RESEARCH ARTICLE ▐▐

Genetic Analysis of Mango (*Mangifera indica*. L) Genotypes for Year-round Flowering and Yield Characters

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ABSTRACT

Mango (*Mangifera indica*. L) is characterized by a high level of genetic variation in seedling population. Estimation of genetic advance is required for the expected genotypic progress of a particular character. Keeping this in view, genetic advances of year-round flowering mango (*Mangifera indica*. L) genotypes was carried out during 2019-2021 in farmer's field at Annur, Coimbatore. High Genotypic Coefficient of Variation (GCV) was found in fruit yield per tree was 30.63 per cent. The low GCV values were found for the traits *viz*., panicle length (6.61 %), days taken for flowering to fruit set (1.75%), days taken for flowering to fruit maturation (1.76 %), percentage of hermaphrodite flowers (5.38 %), sex ratio (5.18%). Whereas high values of heritability estimates were obtained for the traits *viz.,* fruit yield per tree (99.43 %), number of panicles/tree (98.91 %), number of fruits per tree (97.74 %), panicle per sq.m of canopy (97.40 %). The high heritability along with high genetic advance as per cent of mean was observed for fruit yield per tree (99.43, 62.91), number of panicles/tree (98.91, 46.84), number of fruits per tree (97.74, 43.03), panicle per sq.m of canopy (97.40, 28.64) indicates the possibility of improving these traits by selection since there is a wide range of variation and additive gene action exists for these traits. The traits *viz.,* panicle per sq.m of canopy, panicle length, number of panicles/tree, sex ratio, number of fruits per tree were positively correlated with fruit yield per tree. Hence, the selection for these characters would improve fruit yield in mango.

INTRODUCTION

The evaluation of genotypes assumes importance while screening them for a specific region. Although a cultivar may express a unique behavior in a certain area, it may fail to sustain that specific character when grown in a different location. The genetic diversity within mango offers various opportunities to utilize these genomic resources to manipulate desirable traits. Assessment of genetic variation within the natural population and among breeding lines is crucial for effective conservation and exploitation of genetic resources for crop improvement programs. In India, mango occupies an area of around 22.93 lakh hectares with a production of about 207.98 lakh tonnes and the productivity is about 8.39 MT ha^{-1} (Anonymous, 2018-19). In Tamil Nadu, mangoes are cultivated in 1.61 lakh ha, with average productivity of 7.2 MT ha^{-1}. Proper identification of genetic resources is the

basic need for successful improvement work. The development of mango hybrids that are efficient in nutrient utilization, provide better returns and endure adverse environmental conditions, forms the major aim of fruit breeding (Khan, 2004). An ideal mango cultivar should have characteristics like precocious, dwarf, regular and prolific bearing, early flowering and fruit set, attractive fruit color and size, resistance to major diseases and other biotic-abiotic stresses (Litz, 2009). To develop high yielding varieties, it is important to understand the nature and magnitude of genetic variability in the population which is indispensable to assume in any breeding programme. Continuous studies on the performance and evaluation help us to select an ideal cultivar for specific region, which can help us to promote its cultivation and to fetch good price in the market on the based on its quality characters.

Estimating genetic parameters *viz.,* phenotypic and genotypic coefficients of variation, heritability and genetic advance helps to understand the mode of inheritance of quantitative traits and also helps to formulate selection criteria for improving fruit yield in mango. Correlation measures the magnitude of the relationship between yield and other yield contributing traits. Conversely, path coefficient analysis helps split the correlation coefficient into direct and indirect effects of independent traits on the dependent trait. The present study aimed to assess the genetic variability available for different traits among the derivatives of mango genotypes which flowers throughout the year and determine the association of different traits with fruit yield in mango during 2019-2021 at Annur, Coimbatore, Tamil Nadu.

