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GENETIC DIVERGENCE IN COMMERCIAL CUCUMBER (*CUCUMIS SATIVUS* L.) GENOTYPES

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Abstract

Genetic diversity in commercial cucumber genotypes was estimated based on 13 characters. Path analysis revealed that fruits/plant (0.701**)** and fruit weight (0.379) had maximum positive direct effect on yield. Seven cucumber genotypes were grouped into three different clusters. The highest inter-cluster distance (4.078) was observed between cluster I and II whereas lowest inter-cluster distance (1.011) was observed between the clusters I and III. Cluster II showed highest mean for length of main vine, nodes/plant, primary branches/plant, days to 1st male flowering, length of internodes/plant, fruits/plant and yield/plant whereas cluster III produced highest mean for leaf length, leaf breadth, fruit length, fruit diameter and fruit weight. Cluster II and III contributed 53.85 and 38.46%, respectively towards divergence.

Introduction

Cucumber (*Cucumis sativus* L.) commonly known as ‘Shosha’ is one of the most important vegetables belonging to family Cucurbitaceae consumed as a salad (Arankumar *et al.* 2011). Cucumber cultivation goes back to at least 3000 years in India and 2000 years in China (Robinson and Decker-Walters 1997). The crop is grown throughout the world and is the fourth most important vegetable crop after tomato, cabbage, and onion (Tatlioglu 1993). It has tremendous economic and dietic importance. It is a good source of water, minerals, carbohydrates, protein, lipid, ion and vitamin in human diet (Rashid 1999). Demand of cucumber as cooling vegetables is increasing day by day. Everyone is fond of eating this vegetable as raw for refreshment, especially as salad with fast food (Reshma 2011).

In Bangladesh, the yield of cucumber is very low due to lack of high yielding varieties. The total production of cucumber in Bangladesh was about 48,000 metric tons from 19,000 acres during 2010-2011 (BBS 2011). So, intensive research efforts are needed in several areas, particularly, selection of superior genotypes. For an effective breeding program, information concerning the extent and nature of genetic diversity within a crop species is essential. Better knowledge on genetic diversity or genetic similarity could help to sustain long term selection gain in plants (Chowdhury *et al*. 2002). Very few research work relating to diversity of cucumber have been conducted in Bangladesh (Hossain *et al.* 2010). In view of these facts, the present investigation was undertaken to evaluate the potentiality of existing market germplasm of cucumber through the studies of genetic divergence and path analysis.

Materials and Methods

The investigation was conducted during February - May, 2013 at Botanical Garden of Jahangirnagar University, Savar, Dhaka, Bangladesh. The experimental site was at 23° 52' 27.76" north latitude, 90° 16' 5.16" east longitudes, with an altitude of 13.716 m above the sea level.

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Adequate soil fertility was ensured by applying additional quantities of FYM- N-P- K- @ 25-30-50-80kg/ha, respectively. The pit unit was 4 × 4 feet maintaining a plant spacing of 1 × 1 feet. A distance of two feet in the form of drain was maintained between the block and between the plots within a block. The genotypes named Shila, Myabi, Green top, Shufola-1, Green master, Shosa baromasi, Super-1 were used as experimental materials. Data were collected from 3 randomly selected plants basis for length of main vine (cm), no. of nodes/plant, leaf length (cm), leaf breadth (cm), no. of primary branch, days to 1st male flowering, days to 1st female flowering, length of inter node (cm), fruit length (cm), fruit diameter (cm), fruit weight (gm), no. of fruits/plant, yield/plant (gm). Path analysis has been done using programming software R-3.1.1. Mean data of each character was subjected to multivariate analysis *viz.* principal coordinate analysis (PCO), principal component analysis (PCA), cluster analysis, and canonical variate analysis using GENSTAT 5.13 (Mahalanobis 1936, Digby *et al.* 1989).

