

Parental Diversity Study in Cucumber

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Abstract

The present experiment was undertaken to study the parental diversity in 39 (19 parents and 20 F₁s) cucumber genotypes. Among the genotypes, all of them are monoecious in flowering habit. Considerable coefficient of variation were estimated for branches per plant, flesh thickness, placental thickness, fruit length, fruit width, male & female flowers per plant, leaf length, leaf breadth, vine length, fruits per plant, fruit yield per plant indicating the scope of selection for those characters. High Genotypic Coefficient of Variation (GCV) and high heritability coupled with high genetic advance were observed for single fruit weight, fruit length, and vine length. Based on multivariate analysis the 39 genotypes of cucumber were grouped into six clusters. Cluster I comprises 9 genotypes, cluster II had single, cluster III had four, cluster IV had 13 and cluster V and VI had 6 genotypes, respectively. The higher inter cluster distance was between clusters II and VI (38.54) while it was lowest between IV and VI (4.62). The highest and lowest intra cluster distance was displayed in cluster IV (1.386) and cluster II (0.000), respectively. The characters like branches per plant, male and female flowers per plant, fruit length, fruit weight, fruits per plant, fruit yield per plant contributed the maximum variability towards divergence among cucumber genotypes.

Keywords:

Parental Diversity, Genotype, Yield Performance

1. Introduction

Cucumber (*Cucumis sativus* L.) is one of the most popular vegetables of the family Cucurbitaceae (gourd family), with a chromosome number $2n=14$. The cucumber belongs to the genus *Cucumis*, which grown throughout the tropical and subtropical region of the world [1]. Cucumber is one of the important fresh fruit vegetables and salad crops in Bangladesh. Two types of cucumber are found in Bangladesh – One is known as ‘Khira’ available in late winter and other is ‘Shosha’ grown round the year. There are

4.61 thousand ha of land under cultivation in Bangladesh and production is about 49 thousand tons [2]. It is also an ideal summer vegetable crop chiefly grown for its edible tender fruits, preferred salad ingredient, pickles, and desert fruit and as a cooked vegetable. Cucumber contains 0.50 g fibre, 0.65 g protein, 14.3 kilo calories, 16 mg Ca, 24 mg P, 13 mg Mg and 147 mg K per 100 gm of edible portion. It also contains Vitamin B (B1-0.027 mg and B6-0.040 mg per 100 g of edible portion and a considerable amount of Niacin and Vitamin-C [3]. Although cucumber is not rich in nutrient contents, yet it is considerable as a good source of nutrients for human body as it is mostly taken without cooking. Cucumber has some therapeutic properties as well as its leaves and seeds contain cucurbitacin B and C [4] which is used for treating different ailments. It is also consumed by diabetic patients and known as fat reducing food. It is ideal for suffering from jaundice and allied diseases and very much useful in preventing constipation. Seeds contain oil, which is helpful for brain development and body smoothness. Hence, it is being used in Ayurvedic preparations [5]. The major limitations of increasing yield are related to the lack of genetic variability in the cucumber accessions. The lack of process to increase fruit of cucumber might be partially due to the major breeding effort relative to the other crop or lack of variability for yield [6]. Transfer of quantitatively inherited characters into commercially adapted cultivars from exotic germplasm can be an effective way to obtain greater genetic variation and response to selection. Precise information on the nature and degree of genetic divergence of the parents is the prerequisite for variety development program. The importance of genetic diversity in the improvement of a crop has been stressed in both self and cross-pollinated crop [7,8,9]. Genetic variability with respect to genetic diversity has been considered as an important factor which is also an essential prerequisite for crop improvement program for obtaining high yielding progenies. Based on the information, the present study was undertaken to estimate the parental diversity and character association in crosses, obtained from 19 diverse-cucumber parental lines.

2. Materials and Methods

A total of 19 genotypes of cucumber representing samples of different districts of the country, namely Piyas, Yuvraj, Himaloy, Shilla, Hreo, Modhumoti, Baromashi, Greenboy, Sobujsathi, Tripti, Greenking, Khira, 4307, 4315, 4240, 4239, 4308, 4249 and 4263 were collected from Bangabandhu Sheikh Mujibur Rahman Agricultural University and 20 F1s namely Modhumoti × Tripti, Baromashi × Greenking, Baromashi × Hero, Modhumoti × Baromashi, Modhumoti × Hero, Hero × Piyas, Modhumoti × Khira, Baromashi × Khira, Yuvraj × Khira, Himaloy × Tripti, Himaloy × Yuvraj, Himaloy × Baromashi, Sobujsathi × Khira, Himaloy × Khira, Sobujsathi × Baromashi, Greenboy × Tripti, Hreo × Khira, Hero × Tripti, Tripti × Khira and Shilla × Khira were used in this experiment. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications at the experimental field, Department of Genetics and Plant Breeding, Bangabandhu Sheikh & Mujibur Rahman Agricultural University (BSMRAU), Salna, Gazipur during the summer season March 2013 to November 2013 on an upland soil. Seeds of cucumber were sown in 10 cm x 5.5 cm earthen poly-bag. The unit plot size was 7.5 m x 1.2 m accommodating 5 plants in each plot. The pits were dug prior to two weeks of planting in a dimension of 0.5 m x 0.5 m x 0.5 m at spacing of 1.5 m pit to pit. The treatments were randomly assigned to different plots of each block separately. The healthy seedling of 20 days old was transplanted in the pit of the

