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Abstract

Different genotypes are to be classified into clusters based on genetic diversity for any plant improvement programme. Further the extent of genetic divergence between them needs to be estimated. D^2 statistics is one of the powerful tools to assess the relative contribution of different component traits to the total diversity, to quantify the degree of divergence and to choose genetically diverse parents for obtaining desirable recombinants. The present study was conducted at Horticultural College and Research Institute (Tamil Nadu Agricultural University), Periyakulam during 2017-18 on 27 genotypes of mango for genetic divergence with respect to forty six yield contributing traits. The analysis of variance exhibited significant differences among genotypes for all the forty six characters studied. Twenty seven genotypes were grouped into six clusters. The cluster size varied from single genotype (cluster III and VI) to thirteen genotypes (cluster I). Cluster II and IV had three genotypes each. Cluster V consisting of six genotypes. No relationship between geographic and genetic diversity was revealed as genotypes from same geographic area fell in different clusters and *vice versa*. The intercluster distances were more than intracluster distances. The highest intercluster distance was observed between cluster II and III followed by clusters II and IV. The other intercluster distances were of low magnitude. Hence crossing between genotypes of cluster II with those from cluster III and IV will be rewarding. Based on intercluster distances and cluster mean for different characters, parents were identified which upon crossing may yield desirable recombinants.

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Introduction

Genetic variability in a base population is a prerequisite for effective selection and recombination breeding. When existing variability has been exploited, a breeder resorts to create variability through hybridization as a population with more diverse genotypes is of considerable value for the success of any breeding programme. The relatedness and genetic distance between accessions can be obtained through cluster analysis. Cluster analysis is grouping of accessions which have the same characteristics in homogeneous categories of each stratum (Crossa et al. 1995). 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. It originated in the Indo-Burma region during the earlier period of the Cretaceous era (Yonemori et al. 2002; Kumar et al. 2016; 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. Information on the nature and degree of divergence among the genotypes helps the breeders in choosing right type of parents for initiating a breeding programme to recover better varieties or hybrids, since the degree of heterosis is believed to be correlated with genetic divergence among the parents. Earlier geographic diversity was considered to be an index of genetic diversity. However genetic diversity of parents is not necessarily associated with geographic diversity or place of origin. Multivariate analysis using Mahalanobis D^2 technique is a powerful tool in identifying the degree of divergence among the genotypes (reference). The present study was undertaken to assess genetic relatedness of 27 genotypes of mango into different clusters based on genetic divergence.

Materials and Methods

The experimental materials comprised of 27 mango genotypes. 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 Randomized Block Design with three replications. The spacing from row to row and plant to plant was 5.5 m and 5.5 m respectively. 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 (hermaphrodite) per panicle, percentage of perfect flowers, total number of flowers, sex ratio (male: hermaphrodite flowers), period (time) at fifty per cent flowering, period at 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 analysis of variance was carried out for all characteristics and data were analyzed using following multivariate analysis of Mahalanobis (1936) and the genotypes were grouped into different clusters following Tocher's method (Rao 1952).

Results and Discussion

The analysis of variance (ANOVA) exhibited significant differences among the genotypes for all the characters studied. Based on D^2 values, 27 genotypes were grouped into 6 clusters (Table1). The cluster strength varied from single/solitary genotype (cluster III and VI) to 13 genotypes (cluster I). Cluster II and IV had three genotypes each. Cluster V consisting of six genotypes. Raina et al. (2015) also reported the similar findings in pomegranate. The pattern of distribution of genotypes into six clusters confirmed the existence of diversity among the genotypes, as indicated by analysis of variance. It also revealed that geographical diversity was not related to genetic diversity as genotypes of same geographical region were grouped into different clusters and vice versa. It may be due to distribution of different gene constellations within a geographical region or due to differences in adaptation, selection criteria, selection pressure and environmental conditions. This genetic diversity among the genotypes could be due to factors like heterogeneity, genetic architecture of the populations and developmental traits (Murty & Arunachalam 1966).

