

Variability studies in seedling progenies of mango (*Mangifera indica* L.)

CT.SATHAPPAN AND D.DHANASEKARAN

Department of Horticulture, Faculty of Agriculture, Annamalai University, Annamalai nagar,
Tamil Nadu-608002, India

Received: December, 2019; Revised accepted: February, 2020

ABSTRACT

Twenty genotypes of mango more than 15 years were selected from farmer's field in Krishnagiri district for variability studies in seedling progenies of mango (*Mangifera indica*) at Annamalai university, Annamalai nagar. From the experiment, it was inferred that variability studies showed significant differences among the twenty genotypes for all the 12 characters. Yield per tree was maximum (752.6 kg) in G6 genotype and minimum (283.2 kg) in G14.. Inflorescence length (36.1 cm), number of flowers per panicle (114.8), fruit length (15.4 cm) and fruit weight (308.1 cm) were also recorded maximum in the same genotypes (G6). In general, minimum values of these parameters were recorded in G14 genotype. Genetic analysis indicated maximum phenotypic and genotypic coefficient of variation for yield per tree followed by fruit weight. Low GCV and PCV were observed for fruit girth and percentage of non-edible portion. The other eight traits were recorded as moderate GCV and PCV.

Keywords: Mango, Variability studies, seedling progenies

INTRODUCTION

Mango (*Mangifera indica* L.) 'King of fruits' is the most popular fruit in the orient particularly in India, it is considered as the best choice among the indigenous fruit. India is the largest producer and consumer of mango in the world. The country produces about 50 varieties of mango. Uttar Pradesh is known for growing a host of mango varieties which are not found elsewhere. It was observed that significant variation exists, among trees of the same clone in an orchard with respect to fruit shape, size and colour, which is ascribed to bud mutation. It becomes necessary to establish the phylogenetic relationship and investigate any possible differences at molecular level in the mango varieties from different pockets. Simultaneously, it may also help to assess the extent of variability for morphological traits according to Geographical variability. Mango has been reported to have extensive diversity due to allopolyploidy, out breeding, continuous grafting and phenotypic differences arising from varied agro climatic conditions in different mango growing regions. However, most of the cultivars have arisen through the process of selection of desirable types of natural seedlings (Karihaloo *et al.*, 2003) where each cultivar are identified through the combination of characters viz., fruit size, colour, taste, flavor etc. (Anu *et al.*, 2015). In the light of above, the present investigation

was undertaken to study the morphological, qualitative traits and genetic divergence of mango clones from a geographical location in Krishnagiri district.

MATERIALS AND METHODS

The experiment with twenty genotypes selected from Krishnagiri and Uthangari taluk of Krishnagiri district for the study during 2015-16. Among the genotypes six were selected from Mallipatti, eight from Pudhur and six from Singarpattai. The genotypes selected were more than 15 years old and were seedling progenies. The data on morphological characters like leaf length, leaf width, inflorescence length, number of flowers per inflorescence, fruit length, fruit girth, fruit weight, number of fruits per panicle, total soluble solids, percentage of edible portion, percentage of non-edible portion, yield per tree were recorded. The ranges of coefficient of variation (PCV & GCV) were recorded by adopting methods suggested by Burton (1952).

RESULTS AND DISCUSSION

General analysis of variance showed significant differences among the 20 genotypes of mango for all the 14 characters studied. The genotype G17 recorded maximum leaf length (30.1cm) while the genotype G3 recorded wider leaf width (6.17cm). The genotypes G6 recorded

the longest inflorescence (36.1 cm). The genotypes G6 had higher mean value than the grand mean for the character number of flowers per inflorescence (114.8). The best performing genotypes for fruit length was G6 (15.4 cm) followed by G5 (14.7cm). For the character fruit girth, the genotype G7 (24.2 cm) was significantly superior to the grand mean. The maximum fruit weight (308.1g) was observed in the genotypes G6 (Table.1). The best performing genotypes for number of fruits per panicle (3.26) in G12 The highest total soluble solids (26.0)

were noticed in the genotype G8. The genotype G7 recorded the highest percentage of edible portion (47.7%). The highest mean values for yield per tree (752.6 kg) were found in the genotypes G6. Based on the mean values of the various traits, the genotypes G6 was found to be superior. Hence, the genotype may be utilized for the improvement of yield and other useful traits. Similar results have been reported by Majumdar *et al.* (2013) in mango and Patel *et al.*(2012) in guava.

