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## Assessment of genetic variability, heritability and character association in yield and yield attributing traits of pickling mango (*Mangifera indica* L.) genotypes

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### Abstract

The present experiment was carried out in Horticultural College and Research Institute, Periyakulam during the year of 2019-21, to evaluate morphological, flowering, yield and yield attributing characters of 36 pickling mango genotypes, collected from southern parts of the Western Ghats and farmer's fields. Because of open pollination, seedling origin and heterozygous conditions, most of the trees exhibit a wide range of variability. A high level of GCV, PCV along with a moderate to a high level of heritability were recorded for different traits under this study. Magnitude and range of phenotypic coefficient of variation were higher than genotypic coefficient of variation for every trait. High heritability coupled with high genetic advance was exhibited by pulp weight, fruit weight, fruit yield/tree, stone weight, acidity percentage and its mainly due to additive gene action. Association study revealed that fruit yield per tree had a significant and positive correlation with panicle width, fruit weight, fruit length, fruit width, pulp weight, stone weight, and negative association with tree height, tree girth, canopy spread E-W, days to 50% and 100% flowering, and selection may be effective.

**Keywords:** Correlation, GCV, heritability, PCV, pickling mango, selection

### Introduction

Mango (*Mangifera indica* L.) is an allopolyploid fruit crop having chromosome number of  $2n=40$  (Mukherjee, 1953) [16], in the order of Sapindales and Anacardiaceae family. It is the world's most commercially cultivated evergreen tree in tropical and subtropical climates. It has a great economic value because of its adaptability, high nutritional content, colourful fruits, diversity, wonderful juicy taste, and outstanding flavour. It has been grown for four to six thousand years ago. It is now grown in 112 countries across the world, with its origins in the Indo-Burma area (Mukherjee, 1953) [16]. Edible mango fruit has 20% TSS, 0.2-0.5 percent acidity, 1% protein, and a greater quantity of vitamin A and a moderate amount of vitamin C. The existing climatic condition, cross-pollination and a high degree of heterozygosity makes the trees to exhibit wide range of variability in seedling populations. Most of the cultivars at present were developed, mainly through continuous selection for different qualitative and quantitative traits (fruit size, shape, flavour, taste, aroma, juice content, TSS etc.). *Mangifera indica* and *M. Sylvatica* are the two wild forms that occur in the Western Ghats of Indian subcontinents (Kostermans and Bombard, 1993) [10]. They produce small-sized fruits with a big stone, acidic flesh and high fibre thus make them suits for tender whole fruit pickle making. In addition, these species have a wide range of variability for different economically important horticultural traits and had some genes for resistance against various biotic and abiotic stresses related to mango production. Most of them are present in forestlands, riverbanks, the strip of roads, mountainous tracts and undulated topography. Because of rapid deforestation, most of these wild forms are extinct, so attention is needed to conserve these vital genetic resources. A survey was conducted in southern parts of Western Ghats (Tamil Nadu) to characterize these wild forms in our institute, and collected genotypes are evaluated for the further breeding programme.

Selection based crop improvement is one of the primary ways to utilize genetic resources for commercial aspects. Due to existence of wide range of diversity in mango, clonal selection and selection from chance seedlings are precise and ultimately it reduces the breeding cycle. Understanding of particular traits and their genetic constitution are important for crop improvement programmes such as selection and hybridization.

Collection and characterization of available genotypes might be a pre-requisite step in achieving this since they offer the information needed to assess variability. The genetic makeup of the plant and related specific environment, which is constituted of additive and non-additive variation, including dominance and epistasis (non-allelic) interaction, controls the phenotypic expression of plant characteristics and yield. As a result, appropriate metrics like genotypic and phenotypic coefficients of variation, heritability, and genetic advance must be used to assess the phenotypic variability into heritable and non-heritable components. Furthermore, genetic advances can be utilized to get effective selection. With this background, the present investigation was carried out to assess the extent of genetic variability in wild aromatic pickling mango genotypes for yield and its component traits.

