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Abstract

Thirty mango genotypes were studied to find out their variability, heritability, and genetic advance. Significant variations were observed in 46 characters. There were also considerable differences between the genotypic and the phenotypic coefficients of variation for almost all the characters which indicated the influence of environment on the expression of these traits. Among the studied characters, GCV and PCV were high for 40 characters. All the characters showed considerably high heritability except leaf width which ranged from 21.32 to 99.85 % and the genetic advance (as % of mean) was high for 44 traits. High heritability coupled with high genetic advance was observed in 44 traits except leafwidth and chlorophyll content which indicated that these characters were less influenced by environment confirming predominance of additive gene action and therefore, selection in favour of these 44 characters would be feasible for yield improvement of mango.

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Introduction

Mango (*Mangifera indica* L.) is the most important commercial fruit crop of the tropical and subtropical regions of the world. It is considered as the “king of fruits” due to its excellent flavour, beautiful colour, attractive fragrance and delicious taste. Mango belongs to the genus *Mangifera*, family Anacardiaceae and order Sapindales. The edible species *Mangifera indica* L. bears good quality fruits and is commonly referred to as cultivated mango. The other edible *Mangifera* species generally have lower quality fruits and are commonly referred to as wild mangos. It originated in the Indo-Burma region during

the earlier period of the Cretaceous era (Yonemori et al. 2002; Anusuya et al. 2018). It gradually spread and become naturalized and adapted throughout the tropics and subtropics and has been grown commercially for centuries. Today, mangos are recognized and eaten throughout the world and are regarded as one of the most popular and esteemed tropical fruits. Mango is diploid with $2n=40$ having a genome of 8.8×10^8 bp. phenomenon of allopolyploidy, out breeding, and the different agro-climatic conditions in mango growing areas, has resulted in a high level of genetic diversity in mangos (Krishna

& Singh 2007). Mango has rich intra-specific diversity and there are about 1600 cultivars in the world (Pandey & Majumder 1988; Kumar et al. 2019), of which some 350 cultivars are in commercial production and the rest are limited to mixed orchards or home gardens. India is thought to be the primary centre of diversity for mango (NBPGR 2007). It is a major fruit crop of India and occupies an area of 2.263 million hectares with an annual production of 19.68 million tonnes and the productivity is 8.71 MT/hac. The export potential of India is 52761 MT of fresh and dried products of mango with the benefit cost of Rs.44,366 Lacs. (APEDA, 2016-17) The area, production and productivity of mango in Tamilnadu is 160.49 thousand hac, 1.157 million tonnes and 7.19 MT/hac (India stat 2016-17).

An understanding of the nature and magnitude of variability among the genetic stocks of a crop is of prime importance to breeders. Evaluation of genetic variability is important to know the source of gene for a particular trait within the available germplasm (Tomooka 1991). A good knowledge of genetic wealth might also help in identifying desirable cultivars for commercial cultivation. Improvement of yield and other traits depends upon the amount of genetic variability present in the breeding materials for the required traits. High heritability generally enables the breeder to select plants on the basis of the phenotypic expression (Johnson et al. 1955). As the heritability estimates are often subjected to genotype-environment interaction, estimation of genetic advance is required for expected genotypic progress of a particular character. Studies on the variability

using genetic parameters are essential for initiating an efficient breeding programme. The present study was an attempt to gather information on genetic variability, heritability, and genetic advance among the important traits of mango crop.

Materials and Methods

The experimental materials comprised of 30 mango genotypes (Table 1). The study was conducted on the pre-established 10 year old mango orchard of central block, Department of Fruit crops, Horticultural College and Research Institute, Periyakulam, Tamil Nadu Agricultural University (TNAU), during August 2017- June 2018. The experiment was laid out in the RBD with three replications. The distance from plant to plant was 5.5 m and row to row was 5.5 m. Data were recorded on tree height, tree girth, tree spread, leaf length, leaf width, petiole length, chlorophyll content, leaf area, inflorescence length, inflorescence width, number of male flowers per panicle, number of perfect flowers per panicle, percentage of perfect flowers, total number of flowers, sex ratio, duration of fifty per cent flowering, duration of hundred per cent flowering, number of fruit set at marble stage, fruit set percentage at marble stage, fruit retention percentage, fruit drop percentage, fruit length, fruit width, fruit weight, fruit volume, specific gravity, stone length, stone width, stone weight, pulp weight, peel weight, peel thickness, pulp per cent, stone per cent, peel per cent, pulp to stone ratio, pulp to peel ratio, number of fruits per tree, yield per tree, TSS, acidity, reducing sugar, non-reducing sugar, total sugar, total carotenoid content and ascorbic acid content. TSS was measured with the help of a hand refractometer. Genotypic

