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GENETIC DIVERSITY ANALYSIS IN BITTER GOURD (*Momordica charantia L.*)

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Abstract

Seventeen genotypes of bitter gourd (*Momordica charantia* L.) were studied in a field experiment conducted at the experimental field of Sher-e-Bangla Agricultural University, Dhaka, during April 2010 to September 2010. The objectives of the study were to estimate the genetic variation among the genotypes for different characters including fruit yield. There was a great deal of significant variation among the genotypes for all the characters. The inter cluster distance between II and III (12.97) was the highest and distance between other clusters were more or less intermediate. Intermediate diverse parents have more chance to contribute heterosis in the subsequent generations. Cluster II had the highest cluster mean for vine length, number of nodes per vine, branches per vine, days to first male & female flowering, weight per fruit and yield per plant, but the characters days to first male and female flowering were the most important yield contributing character. Hybridization between the genotypes of cluster II and cluster VI manifests the maximum heterosis and creates wide genetic variability. Genetically distant parents are usually able to produce higher heterosis. Considering magnitude of genetic distance, magnitude of cluster means for different characters and field performance the genotypes G_2, G_5, G_{14} G_{15} from cluster II, genotypes G_1 and G_3 from cluster I, genotypes G_8 and G_9 from cluster III and genotypes G_{10}, G_{11}, G_{13} from cluster IV suitable for future hybridization programme.

Keywords: Biter gourd, genetic variation, fruit yield and other characteristics

Introduction

Bitter gourd *(Momordica charantia L.*), is one of the most important and popular cucurbit vegetable grown in Bangladesh. Bitter gourd contains a reasonable amount of different nutrients such as proteins, carbohydrates, fats, minerals and vitamins A, B2, and C etc. Raja *et al.* (1984) reported very high amount of vitamin C (95mg/100g) and protein (930mg/100g) in some Indian bitter gourd varieties. The fruits are bitter to taste due to the presence of a substance called cucurbitacin. Bitter gourd is also reported as beneficial against diseases like paralysis, indigestion and vomiting pain and diabetes (Mier and Yaniv, 1985). Bitter gourd may contribute to the nutritional shortage of the people of Bangladesh. Particularly, it can provide added proteins, minerals and vitamins to the diet. There are a lot of variability's among the existing bitter gourd germplasms of Bangladesh. An understanding of the nature and magnitude of the variability among the genetic stocks of bitter gourd is of prime importance for the breeder. A good knowledge of genetic wealth might also helps in identifying desirable cultivars for commercial production. Because of its nature of high cross pollination, hardly any genetically pure strain is available to the growers. The basic key to a breeder is to develop high yielding varieties through selection, either from the genotypes or from the segregants of a crop. Expression of different plant characters are controlled by genetic and environmental factors. So, the study of genetic parameters is necessary for a successful breeding program which will provide valuable information on the mode of inheritance of different characters which would be useful in selecting plants having desirable characters to develop new varieties. In a hybridization program knowledge of interrelationship between yield and yield components is necessary. Estimation of genetic diversity is considered as an important factor, which is also essential prerequisite for hybridization program for developing high yielding variety. Multivariate analysis is a useful tool in quantifying the degree of divergence among biological population at genotypic level. Very few research efforts related to estimate the variability in bitter gourd have been conducted in the country. Considering the scope of study and available genetic resources of bitter gourd the present investigation was under taken with a view to estimate genetic diversity using multivariate techniques.

Materials and Methods

Seventeen genotypes of bitter gourd were used for the present research work. The genetically pure and physically healthy seeds of these genotypes were collected from different location. The name and sources of these genotypes are presented in Table 1. The experiment was laid out in a Randomized Complete Block Design (RCBD) with three

replications. The individual plot was 3 m × 1 m in size. The distance maintained for spacing was row to row 50 cm, plant to plant 2m and between two blocks 1 m. Seeds of different accessions were sown in the pit on 5thMay, 2010.Germination of seeds were completed within twelve days and in each pit four seeds were sown and the soil around the plant was firmly pressed by hand.