experimental field. All the recommended agronomic practices WERE adopted to ensure a good crop. Data were recorded as per IBPGR (International Board of Plant Genetic Resources) descriptors on following qualitative characters: Grow of the main stem, Flowering habit, Leaf shape, Leaf color, Flower color, Fruit shape, Fruit skin color and Quantitative characters: Days to first male flowering, Days to first female flowering, Male flowers per plant, Female flowers per plant, Days to 50% male flowering (staminate flowers), Days to 50% female flowering (pistillate flowers), Leaf length (cm), Leaf width (cm), Petiole length (cm), Branches per plant, Vine length, Fruit length (cm), Fruit diameter (cm), Fruit weight (g), Flesh thickness (cm), Placental thickness (cm), Fruits per plant, Yield per plant (gm), 1000 seed weight (g) (dried seed). The collected data were statistically analyzed. The mean, range and standard deviation (σ_x) for each character have been calculated and analysis of variance for each of the character was performed. Genotypic means were compared by Duncan's Multiple Range Test (DMRT) and coefficient of variation (CV %) were also estimated as suggested by [10]. The mean square (MS) at error and phenotypic variances were estimated as per [11].

3. Results and Discussion

Performance of 39 genotypes (19 parents and 20 crosses) of cucumber was investigated and the findings of the present study have been discussed character wise under separate headings. The results of the study showed marked variation in different characters are presented in Table 2 to Table 8 and Figure 1 to 2.

3.1. Morphological Characteristics

Among the 39 genotypes (19 parents and 20 crosses) 27 were indeterminate and 12 was dwarf type plant (Table 1&2). In case of leaf shape 39 genotypes was sharp pentagonal (Table 1&2). Three distinct different types of leaf color were found, namely, green (18), dark green (20) and light green (1). All genotypes were monoecious in flowering habit and flower color was yellow. Two types of fruits viz. cylindrical and elliptical were found among the genotypes and 32 genotypes produced cylindrical, 7 elliptical. There were six types of fruit skin color observed in the germplasm. These were green, light green, brown, yellow, white, cream. Six genotypes were fallen in the group green, 13 were light green, 10 were brown, 4 were cream, and 5 were yellow, only one was in the white group. There were four types (brown, black and white) of fruit spine color observed among the germplasm and categorized 24 genotypes were white spine, 11 black, and 4 brown. Stem end of the fruits were categorized into rounded, flattened, pointed and 31, 6 and 2 genotypes, respectively were fallen in the above-mentioned group.

Based on leaf, flower and fruit characteristics, hybrids were rated good. Among the hybrids Modhumoti \times Khira, Himaloy \times Yuvraj, Sobujsathi \times Khira, Modhumoti \times Baromashi, Sobujsathi \times Baromashi, Shilla \times Khira were found very good.

3.2. Analysis of Variance

The analysis of variance (Table 3) of different yield edits compound characters of 39 cucumber genotypes revealed highly significant difference among the genotypes.

Table 1. Morphological characteristics of parental lines of cucumber.

