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A Study Of Genetic Diversity In Bottle Gourd (Lagenaria Siceraria L.)

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Abstract
Genetic divergence of 31 bottle gourd genotypes was studied through multivariate analysis. The genotypes under this study fall into five clusters. Cluster I contained lowest number (2) of genotypes, whereas cluster II contained highest number (10) of genotypes. Cluster III had the highest mean value for the characters such as days to first male flowering, days to first female flowering, fruit weight, fruit length and fruit peduncle length. Inter-cluster distances were much higher than the intra-cluster distances. Cluster II exhibited the highest intra-cluster distance while the lowest distance was observed in cluster I. The highest inter-cluster distance was observed between cluster I and III, while the lowest distance was observed between cluster II and IV. The highest intra-cluster mean for weight fruit^{-1} and four important yield contributing characters were obtained from cluster III. Therefore, more emphasis should be given on the cluster for selecting genotypes as parents for crossing with the genotypes of cluster III which may produce new recombination with desired traits. Considering all the characters G_4 (BD-4580), G_{31} (BD-8948), G_{26} (BD-4560) and G_{28} (BD-4569) were selected for future breeding program.

Keywords: *Bottle gourd (Lagenaria siceraria L.), genetic divergence, multivariate analysis*

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I. Introduction

Bottle gourd (*Lagenaria siceraria* L.), locally known as *Lau*, is an important kitchen garden vegetable in Bangladesh. It is a fast-growing winter season climbing annual, native to Africa. Bottle gourd is a tropical and sub-tropical vine of the Cucurbitaceae family. It is widely grown for edible fruit. 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 south-east 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 separated lobes and velvety texture because of the fine hairs. Each plant bears separate white male and female flowers [1].

Bottle gourd is usually grown under kitchen garden as a winter 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, bottle gourd can be considered as nutrient rich fruit vegetable. It contains considerable amount of water (96.1 g), carbohydrates (2.5 g), protein (0.2 g), fat (0.1 g), minerals (0.5 g), fiber (0.6 g) and energy (12 kcal) 100 g^{-1} of edible fruit [2]. Bottle gourd is a rich source of minerals and vitamins. It is gaining popularity as a healthy food because of its easy digestibility, diuretic and cardiatonic effects [3].

At present the acreage and annual production of bottle gourd is 7,217 ha and 85,267 tons respectively in Bangladesh with an average yield of 11.81 tons per hectare, which is very low compared to other countries [4]. Interestingly, yet no comprehensive systematic research has been done in this crop in Bangladesh. Bottle gourd is monoecious (flowers of both sexes carried on a single plant) 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 (Open pollination) varieties utilizing the existing variability. As a minor vegetable, bottle 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 31 genotypes of bottle gourd, and to screen out the suitable parental groups which are likely to provide superior segregates on hybridization.

II. Materials and Methods

The experiment was conducted at Agricultural Farm, Sher-e-Bangla Agricultural University, Dhaka (23°77'N latitude and 90°33'E longitude, 8.6 masl), Bangladesh during winter season (October to March). The experimental field belongs to the agro-ecological zone of 'Modhupur Tract', AEZ-28 in Bangladesh (Anonymous, 1988a). The soil pH ranged from 6 to 6.6 with 0.84%. organic matter. Thirty-one genotypes of bottle gourd were used in the present study. The genetically pure and physically healthy seeds of these genotypes were collected from Plant Genetic Resources Center (PGRC) of Bangladesh Agricultural Research Institute (BARI), Gazipur, Bangladesh (**Table 1**).