Table 1. Name and sources of seventeen Bitter gourd genotypes used in the present study

Sl. No.	Genotypes No.	Sources
1	G_1	Siddiq Bazar, Gulistan, Dhaka
2	G_2	Siddiq Bazar, Gulistan, Dhaka
3	G_3	Narayanganj local market
4	G_4	Agargaon local market, Agargaon, Dhaka
5	G_5	Siddiq Bazar, Gulistan, Dhaka
6	G_6	Agargaon local market, Agargaon, Dhaka
7	G_7	Agargaon local market, Agargaon, Dhaka
8	G_8	Siddiq Bazar, Gulistan, Dhaka,
9	G_9	Narayanganj local market
10	G_{10}	Kawran bazar,Dhaka
11	G_{11}	Kawran bazar,Dhaka
12	G_{12}	Narayanganj local market
13	G_{13}	Agargaon local market, Agargaon, Dhaka
14	G_{14}	Siddiq Bazar, Gulistan, Dhaka,
15	G_{15}	Kawran bazar,Dhaka
16	G_{16}	Agargaon local market, Agargaon, Dhaka
17	G_{17}	Narayanganj local market

After final land preparation, pits of 50 cm × 50 cm × 45 cm were prepared in each plot with a spacing of 3 m × 1.25 m. The dose of manure and fertilizers used in the study are Cow dung 10 ton/ha, Urea 150 kg/ha, TSP 100 kg/ha, MOP 150 kg/ha, Gypsum 80 kg/ha, Zinc Oxide 8 kg/ha. The intercultural operations were done from time to time throughout the cropping season for proper growth and development of the plants. Only one healthy seedling was kept per pit for the proper development. Fruits were picked on the basis of horticultural maturity, size, color and age. Frequent picking was done throughout the harvesting period. The following data such as, Days to first male flowering, Days to first female flowering, Vine length (m), Number of nodes per vine, Branches per vine, Fruit length (cm), Fruit diameter (cm), Number of fruit per plant, Weight per fruit (g), Yield per plant (kg), were recorded on parameters from the studied plants during the experiment. Mean data of the characters were subjected to univariate analysis using MSTAT-C computer program me. Multivariate analysis was done by computer using GENSTAT 5.13 and Microsoft Excel 2000 software through four techniques viz., Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CA) and Canonical Vector Analysis (CVA). The genetic diversity among the genotypes was assessed by Mahalanobis's(1936) general distance (D^2) statistic and its auxiliary analyses. Principal Coordinate analysis is equivalent to PCA and used to calculate inter unit distances. Through the use of all dimension of p it gives the minimum distance between each pair of the n points using similarity matrix (Digby *et al.,* 1989). The Mahalanobis's distance (D^2) values were calculated from transformed uncorrelated means of characters according to Rao (1952), and Singh and Chaudhury (1985). The D^2 values were estimated for all possible combinations between genotypes. Average intra-cluster distances were calculated by the following formula as suggested by Singh and Chuadhury (1985). Using the values of intra and inter-cluster distances ($D = \sqrt{D^2}$), a cluster diagram was drawn as suggested by Singh and Chuadhury (1985). It gives a brief idea of the pattern of diversity among the genotypes included in a cluster.

Results and Discussion

The experiment was conducted to investigate the yield performance, genetic divergence for yield and yield contributing characters of seventeen bitter gourd genotypes. Some of the analyzed data have been presented in Table (s) and other in figures for ease of discussion, comparison and understanding. Maximum vine length was observed in genotype 9 (4.53m) and minimum in genotype 15 (2.13m). Maximum branch per vine was observed in genotype 5 (45.60) and minimum in genotype 2 (30.67). Maximum nodes per vine were observed in genotype 2 (91.23) and minimum in genotype 11 (81.33). Maximum days of 1st male flowering were observed in genotype 1 (61 days) and minimum in genotype 14 and genotype 16 (54 days). Maximum days of 1st female flowering were observed in genotype 1 (71 days) and minimum in genotype 9, genotype 11, genotype 15 and genotype 16 (63 days). Maximum fruit length was observed in genotype 11 (21.59cm) and minimum in genotype 5 (15.55cm). Maximum fruit diameter was observed in genotype 3 (11.84cm) and minimum in genotype 4 (9.86cm). Maximum fruit weight was observed in genotype 3 (130.2g) and minimum in genotype 5 (102.7g). Maximum no. of fruits per plant was observed in genotype 8 (30) and minimum in genotype 2 (19.67). Maximum fruits per plant was observed in genotype 8 (3.42kg) and minimum in genotype 2 (2.2kg) (Table 2). The result of the experiment have been presented and interpreted under the following headings.