MATERIAL AND METHODS

The present study was performed with ten selected genotypes based on their uniformity and yield related attributes carried out in 2019-2021 at Annur, Coimbatore, Tamil Nadu. The observations were taken on selected trees and recorded for nine quantitative traits. Panicle per sq.m of canopy, panicle length, number of panicles/tree, days taken for flowering to fruit set, days taken for flowering to fruit maturation, percentage of hermaphrodite flowers, sex ratio, number of fruits per tree, fruit yield per tree. Variability present among the twenty-five genotypes was studied through morphological markers, fruit parameters and yield attributes.

The statistical analysis was done according to the procedure outlined by Panse and Sukhatme (1967). Genetic variability parameters like the phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), genetic advance and genetic advance as per cent of mean were estimated according to the procedure outlined by Johnson *et al.* (1955). Heritability in a broad sense was calculated according to the method given by Lush (1940). Correlation and path coefficient analyses were carried out based on the method proposed by Dewey and Lu (1959).

RESULTS AND DISCUSSION

Analysis of variance revealed that a vast range of variability was recorded for all the traits in mango genotypes (Table 1). The results on variability parameters are given in Table 2. Mean performance of all genotypes exhibited a wide range of variation for all the biometrical traits *viz.,* panicle per sq.m of canopy (15.67-23 numbers), panicle length (22.31-29.65 cm), number of panicles/tree (312-590 numbers), days taken for flowering to fruit set (12 days), days taken for flowering to fruit maturation (76 days), percentage of hermaphrodite flowers (6.34-7.85 %), sex ratio (0.073-0.085), number of fruits per tree (257-451 numbers), fruit yield per tree (26.47-58.69 kg/tree).

Table 1. Analysis of variance for flowering and yield related traits of mango

Source	df	Panicle per sq.m of canopy	Panicle length	Number of panicles/ tree	Days taken for flowering to fruit set	Days taken for flowering to fruit maturation	Percentage of hermaphrodite flowers (%)	Sex ratio	Number of fruits per tree	Fruit yield per tree (kg/ tree)
Genotypes	9	21.56*	1.19*	262.96*	0.002	0.110	0.50	0.01	158.58*	461.37*
Replication	2	0.47	30.42	56.20	0.113	1.17	0.01	0.00	201.77	1.38
Error	18	0.19	27.21	103.91	0.133	5.38	0.03	0.00	110.40	1.00

*Significant at 5 per cent level

The number of lines that exhibited more than the general mean values for yield attributing traits was: panicle per sq.m of the canopy (5), percentage of hermaphrodite flowers (5), fruit yield per tree (4). This showed that significant amount of variation was observed for all the traits studied. The genotypic coefficient of variation for various traits studied ranged from 1.75 to 30.63 per cent. High GCV as found in fruit yield per tree was 30.63 per cent. Moderate GCV was found in the characters *viz.* panicle per sq.m of canopy (14.08 %), number of panicles/tree (22.86 %), number of fruits per tree (21.11 %). The low GCV values were found in the traits like panicle length (6.61 %), days taken for flowering to fruit set (1.75%), days taken for flowering to fruit maturation (1.76 %), percentage of hermaphrodite flowers (5.38 %), sex ratio (5.18%). The genotypic coefficient of variation was found to be lower than the phenotypic coefficient of variation for all the traits studied. This showed that these characters are expressed by means of genotype and influenced by the environment. Similar types of the report was observed by Sankaran *et al.* (2020).

The phenotypic coefficient of variation for various traits ranged from 2.49 to 30.71 per cent. The high PCV as found in fruit yield per tree 30.71 per cent. Moderate PCV was found in the characters *viz.,* panicle per sq.m of canopy (14.27 %), panicle length (20.06 %), number of panicles/tree (22.99 %), number of fruits per tree (21.33 %). The low PCV values were found in the traits like days taken

for flowering to fruit set (2.49 %), days taken for flowering to fruit maturation (2.49 %), percentage of hermaphrodite flowers (6.02 %), sex ratio (7.20 %). The high phenotypic coefficient of variation and genotypic coefficient of variation was observed for petiole length, inflorescence width, fruit weight, pulp content, stone weight, seed width, seed weight, reducing sugars, non-reducing sugars, titratable acidity, TSS: acid ratio, ascorbic acid and yield (Sridar *et al.,* 2018).

