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GENOTYPIC AND PHENOTYPIC VARIABILITY IN MANGO (*Mangifera indica* L.)

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Abstract

Sixty mango genotypes were studied to find out their variability, heritability, and genetic advance. Significant variations were observed in 20 characters. There were also considerable differences between the genotypic and the phenotypic coefficients of variation for almost all the characters which indicated the influence of environment on the expression of these traits. Among the studied characters, GCV and PCV were high for weight of harvested fruits per plant, % fruit harvest per inflorescence, % initial fruit set per inflorescence, number of fruits per plant and number of main branches per inflorescence. All the characters showed considerably high heritability which ranged from 56.21 to 98.24% and the genetic advance (as % of mean) was high for the maximum traits. High heritability coupled with high genetic advance was observed in weight of harvested fruits per plant, % initial fruit set per inflorescence, % of flowering shoot, number of inflorescences per shoot, percent fruit harvest per inflorescence, number of main branches per inflorescence, number of fruits per plant, number of inflorescences per shoot, plant height (cm), and percent perfect flowers which indicated that these characters were less influenced by environment confirming predominance of additive gene action and therefore, selection in favour of these characters would be feasible for yield improvement of mango.

Keywords: Variability, heritability, genetic advance and mango.

Introduction

Mango (*Mangifera indica* L.) is the king of the fruits of Bangladesh. It has got a unique position in respect of nutritional quality, taste, and consumer preference among the fifty kinds of fruits grown in Bangladesh (Ahmad, 1985). In Bangladesh, mango ranks second in area and first in respect of fruit production. According to BBS (2009), Bangladesh produces 600 thousand metric tons of mango from 64 thousand hectares of land.

An understanding of the nature and magnitude of variability among the genetic stocks of a crop is of prime importance to breeders. Evaluation of genetic

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variability is important to know the source of gene for a particular trait within the available germplasm (Tomooka, 1991). A good knowledge of genetic wealth might also help in identifying desirable cultivars for commercial cultivation. Improvement of yield and other traits depends upon the amount of genetic variability present in the breeding materials for the required traits. High heritability generally enables the breeder to select plants on the basis of the phenotypic expression (Johnson *et al.*, 1955). As the heritability estimates are often subjected to genotype-environment interaction, estimation of genetic advance is required for expected genotypic progress of a particular character. Studies on the variability using genetic parameters are essential for initiating an efficient breeding programme. The present study was an attempt to gather information on genetic variability, heritability, and genetic advance among the important traits of mango crop.

Materials and Method

The experimental materials comprised of 60 mango genotypes (Table 1). The study was conducted on the pre-established mango orchard of BAU- Germplasm Centre, Department of Horticulture, Bangladesh Agricultural University (BAU), Mymensingh during December to July 2006-2007 and 2007-2008. The experiment was laid out in the RCBD with three replications. The distance from plant to plant was 5 m and row to row was 5 m. Data were recorded on plant height, leaf area, duration of flowering, percent of flowering shoot, number of inflorescence per shoot, number of main branches per inflorescence, percent perfect flowers, percent fruit set per inflorescence, percent fruit dropping at pea stage, days to maturity (from flowering to harvesting), percent fruit harvest per inflorescence, number of fruits harvested per plant, weight of harvested fruits per plant, fruit weight, fruit length, fruit breadth, fruit thickness, percent edible portion, percent non-edible portion, and percent total soluble solids (TSS). TSS was measured with the help of a hand refractometer. Genotypic and phenotypic coefficient of variation was calculated according to Singh and Chaudhury 1985. Heritability in broad sense (h^2b), genetic advance (GA) and genetic advance in percent of mean (GA %) were estimated as proposed by Johnson *et al.* (1955), Hanson *et al.*(1956), Allard (1960) and Comstock and Robinson (1952), respectively.

Results and Discussion

Wide range of variation was observed in growth, floral, and different fruit characters of mango which indicated the presence of genetic divergence of the crop (Table 2). Range, mean with standard error, genotypic and phenotypic coefficient of variation, heritability in broad sense and genetic advance in percent mean of some morphological and biochemical traits of mango are presented in Table 3 and Table 4. The estimates of phenotypic coefficient of variation were higher than the genotypic coefficient of variation for all the characters studied. The results indicated the influence of environment on the expression of the characters under investigation.