Cluster analysis

On the basis of D^2 analysis, 17 genotypes of bitter gourd were grouped into four clusters (Table 3). Cluster I contained the highest number of 6 genotypes followed by cluster II and III having 4 genotypes in each while cluster IV contained the lowest number of 3 genotypes. The clustering pattern of different genotypes did not follow their origin of distribution and was fairly at random. This suggests that falling of materials of same origin into different clusters was an indication of broad genetic base of the genotypes. Prasad *et al.*, (2001) reported the similar result when they studied 60 inbreed lines of bitter gourd. Study showed considerable diversity in the material analyzed.

Principal component analysis (PCA)

The principal component analysis was carried out with 17 genotypes of bitter gourd. PCA produce Eigen values of principle component axes of coordination of genotypes with the first axes totally accounted for the among the genotypes. First 3 Eigen values for 3 principal coordination axes of genotypes accounted for 88.12% variation (Table 4). Precise information about the extent of genetic divergence is crucial for an effective breeding programme. The multivariate analysis is helpful in quantifying the degree of divergence between populations and to determine the forces operating at intra and inter cluster levels (Murthy and Quadri, 1966).

Table 2. Mean performance in respect of vine length, branches per vine, nodes per vine, days of 1st flowering male, days of 1st flowering female, fruit length, fruit diameter, fruit weight, no of fruits per plant and fruits per plant of seventeen bitter gourd genotypes

Genotypes	Vine length (m)	Branches per vine	Nodes per vine	Days of 1st male flowering	Days of 1st female flowering	Fruit length (cm)	Fruit diameter (cm)	Fruit weight (g)	No of fruits per plant	Fruits per Plant (Kg)
Genotype-1	4.20	30.87	85.00	61	71	20.19	11.77	119.3	23.33	2.267
Genotype-2	3.63	30.67	91.23	60	69	21.40	11.33	127.8	19.67	2.200
Genotype-3	3.80	41.03	89.60	56	68	21.10	11.84	130.2	22.33	2.640
Genotype-4	3.27	34.10	82.10	57	69	19.08	9.86	105.8	24.67	2.777
Genotype-5	4.07	45.60	85.37	56	67	15.55	10.75	102.7	20.67	2.290
Genotype-6	3.57	39.70	83.33	58	69	21.43	11.13	110.5	27.67	3.093
Genotype-7	3.77	40.83	82.47	55	65	20.86	10.67	113.7	27.33	3.170
Genotype-8	3.37	35.63	85.37	57	70	20.72	10.47	114.2	30.00	3.420
Genotype-9	4.53	43.70	82.87	56	63	20.75	10.42	117.0	29.33	3.290
Genotype-10	3.73	39.13	87.20	54	65	20.38	10.65	116.8	29.33	3.110
Genotype-11	3.23	37.60	81.33	55	63	21.59	10.52	117.3	27.33	2.797
Genotype-12	3.53	34.93	82.43	59	66	20.77	10.82	112.5	25.00	2.587
Genotype-13	3.20	37.07	90.50	55	64	20.63	10.22	110.7	28.33	2.880
Genotype-14	4.30	39.50	86.50	54	65	21.20	10.73	119.3	26.00	2.973
Genotype-15	2.13	36.23	90.73	55	63	21.32	10.69	116.7	23.33	2.440
Genotype-16	4.27	43.47	87.30	54	63	20.83	10.65	112.5	21.00	2.327
Genotype-17	3.50	39.47	83.10	56	65	20.54	9.87	110.8	25.00	2.747
LSD(0.05)	0.97	5.58	2.71	3.02	2.20	0.97	0.65	9.25	3.74	0.40
Maximum	4.53	45.6	91.23	61	71	21.59	11.84	130.2	30	3.42
Minimum	2.13	30.67	81.33	54	63	15.55	9.86	102.7	19.67	2.2
Mean	3.61	38.2	85.73	56.59	66.29	20.28	10.74	115.3	25.26	2.76

Table 3. Distribution of 17 genotypes of bitter gourd genotypes in four clusters

Cluster no.	No. of associations	Genotypes
I	6	Genotype 1, Genotype 3, Genotype 6, Genotype7, Genotype 16 and Genotype 17
II	4	Genotype 2, Genotype 5, Genotype 14 and Genotype 15
III	4	Genotype 4, Genotype 8, Genotype 9 and Genotype 12
IV	3	Genotype 10, Genotype 11 and Genotype 13

Table 4. Eigen values and percentage of variation for corresponding 10 components characters in seventeen genotypes of Bitter gourd