Results and Discussion

The interrelationships among different traits along direct and indirect effects were worked out using path coefficient analysis in respect to yield. Path coefficient analysis revealed the causes and effects of chain relationships of different yield contributing characters with yield. The estimates of direct effects of these characters on yield based on genotypic correlation are presented in Fig. 1. Path coefficient analysis showed that number of fruits/plant had maximum positive direct effect (0.701**)** on yield/plant (Fig. 1). Similar result was obtained by Hossain *et al.* (2010), Rao *et al.* (2004), Arunkumar *et al.* (2011) and Golabadi *et al.* (2013). Length of main vine (0.045), nodes/plant (0.006), leaf length (0.063), fruit length (0.020), fruit diameter (0.066) and fruit weight (0.379) also showed positive direct effect upon yield. The direct effect of above mentioned characters were negligible except number of fruits/plant and fruit weight as in comparison to correlation with yield. It is suggested that selection of these two characters would give better response for yield improvement.

After computing D^2 values for all the possible pairs, 7 genotypes were grouped into 3 clusters, which indicated a considerable genetic diversity (Table 1). The clustering pattern of different genotypes did not follow their geographical distribution and was fairly at random. This suggested that the materials of same origin into different clusters were an indication of broad genetic base of the genotypes. Prasad *et al.* (2001) reported the similar result when they studied 60 inbreed lines of cucumber.

Based on PCA score I, II and III a three dimensional scattered diagram was developed where the positions of 7 genotypes were apparently distributed into three groups (Fig. 2). Inter-genotypic distance (D^2) was obtained from principal coordinate analysis for all possible combinations among genotypes. The highest inter-genotype distance (2.6164) was observed between Sufoa-1 and Mayabi followed by (2.0299) and (1.7773) distance observed between Sufoa-1 and Shila and between Sufoa-1 and Green top, respectively (Fig. 3). The lowest distance (0.3337) was observed between Shila and Green top followed by the distance (0.44) was observed between the Green master and Super-1. The highest inter genotypic distance indicated the presence of dissimilarity among the concerned genotypes of cucumber.

Maximum numbers of genotypes were accommodated in clusters I and III comprising 3 genotypes while cluster II containing single genotype (Table 1). Intra-cluster distance revealed that, cluster I showed maximum intra-cluster distance (0.165) followed by cluster III (0.142) but cluster II (0.00) showed no intra-cluster distance due to solitary genotype. Based on distance between clusters, the inter cluster D^2 values also ranged from 1.011 to 4.708 (Table 2). The inter-cluster distances were larger than the intra-cluster distances which indicated wider genetic diversity among the genotypes of different groups. Clusters I and II were strikingly diverse from rest of the clusters, the divergence between these two clusters was high as evident from their high