### Materials and Methods

The present experiment was carried out in the Department of fruit Science, Horticultural College and Research Institute, Periyakulam, Tamil Nadu, India during the year 2019-2021. Thirty-six genotypes were evaluated using RBD with two replications. Most of the pickling mango genotypes included in these studies were seedling originated, more than 20 years old and present at pre-established orchards. These genotypes were collected from various location viz., Sothuparai, Kumbakkarai, Manjalar, Adukkam, Agamalai, Allinagaram, Bodinayakkanur, Kurangini, Trichy and some parts of Western Ghats (Table 1). The observation regarding morphological traits viz., tree height (m), tree girth (m), canopy spread E-W (m), canopy spread N-S (m), leaf length (cm), leaf width (cm), petiole length (cm), flowering traits viz., panicle length (cm), panicle width (cm), number of hermaphrodite flowers per panicles, days to 50% flowering and days to 100% flowering, yield characters viz., fruit set percentage, number of fruits at marble stage/panicle, total number of fruits per tree, fruit weight (g), fruit length (cm), fruit width (cm), peel weight (g), pulp weight (g), stone weight (g) and fruit yield/tree) were recorded by adopting standard evaluating procedures using vernier caliper and visual observations on those particular trees. Biochemical trait acidity was recorded by titrating fruit juice, against 0.1N NaOH using Phenolphthalein as an indicator.

GCV, PCV, heritability and genetic advance were calculated as per the method suggested by Burton & De Vance (1952)<sup>[2]</sup>, Johnson *et al.* (1955)<sup>[9]</sup> and categorized the PCV and GCV values as 0-10%-low, 10-20%- moderate, more than 20% for high, as per the method suggested by Siva Subramanian & Madhavamenon (1955). Heritability in broad sense were calculated as per the method suggested by Allard (1960)<sup>[1]</sup> and classified the range as 0-30%-Low, 30-60%- Moderate and more than 60% for High. GAM were worked out using the formula suggested by Millar *et al.*(1958)<sup>[15]</sup>, Phenotypic and Genotypic correlations of pickling mango genotypes using the genotypic coefficient of variation were worked out by using the formula suggested by Falconer (1964)<sup>[7]</sup>.

### Results and Discussion

The degree and magnitude of variability have been measured by the means of range, coefficient of variation, heritability and genetic advance. Data pertained for all the morphological, flowering and fruit characteristics of pickling mango genotypes were given in Table.2. In these experimented results showed that, existence of significant difference among all the polygenetic traits under this study.

Mean values of different genotypes are ranging from 11.27 to 40.40 for tree height, to 5.40 for tree girth, 10.42 to 19.715 for canopy spread E-W, 12.54 to 25.49 for canopy spread N-S, 17.38 to 21.62 for leaf length, 4.03 to 6.43 for leaf width, 2.43 to 3.81 for petiole length, 11.82 to 14.97 for days to 50% flowering, 18.81 to 27.95 for days to 100% flowering, 14.39 to 37.7 for panicle length, 12.32 to 23.56 for panicle width, 221.65 to 443.71 for hermaphrodite flowers per panicle, 11.40 to 21.10 for number of fruits at marble stage, 3.24 to 5.78 for fruit setting percentage, 147.29 to 133.42 for number of fruits per tree, 38.88 to 292.88 for fruit weight, 4.47 to 14.67 for fruit length, 3.51 to 11.75 for fruit width, 21.76 to 219.86 for pulp weight, 4.96 to 73.73 for stone weight, 1.66 to 7.02 for pulp stone ratio, 0.27 to 3.32 for acidity percentage, 2.01 to 22.29 for yield per tree.

