

Multivariate Analysis of Bitter Gourd (*Momordica charantia* L.)

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Abstract: Genetic divergence of twenty bitter gourd genotypes was studied through Moahalanobis's D^2 and principal component analysis. The genotypes under study fall into four clusters. The cluster I contained the highest number of genotypes and it was 10. Cluster IV contained the lowest number of genotypes. Cluster II produced the highest mean value for weight per fruit. The inter cluster distances were much higher than the intra cluster distances. Cluster I exhibit the highest intra cluster distance while the lowest distance was observed in cluster III. The highest inter cluster distance was observed between I and II while the lowest distance was observed between the cluster II and IV. The highest intra cluster means for weight per fruit and five important yield contributing characters were obtained from cluster II. Therefore, more emphasis should be given on the cluster for selecting genotypes as parents for crossing with the genotypes of cluster II which may produce new recombination with desired traits. Considering all the characters the G_1 (Shaparan), G_5 (Rampali gaj), G_9 (Nabil), G_{12} (Nandita), G_{14} (Eureca), G_{16} (Tia) and G_{19} (Maharaj) were selected for future breeding programme.

Key words: Bitter gourd (*Momordica charantia* L.) • Genetic divergence • Multivariate • D^2 statistics

INTRODUCTION

Bitter gourd (*Momordica charantia* L.) locally known as karala/uchha is an important home garden vegetable. It is a fast growing warm seasonal climbing annual, native to South Asia. Bitter gourd is a tropical and subtropical vine of the Cucurbitaceae family. It is widely grown for edible fruit, which is among the most bitter of all vegetables. The original home of the species is not known, other than that it is a native of the tropics. It is widely grown in South and Southeast Asia, China and Africa. The herbaceous tendril-bearing vine grows to 5 m. It bears simple; alternate leaves 4-12 cm across, with 3-7 deeply separated lobes. Each plant bears separate yellow male and female flowers [1]. Compared to other cucurbits, bitter gourd has relatively high nutritional value, in respect of iron and ascorbic acid contents.

Bitter gourd is usually grown under kitchen garden as a summer vegetable. But at present it is also being grown as commercial crop near the urban areas. Moreover, it can also be grown in any type of soil having good drainage system. From nutritional point of view, bitter gourd can be

considered as nutrition rich fruit vegetable. It contains considerable amount of water (83-92%), carbohydrates (4.0-10.5%), protein (1.5-2.0%), fat (0.2-1.0%), minerals (0.5-1.0%) and fiber (0.8-1.7 %) [2]. Ripe fruits are rich in vitamin A. Among all cucurbits vegetables bitter gourd contains the maximum amount of minerals and vitamins.

Yet no comprehensive systematic research has been done in this crop in Bangladesh. Present harvestable yield of bitter gourd is very low (3.72 t/ha) [3] due to unavailability of high yielding varieties. Bitter gourd is monoecious and highly cross-pollinated in nature. Such pollination mechanism can be exploited for hybrid seed production commercially. Moreover, there is a great scope of development of OP varieties utilizing the existing variability. As a minor vegetable, bitter gourd did not get proper attention for its genetic improvement in the past. Considering the availability of genetic variability, its scope of yield improvement and export potential, the present investigation was undertaken to study the genetic divergence among twenty genotypes of bitter gourd and to screen out the suitable parental groups which are likely to provide superior segregates on hybridization.

MATERIALS AND METHODS

The research work relating to determine the genetic diversity of bitter gourds was conducted at the Sher-e-Bangla Agricultural University Farm, Dhaka-1207 during April 2008 to September 2008. The experimental area was situated at 23°77'N latitude and 90°33'E longitude at an altitude of 8.6 meter above the sea level [4]. The experimental field belongs to the Agro-ecological zone of "The Modhupur Tract", AEZ-28 [5]. Soil pH ranged from 6.0- 6.6 and had organic matter 0.84%. Twenty genotypes of bitter gourd were used for the research work. The genetically pure and physically healthy seeds of these genotypes were collected from Plant Genetic Resources Centre (PGRC) of Bangladesh Agricultural Research Institute (BARI). Parar Bond of Meghna, Comilla, Siddiq Bazar, Dhaka (collected from Thailand), Agargaon local market, Agargaon, Dhaka. The experiment was laid out RCBD design with three replications. The individual plot was 3 m × 1 m in size. The twenty genotypes of the experiment were assigned at random into plots of each replication. The distance maintained spacing row to row 50 cm and plant to plant 2 m. The distance maintained between two blocks was 1 m. Due to uncertain rainfall during the period of the study, the seeds were dibbled in poly bag for higher germination percentage and to get healthy seedlings and when the seedlings the seedlings become 25 days old, those were transplanted in the main field in the pit. Seeds were sown 17th. March, 2008. The experiment plot was prepared by several ploughing and cross ploughing followed by laddering and harrowing with tractor and power tiller to bring about good tilth in the middle week of February 2008. After final land preparation, pits of 50 cm × 50 cm × 45 cm were prepared in each plot with a spacing of a spacing of 3 m × 1.25 m. To control field cricket 5 mg Furadan was also mixed with the soils of each pit before making it ready for dibbling. The doses of manure and fertilizers such as Cowdung, Urea, TSP and MOP applied @ 10 ton/ha, 150 Kg/ha, 100 Kg/ha and 150 Kg/ha respectively to the plots for bitter gourd cultivation [6]. Total cowdung, half of TSP and one third MOP were applied in the field during final land preparation. Remaining TSP and one third MOP and whole gypsum and zinc oxide and one third of urea were applied in pit one week prior to transplantation. Remaining urea and MOP were applied as top dressing in four installments at 20, 40, 60 and 75 days after transplanting. Germination of seeds was completed within 12 days