Parents	Plant Type	Leaf shape	Leaf color	Fruit shape	Fruit skin color	Fruit skin mottling	Stemend fruitshap e	Fruit spine color	Flowe rcolor	Flowe ring habit	Male sterility
Piyas	Indeter minate	Sharp pentag onal	Green	Cylind rical	Brown	Absent	Round	Black	Yello w	Mono ecious	Absent
Yuvraj	Semi dwarf	Sharp pentag onal	Green	Cylind rical	White	Absent	Flattened	White	Yello w	Mono ecious	Absent
Himaloy	Semi dwarf	Sharp pentag onal	Green	Cylind rical	Light green	Absent	Pointed	White	Yello w	Mono ecious	Absent
Shilla	Indeter minate	Sharp pentag onal	Dark green	Cylind rical	Light green	Absent	Round	Brown	Yello w	Mono ecious	Absent
Hero	Indeter minate	Sharp pentag onal	Green	Cylind rical	Light green	Absent	Round	White	Yello w	Mono ecious	Absent
Modhu moti	Semi dwarf	Sharp pentag onal	Dark green	Ellipti cal	Light green	Absent	Round	White	Yello w	Mono ecious	Absent
Baroma shi	Indeter minate	Sharp pentag onal	Dark green	Cylind rical	Brown	Present	Round	Black	Yello w	Mono ecious	Absent
Greenbo y	Semi dwarf	Sharp pentag onal	Light green	Ellipti cal	Cream	Absent	Flattened	White	Yello w	Mono ecious	Absent
Sobujsat hi	Indeter minate	Sharp pentag onal	Dark green	Cylind rical	Green	Absent	Round	White	Yello w	Mono ecious	Absent
Tripti	Indeter minate	Sharp pentag onal	Green	Cylind rical	Yello w	Absent	Flattened	Black	Yello w	Mono ecious	Absent
Greenki ng	Indeter minate	Sharp pentag onal	Green	Cylind rical	Light green	Absent	Round	White	Yello w	Mono ecious	Absent
Khira	Semi dwarf	Sharp pentag onal	Green	Cylind rical	Brown	Present	Round	Black	Yello w	Mono ecious	Absent
4307	Semi dwarf	Sharp pentag onal	Green	Ellipti cal	Green	Absent	Round	White	Yello w	Mono ecious	Absent
4315	Indeter minate	Sharp pentag onal	Dark green	Cylind rical	Brown	Present	Round	Black	Yello w	Mono ecious	Absent
4240	Indeter minate	Sharp pentag onal	Dark green	Cylind rical	Light green	Absent	Round	Brown	Yello w	Mono ecious	Absent
4239	Indeter minate	Sharp pentag onal	Green	Cylind rical	Yello w	Absent	Round	White	Yello w	Mono ecious	Absent
4308	Indeter minate	Sharp pentag onal	Dark green	Cylind rical	Cream	Absent	Round	Brown	Yello w	Mono ecious	Absent
4249	Indeter minate	Sharp pentag onal	Dark green	Cylind rical	Light green	Absent	Round	White	Yello w	Mono ecious	Absent
4263	Indeter minate	Sharp pentag onal	Dark green	Cylind rical	Green	Absent	Round	White	Yello w	Mono ecious	Absent

Table 2. Morphological characteristics of F1 s hybrids of cucumber.

Crosses	Plant Type	Leaf shape	Leaf color	Fruit shape	Fruit skin color	Fruit skin mottling	Stem end fruit shape	Fruit spine color	Flower color	Flowering habit	Male sterility
Modhu moti × Tripti	Indeterminate	Sharp pentagonal	Green	Cylindrical	Green	Absent	Round	White	Yellow	Monoecious	Absent
Baromashi × Greenking	Indeterminate	Sharp pentagonal	Dark Green	Cylindrical	Brown	Present	Round	Black	Yellow	Monoecious	Absent
Baromashi × Hero	Indeterminate	Sharp pentagonal	Green	Cylindrical	Brown	Present	Round	Black	Yellow	Monoecious	Absent
Modhu moti × Baromashi	Indeterminate	Sharp pentagonal	Dark green	Cylindrical	Brown	Present	Round	Brown	Yellow	Monoecious	Absent
Modhu moti × Hero	Semi dwarf	Sharp pentagonal	Green	Elliptical	Light green	Absent	Round	White	Yellow	Monoecious	Absent
Hero × Piyas	Semi dwarf	Sharp pentagonal	Green	Cylindrical	Light green	Absent	Round	White	Yellow	Monoecious	Absent
Modhu moti × Khira	Semi dwarf	Sharp pentagonal	Green	Elliptical	Light green	Absent	Round	White	Yellow	Monoecious	Absent
Baromashi × Khira	Indeterminate	Sharp pentagonal	Dark green	Cylindrical	Brown	Present	Round	Black	Yellow	Monoecious	Absent
Yuvraj × Khira	Semi dwarf	Sharp pentagonal	Green	Cylindrical	Green	Absent	Flattened	White	Yellow	Monoecious	Absent
Himaloy × Tripti	Indeterminate	Sharp pentagonal	Green	Cylindrical	Yellow	Absent	Flattened	Black	Yellow	Monoecious	Absent
Himaloy × Yuvraj	Semi dwarf	Sharp pentagonal	Green	Cylindrical	Cream	Absent	Round	White	Yellow	Monoecious	Absent
Himaloy × Baromashi	Indeterminate	Sharp pentagonal	Dark green	Cylindrical	Brown	Present	Round	Black	Yellow	Monoecious	Absent
Sobhuathi × Khira	Indeterminate	Sharp pentagonal	Dark green	Cylindrical	Green	Absent	Round	White	Yellow	Monoecious	Absent
Himaloy × Khira	Semi dwarf	Sharp pentagonal	Green	Cylindrical	Light green	Absent	Round	White	Yellow	Monoecious	Absent
Sobujathi × Baromashi	Indeterminate	Sharp pentagonal	Dark green	Cylindrical	Brown	Present	Round	Black	Yellow	Monoecious	Absent
Greenboy × Tripti	Indeterminate	Sharp pentagonal	Green	Cylindrical	Cream	Absent	Round	White	Yellow	Monoecious	Absent
Hreo × Khira	Indeterminate	Sharp pentagonal	Dark green	Cylindrical	Light green	Absent	Round	White	Yellow	Monoecious	Absent
Hero × Tripti	Indeterminate	Sharp pentagonal	Dark green	Cylindrical	Yellow	Absent	Round	White	Yellow	Monoecious	Absent