### GCV, PCV, heritability and GAM

Assessment of existing variability for the different traits is a prerequisite step in a breeding programme for selecting desirable genotypes. The range of variation, average mean performance, genotypic and phenotypic coefficients of variation, heritability and genetic advance as percentage of the mean (Table 2) revealed that wide range of differences for most of the traits. Magnitude of phenotypic and genotypic coefficient of variation were high for different traits like pulp weight (72.17 and 71.84%), stone weight (70.07 & 69.81%), fruit yield per tree (65.02 & 63.89%), fruit weight (64.47 and 64.45%), acidity (60.89 & 56.26%), pulp stone ratio (41.37 & 38.94%), fruit length (41.33 and 38.99%), fruit width (35.30 & 33.62%), tree height (31.91 and 30.84%), tree girth (28.83 & 24.45%), number of fruits per tree (26.40 & 24.56%), and perfect flowers per panicle (25.33 & 25.31%). Similar findings were obtained by Attari *et al.* (1999)<sup>[2]</sup>, Singh (2002)<sup>[22]</sup>, Simi (2006)<sup>[21]</sup> and Himabindu *et al.* (2016) for the traits of fruit length, fruit width, fruit weight. Similarly, Rajan *et al.* (2009)<sup>[19]</sup> observed a high range of PCV and GCV for pulp weight, fruit weight, stone weight and fruit yield per tree. In these results, most of the traits having minimum deviation between PCV and GCV at increased level so, that the increased PCV than GCV indicates existence of variation is not only controlled by the genetic constitution of particular genotype but also it had least influence by favorable environmental condition. So, selection-based crop improvement on phenotypic basis will be effective.

PCV and GCV values were moderate for Canopy spread N-S, Canopy spread E-W, fruit set percentage and panicle width. This result indicates that there was a variation among different accessions under this experiment, it is important to select these traits for further breeding programmes. While PCV and GCV were low for other traits namely, Leaf length, days to 50% flowering and days to 100% flowering. Almost all the traits had a more phenotypic coefficient of variation value than the genotypic coefficient of variation, suggests that the environment has a significance impact on the various traits that are investigated and that their expression is consistent regardless of growth conditions. High PCV and moderate GCV values were recorded for panicle length (20.42 and 19.39%) and number of fruits per tree (20.67 & 15.76%), while Moderate PCV and Low GCV were recorded for leaf width (15.72 & 7.97%) and petiole length (11.71 & 5.82%). Among these estimates, PCV and GCV values are closer for tree height, panicle length, panicle width, perfect flowers per panicle, fruit weight, pulp weight and stone weight, it gets the least environmental influence and selection on phenotypic

basis will effective for further generation.

Heritability is a crucial characteristic for breeders since its magnitude reflects the consistency with which a genotype may be identified through its phenotypic manifestation. Heritability estimations combined with genetic advance as a percentage of the mean are more relevant for evaluating the true effect of selection (Johnson *et al.* 1955)<sup>[8]</sup>. Heritability in broad sense value is given in Table 2. Revealed that estimates of every morphological, flowering and fruit trait had moderate to high heritability. The range of heritability was high for fruit weight, perfect flowers per panicle, pulp weight, stone weight, fruit yield per tree, tree height, panicle length, fruit length, pulp stone ratio, number of fruits per tree, panicle width, acidity, tree girth, and this results revealed that in these traits are most leastly influenced by that particular environment, so selection may useful for improvement and this is due to broad sense heritability includes non-fixable dominance and epistatic variation. Obtained results for heritability are similar to findings of Attari *et al.* (1999)<sup>[2]</sup>, Singh (2002)<sup>[22]</sup>, Simi (2006)<sup>[21]</sup>, Majumdar *et al.* (2012) and Himabindu *et al.* (2016) for the traits of perfect flower per panicle, tree height, no. of fruits per plant, fruit yield, fruit weight, fruit length, fruit width, stone weight and pulp weight. Moderate heritability should be recorded for number of fruits at marble stage, canopy spread E-W, canopy spread N-S and fruit set percentage, while a low range of heritability has been observed for days to 100% flowering, leaf length, leaf width, petiole length, leaf length and days to 50% flowering, it is due to the masking effects of environment on that particular genotype, so it may not use in the selection programme or more specifically difficult for selection.