and phenotypic coefficient of variation was calculated according to Johnson et al. (1955). Heritability in broad sense (h^2_b) and genetic advance as percent of mean (GA %) were estimated as proposed by Lush (1940) and Johnson et al. (1955) respectively.

Results and Discussion

Wide range of variation was observed in growth, floral and different fruit characters of mango which indicated the presence of genetic divergence of the crop (Table 2).

Range, mean with standard error, genotypic and phenotypic coefficient of variation, heritability in broad sense and genetic advance in percent mean of some morphological and biochemical traits of mango are presented in Table 3. The estimates of phenotypic coefficient of variation were higher than the genotypic coefficient of variation for all the characters studied. The results indicated the influence of environment on the expression of the characters under investigation.

Table 1. Details of the genotypes used in the present study

Treatments	Genotypes	Source
T ₁	Alphonso	Horticultural College and Research Institute, periyakulam
T ₂	Amarapali	Horticultural College and Research Institute, periyakulam
T ₃	Arka Aruna	Horticultural College and Research Institute, periyakulam
T ₄	Arka Puneet	Horticultural College and Research Institute, periyakulam
T ₅	Au Rumani	Horticultural College and Research Institute, periyakulam
T ₆	Banganapalli	Aranmanaithottam, Dindigul
T ₇	Duraipandi	Rajapalayam, Virudhunagar
T ₈	Imam Pasand	Manjakuppam, Virudhachalam
T ₉	Iswarya	Rajapalayam, Virudhunagar
T ₁₀	Javari	Mathuranthagam, Chennai
T ₁₁	Komangai	Shenbagathoppu, Srivilliputhur
T ₁₂	KovanKachi	Shenbagathoppu, Srivilliputhur
T ₁₃	KundurPacharisi	Shenbagathoppu, Srivilliputhur
T ₁₄	KuruviNeelum	Shenbagathoppu, Srivilliputhur
T ₁₅	Mallika	Horticultural College and Research Institute, periyakulam
T ₁₆	Malpacharisi	Rajapalayam, Virudhunagar
T ₁₇	Mohandhas	Shenbagathoppu, Srivilliputhur
T ₁₈	NathamPalamani	Pattiveeranpatty, Dindigul
T ₁₉	Neelum	Kuthukkalvalasai, Tirunelveli
T ₂₀	P.K.Patti	Rajapalayam, Virudhunagar
T ₂₁	Pedharasam	Anantharajupet, Andrapradesh
T ₂₂	PKM 1	Horticultural College and Research Institute, periyakulam

T ₂₃	PKM 2	Horticultural College and Research Institute, periyakulam
T ₂₄	Ratna	Horticultural College and Research Institute, periyakulam
T ₂₅	Samba Kooja	Rajapalayam, Virudhunagar
T ₂₆	Senthuram	Horticultural College and Research Institute, periyakulam
T ₂₇	Shajahan	Mathuranthagam, Chennai
T ₂₈	Sindhu	Horticultural College and Research Institute, periyakulam
T ₂₉	SothuparaiVadumangai	Sothuparai,Theni
T ₃₀	SundarLangra	Shenbagathoppu, Srivilliputhur