		onal									
Tripti × Khira	Indeterminate	Sharp pentagonal	Dark green	Cylindrical	Yellow	Absent	Round	White	Yellow	Monoecious	Absent
Shila × Khira	Indeterminate	Sharp pentagonal	Dark green	Cylindrical	Light green	Absent	Round	White	Yellow	Monoecious	Absent

Table 3. Analysis of variance for yield and yield related characters in cucumber.

Source of variation	Df	LL	LW	VL	LP	NBPP	DFMF	DFFF	DHMF	DHFF	NMF	NFF
Replication	2	5.16	6.93	2438.32	2.84	1.92	9.21	3.87	8.05	13.62	36.98	26.02
Genotype	38	7.02**	8.09**	6026.92**	5.03**	3.01**	20.03**	1.32*	31.93**	29.43**	51.09**	3.87**
Error	76	1.99	1.74	8.02	1.47	3.35	9.52	37.71	9.03	6.61	81.72	60.32

** & * Significant at 5% and 1% level of probability, respectively; NS- Non Significant

Table 3. Analysis of variance for yield and yield related characters in cucumber (Contd.).

Source of variation	df	FT	PT	FL	FW	NFPP	SFW	YPP	100 SW
Replication	2	27.90	13.75	23.09	6.21	15.94	264.47	8.32	0.92
Genotype	38	31.23**	19.78**	58.13**	8.03**	52.09**	1619.32**	10.42**	1.32**
Error	76	1.92	2.31	4.31	0.65	1.03	27.38	16.5	0.06

** & * Significant at 5% and 1% level of probability, respectively; NS- Non Significant

Note: LL= leaf length, LW= leaf width, VL=Vine length, LP=Length of petiole, NBPP= No. of branches/plants, NMF=Number of male flower, NFF= Number of female flower, DFMF= Days to first male flower, DFFF=Days to first female flower, DHMF=Days to 50% male flowering, DHFF =Days to 50% female flowering , FT = Flesh thickness , PT= Placental thickness, NFPP=No .of fruit/plant, SFW=Single fruit weight , FL=Fruit length, FW=Fruit width , YPP=Yield per plant.

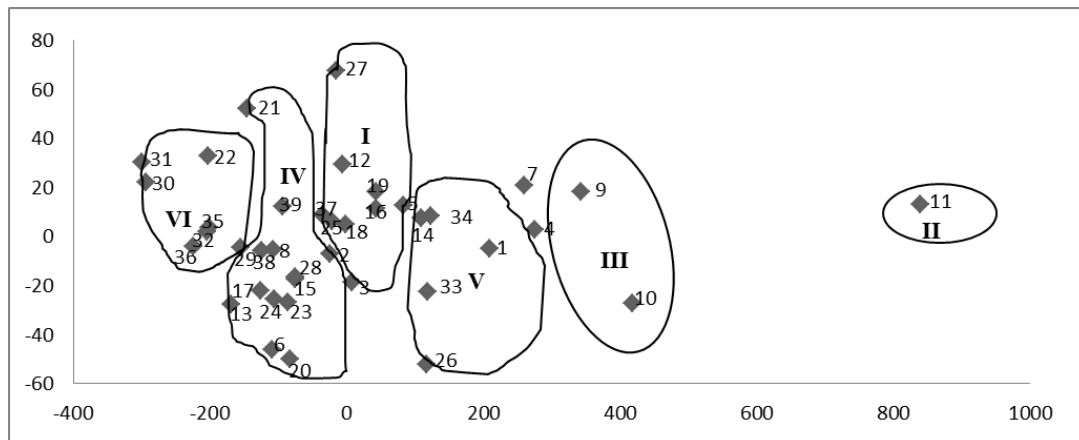


Figure 1. Scatter distribution of 39 genotype of cucumber based on their principal component scores.

