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GENETIC DIVERSITY IN MANGO (*Mangifera Indica* L.) THROUGH MULTIVARIATE ANALYSIS

D. A. N. MAJUMDER[1], L. HASSAN[2], M. A. RAHIM[3] AND M. A. KABIR[4]

Abstract

The genetic divergence was assessed in 60 mango genotypes through D^2-statistics and principal component analysis. The genotypes under study were grouped into eight clusters and the diversity was influenced by the morphological characters, not by the geographical distribution of the genotypes. The clustering pattern revealed that the genotypes collected from the same region did not fall in the single cluster. The maximum inter cluster distance was noticed between cluster II and cluster VIII, and the lowest between clusters VII and cluster VIII. From the cluster means, cluster I was high yielding and ranked first in terms of number of secondary branches per inflorescence, percent fruit set per inflorescence, and yield per plant. Cluster VIII had only one genotype which produced the highest percentage of flowering shoots, % perfect flowers, number of fruits per plant, and %TSS. The genotypes of cluster VII produced the biggest sized fruits. The first nine characters of the principal component axes with eigen values above unity accounted for 88.3% of the total variation among the fifteen characters. Weight of harvested fruits per plant (0.990 and 0.181), number of fruits per plant (0.101 and 0.607) and individual fruit weight (0.027 and 0.107) for both the vectors were positive across two axes indicating the important components of genetic divergence. The genotypes belonging to clusters I, VII and VIII with high to moderate genetic distances might be recommended for use in crossing programs to produce new recombinants with desired traits.

Keywords: Genetic diversity, multivariate analysis, cluster analysis, and mango.

Introduction

Mango (*Mangifera indica* L.), "the king of the fruits", has got a unique position due to its nutritional quality, taste and consumer's preference among the fifty types of fruits grown in Bangladesh (Ahmad, 1985). Though mango is a very common fruit of Bangladesh very limited work has been done for its genetic improvement.

Before taking up any improvement programme for a crop through breeding, information about the relationship among elite breeding populations and the

[1]Manager, Plant Biotechnology Laboratory, BRAC Agricultural Research and Development Centre, Gazipur, [2]Professor, Dept. of Genetics and Plant Breeding, Bangladesh Agricultural University (BAU), Mymensingh, [3]Professor, Dept. of Horticulture, BAU, Mymensingh, [4]Professor, Dept of Horticulture, Hajee Mohammad Danesh Sci. & Tech. University, Dinajpur-5200, Bangladesh.

genetic diversity in available germplasm are important criteria for the optimal design of a breeding programme. This helps in the choice of desired parents for establishing new breeding population. Better knowledge on genetic diversity or genetic similarity can help in sustaining long term selection gain (Chowdhury *et al.,* 2002). Genetic diversity within a population depends on the number and frequency of all loci and the genetic constitution of the population (Crossa *et al.*, 1993). In other words, it is the genetic stock of the plant breeder. In recent years, scientists have been studying the genetic diversity of different crop species for their efficient utilization and conservation.

It is an established fact that genetically diverse parents are likely to contribute desirable segregates and produce high heterotic crosses. More diverse, the greater chances of obtaining high heterotic F_1s and broad spectrum of variability in segregating generations (Arunachalam, 1981). In spite of many valuable morphological traits, genetic diversity conserved in local mango cultivars and in its exotic germplasm has not been assessed in Bangladesh either by using morphological characters or DNA-based genetic markers. Therefore, the objective of the study was to find out the genetic diversity and pattern of variation present among the collected germplasm of mango.

Materials and Method

The study was conducted on the pre-established mango orchard of BAU-Germplasm Centre, Department of Horticulture, Bangladesh Agricultural University, Mymensingh during the period of December to July 2006-2007 and 2007-2008. This study was conducted with 60 mango genotypes in RCBD with three replications. One genotype represented one treatment and five plants in a genotype represented one replication. The distance from plant to plant was 5m and row to row was 5m. Normal recommended cultural practices were adopted during experimentation. Data were recorded on fifteen important parameters. Genetic diversity was estimated using Mahalanobi's D^2-statistics (Mahalanobis, 1936) extended by Rao (1952). Tocher's method was followed to determine group constellation. Canonical vitiate analysis was also performed as per Rao (1964) to confirm the results of cluster and D^2- analysis. The data were analysed using Genstat 5 (Release 4.1) and Microsoft Excel 2000 software.