Table 2. Analysis of variance for different characters in mango

S. No.	characters	Treatment MS (df=29)	Replication MS (df=2)	Error MS (df=58)
1	Tree height (m)	4.033**	0.065	0.177
2	Tree girth (cm)	1,015.02**	27.656	33.311
3	Tree spread (m)	6.263**	2.202	0.309
4	Leaf length (cm)	53.678**	23.14	1.29
5	Leaf width (cm)	5.892**	5.429	3.25
6	Petiole length (cm)	3.101**	1.604	0.291
7	Chlorophyll content (SPAD value)	94.997**	7.672	6.806
8	Leaf area (cm ²)	2,656.33*	325.541	59.282
9	Inflorescence length (cm)	67.865**	15.058	2.424
10	Inflorescence width (cm)	49.956**	17.194	3.018
11	Number of male flowers per panicle	85,543.32**	6,146.85	2,524.86
12	Number of perfect flowers per panicle	9,172.64**	971.775	504.268
13	perfect flower %	47.34**	2.232	0.351
14	Total number of flowers	122,270.75**	1,283.23	607.743
15	Sex ratio (Perfcet to male flowers)	1.916**	0.015	0.008
16	Duration of 50% flowering	225.064**	0.052	0.132
17	Duration of 100% flowering	360.957**	0.885	0.439
18	Number of fruit set at marble stage	9.434**	1.553	0.233
19	Fruit set % at marble stage	0.094**	0.005	0.001
20	Fruit retention %	705.533**	0.941	0.345
21	Fruit drop %	2,204.04**	8.675	3.192

22	Fruit length (cm)	47.465**	0.015	0.076
23	Fruit width (cm)	17.125**	0.407	0.028
24	Fruit weight (g)	19,896.02**	49.108	24.851
25	Fruit volume (cc)	22,775.50**	19.32	27.226
26	Specific gravity (g/cc)	0.400**	0.002	0.001
27	Stone length (cm)	14.068**	0.003	0.033
28	Stone width (cm)	3.851**	0.018	0.006
29	Stone weight (g)	258.539**	2.261	0.488
30	Pulp weight (g)	12,826.55**	23.149	18.546
31	Peel weight (g)	201.364**	1.997	0.366
32	Peel thickness (mm)	0.664**	0	0.001
33	Pulp %	1,627.09**	14.095	2.685
34	Stone %	64.155**	0.082	0.1
35	Peel %	45.164**	0.054	0.086
36	Pulp to stone ratio	13.356**	0.077	0.018
37	Pulp to peel ratio	16.325**	0.015	0.035
38	Number of fruits per tree	15,470.18**	512.067	83.746
39	Yield per tree (Kg/tree)	746.335**	1.848	0.384
40	TSS (⁰ Brix)	93.1**	1.019	0.206
41	Acidity (%)	0.033**	0	0
42	Reducing sugar (%)	5.986**	0	0.01
43	Non-reducing sugar (%)	50.324**	0.05	0.078
44	Total sugar (%)	82.203**	0.152	0.136
45	Total Carotenoid content (mg/100g)	42.934**	0.028	0.029
46	Ascorbic acid content (mg/100g)	671.194**	0.486	1.172

* - Significant at 5 %, ** - Significant at 1 %

Table 3. Genetic variability for different characters of mango

S. No.	characters	Mean	Range	GCV	PCV	h^2b (%)	Genetic advance as % of mean
1	Tree height (m)	5.32	3.57-8.36	21.31	22.73	87.89	41.15
2	Tree girth (cm)	49.98	25 -103.97	36.19	37.99	90.76	71.03
3	Tree spread (m)	5.81	3.35 -8.99	24.24	26.05	86.53	46.44
4	Leaf length (cm)	23.05	15.88-32.85	18.13	18.79	93.12	36.04
5	Leaf width (cm)	5.98	2.64 - 10.24	15.69	33.97	21.32	14.92
6	Petiole length (cm)	3.87	2.55 -6.28	25.04	28.66	76.32	45.06
7	Chlorophyll content	52.58	39.05-63.83	10.31	11.44	81.2	19.14