Table 1: Name and origin of 31 genotypes of Bottle gourd used in the present study

Sl. No.	Genotypes No.	BARI ACC. Number	Origin	Sl. No.	Genotypes No.	BARI ACC. Number	Origin
1	G_1	BD-4577	PGRC, BARI	17	G_{17}	BD-4602	PGRC, BARI
2	G_2	BD-4578	PGRC, BARI	18	G_{18}	BD-4604	PGRC, BARI
3	G_3	BD-4579	PGRC, BARI	19	G_{19}	BD-4603	PGRC, BARI
4	G_4	BD-4580	PGRC, BARI	20	G_{20}	BD-8965	PGRC, BARI
5	G_5	BD-4581	PGRC, BARI	21	G_{21}	BD-8966	PGRC, BARI
6	G_6	BD-4582	PGRC, BARI	22	G_{22}	BD-8987	PGRC, BARI
7	G_7	BD-4583	PGRC, BARI	23	G_{23}	BD-8988	PGRC, BARI
8	G_8	BD-4584	PGRC, BARI	24	G_{24}	BD-4558	PGRC, BARI
9	G_9	BD-4585	PGRC, BARI	25	G_{25}	BD-4559	PGRC, BARI
10	G_{10}	BD-4596	PGRC, BARI	26	G_{26}	BD-4560	PGRC, BARI
11	G_{11}	BD-4597	PGRC, BARI	27	G_{27}	BD-4561	PGRC, BARI
12	G_{12}	BD-4605	PGRC, BARI	28	G_{28}	BD-4569	PGRC, BARI
13	G_{13}	BD-4598	PGRC, BARI	29	G_{29}	BD-8950	PGRC, BARI
14	G_{14}	BD-4599	PGRC, BARI	30	G_{30}	BD-8949	PGRC, BARI
15	G_{15}	BD-4600	PGRC, BARI	31	G_{31}	BD-8948	PGRC, BARI
16	G_{16}	BD-4601	PGRC, BARI	-	-	-	-

Here, PGRC = Plant Genetic Resources Centre, BARI = Bangladesh Agricultural Research Institute

The experiment was laid out in RCBD design with three replications. The genotypes were distributed into the pit of each block of the prepared layout of the experiment. The thirty-one genotypes of the experiment were assigned at random into pits of each replication. The distance maintained spacing pit to pit 3 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 with soil for higher germination and transplanted in the main field in the pit. Pits of 55 cm × 55 cm × 45 cm were prepared in each plot with a spacing of 3 m × 1 m. To control field cricket (*Gryllus sp.)* 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 cow dung, urea, TSP and MOP applied @ 10 t ha^{-1}, 125 kg ha^{-1}, 125 kg ha^{-1} and 150 kg ha^{-1}, respectively to the plots for bottle gourd cultivation. Total cow dung, half of TSP and one-third MOP were applied in the field during final land preparation. Remaining TSP, one-third MOP, 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 (DAT). Germination of seeds was completed within 12 days and the seedlings of different accessions were planted in the pit. The standard agronomic inter-cultural operations were done from time to time throughout the cropping season for proper growth and development of the plants. In mature stage fruit fly (*Bactrocera cucurbitae*) causes severe damage to the fruit. For protection from fruit fly, MSGT (Mashed Sweet Gourd Trap) and pheromone bait were used along with ripcord, sevin powder. Fruits were picked based on horticultural maturity, size, color and age being determined for consumption as the fruit. Fruits were picked with sharp knife and care was taken to avoid injury of the vine.

Observations were recorded on the parameters such as days to first male flowering, days to first female flowering, number of branches $vine^{-1}$, leaf length, leaf breadth (cm), leaf petiole length (cm), inter-nodes distance (cm), male flower pedicel length (cm), female flower pedicel length (cm), number of male flowers, number of female flowers, ratio of male and female flowers, fruit length (inch), fruit breadth (inch), number of fruit $plant^{-1}$, weight $fruit^{-1}$ (kg) and yield $plant^{-1}$ (kg). Mean data of the characters were subjected to multivariate analysis.

Multivariate analysis was done 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 data obtained on above 17 characters was used for cluster analysis and investigated to select the parents for hybridization using Mahalanobis (1936) D^2 statistics [5]. The genetic diversity among the genotypes was assessed by Mahalanobis's general distance (D^2) statistic and its auxiliary analyses. The genotypes were grouped into different clusters by Tocher's method [6].. The population was arranged in order of their relative distances from each other.

III. Results and Discussion

1. Clustering of Bottle gourd genotypes

Thirty-one (31) genotypes of bottle gourd were grouped into five clusters through cluster analysis. This indicated the existence of genetic diversity among the genotypes. The distribution pattern indicated that the highest number (10) of genotypes were included in cluster II whereas the lowest (2) were in cluster I (**Table 2**).