Results and Discussion

The analysis of variance revealed significant variations among the cultivars of mango for all the characters. The difference among the genotypes were tested according to Wilk's criteria '$\wedge$' and the result of the test indicated that there were significant variations among the genotypes {V (stat.) = χ^2 (885)} = 975.274. Assuming D^2 values as χ^2, it appears that the differences between the genotypes

were always significant, except seven lower genotypic distances (D^2). D^2 values indicated that they were more or less identical (Table 3).

Principal component analysis (PCA): Eigen values of principal component axis, percent of total variation and cumulative variation accounted for them obtained from principal component analysis are presented in Table 1. The results showed that the first principal axis, percent of flowering shoot largely accounted for the variation among the genotypes which alone contributed 27.50% of the total variation.

The first nine characters of the principal component axes with eigen values above unity accounted for 88.3% of the total variation among the fifteen characters. The rest seven characters contributed remaining 11.7% of total variation. Ranpise and Desai (2003) studied genetic diversity of acid lime through morphological characters and reported that fruits per tree, yield per plant, juice volume and juice percentage were major contributor towards divergence. The character contributed the maximum to the divergence should be given greater emphasis for selection in breeding (Jagadev *et al.*, 1991).

Table 1. Latent roots (eigen values) and percent of variation in respect of 15 characters of mango.

Principal component axis	Eigen values	Percentage	
		Total variation accounted for	Cumulative
Percent flowering shoots	4.13	27.50	27.50
Number of inflorescences per shoot	2.40	15.97	43.47
No of secondary branches per inflorescence	1.59	10.59	54.06
Percent perfect flowers	1.20	7.97	62.03
Percent fruit set per inflorescence	0.99	6.62	68.65
Percent fruit harvest per inflorescence	0.94	6.27	74.92
Number of fruits per plant	0.88	4.84	79.76
Weight of harvested fruits per plant	0.73	4.47	84.23
Fruit weight (g)	0.67	4.07	88.3
Fruit length (cm)	0.61	3.83	92.13
Fruit breath (cm)	0.58	3.17	95.30
Fruit thickness (cm)	0.48	1.88	97.18
% Brix (TSS)	0.33	1.61	98.79
Percent edible portion	0.24	0.86	99.65
Percent non-edible portion	0.13	0.35	100.00

A two dimensional scatter plotting diagram (Z_1-Z_2) constructed using component score 1 on X axis and component score 2 on Y axis exhibited that the genotypes fall into eight clusters (Fig. 1).

Non- hierarchical clustering

Non-hierarchical clustering was done using covariance matrix where 60 mango genotypes were grouped into eight clusters. The clustering pattern obtained through different techniques coincided with the grouping patterns done by principal component analysis. So it can be safely stated that the results obtained through PCA were established by non-hierarchical clustering. It is interesting to note that 41.66% genotypes were included in cluster II and III and 35.00% in cluster IV and V, and the remaining 23.34% were in four clusters. The composition of clusters with different genotypes including their source of collection is presented in Table 2. Cluster II obtained the highest number of genotypes (20) which was followed by cluster V (15), cluster VI (7), cluster IV (6), cluster I (3) and cluster VII (3). The lowest number of genotypes (1) was observed in cluster VIII. The clustering pattern of the genotypes revealed that the genotypes collected from the same region did not fall in a single cluster which indicated variation in genotypes irrespective of their site of collection. For example, cluster II included 20 genotypes, but their source of origin were different such as Bangladesh, India, Pakistan and Florida (Table 2). This result suggests that the factor(s) other than geographical separation is responsible for divergence, and the genotypes that have originated from the same place may have different genetic architecture or vice-versa.