Table 1: Mean performance of genotypes for growth and yield characters in mango seedling progenies (cm)

Genotype	Leaf length (cm)	Leaf width (cm)	Inflor-escence length (cm)	Flowers per inflor-escence	Fruit length (cm)	Fruit girth (cm)	Fruit weight (g)	Fruits per panicle	Total Soluble Solids (^o Brix)	Edible portion (%)	Yield / tree (kg)
G1	22.2	4.8	24.3	73.1	9.1	18.6	159.9	2.3	23.0**	34.4	355.4
G2	19.1*	4.1**	28.3	85.6**	10.6	19.2	152.1	2.8**	24.0**	36.8**	438.4
G3	26.7	6.1	23.3	76.1	11.8	23.1**	222.4**	2.4	21.2	40.5**	564.6**
G4	23.9	5.1	25.2	64.1	14.6**	22.9**	260.2**	2.3	16.1	40.4**	635.1**
G5	20.7	4.3*	22.8	88.2**	14.7**	21.0	186.1	2.0	24.2**	32.2	378.1
G6	21.2	4.8	36.1**	114.8**	15.4**	22.2*	308.1**	2.3	17.3	35.8	752.6**
G7	19.8	4.9	26.7	80.2	11.8**	24.2**	230.3**	2.8**	21.0	47.7**	675.5**
G8	18.0**	4.9	32.2**	70.1	10.1	21.2	184.0	2.0	26.0**	32.5	374.4
G9	19.2*	4.1**	34.1**	99.0**	11.8**	22.2*	238.0**	2.7	15.0	44.5**	661.8**
G10	24.1	6.1	22.6	73.7	9.9	20.9	175.0	2.5	23.0**	37.1**	464.8
G11	20.7	5.0	20.3	86.1**	10.8	23.0**	180.1	2.8	22.0	30.6	525.6**
G12	23.1	4.1**	26.6	77.6	9.5	21.3	148.1	3.2**	24.1**	30.3	485.6
G13	24.0	4.1**	31.8**	98.2**	10.9	22.8**	175.2	3.1**	20.1	34.3	545.5**
G14	18.1**	5.2	20.0	58.4	8.8	18.9	142.1	2.0	18.3	31.7	283.2
G15	26.0	6.0	24.7	92.3**	9.8	21.1	155.4	2.7	21.0	32.2	445.5
G16	22.7	5.9	32.1**	67.8	10.7	22.7**	190.0	2.8*	21.0	36.8	535.6**
G17	30.1	5.0	26.0	78.6	9.8	21.2	159.9	2.3	23.1**	28.2	395.3
G18	24.1	4.0**	34.0**	85.1	11.0	22.8**	182.1	2.6	21.0	34.9	496.9
G19	21.7	5.0	23.8	62.6	9.7	21.1	249.9**	2.5	22.2**	36.0	685.6**
G20	23.2	5.1	26.1	93.4**	10.9	20.7	265.0**	2.7*	19.0	40.3**	716.3**
General mean	22.4	4.9	27.0	81.3	11.1	21.5	198.2	2.5	21.1	35.9	520.8
SED	1.4	0.26	1.4	1.4	0.27	0.27	1.43	0.09	0.23	0.33	1.61
CD (P=05)	2.9	0.53	2.9	2.9	0.55	0.55	2.89	0.19	0.48	0.67	3.24
(P=01)	3.95	0.71	3.96	3.86	0.73	0.74	3.85	0.26	0.64	0.90	4.32

* Significant at 5% level, ** Significant at 1% level

High GCV (40.5 %) & PCV (41.6 %) estimates were observed for yield per tree in mango (Majumder *et al.*, 2012) and fruit weight, fruit diameter, seeds per fruit, acidity and sugar in guava (Patel *et al.*, 2012). It indicates the availability of abundant variability for these characters in mango. Thus, the high magnitude

of GCV and PCV indicates a scope for improvement of these traits through selection. Closeness between GCV and PCV for some traits indicates that the phenotypic expression of all the genotypes is mostly under the genetic control of such traits and those are comparatively stable to environmental variations.

Rest of the traits showed the low magnitude of GCV and PCV. Low GCV and PCV were observed for fruit weight, fruit length, fruit breadth, fruit thickness, TSS, skin weight, stone weight and pulp percentage (Dinesh *et al.*, 2013) in mango and (Nagar *et al.*, 2018) in guava. The other eight traits were recorded as moderate GCV (6.79 %) and PCV (6.97%).

Table 2: Magnitude of variability for various characters in mango genotypes

S.No.	Characters	Range	Coefficient of variance	
			Genotype (%)	Phenotype (%)
1.	Leaf length (cm)	18.0-30.1	12.67	15.01
2.	Leaf width (cm)	4.03-6.17	13.35	14.89
3.	Inflorescence length (cm)	20.0-36.1	17.20	18.45
4.	Flowers per inflorescence	58.4-114.8	17.21	17.35
5.	Fruit length (cm)	8.8-15.4	16.60	16.87
6.	Fruit girth (cm)	18.6-24.2	6.79	6.97
7.	Fruit weight (g)	142.1-308.1	23.39	23.40
8.	Fruits per panicle	2.06-3.26	12.58	13.42
9.	Total Soluble Solids (^o Brix)	15.0-26.0	13.43	13.50
10.	Edible portion (%)	28.2-47.7	13.66	13.71
11.	Yield per tree (kg)	283.2-752.6	25.58	25.59