Table 2: Distribution of 31 bottle gourd genotypes in five clusters

Cluster	Number of genotypes	Designation
I	2	BD-4577, BD-4580
II	10	BD-4578, BD-4581, BD-4584, BD-585, BD-4600, BD-4602, BD-4604, BD-4603, BD-8988, BD-4559
III	6	BD-4596, BD-4605, BD-4599, BD-4601, BD-8948, BD-8949
IV	8	BD-4579, BD-4583, BD-4582, BD-4597, BD-4598, BD-8965, BD-4561, BD-8950
V	5	BD-4569, BD-8987, BD-4558, BD-4560, BD-8966

Quamruzzaman et al. studied 17 genotypes of bottle gourd and grouped them into four clusters [7]. Gaffar et al. grouped 15 sponge gourds into five clusters [8]. It was also observed from the distribution pattern that the geographic divergence did not follow the same trend as the genotypes within the same cluster originated from different countries. Murty and Arunachalam reported that the geographic distribution and genetic diversity were not directly related [9].

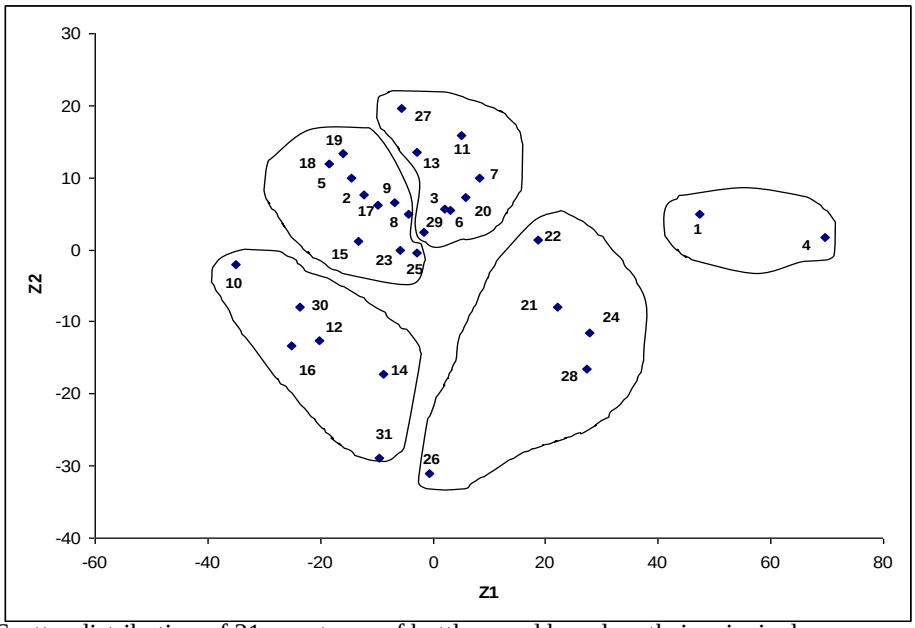

Figure 1. Scatter distribution of 31 genotypes of bottle gourd based on their principal component scores superimposed with clusters

The scatter distribution of 31 genotypes of bottle gourd based on their principal component scores superimposed with clusters was shown in Fig 1. The mean values of the first two vectors for the 31 genotypes were plotted on a two-dimensional graph and the D2 value superimposed over it.

2. Cluster (inter and intra) distances

Average inter and intra-cluster distances were calculated (**Table 3**) by using the formula as suggested by Singh and Chuadhury [10]. It was 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.

Table 3. Average intra and inter-cluster distances (D^2) for 31 bottle gourd genotypes

Cluster	I	II	III	IV	V
I	1.12*				
II	18.34	1.33*			
III	23.65	7.17	1.15*		
IV	16.64	6.16	11.57	1.21*	
V	17.50	6.65	9.99	8.97	1.27*

*Intra-cluster distance

The highest inter-cluster distance was observed between I and III (23.65), while the lowest distance was observed between the cluster II and IV (6.16). Cluster II (1.33) exhibited the highest intra-cluster distance, while the lowest distance was observed in cluster I (1.12). Besides, the intra cluster distance for cluster I, II, III, IV and V was 1.12, 1.33, 1.15, 1.21 and 1.27, respectively.

