SAARC J. Agric., 22(1): 59-71 (2024) *DOI: https://doi.org/10.3329/sja.v22i1.73118*

MORPHOLOGICAL CHARACTERIZATION AND GENETIC DIVERSITY ANALYSIS OF YIELD AND YIELD CONTRIBUTING PARAMETERS IN BRINJAL (S*OLANUM MELONGENA* L.) GENOTYPES

M.A. Zabbar[1], S. Parveen[1], M.A. Rahim[1], K.M.K. Huda[1], M.A.I. Arif[1], M.R. Sharif[3], I. Jahan[1] and M. Harun-Ur-Rashid[1*]

[1]Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka
[3]BS student, Department of Biotechnology and Genetics Engineering, Jahangirnagar University, Savar, Dhaka

ABSTRACT

A field experiment was carried out at Sher-e-Bangla Agricultural University in Dhaka from November 2021 to June 2022 using a Randomized Complete Block Design (RCBD) with three replications to assess the significance of variance, heritability, genetic advance, correlation, path coefficient and genetic diversity for different yield contributing parameters in twenty brinjal genotypes. High heritability associated with high genetic advance and high genetic advance in percentage of mean was found in plant height, individual fruit weight and percent of brinjal shoot and fruit borer infestation, which indicated selection based on phenotype would be effective. Assessments of character association indicated that fruit yield plant^{-1} had highest significant positive correlation with days of last harvesting (r_g= 0.495, r_p= 0.454), number of secondary branches plant-1 (r_g=0.356, r_p=0.315), leaf blade length (r_g = 0.714, r_p = 0.462), leaf blade width (r_g = 0.674, r_p = 0.498) and number of fruits plant-1 (r_g= 0.798, r_p= 0.787) in both genotypic and phenotypic level. Path analysis revealed that the number of flowers plant^{-1} (1.421) had the maximum positive and direct effect on yield plant^{-1}. According to PCA, D^2 and Cluster analysis, twenty brinjal genotypes were grouped into five different clusters- I, II, III, IV and V with three, three, four, six and four genotypes respectively. Considering magnitude of cluster mean performance and genetic parameters genotypes G10 (Choto Katali), G20 (BARI Bt Begun 2), G11 (BARI Hybrid Begun 2), G8 (BARI Begun 6), G5 (BARI Hybrid Begun 4), G18 (Local Black Long) might be used in future breeding program.

Keywords: Brinjal, Characterization, Correlation, Diversity

---

[*] Corresponding author: sumonsau@sau.edu.bd

Received:11.05.2024 *Accepted: 5.06.2024*

INTRODUCTION

Brinjal (*Solanum melongena* L.) is a warm season crop mostly cultivated in tropical and subtropical regions of the world. It is one of the most common, popular and principal vegetable crops of Bangladesh grown throughout the country except at higher altitudes. Brinjal is the most popular vegetable with high nutritional value and lots of health benefits. It is highly beneficial for the regulation of blood sugar levels which helps to control the absorption of glucose (Saha *et al.*, 2019). Fiber contents help in digestion by removing toxins and harmful materials from our stomach thus by reducing stomach and colon cancer (Fraikue, 2016). The extracts of brinjal root and leaves can cure problems such as skin diseases, cough, toothache, piles, inflammation, throat problems, and stomach problems (Barik *et al.*, 2020).

More than 70 different types of insect species attack the brinjal (Subbarathnam, 1982). However, more than 80% yield loss occurs due to Brinjal Shoot and Fruit Borer attack (Mishra, 2008). It feeds internally on the fruit and excretes inside the fruit making worthless for human consumption (Baral *et al*., 2006).

Therefore, brinjal improvement programs need to focus on developing higher yield potential varieties, better fruit quality, good shelf-life, resistance to major insect, pest, and diseases with greater adaptation to different stress conditions. This research aimed to characterize as well as to assess the genetic diversity among different existing genotypes, and to identify the best genotypes for the varietal improvement of brinjal in Bangladesh.

MATERIALS AND METHODS

The brinjal genotypes were distributed randomly in each block. Five plants were planted for each genotype in every single row. From every block, three plants were chosen randomly for each genotype and tagged properly for data collection. At different growth stages, data were recorded on different morphological parameters. The analysis of variance, the mean values of all characters and the significant difference among the treatment means were calculated by using R package (variability, agricolae). The generalized distance method of Mahalanobis (1936) was used to determine genetic diversity (D^2) using GENSTAT software.

