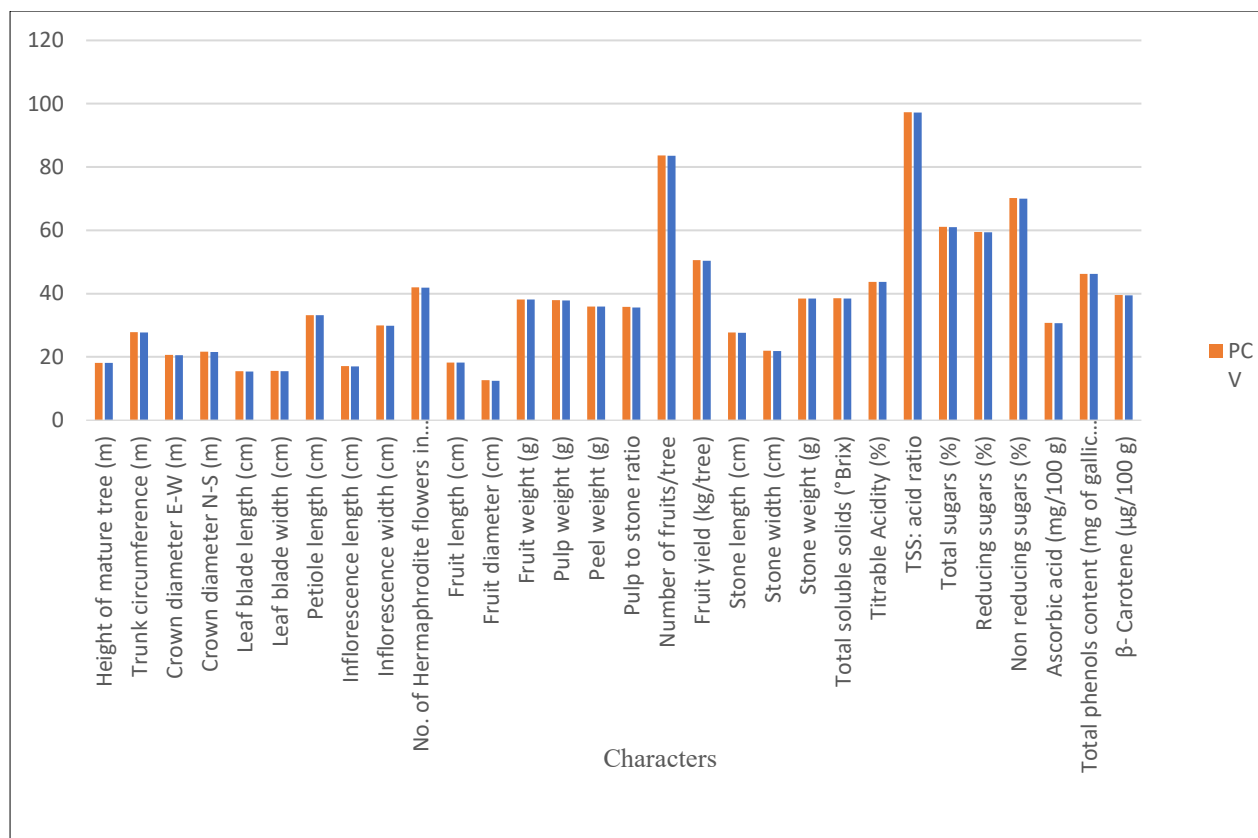


Figure 1. Graphical representation of phenotypic and genotypic coefficients of variation for various characters in mango genotypes.