Principal component axis	Eigen values	% of total variation accounted for	Cumulative percent
Vine length (cm)	5.88	53.63	53.93
Branches per vine	0.96	33.27	86.90
No. of nodes per vine	1.03	1.22	88.12
Days to 1st male flowering	3.66	9.39	56.95
Days to 1st female flowering	2.30	8.83	66.35
Fruit length (cm)	0.88	8.76	92.13
Fruit diameter (cm)	0.96	8.01	96.95
No. of fruit per plant	0.18	1.68	99.25
Fruit weight (gm)	0.15	1.36	99.11
Yield per plant (kg)	0.04	0.41	99.80

Table 5. Ten highest and ten lowest inter genotypic distance among the seventeen genotypes of Bitter gourd

10 higher value D^2 value	Genotypes combination	10 lower D^2 values	Genotypes combination
1.66	G_2-G_{16}	0.21	G_6-G_{13}
1.64	G_5-G_{14}	0.22	G_9-G_{17}
1.61	G_5-G_{10}	0.23	G_{12}-G_{13}
1.43	G_{10}-G_{14}	0.24	G_7-G_{17}
1.42	G_4-G_9	0.25	G_6-G_{12}
1.41	G_9-G_{17}	0.251	G_6-G_{16}
1.40	G_1-G_{10}	0.26	G_{11}-G_{12}
1.39	G_1-G_{17}	0.262	G_{15}-G_{17}
1.37	G_4-G_{14}	0.27	G_7-G_{10}
1.36	G_8-G_9	0.29	G_3-G_{13}

Table 6. Cluster mean for 10 characters of 17 Bitter gourd genotypes

Parameters	Cluster Means			
	I	II	III	IV
Vine length (cm)	35.6	43.5	35.6	41.5
Branches per vine	38.55	42.00	40.23	39.67
No. of nodes per vine	83.44	85.58	84.74	82.25
Days to 1st male flowering	50.37	54	53.00	51.37
Days to 1st female flowering	63.23	64	63.50	62.29
Fruit length (cm)	14.43	16.22	16.23	15.51
Fruit diameter (cm)	9.45	10.20	10.50	10.30
No. of fruit per plant	25.21	24.79	26.83	20.48
Fruit weight (gm)	68.50	82.80	72.46	70.51
Yield per plant (kg)	3.53	3.87	3.66	3.29

Principal coordinates analysis (PCO)

The results obtained from principal coordinate analysis showed that the highest inter genotypic distance was observed between genotype 2 and genotype 16 (1.66) followed by genotype 5 and genotype 14 (1.64) and the lowest distance was observed (0.21) between genotypes 6 and genotype 13 followed by the distance (0.22) between genotypes 9 and genotype 17 (Table 5). The difference between the highest and the lowest inter genotypic distance indicate the presence of moderate variability among the 17 genotypes of bitter gourd. The highest intra-cluster distance was recorded in cluster I (0.46) containing six genotype (G_1, G_3, G_6, G_7, G_{16} and G_{17}) while the lowest was observed in cluster IV (0.21) having three genotype (G_{10}, G_{11} and G_{13}). It favored to decide that intra-group diversity was the highest in cluster I and the lowest in cluster IV (Table 7). Golakiya and Makne (1991) while assessing genetic diversity in 23 genotypes of groundnut and grouped them into six clusters. Reddy and Reddy (1987) reported on 48 genotypes of groundnut and grouped them into 11 clusters.

Non-hierarchical clustering

The computations from covariance matrix gave non-hierarchical clustering among seventeen genotypes of bitter gourd and grouped them into four clusters. The clustering pattern obtained coincided with the apparent grouping patterns performed by PCA. So the results

obtained through PCA were confirmed by non-hierarchical clustering.

Cluster means for 10 characters are shown in Table 7. Among 10 characters highest cluster mean was observed in cluster II for seven characters viz. vine length (43.5 cm), no. of nodes per vine (85.58) , branches per vine (42.00) , days of 1st male flowering (54 days) and female flowering (64 days), weight per fruit (82.80 gm) and yield per plant (3.78kg) (Table 6). Baydar and Bayraktar (1994) reported 35 genotypes of peanut which were divided into 6 clusters of different genetic divergences. Badignnavar *et al*. (2002), Joel and Mylsamy (1998) were found the similar results in groundnut, Islam and Islam. (2000) were found the similar results in mustard.

Canonical variate analysis

The highest inter-cluster distance was observed between cluster II and III (12.97) and intra cluster distance was the highest (0.46) in cluster I (Table 8). The lowest inter-cluster distance was observed between cluster I and IV (6.86). Moderate distance was found between cluster II and IV (10.45) followed by cluster I and IV (10.34) (Table 8). The inter cluster distances were higher than the intra cluster distances suggesting wider genetic diversity among the genotype of different groups. Differently originated genotypes found in same cluster or genotypes from same origin were dispersed in different clusters. Genotypes from same location of Bangladesh being in different clusters, indicating the broad genetic variability.

