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GENETIC DIVERGENCE IN BITTER GOURD (MOMORDICA CHARNTIA L.)

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Abstract

The genetic divergence among 36 genotypes of bitter gourd (*Momordica charantia* L.) was determined through PCA, PCO, CVA, Cluster analysis (CLSA) and Mohalanobis's D^2 analysis. Through multivariate analysis based on 22 characters 36 genotypes were grouped into six distant clusters. Cluster VI includes maximum genotypes (12) followed by cluster I (6) and cluster II (6). Cluster V, cluster III and cluster I comprised 5, 4 and 3 genotypes respectively. The inter-cluster distances were higher than the intra-cluster distances. The inter-cluster distance was maximum between cluster III and IV (28.71) followed by the distance between cluster I and cluster IV (23.61). The intra-cluster distances in all the 6 clusters were more or less low indicating the closeness of genotypes within the same cluster. The highest intra-cluster distance was observed for cluster III (1.84) followed by the cluster I (1.38). The genotypes within the same clusters were collected from different places and genotypes collected in the same place fall in different cluster, which indicated that genetic divergence are not dependent on its geographical position from where the genotypes were collected. The genetic diversity of 36 genotypes was also assessed through PCA. The first three components accounted for 60.04% of the total variation. Days to first male flower opening, number of primary branches per vine, fruit yield per vine, days to green fruit maturity, seed weight per fruit mature seed width had the highest contribution towards the divergence. Cluster diagram exhibited that the genotypes include in the cluster III were far diverse from the genotypes of cluster IV while the genotypes belonging to the cluster II and VI were least diversed.

Key words: D^2 statistics, Cluster, Genetic divergence, Bitter gourd

Introduction

Bitter gourd (*Momordica charantia* L.) locally known as karala/uchha, is an important vegetable and belongs to the family Cucurbitaceae. Compared to other cucurbits, bitter gourd has relatively high nutritional value, in respect of iron and ascorbic acid contents. It has export potentiality because of its excellent keeping quality and grows round the year due to its photo insensitivity (Rashid 1999). As a monoecious crop, bitter gourd is highly cross pollinated and thus, there exists a wide genetic variability in nature. But there is few released varieties of this popular vegetable as per its requirements.

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Genetic diversity is one of the important tools to quantify genetic variability in both cross and self-pollinated crops and also important for crop improvement as well as variety development programme (Matzinger *et al*. 1962, Murty 1965, Marani and Avieli 1973, Anand *et al*. 1975 and Gaur *et al*. 1978). Multivarite analysis by means of Mahalanobis D^2 statistics is an useful tool in quantifying the degree of genotypic divergence among biological populations and to assess the relative contribution of different components to the total divergence both at inter and intra-cluster levels (Murty and Arunachalam 1966, Ram and Panwan 1970, Sachan and Sharma 1971, Jatasra and Paroda 1978 and Das and Gupta 1984). Many researchers have adopted this D^2 technique for measuring divergence among genotypes of pumkin (Masud *et al*. 1995 and Rashid 2000), cucumber (Prasad *et al*. 1993) and snake gourd (Banik 2003).

An understanding of the nature and degree of variability among the germplasm is a pre-requisite for its variety improvement. Therefore, the present study was undertaken to analyze the genetic divergence of a number of bitter gourd genotypes for selecting parents of diverse group for further breeding programme.

Materials and Methods

The experiment was conducted at the experimental farm and laboratory of Bangabandhu Sheikh Mujibur Rahman Agricultural University (BSMRAU) and the experimental farm of Lal Teer Seed Ltd., Gazipur during March to July, 2005. Thirty six genotypes of bitter gourd collected from different parts of Bangladesh as well as India, the Phillipines and AVRDC, Taiwan were used in this study. The experiment was laid out in RCB design with three replications. The inter and intra-row spacing maintained were (2 X 1) m^2. There were three pits per replication and one plant per pit on the raised bed, the pits were prepared and left open for one week prior to transplanting. Seedlings of 36 genotypes of bitter gourd were raised in trays containing a mixture of soil and well decomposed cowdung (1:1). Sowing date was March 03, 2005. Recommended doses and application methods of manure and fertilizers were applied in the experimental field (Anon. 2004). The healthy single seedlings of 30 days old were transplanted in the pits of the experimental field on April 03, 2005. Bamboo stick support was given to the growing plants and allowed them to creep on a rope nets. Necessary intercultural operations and irrigation were done during the crop period to ensure normal growth and development of the plants. Control measures were taken against red pumpkin beetle at seedling stage and fruit fly at fruiting stage (Anon. 1991). Observations were recorded for days to first male flower opening, node number of first male flower, days to first female flower opening, node number of first female flower, main vine length (cm), number of primary branches per vine, nodes on main vine, number of fruits per vine, average single fruit weight (g), fruit yield per vine (kg), fruit length (cm), fruit diameter (cm), thickness of the fruit flesh (mm), thickness of the rind (mm), days to green fruit maturity, days to seed fruit