RESULTS AND DISCUSSION

Variability, heritability and genetic advance

The results of ANOVA showed that the brinjal genotypes varied significantly for all the studied characters (Table 1). The significant differences among the genotypes indicated the presence of genetic variability in the material used and provided a good opportunity for improvement. For all the studied attributes, the existence of genetic variability was investigated using heritability, genetic advance, genetic advance in percentage of mean, genotypic, and phenotypic co-efficient of variation (Table 2).

Table 1. Analysis of variance of fifteen characters of twenty genotypes of brinjal

Source of Variation	df	Mean sum of square														
		DFF	DFPF	DFH	DLH	PH	NPBP	NSBP	LBL	LBW	FW	FL	FD	NFPP	BSFBI	YPP
Replication	2	71.47	32.85	3.35	5.60	220.37	1.07	56.11	12.40	2.04	41.92	0.02	0.12	6.22	101.68	0.02
Genotype	19	327**	243.93**	207.42**	539.87**	575.93**	5.14**	49.28*	13.76**	14.08**	1363.24**	51.86**	7.73**	70.77**	1232.14**	0.19**
Error	38	12.26	12.38	11.82	23.06	55.00	1.71	25.72	3.65	2.68	51.20	1.28	0.12	3.84	121.90	0.01

df = Degrees of freedom, ** = 1% level of significance, * = 5% level of significance

Table 2. Estimation of genotypic and phenotypic variation, genotypic and phenotypic co-efficient of variations, heritability, genetic advance and genetic advance percentage over mean for fifteen characters of brinjal

Characters	σ^2_g	σ^2_p	GCV	PCV	h^2b	GA	GAPM
DFF	104.92	117.17	9.66	10.21	90	19.97	18.82
DFPF	77.19	89.56	7.81	8.42	86	16.80	14.94
DFH	65.20	77.02	6.14	6.67	85	15.30	11.64
DLH	172.27	195.33	6.63	7.06	88	25.39	12.82
PH	173.64	228.64	17.51	20.09	76	23.66	31.43
NPBP	1.15	2.85	12.76	20.13	40	1.40	16.65
NSBP	7.86	33.57	17.37	35.92	23	2.79	17.31
LBL	3.37	7.03	10.08	14.55	48	2.62	14.38
LBW	3.80	6.48	15.34	20.03	59	3.08	24.20
FW	437.35	488.54	31.49	33.28	90	40.76	61.37
FL	16.86	18.14	29.79	30.90	93	8.16	59.16
FD	2.54	2.65	37.69	38.54	96	3.21	75.94
NFPP	22.31	26.15	46.36	50.19	85	8.99	88.20
BFSBI	370.08	491.98	59.50	68.60	75	34.37	106.30
YPP	0.06	0.07	48.38	53.67	81	0.46	89.85

(σ^2_g - Genotypic variation, σ^2_p - Phenotypic variation, GCV- Genotypic co-efficient of variation, PCV- Phenotypic co-efficient of variation, h^2b- Heritability percentage in broad sense, GA- Genetic advance, GAPM- Genetic advance percentage over mean), DFPF- Days to first flowering, DFPF- Days to 50% flowering, DFH- Days to first harvesting, DLH- Days to last harvesting, PH- Plant height (cm), NPBP- No. of primary branches plant^{-1}, NSBP- No. of secondary branches plant^{-1}, LBL- Leaf blade length (cm), LBW- Leaf blade width (cm), FL- Fruit length (cm), FD- Fruit diameter (cm), FW- Individual fruit weight (g), NFPP- No. of fruits plant^{-1}, BSFB- Percent of BSFB infestation, YPP- Yield

For all studied characters, the phenotypic variance was higher than the corresponding genotypic variance, indicating a greater influence of the environment on these characters' expression. Characters like individual fruit weight, fruit length, fruit diameter, number of fruits plant^{-1}, percent of BSFB infestation and yield plant^{-1} exhibited high genotypic and phenotypic co-efficient of variation. Plant height, number of primary branches plant^{-1} and number of secondary branches plant^{-1} exhibited high phenotypic co-efficient of variation. The phenotypic co-efficient of variation was higher than the genotypic co-efficient of variation for all the characters. The maximum difference between phenotypic and genotypic coefficient of variation were 35.92 and 17.37, respectively which indicated that the number of secondary branches plant^{-1} was mostly depended on the environmental condition. Highest phenotypic co-efficient of variation (68.60) was found in percent of BSFB infestation and genotypic co-efficient of variation (59.50) was found in percent of BSFB infestation. High heritability associated with high genetic advance and high genetic advance in percentage of mean was found in plant height, individual fruit weight and percent of BSFB infestation which indicated that additive gene expression on this character and selection methods can be accomplished for the improvement of these traits. Fruit length, fruit diameter, number of fruits plant^{-1} and yield plant^{-1} showed high heritability with low genetic advance and high genetic advance in percentage of mean that might be presence of additive and non-additive gene expression. High heritability with high genetic advance and low genetic advance in percentage of mean were found in days to last harvesting**.**