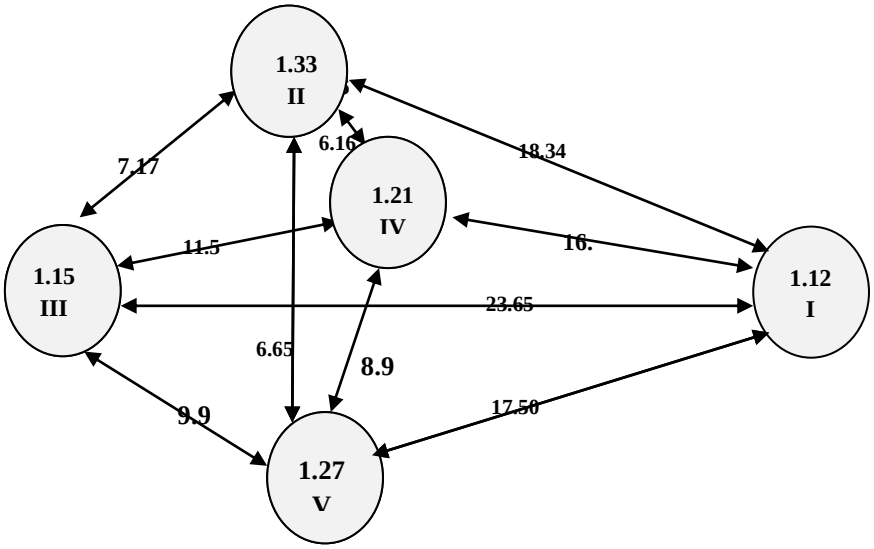

Figure 2. Cluster diagram showing intra and inter-cluster distances of 31 genotypes of bottle gourd

In the present study, it was observed that cluster III was highly diverge. So, 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 got segregants with wider variations among the genotypes in Niger from the crossing between the clusters involving the parents which belonged to distant clusters [11]. It is expected that the crosses between the clusters I and III would exhibit higher heterosis and also likely to produce new recombinants with desired traits. Somayajullu et al. reported that clustering revealed instability due to relatively lesser divergence, whereas widely divergent clusters remained distinct in different environments [12]. These results are in general agreement with the findings of Singh et al. [13] and Bhardwaj et al. [14].

3.Mean performance of clusters

The mean performance for different clusters of genotypes for fruit yield and its components are presented in Table **4.** Total 18 characters were considered for calculating the cluster mean of 31 genotypes of bottle gourd. The data of cluster means for all the characters showed appreciable differences.

Table 4. Cluster mean of 18 characters of 31 bottle gourd genotypes

No.	Character	I	II	III	IV	V
1	Days of first male flowering	58.00	73.30	**83.50**	75.79	66.20
2	Days of first female flowering	66.50	87.70	**101.67**	77.67	74.00
3	Number of branches vine^{-1}	9.00	8.83	11.83	10.50	**17.50**
4	Leaf length (cm)	19.98	17.42	16.15	20.09	**21.57**
5	Leaf breadth (cm)	26.75	20.72	21.49	24.13	26.13
6	Leaf petiole length (cm)	13.00	10.60	11.17	12.62	**14.40**
7	Inter-nodes distance (cm)	10.00	**11.25**	8.71	9.04	8.82
8	Male flower pedicel length (cm)	4.00	6.05	6.21	4.57	**6.59**
9	Female flower pedicel length (cm)	**20.00**	17.84	16.18	19.02	17.59
10	Number of male flowers	**91.34**	27.90	26.28	37.83	49.00
11	Number of female flowers	**29.00**	17.03	16.33	17.71	27.40

12	Ratio of male and female flowers	**3.18**	1.68	1.64	2.26	1.83
13	Number of fruits plant^{-1}	8.50	8.70	13.00	7.87	**15.60**
14	Fruit weight (kg)	2.30	1.85	**2.38**	1.70	2.20
15	Fruit length (inch)	9.03	11.92	**14.40**	12.53	11.48
16	Fruit breadth (inch)	18.51	17.12	15.46	14.98	**18.85**
17	Fruit peduncle length (inch)	4.27	5.00	**5.33**	4.91	4.68
18	Yield plant^{-1} (kg)	19.20	15.89	31.47	13.49	**34.75**

The highest mean values are **bolded**, and the lowest mean values are underlined.