maturity, number of seeds per fruit, seed weight per fruit (g), 100-seed weight (g), mature seed length (mm), mature seed width (mm), mature seed thickness (mm)

Genetic Diversity was studied following Mahalanobis's (1936) D^2 statistics extended by Rao (1952). Clustering of genotypes was done according to Tocher's method (Rao 1964) and Principal component analysis (PCA), Principal coordinate analysis (PCO), Canonical vector analysis (CVA) were done by computer using GenStat 5.13 (Payne *et al*. 1993). The intra-cluster distances were computed by using the values of inter-genotype distance from distance matrix of PCO according to Singh and Chaudhary (1985).

Results and Discussion

Analysis of variance exhibited significant differences among the genotypes for all the characters under this investigation. Thus, it indicated considerable amount of genetic variability among 36 genotypes. Eigen values of 22 principal component axes and percentage of variation accounting for them obtained from the principal component analysis are presented in Table 1. The results revealed that the first axis largely accounted

Table 1. Latent roots (Eigen values) and percent of variation for corresponding 22 component characters in 36 genotypes of bitter gourd.

Principal component axis	Eigen values	Percentage	
		Total variation accounted for	Cumulative
Days to first male flower opening	7.67	34.85	34.85
Node number of first male flower	3.31	15.05	49.90
Days to first female flower opening	2.23	1014	60.04
Node number of first female flower	1.72	7.80	67.84
Main vine length (m)	1.49	6.79	74.63
Number of primary branches per vine	1.24	5.64	80.27
Nodes on main vine	0.98	4.43	84.70
Number of fruits per vine	0.68	3.09	87.79
Average single fruit weight (g)	0.67	3.02	90.81
Fruit yield per vine (kg)	0.45	2.02	92.83
Fruit length (cm)	0.42	1.90	94.73
Fruit diameter (cm))	0.27	1.23	95.96
Thickness of fruit flesh (mm)	0.24	1.07	97.03
Thickness of rind (mm)	0.19	0.88	97.91
Days to green fruit maturity	0.16	0.72	98.63
Days to seed fruit maturity	0.09	0.42	99.05
Number of seed per fruit	0.06	0.28	99.33
Seed weight per fruit (g)	0.06	0.27	99.60
100 seed weight (g)	0.05	0.21	99.81
Mature seed length (mm)	0.02	0.11	99.92
Mature seed width (mm)	0.01	0.05	99.97
Mature seed thickness (mm)	0.01	0.03	100.0

for the variation among the genotypes (34.85%) followed by second axis (15.05%). The first ten axes accounted for 92.83% of the total variation among the 22 characters describing in 36 bitter gourd genotypes while the former two accounted for 49.90%.

Thirty six genotypes of bitter gourd were grouped into 6 clusters according to Tocher method by using distance matrix obtained from principal coordinate analysis (Rao 1952) and shown in Table 2. The cluster VI enclosed the highest number (12) of genotypes. The second possessed six genotypes in I and II. The cluster IV contained three genotypes and occupied least position. The genotypes within the same cluster although formed specific cluster but were collected from different places. The clustering pattern of the genotypes revealed that the genotypes collected from the same place did not form a single cluster. This indicates that geographic diversity is not always related to genetic diversity. Similar results had been reported by Chowdhury *et al.* (1998) in soybean, Bhadra and Akhtar (1991) in mungbean, Natarajan *et al.* (1988) in green gram, Rashid (2000) in pumpkin, Mannan (2000) in country bean and Banik (2003) in snake gourd. Shanmugam and Rangasmy (1982) reported that falling of materials of same origin into different clusters was an indication of broad genetic base of the genotypes belonging to that origin.