Table 3. Mean performance, range, standard error and coefficient of variation in respect of fifteen characters of twenty brinjal genotypes

Genotypes	DFF	DFPF	DFH	DLH	PH	NPBP	NSBP	LBL	LBW	FW	FL	FD	NFPP	BFSBI	YPP
G1	105.34fg	111ef	128ef	176.33fg	71.23d-f	8.55a-d	12.77c-e	16.9c-e	10ef	50.44ij	14.07de	3.2e	10.22d-g	10.26e-h	0.29f-h
G2	109.67d-f	113de	130d-f	183f	68.46ef	9a-c	17.1a-d	18.56bc	13.37a-c	61.22g-i	14.49d	3.85d	8.88e-g	43.83bc	0.34e-g
G3	109.67d-f	113.67de	129ef	196de	61.25fg	7.44b-d	15.88a-e	18.67a-c	14.03a-c	61.45g-i	14.06de	3.82d	12.78cd	12.31d-h	0.65c
G4	96.34h	106.67f	126f	197cde	71.81d-f	9.11ab	9.88de	18.63a-c	12.1c-e	70.03e-g	9.45g	6.07bc	8.55fg	49.19b	0.43d-g
G5	106.33e-g	111.33ef	128ef	207.67ab	85.68b	9.abc	24.22a	20.76ab	15.27ab	75.58de	10.07g	5.95bc	22.33a	29.06cd	1.10a
G6	106e-g	117.33b-d	128ef	204bc	62.58fg	9.22ab	13.21c-e	16.93c-e	10.17d-f	79.67de	9.62g	6.92a	7.33gh	22.6def	0.44d-g
G7	103.34g	114.67de	129.33d-f	204bc	78.68b-e	8.55a-d	15.49b-e	18.7a-c	13.23a-c	63.07f-h	12.7d-f	3.92d	13.05b-d	20.49d-g	0.53c-e
G8	117.33ab	121.33ab	140b	203b-d	70.15d-f	9.a-c	19.61a-c	17.63b-d	13.7a-c	117.3a	10.57g	6.78a	2.39j	29.96cd	0.38e-g
G9	119a	120.67bc	139b	196de	81.21b-d	6.94cd	12.33c-e	18.43bc	13.57a-c	93.11bc	10.5g	6.07bc	3.83ij	28.33c-e	0.32fg
G10	70.67i	82h	105g	168.33h	39.76h	7.55b-d	17a-d	14.06ef	8.73f	29.42l	9.35g	3.08e	11.33c-f	7.48f-h	0.42d-g
G11	113b-d	115c-e	146a	204bc	99.75a	9.a-c	23.5ab	20.2ab	14.57a-c	101.33b	12.6ef	3.92d	4.78h-j	45.23bc	0.43d-g
G12	108.33d-g	114de	132c-e	204.33bc	84.7bc	9.a-c	19.66a-c	21.73a	14.83ab	74.1d-f	11.09fg	5.52c	13.88bc	48.69b	0.87b
G13	108.67d-g	113.67de	139b	210.33ab	78.75b-e	8.5a-d	15.88a-e	20.53ab	13.9a-c	55.92h-j	19.12bc	2.78e	8.16fg	61.46ab	0.40d-g
G14	105.67e-g	112d-f	128ef	206.67ab	72.90c-f	8.33a-d	15.88a-e	19.6a-c	14.2a-c	84.67cd	10.58g	6.38ab	14.11bc	28.92cd	1.06ab
G15	106e-g	111.67d-f	135b-d	207.67ab	87.05b	9.77a	19.66a-c	19.13a-c	15.67a	53.8h-j	18.52bc	2.78e	16.05b	52.93b	0.66c
G16	111.33c-e	115.67b-e	139b	209ab	80.4b-e	8.78a-d	16.33a-e	18.3bc	13.06a-c	56.11h-j	20.01ab	2.08f	7g-i	72.92a	0.26gh
G17	106.33e-g	114.67de	132cde	213a	87.65ab	9.22ab	15.1c-e	17.96bc	12.8b-d	61.31g-i	19.93ab	2.75e	11.9c-e	50.85b	0.59cd
G18	109.66d-f	114de	132.33c-e	207.67ab	89ab	9.89a	18.1a-d	19.3a-c	13a-c	56.39h-j	17.27c	2.87e	11.11c-f	28.97cd	0.47c-f
G19	92.34h	99.67g	127ef	193e	52.49g	4.11e	12.88c-e	14.8d-f	9.47ef	46.11jk	21.72a	2.88e	13.11b-d	3.2gh	0.39e-g
G20	116.33a-c	127a	137.33bc	170gh	81.7b-d	6.83d	8.11e	13.56f	8.53f	37.33kl	9.98g	2.93e	3j	0h	0.12h