In the present investigation, all the 12 characters showed high heritability indicating low environmental effect and high capacity of the characters for the transmission to subsequent generation. All the characters, except fruit girth, recorded high heritability with high genetic advance, suggesting these characters are governed by additive genetic effect to a great extent and improvement of these characters would be effective through phenotypic selection. Similar results were observed by Singh *et al.* (2015) and Dubey *et al.* (2016) in guava. High heritability and moderate genetic advance were observed for fruit girth. Similarly, high heritability, genetic advance were also recorded for tree and panicle characters (Sachin Kishor *et al.*, 2019). The genetic divergence studies in combination with variability studies will give a better understanding of the traits and types thereby paving the way for the final task of crop improvement. In this study, yield per tree and fruit weight showed higher heritability and also

contributed maximum towards genetic divergence. So these characters could be relied upon for further improvement by phenotypic selection. The genotypes G6, G20 and G9 recorded significant and maximum mean values for the above said two characters, yield per tree and fruit weight and thereby utilized for crossing programme to generate desirable segregants and recombination types for yield and its attributing traits.

From the experiment, it may be inferred that variability studies showed significant differences among the twenty genotypes for all the 12 characters. Among the genotypes G6 proved superior in respect of almost all parameters. Genetic analysis indicated maximum phenotypic and genotypic coefficient of variation for yield per tree followed by fruit weight. Low GCV and PCV were observed for fruit girth and percentage of non-edible portion. The other eight traits were recorded as moderate GCV and PCV.

REFERENCES

- Anu, A., Prasad, B.D., Kumar, R., Kumar, P., Patel, V.B., and Jha, R.N. (2015) Clonal variability studies in 'Langra' mango (*Mangifera indica* L.) using morphological, biochemical and molecular markers. *International Journal of Agriculture Environment and Biotechnology* 8 (3): 567- 581.
- Burton, G.W. and De vane, E.W. (1952). Estimation of heritability in tall fescue (*Festuca arundinances*) from replicated clonal material. *Agronomy Journal* 45: 478-481.
- Dinesh, M.R., Vasugi,C., and Venugopal,R (2013) Heritability studies in mango

- (*Mangifera indica* L.). *Acta Horticulturae* 992: 42
- Dubey, M.C., Kumar, R., Kumar, J. and Kumar, A. (2016) Morphological and physico-chemical characteristics of guava genotypes. *Research on Crops* 17 (2):276- 282.
- Falconer, D.S. (1967) Introduction to quantitative genetics Oliver and Boyd, Lond.P.283.
- Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1953) Estimates of genetic and environmental variability in soybean. *Agronomy Journal* 47: 314-18.
- Karihaloo, J.L., Dwivedi, Y.K., Archak, S., and Gaikwad, A.B. (2003) Analysis of genetic diversity of Indian mango cultivars using RAPD markers. *Journal of Horticulture Science Biotechnology* 78: 285-289.
- Majumder, D. A. M, Hassan, L., Rahim, M.A. and Kabir, M.M. (2012) Genotypic and phenotypic variability in mango (*Mangifera indica* L.). *Bangladesh Journal of Agricultural Research* 37(4): 683-690.
- Majumder, D., Hassan, A.N.L., Rahim, M.A. and Kabir, M.A. (2013) Genetic diversity in mango (*Mangifera indica* L.) through multivariate analysis. *Bangladesh Journal of Agricultural Research* 38(2): 343-353.
- Nagar, P.K., Satodiya, B.N., Prajapati, D.G. and Nagar, S.K. (2018) Assessment of genetic variability and morphological screening of guava (*Psidium guajava* L.) hybrids. *The Pharma Innovation Journal* 7(8): 35-40.
- Patel, R.K., Maiti, C.S., Amrendra Kumar and Kuldeep Srivastava (2015) Genetic variability, character association and path coefficient study guava. *The Ecoscan* (VII): 447-453.
- Sachin Kishor, Deepa H. Dwivedi, Namrata Singh, Sutanu Maji and Manoj K. Sharma (2019) Analysis of Intravarietal variability in mango (*Mangifera indica* L.) Cv. Deshehari. *Annals of Plant and Soil Research* 21(2):193-199.
- Singh, D., Gill, M.I.S., Boora, R.S., Arora, N.K. (2015) Genetic diversity analysis in guava (*Psidium guajava* L.) on the basis of morphological and physico-chemical traits. *Indian Journal of Agricultural Sciences* 85(5):678-683.
- Zaied, N.S., Khafagy, S.A.A and Salah, M.A. (2007) Evaluation of so mango species by fruit characters and fingerprint. *Research Journal of Agriculture and Biological Sciences* 3(4): 316-320.