3.3. Multivariate Analysis (D2 Statistics)

Principal component analysis (PCA), principal coordinate analysis (PCO), cluster analysis (CLU) and canonical vector analysis (CVA) were done by GENSTAT program. The results of parental diversity in 39 cucumber genotypes are presented in this section.

3.3.1. Principal Component Analysis (PCA)

The principal component analysis yielded Eigen values of each principal component axes of coordination of genotype with the first axes totally accounted for 28.35 % variation among the genotypes, while five of these Eigen values above unity accounted for 74.56 % of the total variation among the 19 characters describing 39 genotypes of cucumber (Table 4).

3.3.2. Construction of Scatter Diagram

Based on the values of principal component scores 1 and 2 obtained from the principal component analysis, a two dimensional scatter diagram (Z1 –Z2) using component score 1 as X-axis and component score 2 as Y-axis was constructed, which have been presented in Fig-1. The position of the genotypes in the scatter diagram was apparently distributed into six groups, which indicated that there exists considerable diversity among the genotypes of cucumber. The scattered diagram for the genotypes of six clusters revealed that the cluster II and cluster VI was distantly located which suggested that the genotypes of these two clusters were more diverged.

3.3.3. Non-hierarchical Clustering

With the application of co-variance matrix for non-hierarchical clustering, 39 cucumber genotypes were grouped into six different clusters (Table 5). 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. Table 5 represents the clusters occupied by 39 genotypes of cucumber. The cluster IV had the maximum (13) number of genotypes, followed by cluster I, V VI and III (9, 6, 6 4 genotypes). The cluster II had 1 genotype. These results confirmed the clustering pattern of the genotype according to the principal component analysis. In clusters I, IV, V, VI, the distribution of hybrids and their parents were observed in the same cluster.

3.3.4. Principal Co-ordinate Analysis (PCO)

Principal coordinate analysis (PCO) was done to calculate the inter-genotypic distances of parents using all the dimensions. From Table 6, it was observed that both P6 and P11 produced considerable distances with other genotypes. The inter- genotypic distances between this two genotypes was high (2.162). The longest inter –genotypic distance (2.282) was observed between P11 and P15.

3.3.4. Canonical Vector Analysis (CVA)

Canonical vector analysis was done to compute the inter-cluster Mahalanobis'sD² values. The intra and inter cluster distance (D²) values are presented in Table 8. Statistical distances represent the index of genetic diversity among the clusters. Results indicated that the highest inter-cluster distance was observed between cluster II and VI (38.54) followed by cluster II and IV (35.70) and cluster I and II (31.30). The lowest

inter-cluster distance was observed between the clusters IV and VI (4.62) followed by cluster I and V (5.17), I and IV (5.33), I and VI (8.03). Moderate inter-cluster distance was observed between cluster V and VI (12.28), I and III (12.77). The maximum values of intra-cluster distance indicated that the genotypes belonging to the cluster II was far diverged from those cluster VI and cluster IV. The genotypes belonging to the distant clusters could be used in hybridization program for obtaining a wide spectrum of variation among segregates. Similar reports were also made by Uddin (2008) and Ali (2011). But the present study revealed that the genotypes, Modhumoti, Greenboy, 4308, 4240, 4309, Modhumoti×Tripti, Baromashi×Greenking, Modhumoti×Baromashi, Modhumoti×Hero, Yuvraj × Khira, Himaloy×Tripti, Tripti × Khira, Shila ×Khira were included in the cluster IV and Baromashi× Hero, Himaloy × Yuvraj, Himaloy × Baromashi, Sobujisathi × Khira, Greenboy × Tripti, Hero × Khira were included in the cluster VI.

These relations were also reflected in the following diagram (Fig 2). The inter-cluster distances were bigger than the intra-cluster distances suggesting wider genetic diversity among the genotypes of different groups. The intra-cluster divergence varied from 0.00 to 1.386. The highest being on cluster IV (1.386) and the lowest on cluster II (0.00) (Table 7).