Table 2. Distribution of 36 genotypes of bitter gourd in 6 clusters.

Cluster	No. of genotypes	Genotypes with original place of collection
I	6	BG 002 (Savar), BG 011 (Phillpines), BG 016 (Jhenaidah), BG 018 (Bijbhander, Dhaka), BG 025 (Rangpur), BG 030 (Jessore)
II	6	BG 003 (AVRDC, Taiwan), BG 010 (Chittagong), BG 012 (Chittagong (Potia)), BG 019 (Chittagong), BG 026 (Rangpur), BG 032 (Cox's Bazar)
III	4	BG 004 (Bogra), BG 005 (Brahmanbaria), BG 023 (Barisal), BG 024 (Pirojpur)
IV	3	BG 006 (Thakurgaon), BG 033 (Chittagong), BG 036 (Nawabgonj
V	5	BG 001 (India), BG 013 (Bogra), BG 014 (Narsindi), BG 015 (Jessore), BG 031 (Faridpur)
VI	12	BG 007 (BARI, Gazipur), BG 008 (Rampal), BG 009 (BARI, Gazipur), BG 017 (India), BG 020 (Thakurgaon), BG 0021 (Lal Teer Seed Ltd.), BG 022 (Jessore), BG 027 (Rangpur), BG 028 (Rangpur), BG 029 (Rangpur), BG 034 (Chittagong), BG 035 (Pabna)

The magnitude of the intra-cluster distances was not always proportional to the number of genotypes in the clusters (Table 3) in this study. It was observed that the cluster VI contained twelve genotypes but its intra-cluster distance was not necessarily the highest.

The cluster III had only four genotypes but its intra-cluster distance was the highest. The intra-cluster distances in all clusters were less than inter-cluster distances (Table 3) which revealed that the genotypes within the same cluster were closely related. Sidhu and Brar (1985) obtained larger inter-cluster distance than the intra-cluster distance in watermelon. The lower intra-cluster and high inter-cluster values suggested that the population grouped were homogeneous within and heterogeneous between clusters.

Table 3. Mean intra-(bold) and inter-cluster distance (D^2) for 36 genotypes of bitter gourd obtained on the basis of 22 morphological characters.

Cluster	I	II	III	IV	V	VI
I	**1.38**	10.06	8.38	23.61	3.46	15.17
II		**0.71**	16.50	13.68	6.92	5.99
III			**1.84**	28.71	9.93	19.89
IV				**0.81**	20.27	8.82
V					**0.90**	11.73
VI						**0.83**

The highest inter-cluster distance was obtained between the cluster III and IV (28.71) followed by cluster I and IV (23.61) (Table 3). The lowest inter-cluster distance was noticed between the cluster I and V (3.46), followed by the cluster II and VI (5.99). The maximum value of intra-cluster distance (1.84) indicated that genotypes belonging to cluster III were far diverged from those of cluster I. Similarly the higher inter-cluster values between cluster III and IV, cluster I and IV, cluster IV and V indicated that the genotypes between each pair of clusters were far diversed. These relationships were also reflected in the scatter diagram (Fig. 1). Somayajulu *et al*. (1970) reported that the clustering revealed instability due to relatively lesser divergence, where the widely divergent cluster remain distinct in different environment. From the present study it is evident that the cluster III and IV were highly diverged. So, they would be more suitable. It is expected that the crosses between the genotypes of cluster III and IV would exhibit high heterosis and also likely to produce new recombinant with desired traits.

The genotypes belonging to the distant clusters could be used in hybridization program for obtaining a wide spectrum of variation among the segregant. Wen Xing *et al*. (1994) reported that genetic diversity were more beneficial if crossing was carried out between genotypes belonging to different groups having genetic distance (D^2) greater than 12.5. Thus it could be said that crosses should be made between genotypes belonging to the distant clusters for higher heterotic response. In the present study the inter-cluster distances between cluster IV and other clusters ranged from 13.68 to 28.71 (Table 3). The genotypes of cluster IV crossed with desirable genotypes of other clusters might expressed heterotic effect. Mian and Bhal (1989) reported that parental clusters separated by medium D^2 values exhibited significant positive heterosis in chick pea. Thus, crossing

between genotypes belonging to clusters with moderate diversity like between genotypes of cluster IV and V and cluster II and III could also exploit heterosis. Kadam and Kale (1987) observed highly significant difference between cultivars suggesting considerable divergence among 30 ribbed gourd cultivars. The 30 cultivars were grouped into 20 clusters based on their D^2 values.