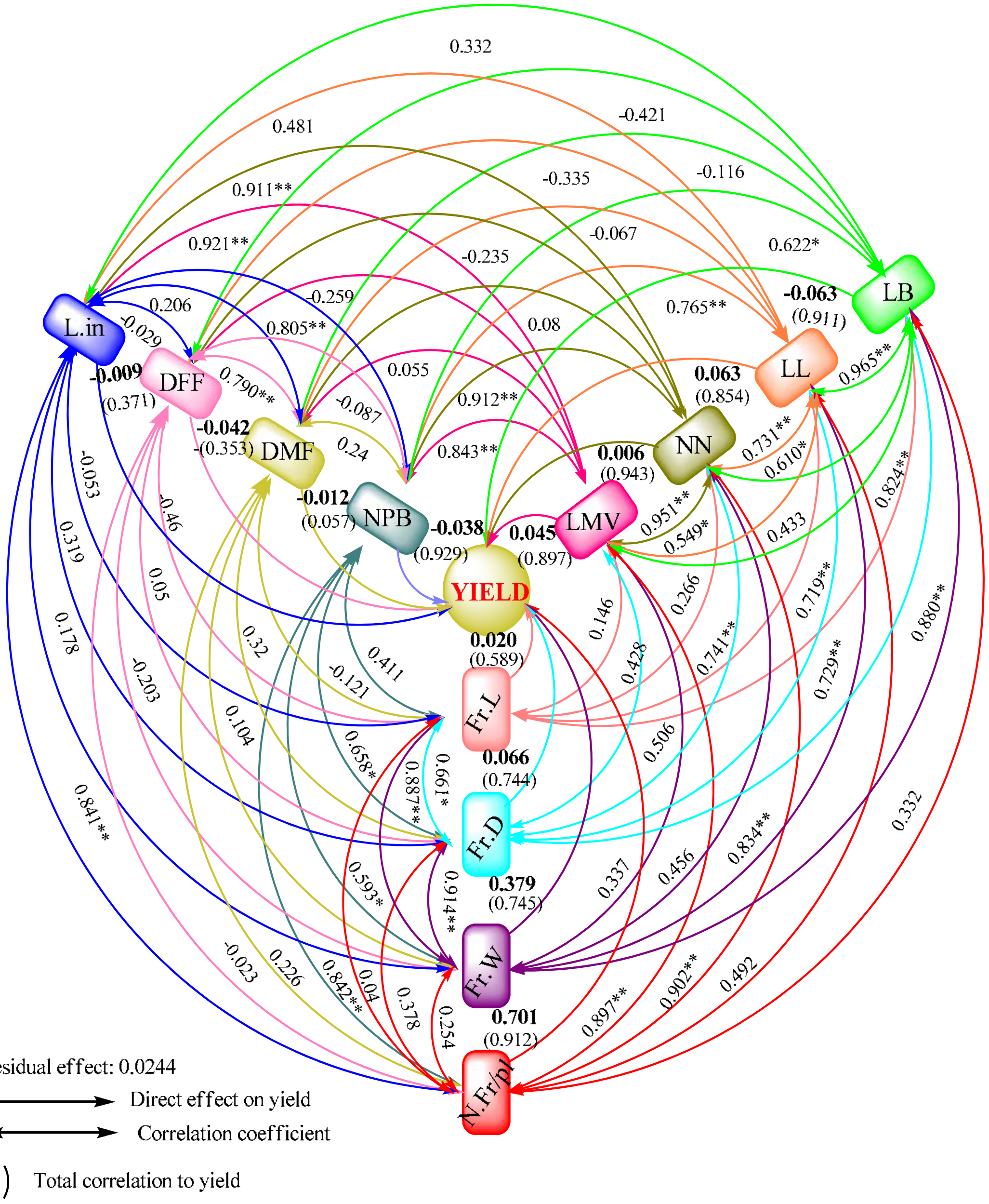

Fig. 1. Path diagram of different yield contributing characters on yield per plant at genotypic level.

LMV = Length of main vine, NN = No. of nodes, LL = Leaf length, LB = Leaf breadth, NPB = No. of primary branch, DMF = Days to 1st male flowering, DFF = Days to 1st female flowering, L. In = Length of internodes, Fr. L = Fruit length, Fr. D = Fruit diameter, Fr. W = Fruit weight, N.Fr/Pl = No. of fruits/plant. ** = Significant at 1% level of probability and * = Significant at 5% level of probability.

inter cluster D^2 value (4.078). Therefore, the genotypes belonging to these clusters were genetically more divergent which suggested intercrossing the genotypes from these two clusters may generate wider variability and is expected to throw high yielding transgressive segregants in improvement programme. The minimum inter-cluster D^2 value (1.011) observed between clusters I and III indicated that genotypes of these two clusters were more or less genetically same. Similar finding was reported by Rao *et al*. (2003).

Table 1. Distribution of different cucumber genotypes.

Cluster	No. of genotypes	Name of the genotype
I	3	Shila, Mayabi, Green top
II	1	Shufola-1
III	3	Green master, Shosa baromasi, Super-1

Table 2. Average intra (bold) and inter-cluster distance (D^2) for cucumber genotypes.