Table 1. List of mango genotypes along with the source of collection.

Sl. no.	No. of genotypes	Name	Source of collection	Sl. no.	No. of genotypes	Name	Source of collection
1.	MI 01	Rad	Philippine	31.	MI 49	Totapuri	India
2.	MI 02	Faraquebhog	Bangladesh	32.	MI 50	Kohitoor	India
3.	MI 03	Anwar-rataul	India	33.	MI51	Dudsar	Bangladesh
4.	MI 04	Shrabani	Bangladesh	34.	MI52	Mishridana	Bangladesh
5.	MI 08	Indian choucha	India	35.	MI54	Laxmanghog	Bangladesh
6.	MI 09	Mallika	India	36.	MI58	Samarbehist	India
7.	MI 12	Pakistani choucha	Pakistan	37.	MI60	Kazla-4	Bangladesh
8.	MI 16	Tommy Atkins	Florida, USA	38.	MI61	Himsagar	Bangladesh
9.	MI 19	Hybrid-10	India	39.	MI64	Baromashi	Bangladesh
10.	MI 20	Seedless	India	40.	MI70	BARI Aam-4	Bangladesh
11.	MI 21	Ratna	India	41.	MI 74	Golapkhash	Bangladesh
12.	MI 22	Mixed special	India	42.	MI 75	Surjapuri	Bangladesh
13.	MI 23	Gopalbhog	Bangladesh	43.	MI 77	Bandiguri	Bangladesh
14.	MI 24	Fazli	Bangladesh	44.	MI 80	Khuda-khirsapat	Bangladesh
15.	MI 25	Langra	Bangladesh	45.	MI 81	Elshapatti	Bangladesh
16.	MI 26	Khirsapat	Bangladesh	46.	MI 82	Kew Sai	Thailand
17.	MI 27	Ashwina	Bangladesh	47.	MI 83	Benishan	FloridaUSA
18.	MI 28	Amrapali	India	48.	MI 84	Kalia	Bangladesh
19.	MI 29	Carabao	Philippine	49.	MI 85	Nam Doc Mai	Thailand
20.	MI33	Bira	Bangladesh	50.	MI 86	Nakfazli	Bangladesh
21.	MI 38	Suborna	India	51.	MI88	Thai Kanchamitha	Philippine
22.	MI 39	Jolchhatra	Bangladesh	52.	MI90	Bhute bomby	Bangladesh
23.	MI 40	Rataul	India	53.	MI91	Golla	Bangladesh
24.	MI 41	Anu-kachamitha	Bangladesh	54.	MI92	Eshordijuthi	Bangladesh
25.	MI 43	Phalam	India	55.	MI93	Bogla	Bangladesh
26.	MI 44	Kent	Florida,USA	56.	MI94	Polyembryony	Bangladesh
27.	MI 45	Keitt	Florida, USA	57.	MI95	Ranguai	Bangladesh
28.	MI 46	Palmer	Florida,USA	58.	MI96	Golapkhash	Bangladesh
29	MI 47	Mishribhog	Bangladesh	59.	MI97	MDS (Neeluddin)	India
30.	MI 48	Sindhi	Pakistan	60.	MI98	Khirmon	Bangladesh

Table 2. Analysis of variance of 20 characters in mango.

Source of variation	Degrees of freedom (df)	Mean sum of squares									
		Plant height (cm)	Leaf Area (cm^2)	Duration of flowering (days)	Percent flowering shoot	Number of inflorescences/ shoot	Number of main branches/ inflorescence	Percent bisexual flowers	Percent fruit set/ inflorescence	Percent fruit dropping at pea stage	Days to maturity (days)
Replication	2	979.91	8.36	4.36	7.07	0.04	0.26	6.09	0.32	5.98	5.54
Treatment	59	24044.30 **	86.78 **	72.10 **	430.43**	0.65**	266.59**	23.77**	115.40**	102.20**	925.36**
Error	118	1113.73	11.88	7.34	11.42	0.02	1.58	2.25	1.85	14.34	100.11
Replication	2	0.08	5.97	1.52	206.67	0.12	0.22	0.19	5.72	5.72	3.18
Treatment	59	3.54**	471.74**	57.56**	5506.25**	2.44**	5.01**	3.36**	244.39**	244.39**	18.69**
Error	118	0.17	19.06	1.12	300.86	0.52	0.14	0.21	3.42	3.42	1.25