Estimates of heritability are not the best way to predict the outcome of particular trait. So, Panse (1957)<sup>[17]</sup> and Johnson *et al.* (1955)<sup>[8]</sup> found that heritability estimates combined with genetic advances are more effective in forecasting the selection of the best genotype than heritability values alone. Genetic advance as percentage of mean is varied from 3.24 to 147.31, among various characters understudy, pulp weight, fruit weight, fruit yield per tree, acidity and stone weight exhibit higher GA as percentage of mean. Higher magnitude of heritability coupled with maximum genetic advance as percentage of mean was recorded for pulp weight, fruit weight, stone weight, fruit yield/tree and acidity stone, results indicating that there was an additive gene action for that traits, selecting progenies based on these traits may be effective for next subsequent generations. Selection based on phenotypic performance for these variables would be beneficial in their population because these features also have a high GCV. High GCV values and heritability estimates along with higher genetic gains are also suggestive of additive gene effects governing the inheritance of such characteristics (Narayan *et al.* 1996); as a result, those traits have higher selective values provide plenty of opportunities for selection. Similar results were obtained by Kulkarni *et al.* (2002)<sup>[11]</sup>, Kumar *et al.* (2002)<sup>[12]</sup>, Doss *et al.* (2006)<sup>[6]</sup>, Lenka *et al.* (2001)<sup>[13]</sup> and Rajan *et al.* (2005)<sup>[20]</sup> in case of estimates of GCV, PCV, heritability and genetic advance as percent of mean in

different crops.

### Association studies

Studying association among different traits helps to determine the relationship and degree of closeness between them and it helpful for selecting superior genotypes. Correlation at the genotypic and phenotypic levels given the advantage to select more than one trait at a time. A correlation coefficient of different traits under this study was worked out at phenotypic and genotypic levels, thus given in Tables 3. and 4. The obtained results indicate that genotypic correlation coefficient values are higher than a phenotypic correlation coefficient, thus indicated that these traits are inherent association between them.

Correlation coefficient at genotypic and phenotypic level of fruit yield per tree had significant and positively correlated with panicle width (0.468G, 0.461P), fruit weight (0.909G, 0.894P), fruit length (0.638G, 0.611P), fruit width (0.635G, 0.595P), pulp weight (0.870G, 0.853P), stone weight (0.750G, 0.643P), and it showed negative association for various traits namely, tree height, tree girth, canopy spread E-W, days to 50% and 100% flowering. Rai *et al.* (2001)<sup>[18]</sup> noticed fruit yield per tree had highly significant and positive association with fruit length, fruit girth, fruit weight, fruit volume and number of fruits per plant, similar report were also suggested by Ojo *et al.* (2006) and Chaubey and Singh (1994)<sup>[4]</sup>.

Positive and significant correlation of pulp weight was observed with fruit weight (0.974G, 0.97P), fruit length (0.736G, 0.696P), fruit width (0.749G, 0.706P), while significant and positively correlated with genotypic levels leaf length, leaf width, days to 50% flowering and, whereas negatively correlated with tree height, stem diameter, canopy spread E-W & N-S, petiole length, fruit set percentage and number of fruits per tree. Among various traits fruit length had significant and positive association with panicle length (0.446G, 0.375P), panicle width (0.576G, 0.490P) and fruit weight (0.812G, 0.769P), similarly fruit width had significant association with panicle length (0.484G, 0.444P), panicle width (0.532G, 0.495P), fruit weight (0.821G, 0.781P) and fruit length (0.960G, 0.890P). Likewise stone weight was significant and highly correlated with fruit weight (0.904G, 0.900P), fruit length (0.729G, 0.686P), fruit width (0.769G, 0.725G), pulp weight (0.799G, 0.790P). Other traits namely fruit set percentage had significant association with number of perfect flowers per panicle (0.861G, 0.658P).

Based on these results, fruit yield per tree was highly correlated with many numbers of traits, and these traits were poly genically controlled. For this character, direct selection is difficult, so selection based on that particular economic trait with their association trait will be helpful to get a good economical yield. The present investigation revealed that fruit weight, fruit length, fruit width, pulp weight, stone weight, number of perfect flowers per panicle, panicle length, panicle width, number of fruits per tree and fruit fruit set percentage are the traits that help improve the yield of particular genotypes.