Cluster	I	II	III
I	**0.165**		
II	4.708	**0.000**	
III	1.011	1.941	**0.142**

Character wise mean were estimated for all the genotypes spread over three clusters (Table 3). Among the 13 characters the following characters such as; length of main vine, nodes/plant, primary branches/plant, fruit weight, fruits/plant and yield/plant were considered as superior characters based on maximum range of variability observed in different cluster mean (Table 3). Cluster I showed lowest mean value for almost all the characters except one character (Days to 1st female flowering) indicating selection of parental lines from this cluster for future hybrid cucumber breeding programme is ineffective.

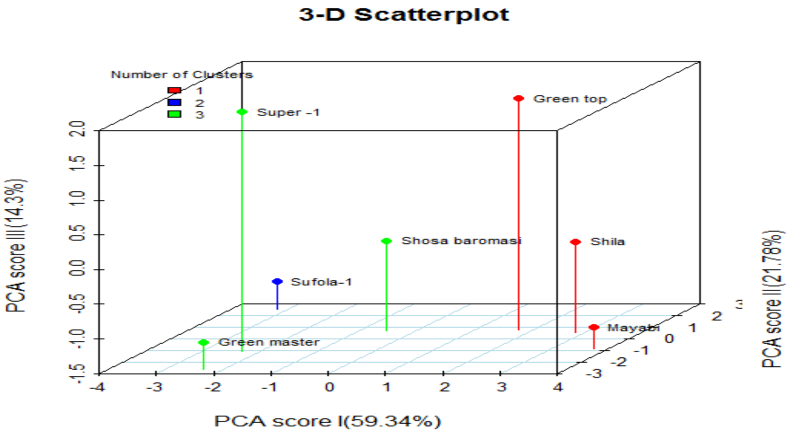

Fig. 2. Three dimensional scattered diagram based on three PCA scores showing the distribution of different genotypes.

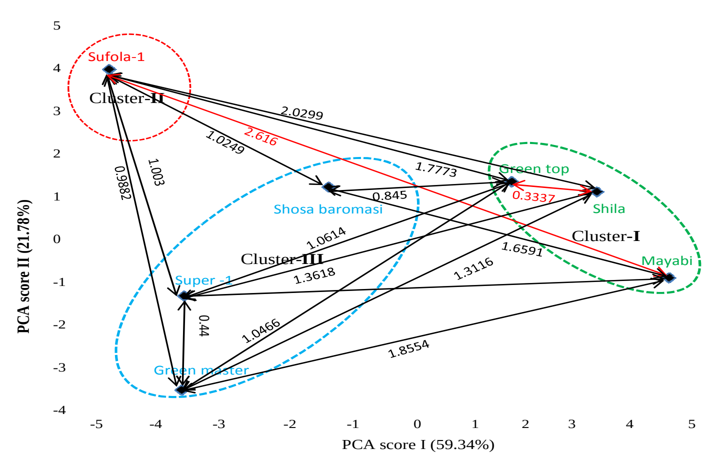

Fig. 3. Inter-genotypic distance (D^2) of different genotypes based on principal coordinate analysis.

Cluster II contained highest mean value for 7 characters and cluster III showed highest mean value for 5 characters, hence, they contributed 53.85 and 38.46% (Table 3) respectively, towards divergence that refers possession of superior characters in these clusters in respect of yield which also indicated the presence of most promising genotypes available in these clusters. Considering the magnitude of genetic distance, character contribution towards divergence and cluster mean for different characters performance, the genotypes Sufola-1, Green master, Shosa baromasi and Super-1 could be selected effectively for further breeding programme (Table 4).

Table 3. Cluster mean for various characters of cucumber genotypes.