The high heritability estimates help in the identification of transmissible traits from one generation to another and have minimal influence by the environment. The high values of heritability estimates were obtained for the traits *viz.,* fruit yield per tree (99.43 %), number of panicles/tree (98.91 %), number of fruits per tree (97.74 %), panicles per sq. m of the canopy (97.40 %). Moderate values of heritability estimates were obtained in the percentage of hermaphrodite flowers (79.90%), sex ratio (51.80%), days taken for flowering to fruit set (49.91 %) and days taken for flowering to fruit maturation (49.85 %). Low heritability estimates were obtained in panicle length (10.89 %).

High heritability along with high genetic advance as per cent of mean was observed for fruit yield per tree (99.43, 62.91), number of panicles/ tree (98.91, 46.84), number of fruits per tree (97.74, 43.03), panicles per sq. m of the canopy (97.40, 28.64) (Table 2). The coupled action of high heritability and high genetic advance as per cent of mean indicated the additive gene effects that would be improved by selecting these traits. High heritability coupled with high genetic advances was observed for all characters studied indicating these characters are governed by additive gene action and phenotypic selection may be more fruitful (Sridar *et al.,* 2018).

Table 2. Mean, Range, Coefficient of variations, heritability and genetic advance as per cent mean for different traits in mango

Character	Mean	Range	Number of lines above mean value	GCV%	PCV%	SED	CD	Heritability (h²%)	Genetic advances of mean
Panicle per sq.m of canopy	18.94	15.67-23	5	14.08	14.27	0.35	0.74	97.40	28.64
Panicle length	25.69	22.31-29.65	3	6.61	20.06	4.25	8.94	10.89	4.50
Number of panicles/ tree	423.70	312-590	3	22.86	22.99	8.32	17.48	98.91	46.84
Days taken for flowering to fruit set	12.00	12.00-12.00	-	1.75	2.49	0.29	0.62	49.91	2.56
Days taken for flowering to fruit maturation	75.97	76.00-76.00	-	1.76	2.49	1.89	3.98	49.85	2.56
Percentage of hermaphrodite flowers (%)	7.28	6.34-7.85	5	5.38	6.02	0.16	0.33	79.90	9.92
Sex ratio	0.07	0.073-0.085	3	5.18	7.20	0.03	0.07	51.80	7.68
Number of fruits per tree/ season	342.30	257-451	3	21.11	21.33	8.57	18.02	97.94	43.03
Fruit yield per tree (kg/ tree)	40.44	26.47-58.69	4	30.63	30.71	0.76	1.61	99.43	62.91

High heritability and low genetic advance as per cent of the mean was observed for percentage of hermaphrodite flowers (79.90, 9.92) which indicates non-additive gene action. Low heritability and low genetic advance as per cent of the mean was observed in panicle length (10.89, 4.50) indicating ineffectiveness of selection if practiced for this trait.

Correlation analysis is a statistical tool exploited to determine degree of relationship between two or more variables. The values of genotypic correlation coefficients among the yield and yield attributing traits are indicated in Table 3. In the present study, out of 45 total associations, 17 associations were positively significant which highlights the additive genetic effect. The traits *viz*., panicle per sq. m of canopy, panicle length, number of panicles/tree, sex ratio, number of fruits per tree were positively correlated with fruit yield per tree. The correlation study revealed a significant and positive correlation of fruit yield per tree with the number of fruits per tree at both genotypic and phenotypic levels, hence it could be given due weightage during the selection process for yield improvement of mango (Patel *et al.,* 2015).

The correlation coefficient describes only the relationship between the yield and other yield attributing traits but it fails to show the direct as well as indirect effects for various traits on yield because the characters that are in association do not exert effects by themselves but are linked to other component traits. So, in order to get direct as well as the indirect contribution of yield over other traits, path coefficient analysis need be taken into consideration (Table 4).