** $P< 0.01$

Table 3. Estimation of genetic parameters for different vegetative and floral characters of 60 mango genotypes

Characters	Range	Mean ± SE	GCV (%)	PCV (%)	h^2b (%)	GA in % mean (5%)
Plant height (cm)	578.33-211.31	356.66 ± 19.27	24.51	26.24	87.28	47.18
Leaf area (cm^2)	52.59-74.32	60.30 ±1.99	8.29	10.07	67.77	14.05
Duration of flowering	17.67-35.33	24.68 ± 1.57	18.83	21.80	74.61	33.50
% of flowering shoot	24.00-71.33	42.41± 1.95	27.87	28.99	92.44	55.20
No. of Inflorescence / shoot	1.13-2.77	1.74 ± 0.08	26.41	27.57	91.76	52.12
No of main branches/inflorescence	21.57-52.53	30.78± 0.73	30.53	30.81	98.24	62.35
% perfect flowers	8.10-19.17	12.07± 0.87	22.24	25.53	75.94	39.93
% initial fruit et/inflorescence	9.07-29.27	18.50 ± 0.79	33.24	34.06	95.26	66.84
% fruit dropping at pea stage	69.90-88.43	78.96 ± 2.19	6.85	8.37	67.12	11.57
Days to maturity	117.00-178.00	141.07± 5.78	11.76	13.73	73.32	20.74

GCV-Genotypic coefficient of variation h^2b- Heritability in broad sense
PCV- Phenotypic coefficient of variation GA- Genetic Advance

The higher estimates of genotypic and phenotypic coefficient of variation and medium difference between GCV and PCV were obtained for weight of harvested fruits (40.50% & 41.69%), percent initial fruit set (33.24% & 34.06%), fruit harvest per inflorescence (34.89% and 37.43%), number of fruits per plant (31.72% and 33.68%), number of main branches per inflorescence (30.51% & 30.81%), percent flowering shoots (27.87% and 28.99%), number of inflorescence per shoot (26.41% and 27.57%) and plant height (24.51% & 26.24%) (Table 3 and Table 4) which indicated the presence of environmental effect on these characters and wide scope of improvement through selection.

Estimates were very low for leaf area, days to maturity, percent fruit dropping at pea stage, fruit length and TSS suggesting the very limited scope for improvement of these traits through selection. Ranpise and Desai (2003) found high estimates of phenotypic coefficient of variation and genotypic coefficient of variation in lime for number of fruits per plant, flower twig, tree volume and yield per plant. Prasad and Rao (1989) observed high estimates of genotypic coefficient of variation and phenotypic coefficient of variation in lime for rind thickness, juice weight and juice volume in July crops and high estimates for TSS, fruit weight, and number of seeds in December crops.

Considerable difference was found between genotypic coefficient of variation (22.24%) and phenotypic coefficient of variation (25.53%) indicating high environmental effect upon the expression of percent perfect flowers. The medium estimates of genotypic and phenotypic coefficient of variation were obtained by days to flowering, fruit weight, fruit breadth, fruit thickness, and percent edible portion suggesting a hopeful scope for improvement of these traits through selection.

Table 4. Estimation of genetic parameter for different fruit characters of 60 mango genotypes.

Characters	Range	Mean ± SE	GCV	PCV	h^2b (%)	GA in % Mean (5%)
Fruit weight (g)	219.00-365.33	283.36 ± 10.01	14.70	15.92	85.20	27.95
Fruit length (cm)	6.86-11.50	8.92 ±0.42	9.08	12.11	56.21	14.02
Fruit breadth (cm)	5.37-10.96	7.19 ± 0.21	17.72	18.45	92.22	35.05
Fruit thickness (cm)	5.10-9.71	42.41± 1.95	16.10	17.66	83.12	30.24
% TSS (Brix)	16.90-28.26	23.07± 0.65	10.45	11.52	82.29	19.53
% Edible portion	45.22-79.83	63.67± 1.07	14.08	14.31	95.91	28.40
% Non-edible portion	20.17-54.78	36.33± 1.07	24.67	25.19	95.91	49.77
%Fruit harvest / Inflorescence	1.56-5.46	10.71 ± 0.61	34.89	37.43	86.92	67.02
No. of fruits / plant	21.33-60.33	38.64 ± 2.53	31.72	33.68	88.69	61.53
Weight of harvested fruits /plant (kg/plant)	6.33-25.04	10.71±0.61	40.50	41.69	94.41	81.07