The result revealed that cluster V had the highest mean value for the characters such as number of branches vine^{-1}, leaf length, leaf petiole length, male flower pedicel length, number of fruit plant^{-1}, fruit breadth, and yield plant^{-1}. Cluster III had the highest mean value for the characters such as days to first male flowering, days to first female flowering, fruit weight, fruit length and fruit peduncle length. The highest intra-cluster mean for important yield contributing characters were obtained from cluster III. Cluster I had the lowest mean value for the characters days to first male flowering, days to first female flowering, and the highest mean value for the characters number of male and female flowers, ratio of male and female flowers. The most divergence group means were found for days to first male flowering between cluster I and III, days to first female flowering between cluster I and III, number of branches vine^{-1} between cluster II and V, number of fruit plant^{-1} between cluster IV and V, fruit weight between cluster III and IV, fruit length between cluster I and III, fruit diameter between cluster IV and V, and yield plant^{-1} (kg) between cluster IV and V (**Table 4**). The better genotypes can be selected for most of characters on the basis of mean performance in the cluster.

4. Contribution of the characters towards divergence

The Canonical Vector Analysis (CVA) revealed that in vector I, days to first male flowering, days to first female flowering, inter-nodes distance, male flower pedicel length, fruit length and fruit peduncle length were positive. Days to first male flowering, days to first female flowering, number of branches vine^{-1}, leaf breadth, male flower pedicel length, number of female flower, number of fruit plant^{-1}, fruit weight, fruit length, fruit width, fruit peduncle length and yield plant^{-1} were positive in case of vector II. Such results indicated that these characters contributed maximum towards divergence (**Table 5**). 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 bottle gourd genotypes.

Table 5: Latent vectors for 18 principal component characters of 31 genotypes of bottle gourd

Character	Vector I	Vector II
Days of first male flowering	0.3785	0.0279
Days of first female flowering	0.3649	0.1008
Number of branches vine^{-1}	-0.1321	0.3340
Leaf length (cm)	-0.3303	-0.0269
Leaf breadth (cm)	-0.3406	0.0457
Leaf petiole length (cm)	-0.2652	-0.0008
Inter-nodes distance (cm)	0.0478	-0.1035
Male flower pedicel length (cm)	0.0719	0.1770
Female flower pedicel length (cm)	-0.1465	-0.2952
Number of male flowers	-0.3886	-0.0703
Number of female flowers	-0.3298	0.0847
Ratio of male and female flowers	-0.2272	-0.1918
Number of fruit plant^{-1}	-0.1036	0.5048
Fruit weight (kg)	-0.0202	0.3610
Fruit length (inch)	0.2003	0.0996
Fruit breadth (inch)	-0.1065	0.1345
Fruit peduncle length (inch)	0.0467	0.0540
Yield plant^{-1} (kg)	-0.0743	0.5296

IV. Conclusion

Findings of the present study indicated significant variation among the genotypes for all the character studied. The D2 values recorded for 31 genotypes indicated the presence of appreciable amount of genetic diversity among the genotypes. Considering diversity pattern and other field performances, the genotypes G_{28} (BD-4569), G_{26} (BD-4560) from cluster V, G_{31} (BD-8948) from cluster III and G_4 (BD-4580) from cluster I could be best choice as suitable parents for efficient hybridization programme. The inter genotypic crosses between G_4 (BD-4580) & G_{31} (BD-8948); G_4 (BD-4580) & G_{28} (BD-4569); G_4 (BD-4580) & G_{26} (BD-4560); G_{31} (BD-8948) & G_{28} (BD-4569), and G_{31} (BD-8948) & G_{26} (BD-4560) might be suitable choice for future hybridization programme.

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