Characters	Cluster I	Cluster II	Cluster III	Contribution towards divergence (%)
Length of main vine (cm)	287.9	918.6*	490.6	0
Nodes/plant	24.5	66.4*	46.4	0
Leaf length (cm)	12.3	14.1	15.1*	0
Leaf breadth (cm)	13.7	15.7	18.2*	0
Primary branch	2.5	7.1*	5.3	0
Days to 1st male flowering	37	37.3*	36.8	0
Days to 1st female flowering	48.4*	46.7	46.8	0
Length of inter-node (cm)	10.9	14.4*	12.1	0
Fruit length (cm)	18.9	19.1	21*	0
Fruit diameter (cm)	16.9	18.3	19.1*	14.29
Fruit weight (g)	281.9	310.3	362.5*	0
Fruit /plant	5.1	11.6*	7.3	47.61
Yield/plant (g)	1453.3	3585*	2653.3	38.10
Contribution (%)	7.69	53.85	38.46	100

*= Highest mean value.

Table 4. Finally selected cucumber genotypes for important traits.

Sl. No.	Selection traits	Genotypes	Cluster	Mean value
1	Length of main vine (cm)	Sufola-1	II	918.6
2	Primary branches/plant	Sufola-1	II	7.1
3	Fruit weight (g)	Green master, Shosa baromasi, Super-1	III	362.5
4	Fruit diameter (cm)	Green master, Shosa baromasi, Super-1	III	19.1
5	Fruits/plant	Sufola-1	II	11.6
6	Yield/plant (g)	Sufola-1	II	3585

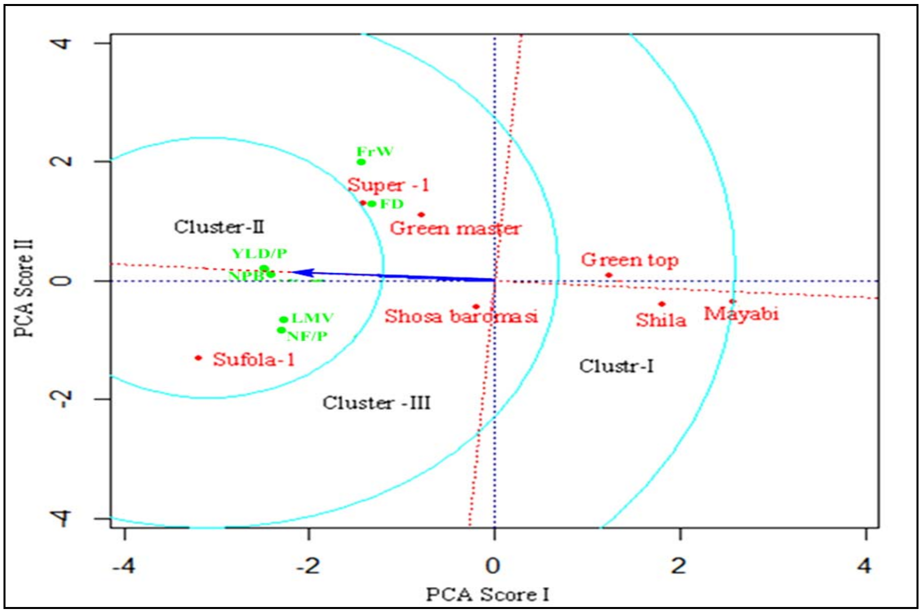

Fig. 4. Ranking of cucumber genotypes having important characters.

LMV = Length of main vine, NPB = No. of primary branch, NF/Pl = No. of fruits/plant, Fr.W = Fruit weight, FD = Fruit diameter, YLD/P = Yield/plant.

Genotypes were ranked using biplot method (Fig. 4). A genotype is ideal if it is located at the center of the concentric circles and closer to the line passing through the biplot origin called the indicator of superiority (blue line) which is defined by the average PCA scores I and II of the selected characters. Therefore, Sufola-1 was more reliable followed by Super-1, Green master and Shosa baromasi. These genotypes can be developed as parental line for further breeding programme.

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