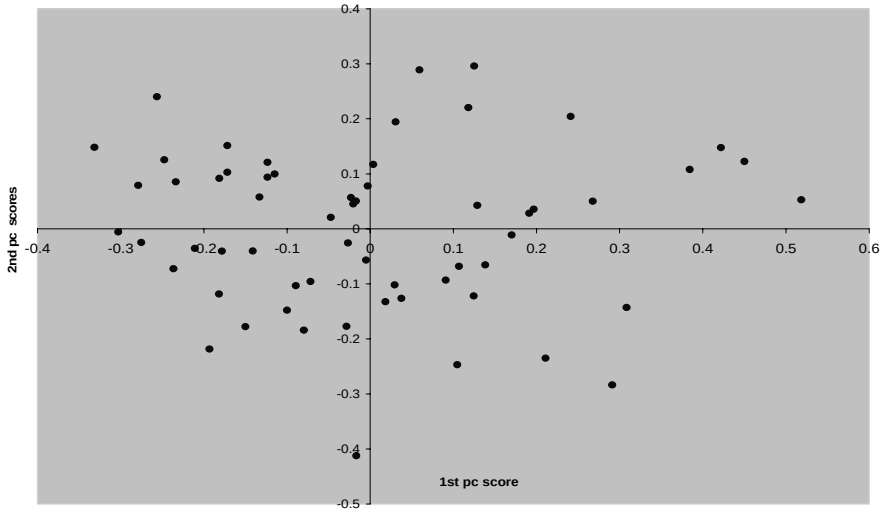

Fig. 1. Scattered distribution of 60 mango genotypes based on the principal component score.

These findings are in agreement with those of Ismail (2008) and Rahman *et al.* (2006). Lack of true relationship between geographical and genetic diversity was also explained by Murthy and Arunachalam (1966) and Upadhya and Murty (1970) who explained that genetic drift and natural selection in different environment can cause high diversity among the genotypes than geographical isolation can.

Table 2. Distribution of 60 mango genotypes in 8 clusters.

Cluster	No. of Genotype	Genotypes	Source of collection
I	3	MI61, MI94, MI95	Bangladesh
II	20	MI22, MI33, MI39, MI41, MI52, MI60, MI80, MI91	Bangladesh
		MI03, MI8, MI21, MI38, MI40, MI43, MI58	India
		MI12	Pakistan
		MI29, MI45, MI83, MI85	USA (Florida)
		MI24, MI26, MI27	Bangladesh
III	5	MI19	India
		MI16	USA (Florida)
IV	6	MI02, MI25, MI93, MI98	Bangladesh
		MI49. MI90	India
V	15	MI04, MI47, MI51, MI64, MI74, MI77, MI96	Bangladesh
		MI20, MI54, MI84, MI97	India
		MI88	Philippine
		MI44, MI46	USA (Florida)
		MI48	Pakistan
VI	7	MI23, MI75, MI81, MI86	Bangladesh
		MI50	India
		MI01	Philippine
		MI82	USA (Florida)
VII	3	MI70, MI92	Bangladesh
		MI09	India
VIII	1	MI28	India

Principal co-ordinate analysis (PCO)

Principal coordinate analysis was performed to get the inter-genotypic distance (D) for all 1770 possible combinations among the genotypes, and the values

ranged from 98.23 (MI23 and MI27) to 0.88 (MI22 and MI45) (Table 3). The difference between the highest and lowest inter genotypic distance was wide indicating the presence of wide genetic diversity among the genotypes. The intra-cluster distance was computed from these inter genotypic distance matrix as per Singh and Chowdhury (1985). The intra cluster distance was maximum in cluster V (55.42), followed by cluster II (54.02) and cluster VI (53.44). On the other hand the minimum was in cluster VIII (0.00) which included a single genotype MI28. The genotypes in cluster II, V and VI were most heterogeneous than those of cluster I and VII. Statistical distances represent the indices of genetic diversity among the clusters. The hybrid variety, MI28 formed a single cluster (cluster VIII) which was far diverged with the rest of the clusters indicating that this genotype could be crossed with other genotypes in order to incorporate the desired characters like percentage of flowering shoot, percent perfect flower, individual fruit weight, %TSS, number of fruits per plant and yield into the cultivated types.