**Table 1:** Local pickling mango genotypes taken for the study

<b>S. No</b>	<b>Accession number</b>	<b>Location and site of collection</b>
1.	MI-PKM-01	Sothuparai forest areas, Periyakulam, Theni
2.	MI-PKM-02	Sothuparai forest areas, Periyakulam, Theni
3.	MI-PKM-03	Sothuparai local, Periyakulam, Theni
4.	MI-PKM-04	Kumbakkarai forest areas, Periyakulam, Theni.
5.	MI-PKM-05	Kumbakkarai forest areas, Periyakulam, Theni.
6.	MI-PKM-06	Kumbakkarai forest areas, Periyakulam, Theni.
7.	MI-PKM-07	Adukkam forest areas, Periyakulam, Theni.
8.	MI-PKM-08	Adukkam forest areas, Periyakulam, Theni.
9.	MI-PKM-09	Agamalai forest area, Theni.
10.	MI-PKM-10	Manjalar forest areas, Devadhanapatti, Dindugal.
11.	MI-PKM-11	Manjalar forest areas, Devadhanapatti, Dindugal.
12.	MI-PKM-12	Manjalar forest areas, Devadhanapatti, Dindugal.
13.	MI-PKM-13	Veerappa ayyanar kovil, Allinagaram, Theni.
14.	MI-PKM-14	Veerappa ayyanar kovil, Allinagaram, Theni.
15.	MI-PKM-15	Veerappa ayyanar kovil, Allinagaram, Theni.
16.	MI-PKM-16	Velappar areas, Andipatti, Theni
17.	MI-PKM-17	Velappar areas, Andipatti, Theni
18.	MI-PKM-18	Velappar areas, Andipatti, Theni
19.	MI-PKM-19	Kurangini foot hills, Theni
20.	MI-PKM-20	Kurangini foot hills, Theni
21.	MI-PKM-21	Kurangini foot hills, Theni
22.	MI-PKM-22	Marudhanadhi dam local
22.	MI-PKM-23	Marudhanadhi dam local
24.	MI-PKM-24	Devadhanappatti local, Dindugal
25.	MI-PKM-25	Devadhanappatti local, Dindugal
26.	MI-PKM-26	Munthal, Bodinayakkanoor local, Theni
27.	MI-PKM-27	Munthal, Bodinayakkanoor local, Theni
28.	MI-PKM-28	Selayampatti local, Chinnamanoor, Theni
29.	MI-PKM-29	Selayampatti local, Chinnamanoor, Theni
30.	MI-PKM-30	Kottoor local, Cumbum, Theni
31.	MI-PKM-31	Kottoor local, Cumbum, Theni
32.	MI-PKM-32	Shenbagathoppu, Srivilliputhur.
33.	MI-PKM-33	Shenbagathoppu, Srivilliputhur.
34.	MI-PKM-34	Shenbagathoppu, Srivilliputhur.
35.	MI-PKM-35	Natham, Dindugal.
36.	MI-PKM-36	Rajapalayam, virudhunagar.

**Table 2:** Mean performance, co-efficient of variation, heritability and GAM for different characteristics of pickling mango genotypes

Characters	Mean	Range		Co-efficient of variation		h <sup>2</sup> (%)	GAM
		Min.	Max.	PCV	GCV		
Tree height (m)	27.33	11.27	40.40	31.91	30.84	93.39	61.40
Tree girth (m)	03.78	0.99	05.40	28.83	24.55	72.50	43.05
Canopy spread E-W (m)	15.41	10.42	19.71	18.32	13.74	56.22	21.22
Canopy spread N-S (m)	15.82	12.54	25.49	16.84	11.83	49.35	17.12
Leaf length (cm)	19.71	17.38	21.62	6.41	3.17	24.52	3.24
Leaf width (cm)	04.71	04.01	06.43	15.72	7.97	25.66	8.31
Petiole length (cm)	03.37	02.43	03.81	11.71	5.82	24.74	5.97
Days to 50% flowering	13.20	11.82	14.97	8.77	4.16	22.53	4.07
Days to 100% flowering	24.77	18.81	27.95	9.88	5.32	29.05	5.91
Panicle length (cm)	22.13	14.39	37.70	20.42	19.39	90.14	37.92
Panicle width (cm)	17.71	12.32	23.56	18.80	17.43	86.00	33.30
Perfect flowers per panicle	321.56	221.65	443.71	25.33	25.31	99.85	52.11
No. of fruits at marble stage	14.785	11.40	21.40	20.67	15.76	58.11	24.75
Fruit set percentage	04.72	03.24	05.78	17.92	11.42	40.59	14.98
No. of fruits per tree	80.47	47.29	133.42	26.40	24.56	86.56	47.06
Fruit weight (g)	132.19	38.88	292.88	64.47	64.45	99.95	132.74
Fruit length (cm)	7.09	04.47	14.67	41.13	38.99	89.88	76.16
Fruit width (cm)	05.64	03.51	11.25	35.30	33.62	90.68	65.94
Pulp weight (g)	81.92	21.76	219.86	72.17	71.84	99.09	147.31
Stone weight (g)	28.15	04.96	73.73	70.07	69.81	99.26	143.27
Pulp: Stone ratio	3.15	1.66	7.02	41.37	38.94	88.62	75.52
Acidity (%)	1.83	0.27	3.32	60.89	56.26	85.35	107.06
Fruit yield/ tree (Kg)	10.14	02.01	22.29	65.02	63.89	96.55	129.32