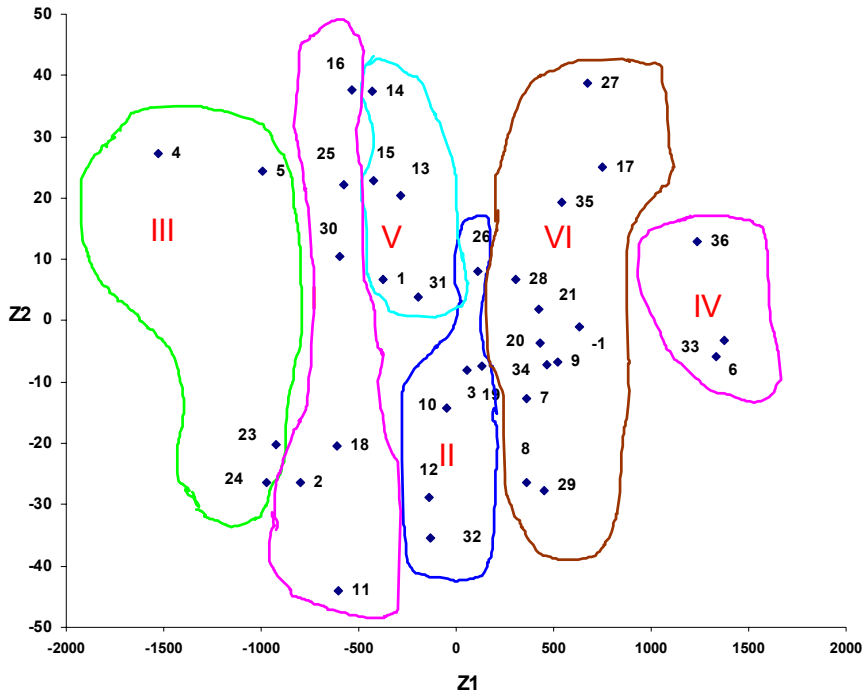

Fig. 1. Scattered distribution of 36 genotypes of bitter gourd based on their principal component scores super imposed with clustering.

Cluster means for 22 characters are presented in Table 4. Among the 22 studied characters the highest cluster mean was maximum (9) in cluster IV, followed by cluster III, cluster II and cluster VI. Cluster V occupied the only one highest cluster mean but which is the most important characters "Number of fruits per vine". The minimum days (50.6) required for first female flower opening in cluster I whereas Cluster III required the maximum (58.4). The highest number of fruits per vine (36.4) was harvested from the genotypes included in cluster V followed by cluster IV and cluster VI. The lowest number of fruits (25.8) was harvested from the plants of cluster II. The highest fruit weight was recorded by the genotypes included in cluster IV followed by cluster II and cluster VI and the lowest was in cluster III. The biggest fruit was produced by the

genotype under cluster IV. The maximum and minimum days required for green fruit maturity for fruits of cluster VI (12.9) and III (12.1), for seed fruit maturity for cluster IV (22.3) and I (21.3), respectively.The minimum number of seeds and seed weight per fruit was noticed for cluster III. The highest number of seed per fruit as well as seed weight was produced by cluster IV. The maximum 100-seed weight was observed for cluster I followed by cluster II and cluster IV. The minimum 100- seed weight was found for cluster III. The highest mature seed length and width was recorded in group II and lowest in III whereas highest thickness in cluster I and lowest in VI.

Table 4. Cluster means and Relative contributions of 22 characters to the total divergence in bitter gourd.