	(SPAD value)						
8	Leaf area (cm ²)	94.23	34.28-166.35	31.23	32.28	93.59	62.23
9	Inflorescence length (cm)	25.3	17.52-39.50	18.46	19.46	90	36.07
10	Inflorescence width (cm)	15.94	11.49-28.53	24.81	27.09	83.83	46.79
11	Number of male flowers per panicle	788.11	528.47-1063.53	21.11	22.05	91.64	41.63
12	Number of perfect flowers per panicle	234.35	164.33-340.67	22.94	24.86	85.14	43.6
13	perfect flower %	19.39	15.55-31.43	17.13	17.33	97.81	34.91
14	Total number of flowers per panicle	1187.4	700-1346.80	19.7	19.84	98.52	40.27
15	Sex ratio	4.16	2.18 -5.43	23.05	23.2	98.71	47.18
16	Duration of 50% flowering	14.47	7-39	59.85	59.91	99.82	123.19
17	Duration of 100% flowering	27.23	15-53	40.25	40.33	99.64	82.77
18	Number of fruitset at marble stage	3.06	0.40-6.13	57.31	59.45	92.94	113.82
19	Fruitset % at marble stage	0.30	0.03-0.74	59.55	59.61	99.78	122.54
20	Fruit retention %	20.86	12.20-83.33	73.51	73.56	99.85	151.31
21	Fruit drop %	69.14	16.67-87.80	39.17	39.26	99.57	80.52
22	Fruit length (cm)	10.24	5.7-15.2	38.82	38.92	99.52	79.78
23	Fruit width (cm)	6.29	3.2-9.2	37.93	38.04	99.44	77.93
24	Fruit weight (g)	189.89	119.56-315.08	42.86	42.94	99.63	88.12
25	Fruit volume (cc)	191.17	115-345	45.55	45.63	99.64	93.66
26	Specific gravity (g/cc)	0.92	0.72-1.76	39.79	39.89	99.5	81.76
27	Stone length (cm)	5.94	5-8.36	36.42	36.55	99.29	74.77
28	Stone width (cm)	3.16	2.69-4.48	35.89	35.97	99.55	73.77
29	Stone weight (g)	24.17	15.38- 33.82	38.37	38.48	99.44	78.82
30	Pulp weight (g)	144.43	91.8-252.85	45.24	45.34	99.57	92.99
31	Peel weight (g)	21.29	12.38-29.86	38.45	38.56	99.46	78.99
32	Peel thickness (mm)	1.21	0.84-1.86	38.82	38.94	99.4	79.73
33	Pulp %	67.85	66.41-80.25	34.3	34.38	99.51	70.48
34	Stone %	11.81	10.73-19.91	39.13	39.23	99.53	80.43
35	Peel %	10.35	9.02-16.25	37.46	37.57	99.43	76.96
36	Pulp to stone ratio	5.35	3.44-7.48	39.41	39.49	99.6	81.02
37	Pulp to peel ratio	6.05	4.18-8.90	38.5	38.62	99.37	79.05
38	Number of fruits per tree	59.90	3.00-252.00	118.7 3	118.7 8	99.9	244.45

39	Yield per tree (Kg/tree)	16.68	0.46-59.67	94.53	94.6	99.85	194.58
40	TSS (°Brix)	16.05	14.58-20.12	34.68	34.8	99.34	71.21
41	Acidity (%)	0.22	0.14-0.43	48.42	48.55	99.48	99.49
42	Reducing sugar (%)	3.63	3.04-5.95	38.93	39.02	99.5	79.99
43	Non-reducing sugar (%)	11.26	9.74-14.71	36.36	36.44	99.54	74.73
44	Total sugar (%)	14.88	13.6-19.47	35.15	35.24	99.5	72.23
45	Total Carotenoid content (mg/100g)	6.40	2.70-15.79	59.06	59.12	99.79	121.54
46	Ascorbic acid content (mg/100g)	35.81	14.84-53.76	41.73	41.84	99.48	85.75

GCV-Genotypic coefficient of variation, h^2b - Heritability in broad sense

PCV- Phenotypic coefficient of variation

The higher estimates of genotypic and phenotypic coefficient of variation and medium difference between GCV and PCV were obtained for tree height, tree girth, tree spread, petiole length, leaf area, inflorescence width, number of male flowers per panicle, number of perfect flowers per panicle, sex ratio, duration of fifty per cent flowering, duration of hundred per cent flowering, number of fruit set at marble stage, fruit set percentage at marble stage, fruit retention percentage, fruit drop percentage, fruit length, fruit width, fruit weight, fruit volume, specific gravity, stone length, stone width, stone weight, pulp weight, peel weight, peel thickness, pulp per cent, stone per cent, peel per cent, pulp to stone ratio, pulp to peel ratio, number of fruits per tree, yield per tree, TSS, acidity, reducing sugar, non-reducing sugar, total sugar, total carotenoid content and ascorbic acid content, which indicates the possibility of selecting superior genotypes. The results are in accordance with the findings of Rai et al. (2001) and Himabindu et al. (2016). Ranpise & Desai (2003) found high estimates of phenotypic coefficient of variation and genotypic coefficient of variation in lime for number of fruits per plant, flower twig, tree volume and yield per plant. Prasad and Rao (1989) observed high

estimates of genotypic coefficient of variation and phenotypic coefficient of variation in lime for rind thickness, juice weight and juice volume in July crops and high estimates for TSS, fruit weight, and number of seeds in December crops. Moderate phenotypic and genotypic coefficient of variations were recorded for leaf length, chlorophyll, inflorescence length, percentage of perfect flower and total number of flowers. High phenotypic and moderate genotypic coefficients of variations were recorded for leaf width. The similar results were also reported by Patel (2002), Rathod (2007); Kumar et al. 2016 and Nayak et al. (2013).