Table 3. Genetic Correlation coefficient among the nine characters for mango

	Number of panicles per square meter of canopy	Panicle length (cm)	Number of panicles/ tree	Days taken for flowering to fruit set	Days taken for flowering to fruit maturation	Percentage of hermaphrodite flowers (%)	Sex ratio	Number of fruits per tree/ season	Fruit yield per tree (kg/tree)
Number of panicles per square meter of canopy	1	-10.67	-0.309	0.012	-0.03	0.255	0.857**	0.180	0.717*
Panicle length (cm)		-1	0.723*	-0.329	0.782**	0.663*	0.729*	0.659*	0.769**
Number of panicles/tree			1	0.011	0.032	0.768**	0.130	0.972**	0.808**
Days taken for flowering to fruit set				-1	0.671*	0.012	0.095	-0.005	0.013
Days taken for flowering to fruit maturation					1	0.026	0.095	0.019	0.036
Percentage of hermaphrodite flowers (%)						1	0.685*	0.698*	0.762*
Sex ratio							1	0.102	0.668*
Number of fruits per tree/ season								1	0.673*
Fruit yield per tree (kg/tree)									1

* Significant at 5 per cent level   ** Significant at 1 per cent level

In this study, the number of fruits per tree (1.378) had very high positive direct effect on fruit yield per tree. Whereas sex ratio (0.791), number of panicles per tree (0.684) and percentage of hermaphrodite flowers (0.526) had a high direct effect on fruit yield per tree. The number of panicles per sq. m of canopy (0.261), panicle length (0.280), days taken for flowering to fruit maturation (0.257) had a moderate direct effect on fruit yield per tree. Days taken for flowering to fruit set (0.020) had a negligible direct effect on fruit yield per tree. Number of panicles per sq. m of canopy, panicle length, number of panicles/ tree, percentage of hermaphrodite flowers (%), sex ratio, number of fruits per tree had an indirect effect on fruit yield per tree. Hence, these characters turn out to be yield attributing characters. The residual effect in the present study was 0.654, which implies that the characters in the path analysis contribute 35 per cent to the variability in single plant yield.

Table 4. Direct and Indirect effect of nine characters on yield of mango

	Number of panicles per square meter of canopy	Panicle length (cm)	No. of panicles/ tree	Days taken for flowering to fruit set	Days taken for flowering to fruit maturation	Percentage of hermaphrodite flowers (%)	Sex ratio	Number. of fruits per tree/ season	Fruit yield per tree (kg/tree)
Number of panicles per square meter of canopy	0.261	0.298	0.519	0.002	0.006	0.133	0.677	0.428	0.717*
Panicle length (cm)	0.279	0.280	-1.217	-0.007	-0.201	-0.033	0.577	1.091	0.769**
Number of panicles/ tree	0.081	-0.202	0.684	0.000	0.008	0.191	0.103	1.311	0.808**
Days taken for flowering to fruit set	-0.003	0.092	-0.019	0.020	-0.095	-0.006	0.075	-0.011	0.013
Days taken for flowering to fruit maturation	0.001	0.219	-0.054	-0.007	0.257	0.014	0.075	0.046	0.036
Percentage of hermaphrodite flowers (%)	-0.067	0.018	-0.611	0.000	0.007	0.526	0.462	0.851	0.762*
Sex ratio	-0.224	0.204	0.219	-0.002	-0.024	0.307	0.791	0.242	0.668*
Number of fruits per tree/ season	0.047	-0.128	-1.636	0.000	0.005	0.188	0.081	1.378	0.673*
									1

Residual Effect= 0.654

CONCLUSION

The mango genotypes performing with better mean values for yield attributing traits could be further used in the breeding program to development high yielding varieties and enhance the genetic base in crop improvement. The cultivation of non-seasonal bearing genotype generates more revenue for the farmers and paves way for mango improvement programme. Since, the mango is propagated through vegetative means, genotypes showing better mean values could be experimented directly or it can be used for further breeding programmes.

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Ethics statement

No specific permits were required for the described field studies because no human or animal subjects were involved in this research.

Consent for publication

All the authors agreed to publish the content.

Competing interests

There were no conflicts of interest in the publication of this content.

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