**Table 3:** Estimation of genotypic correlation coefficient between fruit yield and yield attributing traits of pickling mango genotypes

Trait	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	
1	0.911**	0.561**	0.428*	-0.396	-0.237	-0.065	0.145	0.231	-0.353	-0.598*	-0.437	-0.212	0.631**	0.072	-0.482	-0.631*	-0.493	-0.433	-0.385	-0.115	0.710**	-0.444	
2		0.639**	0.504**	-0.358	-0.168	0.125	-0.007	-0.094	-0.230	-0.407	-0.269	-0.152	0.316	0.175	-0.574*	-0.687*	-0.494	-0.530	-0.461	-0.100	0.747**	-0.508	
3			0.260	-0.436	-0.087	-0.280	0.731**	0.342	-0.159	-0.331	-0.208	-0.155	0.219	-0.128	-0.224	-0.294	-0.136	-0.189	-0.199	0.099	0.405*	-0.249	
4				-0.028	0.254	0.315	0.151	0.199	0.198	-0.171	0.135	0.381*	0.161	0.184	-0.036	-0.188	0.009	-0.083	0.144	-0.203	0.376*	0.043	
5					-0.066	-0.065	-0.167	-0.555	-0.198	0.434*	0.541**	0.579**	-0.470	-0.342	0.623**	0.534**	0.519**	0.583**	0.509**	0.033	-0.620*	0.533**	
6						0.058	0.123	0.670**	0.543**	-0.067	0.279	0.095	-0.483	0.192	0.520**	0.574**	0.474**	0.440*	0.582**	-0.120	-0.394	0.642**	
7							-0.577*	-0.391	0.447*	0.408*	-0.215	0.041	0.351	0.260	-0.007	0.142	0.301	-0.189	0.259	-0.703*	-0.038	-0.024	
8								0.532**	-0.280	-0.551	0.184	-0.139	-0.522	-0.141	0.325	0.077	0.095	0.399*	0.259	0.266	-0.119	0.346	
9									-0.189	-0.507	0.032	0.106	0.184	0.198	0.080	-0.195	-0.102	0.193	-0.039	0.337	0.109	0.141	
10										0.500**	0.283	0.102	-0.419	0.249	0.311	0.446*	0.484**	0.199	0.448*	-0.221	-0.371	0.414*	
11											0.324	0.251	-0.316	-0.048	0.348	0.576**	0.532**	0.275	0.336	-0.068	-0.471	0.307	
12												0.861**	-0.954**	0.293	0.348	0.342	0.315	0.311	0.329	-0.074	-0.348	0.468**	
13														-0.637*	0.372*	0.080	0.051	0.079	0.023	0.120	-0.250	-0.148	0.246
14															-0.084	-0.603*	-0.623*	-0.544	-0.571*	-0.559	-0.069	0.501**	-0.630*
15																-0.299	-0.412	-0.409	-0.305	-0.184	-0.204	0.273	0.053



## Conclusion

High heritability coupled with higher genetic advance as percentage of mean were noticed for pulp weight, fruit weight, fruit yield/tree, acidity, stone weight. Among those traits, fruit weight, pulp weight, stone weight had positive and significant correlation with fruit yield per tree. In this present experiment, pulp weight, fruit weight, fruit length, number of fruits per tree, fruit yield per tree, perfect flowers per panicle and fruit setting percentage are those traits that are had high heritability and high heritability and genetic advance, so phenotypic selection based on these traits may be effective.

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