Table 7. Average intra (bold) and inter cluster distances (D^2) for 17 Bitter gourd genotypes

Cluster	I	II	III	IV
I	0.46			
II	10.34	0.33		
III	7.59	12.97	0.25	
IV	6.86	10.45	5.84	0.21

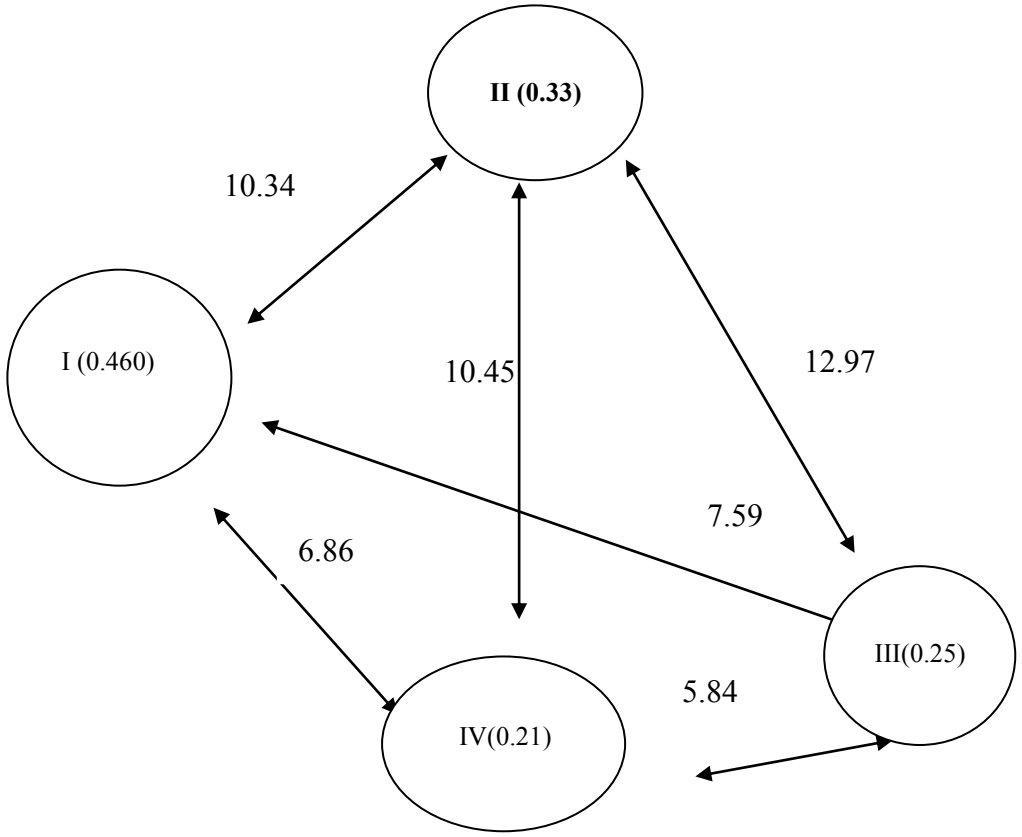

Fig 1. Diagram showing intra and inter-cluster distance of seventeen genotypes of Bitter gourd

There was evidence from Shanmugam and Rangasamy (1982) showed that materials from same origin distributed in different clusters are an indication of broad genetic base of the genotypes belonging to that origin.

Among the inter cluster distance, distance between II and III (12.97) (Fig 1) were the highest and other clusters were bearing more or less intermediate distance. Intermediate diverse parents have the more chance to contribute heterosis in the subsequent generations. Cluster II had the highest cluster mean for vine length, no. of nodes per vine, branches per vine, first male & female flowering, weight per fruit and yield per plant, but average to below average for days to first male and female flowering were not direct yield contributing characters. Hybridization between the Genotype of cluster II and cluster VI will manifest the maximum heterosis and create wide genetic variability. Considering magnitude of genetic distance, magnitude of cluster means for different characters and field performance of the genotypes G_2, G_5, G_{14} G_{15} from cluster II, genotypes G_1 and G_3 from cluster I, genotypes G_8 and G_9 from cluster III and genotypes G_{10}, G_{11}, G_{13} from cluster IV would be suitable for highest yield per plant in future hybridization programme.

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