Canonical vector analysis (CVA)

The vector analysis was done to compute the inter-cluster distance (Mahalanobis D^2 values). The results indicated that the inter-cluster distances between the different clusters of mango genotypes differed widely. The maximum inter cluster distance (151.82) was observed between cluster II and cluster VIII indicating wide range of genetic diversity between these two clusters, which was followed by the distances between cluster IV and V (141.03), cluster I and VIII (99.70) and cluster II and VII (97.93) (Table 4). The lowest (55.47) was between clusters VII and VIII, followed by I and VI (55.81) and II and V (56.05) indicated that genotypes of these clusters were genetically close. Hybridization among the genotypes drawn from widely divergent clusters with high yield potential would likely to manifest maximum heterotic combinations as well as new recombinations with desired traits. Similar results were in agreement with Ismail (2008) in lemon, Rahman *et al*. (2006) in sweet gourd and Saifullah *et al.* (1999) in jackfruit.

Cluster means

A comparison of cluster means for the different characters is presented in Table 5. Cluster I comprising of three (3) genotypes had the extreme mean values for number of secondary branches per inflorescence (51.63%), percent fruit set per inflorescence (25.90%) and weight of harvested fruits per plant (23.88kg). The second extreme mean values were in percent flowering shoot (59.56%), number of inflorescences per shoot (2.44) and number of fruits per plant (53.67 kg.). Though the cluster VIII had only one genotype, it produced the highest percentage of flowering shoot (67.33%), number of inflorescences per shoot

(2.67%), percent perfect flower (17.27%), highest individual fruit weight (317.00g) and in brix content (27.50%). Cluster VII possessed first position in case of fruit length (9.52cm), fruit breath (9.12 cm) and fruit thickness (7.43cm). Although cluster II (20) and cluster V (15) had the maximum number of genotypes, no remarkable feature was noticed in these two clusters for different characters. Similar results were also noticed by Ismail (2008) in case of lemon. None of the fifteen characters had the highest mean value under cluster IV and cluster V. Moreover, the genotypes belonging to cluster V had the lowest mean values for number of secondary branches per inflorescence, percent fruit set per inflorescence, percent brix and percent edible portion. Cluster IV had the lowest mean values for percent flowering shoot and number of inflorescences per shoot.

Table 3. Ten of each lower and higher inter-genotypic distance ($D = \sqrt{D^2}$) between pair of genotypes.

10 lower D values	Genotype combination	10 higher D values	Genotype combination
0.88	MI22 and MI45	98.23	MI23 and MI27
0.90	MI51 and MI45	98.20	MI28 and MI27
0.93	MI64 and MI97	98.13	MI51 and MI27
0.93	MI22 and MI51	98.06	MI74 and MI27
0.94	MI22 and MI38	97.89	MI22 and MI27
0.99	MI88 and MI84	97.87	MI20 and MI27
0.99	MI51 and MI84	97.83	MI51 and MI27
1.02	MI97 and MI51	97.83	MI82 and MI27
1.03	MI26 and MI97	97.77	MI23 and MI54
1.04	MI04 and MI20	97.76	MI45 and MI27

Table 4. Average intra (bold) and inter-cluster distance ($D = \sqrt{D^2}$) of 60 mango genotypes.

Cluster	I	II	III	IV	V	VI	VII	VIII
I	**49.989**	58.510	59.529	59.162	58.530	55.805	58.456	99.700
II		**54.018**	66.525	61.300	56.051	95.840	97.931	151.823
III			**51.751**	72.041	62.122	61.477	57.945	58.041
IV				**52.464**	141.031	57.695	71.310	64.543
V					**55.420**	62.093	69.312	59.681
VI						**53.440**	68.00	61.158
VII							**48.986**	55.466
VIII								**00.00**

Intra (bold) and inter cluster D values for nine characters

Table 5. Cluster means of 60 mango genotypes.