and the seedlings of different accessions were planted in the pit on 12th. April, 2008. The standard agronomic intercultural operations were done from time to time throughout the cropping season for proper growth and development of the plants. In mature stage fruit fly caused severe damage to the fruit. For protection from fruit fly, MSGT (Mashed Sweet Gourd Trap) and Pheromone bait was used along with ripcord, sevin powder. Fruits were picked on the basis of horticultural maturity, size, colour and age being determined for the purpose of consumption as the fruit. Fruits were picked with sharp knife and care was taken to avoid injury of the vine. Data were recorded on the parameters from the studied plants during the experiment 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) and yield per plant (kg). Mean data of the characters were subjected to multivariate analysis. 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).

RESULTS AND DISCUSSION

Twenty genotypes of bitter gourd studied were grouped into four Cluster (Table 1). Chaturvedi and Gupta [7] studied 40 genotypes of sponge gourd and grouped them into 11 clusters. Shamsuddin [8] grouped 45 ridge gourds into three clusters. The distribution pattern indicated that the highest number of genotypes (10) was included in cluster I and the lowest were in cluster IV. It was also observed from the distribution pattern that the geographic divergence did not follow the same trend as he genotypes within the same cluster originated from different countries. Murty and Anand [9] reported that the geographic distribution and genetic diversity were not directly related. Inter and intra cluster distances are presented in the (Table 2), which revealed that the inter cluster distances in all cases were larger than intra cluster distances suggesting wider genetic diversity among the genotypes of different groups. The highest inter cluster distance was observed between I and II while the lowest distance was observed between the cluster II and IV. Cluster I exhibit the highest intra cluster distance while the lowest distance was observed in cluster III.

Table 1: Distribution of 20 bitter gourd genotypes in four clusters

Cluster	Number of members	Bitter gourd genotypes
I	10	TB/qt 01-05× 03-01, TB (Q) 07-01× 08-03, BARRI Karla-I, Sagarica,
II	4	Rampali gaj, Nabil, Eureka, Maharaj
III	4	Deshi, Bt (N) 04-07, Nandita, Bt (N) 04-12
IV	2	Shaparan, Tia

Table 2: Average intra (bold) and inter cluster distances (D^2) for 20 Bitter gourd genotypes

Cluster	I	II	III	IV
I	0.490			
II	11.413	0.337		
III	6.517	10.719	0.265	
IV	7.101	4.510	8.354	0.312

Table 3. Cluster mean for ten characters of twenty Bitter gourd genotypes

Parameters	I	II	III	IV
Days to first male flowering	51.37	51.67	52.92	54
Days to first female flowering	60.93	61.17	62.5	64
Vine length (m)	3.56	4.35	3.56	4.15
No. of nodes per vine	85.24	89.58	80.74	82.25
Branches per vine	39.26	43.26	39.67	37.94
Fruit length (cm)	16.79	20.59	20.73	18.51
Fruit diameter (cm)	10.45	10.68	11.19	10.32
No. of fruit per plant	26.2	56.17	26.83	47.84
Weight per fruit (g)	86.5	128.87	122.64	100.5
Yield per plant (kg)	2	4.61	2.4	3.21

Somayajullu *et al.* [10] reported the clustering revealed instability due to relatively lesser divergence, whereas widely divergent clusters remain distinct in different environments. The result was also supported by Raut *et al.* [11]. In this study it was observed that cluster II was highly diverged. So those would be more stable. The genotypes of the distant clusters could be used in crossing programs for obtaining wide range of variation among the segregates. Jagadev and Samal [12] got segregants with wider variations among the genotypes in niger from the crossing between the clusters involving the parents which were belong to distant clusters. It is expected that the crosses between the clusters II and III would exhibit higher heterosis and also likely to produce new recombinants with desired traits. The cluster mean of twenty genotypes of bitter gourd are presented in the (Table 3). The result revealed that the cluster II had the highest mean value for the characters weight per fruit (g), number of nodes per vine, days to first female flowering and days to first male flowering. Cluster IV had the dwarf type plants and cluster III had the minimum no. of fruit per