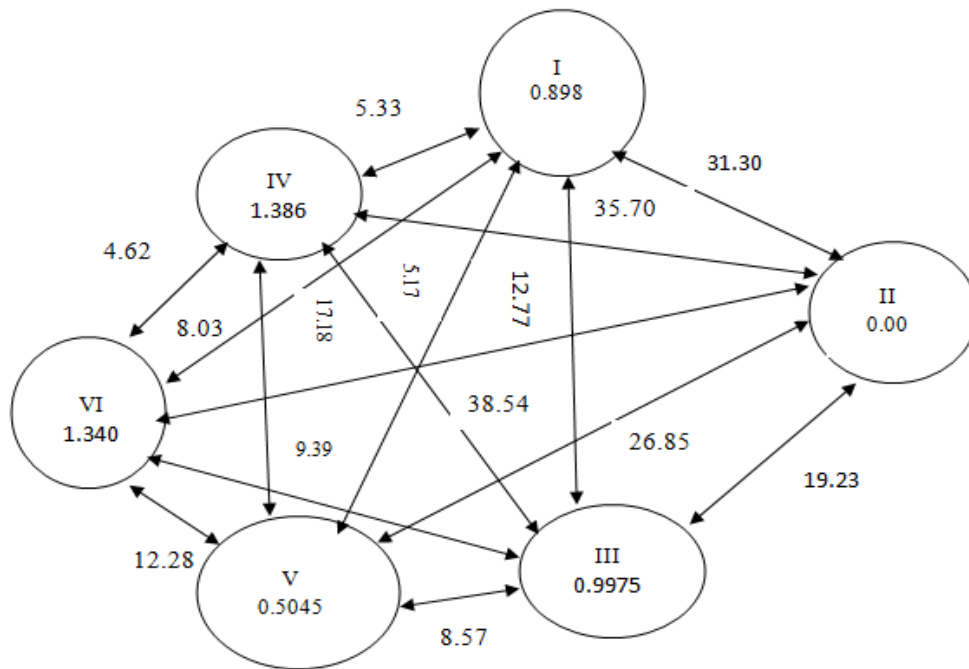


Figure 2. Diagram showing intra-cluster distances of 39 genotypes of cucumber.

3.4. Cluster Mean Value

Mean performances of different genotypes included in different clusters are shown in Table 8. Difference in cluster means existed for almost all the characters. An attempt was made to characterize the individual genotypes in respect of their mean values for different characters with a view to get idea that whether genotypes having similar characteristics

could be disseminated. Cluster I constitute nine genotypes namely Yuvraj, Himaloy, Khira, 4239, 4249, 4263, Hero × Piyas, Baromashi × Khira, Hero × Tripti produces the highest mean value for number of male flower (35.15). Cluster II constituting one genotypes (Greenking) produced the highest mean value for vine length (209.33), length of petiole ((14.00), no. of branches per plant (13.67), no. of female flower (44.33), days to first female flower (12.00), flesh thickness (2.90), placental thickness (4.43), fruit length (35.67), fruit width (8.98), single fruit weight (1246.67) and yield per plant (gm) (1523.00). Cluster III constituting four genotypes (Shilla, Baromashi, Sobujsathi, and Tripti) produced the highest mean value for leaf length (13.87). Cluster IV constituting 13 genotypes (Modhumoti, Greenboy, 4308, 4240, 4309, Modhumoti × Tripti, Baromashi × Greenking, Modhumoti × Baromashi, Modhumoti × Hero, Yuvraj × Khira, Himaloy × Tripti, Tripti × Khira, Shila × Khira) produced the highest mean value for days to first male flowering (32.77), no. of fruit per plant (4.28). Cluster V constituting six genotypes (Piyas, Hero, 4315, Modhumoti × Khira, Himaloy × Khira, Sobujsathi × Baromashi) produced the highest mean value for days to 50% male flowering (37.11) , days to 50% female flowering (47.33), 100 seed weight (37.16). Cluster VI constituting six genotypes (Baromashi × Hero, Himaloy × Yuvraj, Himaloy × Baromashi, Sobujsathi × Khira, Greenboy × Tripti, Hero × Khira) produced the highest mean value for leaf width (16.97).

3.5. Contribution of Characters Toward Divergence of the Genotypes

The character contributing maximum to the divergence are given greater emphasis for deciding on the cluster for the purpose of further selection and the choice of parents for hybridization [12] Contribution of characters towards divergence obtained from CVA is presented in Table 9.

The values of Vector I and Vector II revealed that both the vectors had positive values for leaf length, leaf width, vine length, no. of branches per plant, no. of male flower, no. of female flower, days to 50% male flowering, days to 50% female flowering, days to 1st male flowering. These results indicated that these characters had the highest contribution towards divergence among the 39 genotypes of cucumber. In vector I, the other important characters responsible for genetic divergence in the major axis of differentiation was length of petiole, days to 1st female flowering, flesh thickness, placental thickness, fruit length, fruit width, no. of fruits per plant having positive values. While in vector II (the second axis of differentiation) single fruit weight, yield per plant were important. Negative values in both vectors for 100 seed weight indicated this character had the lowest contribution to the divergence. Similar results were also obtained by Uddin (2008)[12] and Ali (2011) [14] in cucumber.

Table 4. Eigen values and percent of variation for corresponding 19 component characters in 39 genotypes of cucumber.