Characters	Cluster mean						Vector 1	Vector 2
	I	II	III	IV	V	VI		
Days to first male flower opening	48.8	58.7	59.2	57.9	51.5	55.4	0.370	0.186
Node number of first male flower	12.7	17.5	14.9	15.3	12.8	15.6	-0.312	0.163
Days to first female flower opening	50.6	57.7	58.4	57.5	51.3	55.9	-0.317	-0.075
Node number of first female flower	19.7	21.2	20.9	21.6	17.8	20.6	-0.053	-0.025
Main vine length (m)	4.3	5.2	4.5	5.1	4.5	5.4	0.973	-0.122
Number of primary branches per vine	6.9	7.2	8.2	7.3	7.0	7.8	0.289	0.500
Nodes on main vine	76.7	82.4	84.9	84.9	75.6	86.5	-0.003	0.105
Number of fruits per vine	28.7	25.8	29.9	35.1	36.4	34.3	0.154	-0.140
Average single fruit weight (g)	60.9	79.5	37.3	93.4	43.9	76.1	0.120	-0.089
Fruit yield per vine (kg)	1.34	1.95	8.52	3.27	1.61	2.45	0.008	0.004
Fruit length (cm)	13.8	17.0	8.3	19.1	11.8	16.2	0.005	-0.042
Fruit diameter (cm))	3.5	4.3	3.1	4.4	3.7	4.0	4.165	-10.844
Thickness of fruit flesh (mm)	24.0	27.2	20.8	28.5	24.4	25.4	-0.514	1.323
Thickness of rind (mm)	3.7	4.4	3.5	4.6	4.1	4.4	-1.146	2.126
Days to green fruit maturity	12.3	12.7	12.1	12.5	12.8	12.9	0.000	0.391
Days to seed fruit maturity	21.3	21.9	21.6	22.3	21.5	22.2	-0.237	0.629
Number of seed per fruit	13.1	13.0	9.7	14.8	12.7	12.7	-0.297	-1.214
Seed weight per fruit (g)	1.9	2.2	1.3	2.4	1.9	2.0	3.651	3.155
100 seed weight (g)	17.3	17.1	13.8	16.9	15.6	15.8	0.759	-0.952
Mature seed length (mm)	13.1	14.0	12.1	13.8	13.1	13.3	-1.269	-0.442
Mature seed width (mm)	7.5	7.6	7.4	7.5	7.4	7.5	0.595	0.661
Mature seed thickness (mm)	3.8	3.7	3.6	3.6	3.7	3.5	-6.535	0.867

Contribution of characters towards divergence was obtained from canonical variate analysis (CVA) and is presented in Table 4. The values of Vector 1 and Vector II revealed that both the vectors had positive values for days to first male flower opening, number of primary branches per vine, fruit yield per vine, days to green fruit maturity,

seed weight per fruit (g), mature seed width. These results indicated that these five characters had highest contribution towards divergence among the twenty two characters for 36 genotypes of bitter gourd. In vector 1, other important characters responsible for genetic diversity in the major axis of differentiation were main vine length (m), number of fruits vine per vine, average single fruit weight (g), fruit length (cm), fruit diameter (cm), 100 seed weight (g) while in vector 2 (the second axis of differentiation) node number of first male flower, nodes on main vine, thickness of fruit flesh, thickness of rind, days to seed fruit maturity, mature seed thickness contributed positive impact on divergence. Negative values in both the vectors were for days to first female flower opening, node number of first female flower, number of seeds per fruit, mature seed thickness**,** indicated these four characters had lowest contribution to the total divergence.

Sidhu and Brar (1985) studied seven diverse water melon varieties and their hybrids and observed that the average fruit weight contributed maximum towards genetic diversity (28.04%) followed by fruits per plant (23.28%). Mathew *et. al,.* (1986) observed the maximum contribution of fruits per plant (80%) in *Cucumis spp*. They found that selection of botanical varieties based on fruits/plant would be logical in selection of divergent parents. Similar type of results was also obtained by Prasad *et al.* (1993) in cucumber, Masud *et al.* (1995) in pumpkin and Singh and Singh (1979) in okra, Mannan (2000) in country bean and Banik (2003) in snake gourd.

High variability exists among the studied genotypes of bitter gourd. The selection of parents for further breeding programme to the maximum divergent cluster such as cluster III and Cluster IV, Cluster I and Cluster IV, Cluster IV and Cluster V in the present study, which would exert high heterosis and wide variability in genetic architecture in subsequent generatios.

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