plant. The most divergence group means were found days to first male flowering between cluster I and II, days to first female flowering between cluster II and III, vine length (m) between cluster II and IV, No. of nodes per vine between cluster III and IV, Branches per vine between cluster I and III, Fruit length (cm) between cluster II and III, Fruit diameter (cm) between cluster I and IV, No. of fruit per plant between cluster I and III, Weight per fruit (g) between cluster II and III and yield per plant (kg) between cluster I and III (Table 3). Fig. 1 showing the scatter distribution of twenty genotypes of bitter gourd based on their principal component scores superimposed with clusters and Fig. 2 also showing diagram showing intra and inter-cluster distances of twenty genotypes of bitter gourd.

Contribution of the characters towards divergence is presented in (Table 4). The canonical variate analysis revealed that the Vector I, days to first flowering male, Branches per vine and yield per plant were positive. Vine length (m), No. of nodes per vine, Fruit length (cm) and No. of fruit per plant were positive in case of vector II.

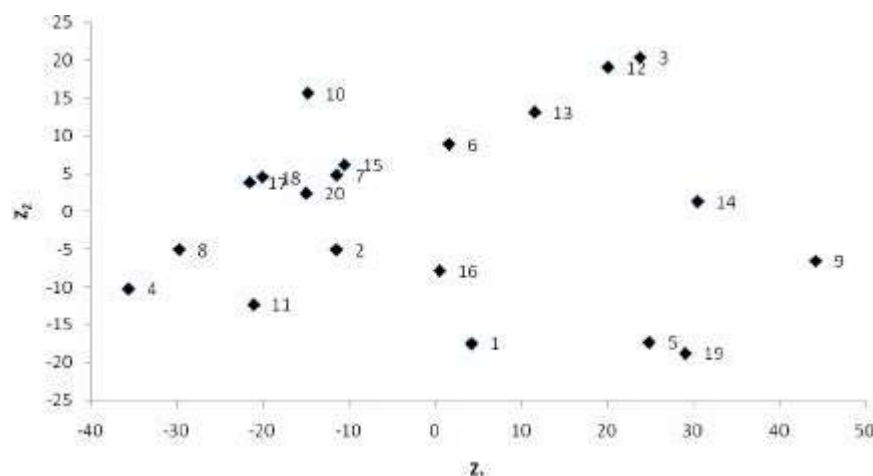


Fig. 1: Scatter distribution of 20 genotypes of bitter melon based on their principal component scores superimposed with clusters

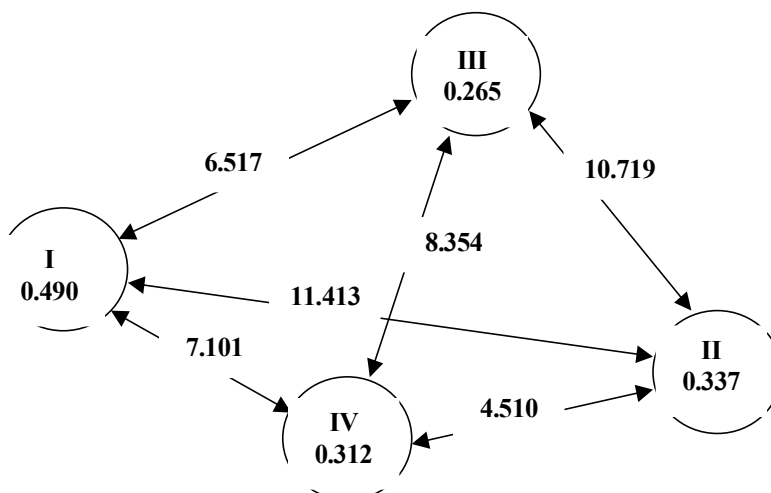


Fig. 2: Diagram showing intra and inter-cluster distances of twenty genotypes of Bitter melon

Table 4: Latent vectors for 10 principal component characters of 20 genotypes of Bitter melon

Characters	Vector1	Vector2
Days to first male flowering	0.451	-0.932
Days to first female flowering	-0.045	-0.275
Vine length (m)	-5.009	5.857
No. of nodes/vine	-0.268	0.143
Branches/vine	0.509	-0.430
Fruit length (cm)	-0.211	0.407
Fruit diameter (cm)	-0.717	-0.461
No. of fruit/ plant	-0.271	0.199
Weight/fruit (gm)	-0.080	-0.155
Yield/ plant (kg)	1.568	-1.942

Such results indicated that these characters contributed maximum towards divergence. It is interesting that greater divergence in the present material due to those characters will offer a good scope for improvement of yield through rational selection of parents for producing heterotic bitter melon genotypes.

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