GCV-Genotypic coefficient of variation h^2b- Heritability in broad sense
PCV- Phenotypic coefficient of variation GA- Genetic Advance

Although the genotypic coefficient of variation and phenotypic coefficient of variation are the measures of genetic variability however, the amount of genetic gain can be estimated from genotypic coefficient of variation and phenotypic coefficient of variation along with heritability. Swarup and Chougule (1962) suggested that the estimates of genotypic coefficient of variation alone was not sufficient to quantify the amount of variation which is heritable and Burton (1952) inferred that genotypic coefficient of variation effects together with heritability estimates would furnish more reliable information. In the present study, heritability estimates were high for most of the characters viz., plant height (87.28 %), duration of flowering (74.61%), percent of flowering shoot (92.44 %), number of inflorescence per shoot (91.76 %), number of main branches per inflorescence (98.24%), percent perfect flower (75.94 %), percent initial fruit set per inflorescence (95.26 %), fruit weight (85.20%), fruit breadth (92.22 %), fruit thickness (83.12 %), percent TSS (82.29%), percent edible portion (95.91%), percent non-edible potion (95.91 %), percent fruit harvest per inflorescence (86.69 %), number of fruits per plant (88.69%), and weight of harvested fruits per plant (94.41%) and moderate estimates for remaining characters. Higher values of heritability indicates that either these were simply inherited characters governed by a few major genes or additive gene effects even if, they were under polygenic control and therefore, selection of these characters would be more effective for improvement (Johnson *et al.,* 1955; Panse , 1957). Ranpise and Desai (2003) observed high values of heritability for fruits per plant, average fruit weight, juice percentage, TSS and acidity. Prasad and Rao (1989) recorded high estimates of heritability in lime for TSS, ascorbic acid, acidity, rind thickness, and fruit volume.

The genetic advance expressed in percent mean was very high for some of the characters, such as weight of harvested fruits per plant (81.07 %)), number of main branches per inflorescence (62.35 %), percent flowering shoot (55.20%), number of inflorescences per shoot (52.12 %), initial fruit set per inflorescence (66.84 %) number of fruits per plant (61.53%), and percent fruit harvested per inflorescence (67.02 %). It might be due to high range of variation among the genotypes. The characters, such as plant height, percent perfect flowers, duration of flowering, fruit weight, fruit breadth, fruit thickness, percent edible portion, and percent non-edible portion expressed moderate genetic advance. The percentage of heritability was 73.32% and genetic advance was 20.74% for days to maturity. These moderate to low values of GCV and PCV indicated to low genetic divergence among the accessions for those mentioned vegetative and floral characters indicating practically little chance for plant selection. There was moderate difference between genotypic (6.85%) and phenotypic (8.37%) coefficient of variation on percent fruit dropping at pea stage. The result indicated low environmental influence upon the expression of this character. The heritability of percent fruit dropping at pea stage was also moderate (67.12%) and genetic advance was low.

The higher values of genetic advance for fruits per plant, yield per plant, tree volume, and flower per twig were reported by Ranpise and Desai (2003). Prasad and Rao (1989) observed moderate values of genetic advance in lime for rind thickness, juice weight, juice volume and fruit volume. Panse (1957) opined that high genetic advance would be obtainable when heritability is chiefly due to dominance and epistasis (non additive gene action), consequently genetic advance would also below.

Heritability and genetic gain (GA) aid in referring valuable conclusion for effective selection based on the phenotypic coefficient of variation (Johnson *et al*., 1955). The characters having high heritability as well as moderate to high genetic advance and narrow difference between GCV and PCV were found in plant height, percent flowering shoot, number of inflorescences per shoot, percent perfect flower, initial fruit set per inflorescence, fruit weight, fruit breadth, fruit thickness, % edible portion, % non-edible potion, fruit harvest per inflorescence, number of fruits per plant, and weight of harvested fruits per plant indicate predominance of additive gene action for these characters and these characters would have possibilities of selection towards desired direction.

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