Although the genotypic coefficient of variation and phenotypic coefficient of variation are the measures of genetic variability however, the amount of genetic gain can be estimated from genotypic coefficient of variation and phenotypic coefficient of variation along with heritability. Swarup and Chougule (1962) suggested that the estimates of genotypic coefficient of variation alone was not sufficient to quantify the amount of variation which is heritable and Burton (1952) inferred that genotypic coefficient of variation effects together with heritability estimates would furnish more reliable information. In the presents tudy,

heritability estimates were high coupled with high genetic advance as per cent of mean for most of the characters viz., tree height, tree girth, tree spread, leaf length, petiole length, leaf area, inflorescence length, inflorescence width, number of male flowers per panicle, number of perfect flowers per panicle, percentage of perfect flowers, total number of flowers, sex ratio, duration of fifty per cent flowering, duration of hundred per cent flowering, number of fruit set at marble stage, fruit set percentage at marble stage, fruit retention percentage, fruit drop percentage, fruit length, fruit width, fruit weight, fruit volume, specific gravity, stone length, stone width, stone weight, pulp weight, peel weight, peel thickness, pulp per cent, stone per cent, peel per cent, pulp to stone ratio, pulp to peel ratio, number of fruits per tree, yield per tree, TSS, acidity, reducing sugar, non-reducing sugar, total sugar, total carotenoid and ascorbic acid and moderate estimates for leaf width and chlorophyll content (GA as % of mean only). Higher values of heritability indicates that either these were simply inherited characters governed by a few major genes or additive gene effects even if, they were under polygenic control and therefore, selection of these characters would be more effective for improvement (Johnson et al. 1955; Panse 1957). Ranpise & Desai (2003) observed high values of heritability for fruits per plant, average fruit weight, juice percentage, TSS and acidity. Prasad & Rao (1989) recorded high estimates of heritability in lime for TSS, ascorbic acid, acidity, rind thickness and fruit volume.

The higher values of genetic advance for fruits per plant, yield per plant, tree volume, and flower per twig were reported by Ranpise & Desai (2003); Indian et al. (2019). Prasad & Rao (1989) observed moderate values of genetic advance in lime for rind thickness, juice weight, juice volume and fruit volume.

Panse (1957) opined that high genetic advance would be obtainable when heritability is chiefly due to dominance and epistasis (non additive gene action), consequently genetic advance would also be low. Heritability and genetic gain (GA) aid in referring valuable conclusion for effective selection based on the phenotypic coefficient of variation (Johnson et al. 1955).

Conclusion

From the above experiment it can be concluded that the characters having high heritability as well as moderate to high genetic advance and narrow difference between GCV and PCV were found in tree height, tree girth, tree spread, leaf length, petiole length, leaf area, inflorescence length, inflorescence width, number of male flowers per panicle, number of perfect flowers per panicle, percentage of perfect flowers, total number of flowers, sex ratio, duration of fifty per cent flowering, duration of hundred per cent flowering, number of fruit set at marble stage, fruit set percentage at marble stage, fruit retention percentage, fruit drop percentage, fruit length, fruit width, fruit weight, fruit volume, specific gravity, stone length, stone width, stone weight, pulp weight, peel weight, peel thickness, pulp per cent, stone per cent, peel per cent, pulp to stone ratio, pulp to peel ratio, number of fruits per tree, yield per tree, TSS, acidity, reducing sugar, non-reducing sugar, total sugar, total carotenoid content and ascorbic acid content. The medium estimates of genotypic and phenotypic coefficient of variation were obtained by Leaf length, leaf width (GCV only), chlorophyll content, inflorescence length, perfect flower per cent and total number of flowers per panicle suggesting a hopeful scope for improvement of these traits through selection.

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