The average intra and inter-cluster distances are given in table 2. The intra-cluster distance ranged from 0.00 in third and sixth cluster to 67.98 in fifth cluster. This apparently indicates that cluster V had genotypes that are relatively distant from each other than the other clusters which had lower intra-cluster D^2 distance. The intra-cluster distance was zero for cluster III and VI as they were made up of single genotype. The maximum intra-cluster distance was observed in cluster V (67.98). Similar findings were also reported by Rajan et al. (2007) in guava. The inter-cluster distances were higher than intra-cluster distances. Shazia et al. (2017) reported that the maximum intra-cluster distance was observed in cluster III (139.24) followed by cluster I (67.77) whereas the inter-cluster distance was maximum between cluster II & V (5213.52) followed by cluster II & IV (4895.20) which is in correspondence with the results of present study. The inter cluster distance ranged from minimum of 56.86 in third & fourth cluster to maximum of 159.02 in second & third cluster. The highest inter-cluster distance was observed between cluster II & III (159.02) followed by clusters II and IV (151.29). Genotypes from such clusters may be utilized in the hybridization programme as crossing between diverse parents is likely to produce wide variability and transgressive segregants with heterotic effects. The minimum inter-cluster distance was observed between clusters III & IV (56.86) revealing that the genotypes of these clusters were relatively closer. The result of

present study was also accordance with the findings of Barhate et al. (2012) in mango, Sharma et al. (2013) in apple and Barholia & Yadav (2014) in mango.

The cluster means for different characters under study revealed considerable differences between the groups (Table 3). Cluster I was characterized with minimum reducing sugar (3.74 %). The maximum tree height (6.45 m), tree girth (69.09 cm), tree spread (7.36 m), fruit retention percentage (6.05 %), fruit weight (248.20 g), stone weight (28.57 g), pulp weight (194.00 g), peel weight (25.63 g), number of fruits per tree (212.33) and yield per tree (48.32 kg/tree) were found in cluster II. The maximum TSS (20.12 ^{0}Brix), reducing sugar (4.95 %), non-reducing sugar (14.57 %) and total sugar (19.47 %) with minimum tree girth (32.37 cm), chlorophyll content (47.03), fruit set percentage at marble stage (1.43 %), fruit weight (148.64 g), stone weight (18.29 g), pulp weight (113.86 g), peel weight (16.49 g), acidity (0.15 %), number of fruits per tree (4.00) and yield per tree (0.46 kg/tree) were noticed in cluster III. The highest mean value for fruit set percentage at marble stage (3.01 %), fruit drop percentage (98.73 %) and ascorbic acid content (48.37 mg/100g) with lowest mean value for tree height (3.85 m), tree spread (3.66 m), leaf length (18.10 cm), leaf width (4.02 cm), number of male flowers per panicle (576.04), number of perfect flowers per panicle (188.93), fruit retention percentage (1.27 %) and TSS (16.58 ^{0}Brix) was recorded in cluster IV. Cluster V was found to be the cluster consisting of genotypes with maximum acidity (0.29 %) and minimum ascorbic acid content (28.61 mg/100g). The maximum mean value for leaf length (26.40 cm), leaf width (10.24 cm), Chlorophyll content (57.47), number of male flowers per panicle (1046.13), perfect flowers per panicle (285.60) with minimum mean value for fruit drop percentage (93.99 %), non-reducing sugar (10.37 %) and total sugar (14.60 %) were noticed in cluster VI. These results are in accordance with the findings of Manchekar et al. 2011; Dimpy et al. 2016; Shazia et al. 2017.

The components of D^2 due to each character were ranked. These ranks would provide indirect information about the order of priority in terms of percentage contribution of the character to the total divergence. These per cent contributions of different characters are presented in table 19. The yield per tree contributed higher towards the genetic divergence (46.72%) followed by fruit retention percentage (15.10 %), number of fruits per tree (7.69 %), pulp weight (6.55 %), acidity (5.98 %), total sugar (3.99 %), fruit set percentage at marble stage (3.42 %), reducing sugar (2.56 %), TSS (0.86 %), fruit weight (0.85 %) and peel weight (0.28%). Characters such as tree height (0.00 %), tree girth (0.00 %), tree spread (0.00 %), leaf length (0.00 %), leaf width (0.00 %), chlorophyll content (0.00 %), number of male flowers per panicle (0.00 %), number of perfect flowers per panicle (0.00 %), fruit drop percentage (0.00 %), stone weight (0.00 %) and non-reducing sugar (0.00 %) had no contribution towards total divergence. Clemilton et al. (2017) reported that the fruit mass (16.88%), fruit equatorial diameter (11.32%) and greatest thickness of

fruit pulp (11.01%) showed the greatest contribution to genetic diversity. On the other hand, yield (2.26%), stem diameter (1.17%) and first fruit insertion height (0.66%) showed the smallest relative contribution in papaya which is in correspondence with the results of the present study.