Characters	Cluster mean							
	I	II	III	IV	V	VI	VII	VIII
% Flowering shoots	59.56	39.25	51.40	37.28	38.18	41.86	55.66	67.33
No. of inflorescences / shoot	2.44	1.58	1.75	1.46	1.63	1.91	2.51	2.67
No. of secondary branches	51.63	26.71	26.73	32.27	26.68	35.49	43.91	49.9
% Perfect flowers	14.47	10.50	11.51	13.05	11.49	15.22	12.78	17.27
% Fruit set/ inflorescence	25.90	17.69	15.65	23.30	14.84	20.53	22.98	24.93
% Fruit harvest / inflorescence	4.26	2.45	3.59	2.32	3.10	4.47	2.08	4.50
No. of fruits per plant	53.67	31.43	38.34	36.22	40.87	55.09	23.33	53.33
Wt. of harvested fruits (kg)	23.88	8.29	12.79	10.84	9.49	13.71	8.27	13.11
Fruit weight (g)	305.22	273.40	252.07	274.28	275.13	261.52	335.33	317.00
Fruit length (cm)	9.04	8.69	9.08	9.23	8.90	8.94	9.52	8.65
Fruit breath (cm)	7.95	6.30	8.82	6.82	7.83	6.57	9.12	5.91
Fruit thickness (cm)	6.51	5.72	7.31	6.32	6.96	5.86	7.43	5.50
% Brix (TSS)	23.36	23.13	22.99	24.46	21.79	23.56	23.48	27.50
% Edible portion	70.22	54.62	77.18	70.15	66.86	71.40	71.40	69.31
% Non-edible portion	29.78	45.36	22.82	29.85	33.14	28.60	28.60	30.69

Contribution of different characters towards divergence

Contributions of different characters responsible for genetic divergence are presented in Table 6. The canonical variate analysis (CVA) revealed that in vector I (Z_1), the important characters responsible for genetic divergence in the major axis of differentiation were weight of harvested fruits per plant, number of fruits per plant, percent of flowering shoot, percent perfect flower and fruit weight. In vector II (Z_2) weight of harvested fruits per plant, number of fruits per plant, fruit weight and percent non-edible portion. Weight of harvested fruits per plant (0.990 and 0.181), number of fruits per plant (0.101 and 0.607), and individual fruit weight (0.027 and 0.107) for both the vectors were positive across the two axes indicating the important component of genetic divergence among the studied characters. Negative values for both the vectors for %TSS and

percent non-edible portion indicated the lowest contribution towards total divergence of mango. Saifullah *et al.* (1999) reported that fruit per primary branch, %TSS, seed diameter, spine density and yield per plant played major role in both axes for determining genetic divergence of jackfruit.

Table 6. Relative contributions of the 15 characters towards genetic divergence of mango.

Character	Vector 1	Vector 2
Percent flowering shoot	0.095	-0.482
No. of inflorescences / shoot	0.001	-0.009
No. of secondary branches per inflorescence	0.032	-0.334
Percent perfect flowers	0.012	-0.089
Percent fruit set/ inflorescence	0.004	-0.116
Percent fruit harvest / inflorescence	0.003	-0.036
No. of fruits/plant	0.101	0.607
Wt of harvested fruits per plant (kg)	0.990	0.181
Fruit weight (g)	0.027	0.107
Fruit length (cm)	0.002	-0.010
Fruit breath (cm)	0.006	-0.015
Fruit thickness (cm)	0.001	-0.005
% Brix (TSS)	-0.004	-0.018
% Edible portion	0.065	-0.333
% Non-edible portion	-0.065	-0.333

Selection of genotypes for hybridization programme

Considering magnitude of genetic distance, contribution of different characters towards the total divergence, magnitude of cluster means for different characters and per se performances, the genotypes of clusters I, VII, and VIII could be considered as parents for hybridization programmes. The genotypes of cluster I ranked first in terms of weight of harvested fruits per plant, the genotypes of cluster VII produced the biggest sized fruits and the genotype of cluster VIII possessed extreme values for % flowering shoot, number of inflorescences per shoot, number of secondary branches, % perfect flower, % fruit harvest per inflorescence, number of fruit per plant, individual fruit weight, %TSS and yield. These characters could be incorporated into the genotypes of clusters I, II and IV

for immediate benefit adopting appropriate breeding techniques. For long term breeding programme, MI28 should be crossed with the genotypes of cluster I to get heterotic effect on yield and related traits.

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