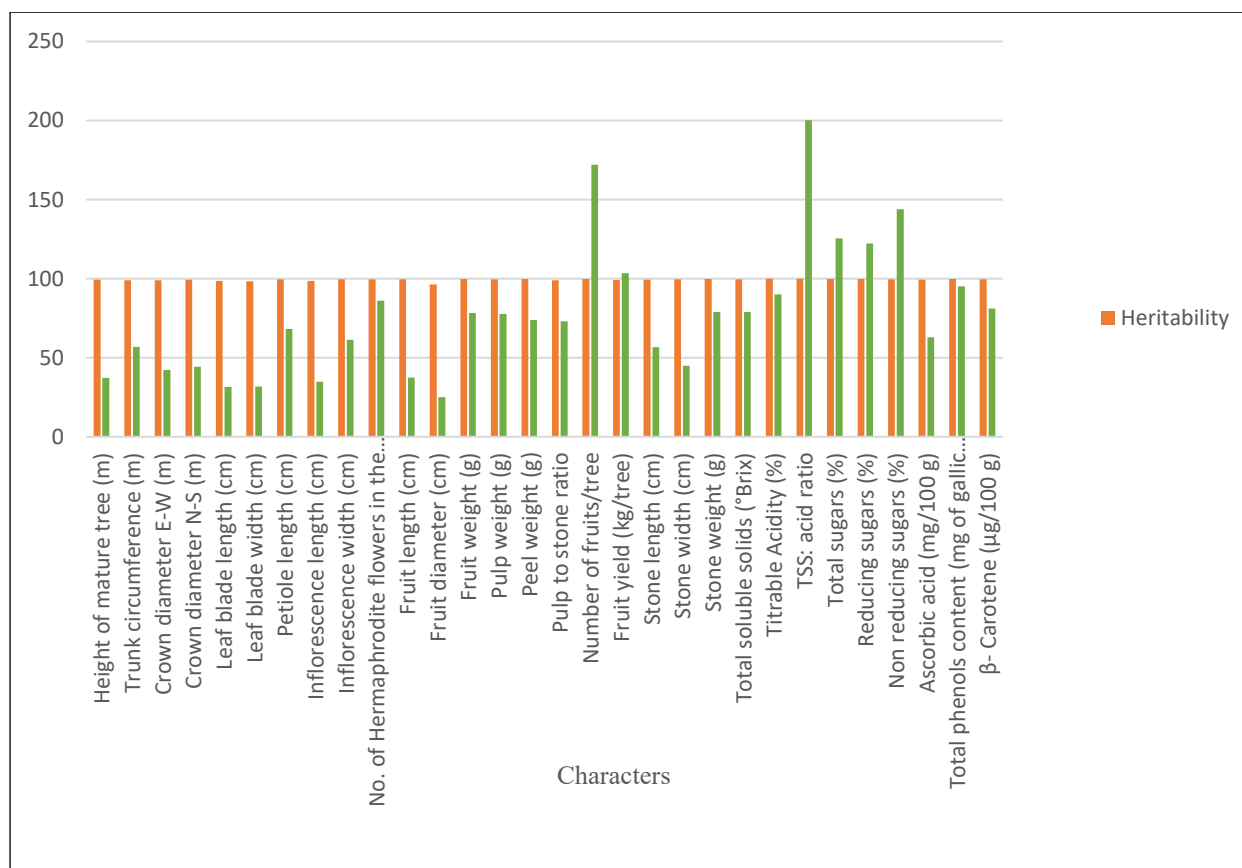


Figure 2. Graphical representation of heritability (broad sense) and genetic advance as per cent mean for various characters in mango genotypes.

CONCLUSION

In the present findings, High PCV and GCV values were recorded for trunk circumference (m), crown diameter E-W (m), crown diameter N-S (m), petiole length (cm), inflorescence width (cm), no. of hermaphrodite flowers in the inflorescence, fruit weight (g), pulp weight (g), peel weight (g), pulp to stone ratio, number of fruits/tree, fruit yield (kg/tree), stone length (cm), stone width (cm), stone weight (g), total soluble solids ($^{\circ}$ Brix), titrable acidity (%), TSS: acid ratio, total sugars (%), reducing sugars (%), non reducing sugars (%), ascorbic acid (mg/100 g), total phenols content (mg of gallic acid/100 g) and β - carotene (μ g/100 g) which suggested the existence of genetic variability among these characters. So, improvement of these characters can be done by selection. Moderate PCV and GCV values were recorded for height of mature tree (m), leaf blade length (cm), leaf blade width (cm), inflorescence length (cm), fruit length (cm) and fruit diameter (cm) indicated the presence of considerable genetic variability as a result of which it can be expected that selection has scope to improve these traits.

High heritability along with high genetic advance as per cent mean was observed for height of mature tree (m), trunk circumference (m), crown diameter E-W (m), crown diameter N-S (m), leaf blade length (cm), leaf blade width (cm), petiole length (cm), inflorescence length (cm), inflorescence width (cm), no. of hermaphrodite flowers in the inflorescence, fruit length (cm), fruit diameter (cm), fruit weight (g), pulp weight (g), peel weight (g), pulp to stone ratio, number of fruits/tree, fruit yield per tree (kg), stone length (cm), stone width (cm), stone weight (g), total soluble solids ($^{\circ}$ Brix), titrable acidity (%), TSS: acid ratio, total sugars (%), reducing sugars (%), non reducing sugars (%), ascorbic acid (mg/100 g), total phenols content (mg of gallic acid/100 g) and β -carotene (μ g/100 g) indicated that the heritability is most likely due to additive gene effects and thus simple selection based on phenotypic performance of these characters may be effective.

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Conflict of interest

The authors declare that they do not have any conflict of interest.

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