Principal component axis	Eigen values	% of total variation accounted for	Cumulative percent of variation
Leaf length(cm)	5.103	28.35	28.35
Leaf Width(cm)	3.029	16.83	45.18
Vine length	2.147	11.93	57.11
Length of petiole(cm)	1.835	10.20	67.31
No. of branches/plant	1.306	7.25	74.56
No. of male flower	0.886	4.92	79.48
No. of female flower	0.751	4.17	83.65
Days to 50% male flowering	0.721	4.00	87.65

Days to 50% female flowering	0.495	2.75	90.40
Days to first male flowering	0.421	2.34	92.74
Days to first female flowering	0.345	1.92	94.66
Flesh thickness(cm)	0.273	1.52	96.18
Placental thickness(cm)	0.210	1.17	97.35
Fruit Length(cm)	0.176	0.98	98.33
Fruit width(cm)	0.136	0.75	99.08
100 seed weight (gm)	0.091	0.51	99.59
No. of fruit per plant	0.055	0.31	99.90
Single fruit weight(gm)	0.021	0.12	100.02
Yield per Plant	0.006	0.00	100.02

Table 5. Distribution of 39 genotypes of cucumber in six clusters.

Cluster	Number of member	Name of the genotypes
I	9	Yuvraj,Himaloy,Khira,4239,4249,4263,Hero ×Piyas,Baromashi ×Khira,Hero ×Tripti
II	1	Greenking
III	4	Shilla, Baromashi, Sobujsathi, Tripti
IV	13	Modhumoti,Greenboy,4308,4240,4309,Modhumoti × Tripti, Baromashi × Greenking, Modhumoti ×Baromashi, Modhumoti ×Hero, Yuvraj × Khira, Himaloy ×Tripti, Tripti × Khira, Shila ×Khira
V	6	Piyas,Hero,4315,Modhumoti × Khira, Himaloy ×Khira, Sobujsathi × Baromashi
VI	6	Baromashi ×Hero,Himaloy ×Yuvraj,Himaloy ×Baromashi,Sobujsathi ×Khira, Greenboy ×Tripti, Hero ×Khira

Table 6. Inter parental distance.

	P2	P3	P4	P5	P6	P7	P8	P9	P10
P1	0.778	0.791	0.739	0.619	1.240	0.905	1.097	0.848	0.869
P2		0.703	1.121	0.762	0.833	1.158	0.623	1.153	1.234
P3			0.791	0.602	0.964	1.300	0.866	0.965	0.935
P4				0.775	1.570	1.194	1.437	0.553	0.532
P5					0.998	0.978	0.836	0.801	0.840
P6						1.400	0.523	1.582	1.629
P7							1.304	0.938	1.246
P8								1.419	1.511
P9									0.577
P10									
P11									
P12									
P13									
P14									
P15									
P16									
P17									
P18									

Table 6. Inter parental distance (Contd.).

	P11	P12	P13	P14	P15	P16	P17	P18	P19
P1	1.234	0.905	1.420	0.693	1.299	0.872	1.165	0.775	0.800
P2	1.699	0.951	1.212	0.901	1.269	0.966	1.062	0.890	0.956
P3	1.511	0.625	0.945	0.659	0.892	0.591	0.819	0.650	0.551
P4	0.911	1.005	1.514	0.893	1.315	0.849	1.356	0.990	0.857
P5	1.348	0.809	1.290	0.590	1.198	0.787	1.005	0.744	0.784
P6	2.162	1.274	1.278	1.086	1.351	1.191	1.038	1.226	1.311
P7	1.343	1.455	2.052	1.016	1.866	1.315	1.592	1.330	1.385

P8	2.028	1.075	1.187	1.029	1.286	1.090	0.899	0.999	1.138
P9	0.686	1.124	1.774	0.899	1.571	1.011	1.500	1.068	1.014
P10	0.824	1.101	1.635	0.907	1.427	0.987	1.447	1.042	0.965
P11		1.615	2.282	1.373	2.068	1.527	2.075	1.561	1.464
P12			0.851	0.687	0.739	0.545	0.743	0.347	0.323
P13				1.275	0.582	0.990	0.691	0.944	0.964
P14					1.137	0.561	0.977	0.708	0.658
P15						0.758	0.685	0.851	0.797
P16							0.801	0.667	0.511
P17								0.723	0.835
P18									0.401

Note: P1 = Piyas, P2 = Yuvraj, P3 = Himaloy, P4 = Shilla, P5 =Hero, P6 = Modhumoti, P7 = Baromashi, P8 = Greenboy, P9 = Sobujathi, P10 = Tripti, P11 = Greenking, P12 = Khira, P13 = 4307, P14 = 4315, P15 = 4240, P16 = 4239, P17 = 4308, P18 = 4249, P19 = 4263

Table 7. Average intra (bold) and inter cluster distances (D₂) for 19 genotypes of cucumber.