Table 1. Composition of clusters based on D^2 values in various characters of mango

Cluster number	No. of genotypes	Name of genotypes
I	13	Javari Natham Palamani Sundar langra Duraipandi Komangai Kovankachi P.K.Patti Iswarya Kundur Pacharisi Banganapalli Amarapali Mallika Pkm 2
II	3	Ratna Sendhuram Arka Aruna
III	1	Mohandhas
IV	3	Kuruvi Neelum Samba kooja Shajahan
V	6	Alphonso Neelum Pedharasam Malpacharisi Pkm 1 Au Rumani
VI	1	Sindhu

Table 2. Intra and inter cluster distance values for different characters in mango

Clusters	I	II	III	IV	V	VI
I	49.82	120.61	69.31	62.45	69.05	75.66
II		54.20	159.02	151.29	105.79	82.21
III			0.00	56.86	95.97	103.03
IV				61.93	92.73	100.72
V					67.98	84.41
VI						0.00

Table 3. Cluster mean values for different characters in mango

Characters / Clusters	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23
I	5.59	50.99	5.95	23.70	5.95	53.23	797.83	246.86	2.63	2.26	97.74	209.29	27.96	157.08	24.25	17.81	0.23	3.74	12.82	16.56	43.27	39.28	14.21
II	6.45	69.09	7.36	26.18	6.55	53.89	818.87	252.20	2.80	6.05	94.01	248.20	28.57	194.00	25.63	18.72	0.25	4.60	11.77	16.38	39.37	212.33	48.32
III	4.19	32.37	4.28	23.34	4.49	47.03	641.00	192.73	1.43	1.68	98.32	148.64	18.29	113.86	16.49	20.12	0.15	4.95	14.57	19.47	38.63	4.00	0.46
IV	3.85	33.89	3.66	18.10	4.02	53.58	576.04	188.93	3.01	1.27	98.73	185.50	21.99	143.17	20.34	16.58	0.20	4.26	12.55	16.81	48.37	6.67	0.88
V	5.31	50.73	6.03	23.40	5.91	49.93	905.78	234.21	2.56	2.21	97.79	216.73	27.58	165.12	24.02	17.53	0.29	4.07	12.19	16.26	28.61	90.33	24.62
VI	5.33	49.00	6.12	26.40	10.24	57.47	104 6.13	285.60	1.83	6.02	93.99	225.88	26.23	174.79	24.86	18.58	0.22	4.23	10.37	14.60	38.28	87.33	19.87

1. Tree height	6. Chlorophyll content	11. Fruit drop percentage	16. TSS	21. Ascorbic acid content
2. Tree girth	7. Number of male flowers per panicle	12. Fruit weight	17. Acidity	22. Number of fruits per tree
3. Tree spread	8. Number of perfect flowers per panicle	13. Stone weight	18. Reducing sugar	23. Yield per tree
4. Leaf length	9. Fruit set percentage at marble stage	14. Pulp weight	19. Non-reducing sugar	
5. Leaf width	10. Fruit retention percentage	15. Peel weight	20. Total sugar	

Table 4. Relative contribution of each character to genetic divergence in mango

Characters	No. of first rank	% of contribution
1	0	0
2	0	0
3	0	0
4	0	0
5	0	0
6	0	0
7	0	0
8	0	0
9	12	3.42
10	53	15.1
11	0	0
12	3	0.85
13	0	0
14	23	6.55
15	1	0.28
16	3	0.85
17	21	5.98
18	9	2.56
19	0	0
20	14	3.99
21	21	5.98
22	27	7.69
23	164	46.72
TOTAL	351	100

1. Tree height	6. Chlorophyll content	11. Fruit drop percentage	16. TSS	21. Ascorbic acid content
2. Tree girth	7. Number of male flowers per panicle	12. Fruit weight	17. Acidity	22. Number of fruits per tree
3. Tree spread	8. Number of perfect flowers per panicle	13. Stone weight	18. Reducing sugar	23. Yield per tree
4. Leaf length	9. Fruit set percentage at marble stage	14. Pulp weight	19. Non-reducing sugar	
5. Leaf width	10. Fruit retention percentage	15. Peel weight	20. Total sugar	

In the present study, D^2 analysis recorded the twenty seven genotypes of mango could be grouped in to six clusters. On the basis of inter-cluster distance and cluster mean values, the genotypes Ratna, Sendhuram and Arka Aruna were identified as the suitable parent for hybridization programme for

improving early flowering, fruit retention, fruit yield per tree, pulp percentage and TSS.

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