Cluster	I	II	III	IV	V	VI
I	0.898					
II	31.30	0.000				
III	12.77	19.23	0.9975			
IV	5.33	35.70	17.18	1.386		
V	5.17	26.85	8.57	9.39	0.5045	
VI	8.03	38.54	19.80	4.62	12.28	1.3403

Table 8. Cluster mean for 19 characters of 39 genotypes in cucumber.

Parameters	Cluster					
	I	II	III	IV	V	VI
Leaf length(cm)	12.46	12.93	13.87	13.24	12.68	12.65
Leaf Width(cm)	15.56	14.03	16.92	15.73	16.07	16.97
Vine length	174.56	209.33	177.42	142.59	159.39	164.89
Length of petiole(cm)	10.49	14.00	13.00	10.63	10.89	12.70
No. of branches/plant	10.91	13.67	11.25	9.82	9.85	10.80
No. of male flower	35.15	32.67	34.92	32.25	32.01	32.18
No. of female flower	40.79	44.33	42.50	40.76	40.36	36.68
Days to 50% male flowering	40.74	40.00	40.42	38.15	37.11	38.50
Days to 50% female flowering	49.33	52.00	48.83	48.95	47.33	47.38
Days to first male flowering	36.78	52.00	49.08	32.77	35.22	39.80
Days to first female flowering	13.70	12.00	17.25	14.54	13.11	14.27
Flesh thickness(cm)	1.60	2.90	2.25	1.39	1.79	1.36
Placental thickness(cm)	3.45	4.43	3.98	3.35	3.67	3.24
Fruit Length(cm)	19.26	35.67	26.21	16.09	21.14	12.11
Fruit width(cm)	5.70	8.98	7.02	5.23	6.31	4.11
100 seed weight (gm)	28.01	23.07	33.40	29.31	37.16	28.42
No. of fruit per plant	3.26	4.00	4.08	4.28	4.00	4.15
Single fruit weight(gm)	406.07	1246.67	731.67	296.38	534.45	169.43
Yield per Plant	653.05	1523.00	832.46	342.73	732.85	360.02

Table 9. Latent vectors for 19 principal component characters of 39 genotypes of cucumber.

Characters	Vector 1	Vector 2
Leaf length(cm)	0.1594	0.3154
Leaf Width(cm)	0.0950	0.2935
Vine length	0.2611	0.1388
Length of petiole(cm)	0.1224	-0.1027
No. of branches/plant	0.2054	0.1649
No. of male flower	0.2190	0.3649
No. of female flower	0.2251	0.2208
Days to 50% male flowering	0.2018	0.3419
Days to 50% female flowering	0.1956	0.0183
Days to first male flowering	0.0222	0.0076
Days to first female flowering	0.3829	-0.1788
Flesh thickness(cm)	0.3059	-0.2670
Placental thickness(cm)	0.3399	-0.2575
Fruit Length(cm)	0.3399	-0.1786
Fruit width(cm)	0.0620	-0.2426
100 seed weight (gm)	-0.0056	-0.0107
No. of fruit per plant	0.3808	-0.2609
Single fruit weight(gm)	-0.0338	0.0110
Yield per plant	-0.1830	0.0139

4. Conclusion

Considerable variability for most of the qualitative and quantitative traits of cucumber observed among the studied genotypes. Two genotypes 4315 and 4240 found early flowering habit. The genotypes Greenking, Baromashi, Piyas, Tripti, and Sobujsathi had higher yield potentiality, while the genotypes Greenboy, 4308, Hero, Sobujsathi, 4263, Tripti, 4249 exhibited as large fruit length. Based on multivariate analysis the 39 cucumber genotypes were grouped into six clusters and the highest inter-cluster distance was observed between clusters II and VI and the highest intra-cluster distance noticed for cluster IV. Among the characters vine length, branches per plant, female flowers per plant, fruits per plant, fruit weight, days of 50% female flowering, yield per plant were major characters that contributed positive impact towards divergence. Based on morphological characterization and genetic diversity eight genotypes viz. Greenking, Modhumoti, Baromashi, Tripti, Shilla, Khira, 4249, 4263 were found superior and may be selected for effective breeding work. Considerable variability for most of the qualitative and quantitative traits of cucumber was observed which would be conserved properly for future exploitation in varietal development program. The cucumber genotypes (Greenking, Modhumoti, Baromashi, Tripti, Shilla, Khira, 4249, 4263) may be recommended for cultivation in Bangladesh.

Conflicts of Interest

The authors declare that there is no conflict of interest regarding the publication of this article.

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