Genotypes	DFF	DFPF	DFH	DLH	PH	NPBP	NSBP	LBL	LBW	FW	FL	FD	NFPP	BFSBI	YPP
MAX	119.00	127.00	146	213	99.75	9.89	24.22	21.73	15.67	117.3	21.72	6.92	22.33	72.92	1.10
MIN	70.67	82.00	105	168.33	39.76	4.11	8.11	13.567	8.53	29.42	9.35	2.08	2.39	0.00	0.12
MEAN	108.48	112.45	131.50	198.05	75.26	8.39	16.13	18.22	12.71	66.42	13.78	4.23	10.19	32.33	0.51
CV%	3.30	3.06	2.67	2.42	9.85	15.54	31.43	10.48	12.88	10.77	8.18	7.84	19.23	34.15	19.70
SE	2.86	2.87	2.81	3.92	6.06	1.07	4.14	1.56	1.34	5.84	0.92	0.28	1.60	9.01	0.10
LSD	5.79	5.81	5.68	7.94	12.26	2.16	8.38	3.16	2.71	11.83	1.87	0.56	3.24	18.25	0.20

SE- Standard error, CV- Co-efficient of variation, LSD- Least Significant Differences, DFPF- Days to first flowering, DFPF- Days to 50% flowering, DFH- Days to first harvesting, DLH- Days to last harvesting, PH- Plant height (cm), NPBP- No. of primary branches plant^{-1}, NSBP- No. of secondary branches plant^{-1}, LBL- Leaf blade length (cm), LBW- Leaf blade width (cm), FL- Fruit length (cm), FD- Fruit diameter (cm), FW- Individual fruit weight (g), NFPP- No. of fruits plant^{-1}, BSFB- Percent of BSFB infestation, YPP- Yield plant^{-1} (kg)

According to the mean performance, G10 (70.67 DAS) had the shortest length needed for first flowering, whereas G9 (119 DAS) had the longest. The maximum time was observed in G20 (127 DAS) and the shortest duration needed for 50% flowering was identified in G10 (82 DAS). G10 had the minimum 105 DAS period needed for first fruit harvesting while G11 had the 146 DAS maximum length. The longest period needed for the last fruit harvesting has been found in G17 (213 DAS), and the shortest period was reported in G10 with 168.33 DAS. The G11 plant measured 99.75 cm in height at its maximum, whereas the G10 plant measured 39.76 cm at its shortest. The genotype G18 scored the most primary branches (9.89), while the genotype G19 recorded the fewest (4.11). G5 was found to have the most secondary branches (24.22), whereas the genotype G20 had the fewest (8.11). The largest fruit weight in G8 was 117.3 g, and the smallest fruit weight in G10 was 29.42 g. The genotype G19 had the longest fruit length at 21.72 cm, while genotype G10 had the shortest fruit length (9.35 cm). The genotype G6 had the largest fruit diameter (6.92 cm), whereas G16 had the smallest (2.08 cm). Genotype G5 produced the most fruits plant-1 (22.33) and the genotype G8 produced the fewest (2.39). G16 had the highest brinjal shoot and fruit borer infestation (72.92%), whereas the genotype G20 had the lowest infestation (0%). The largest fruit yield plant^{-1} 1.10 kg emerged in G5, and the lowest 0.12 kg was found in G20.

Correlation co-efficient

Assessments of character association (Table 4) indicating that fruit yield plant^{-1} had highest significant positive correlation with days of last harvesting (r_g = 0.495, r_p = 0.454), number of secondary branches plant^{-1} (r_g=0.356, r_p=0.315), leaf blade length (r_g = 0.714, r_p = 0.462), leaf blade width (r_g = 0.674, r_p = 0.498) and number of fruits plant^{-1} (r_g= 0.798, r_p= 0. $^{-1}$787) in both genotypic and phenotypic level indicating the importance of these trait in selection for increasing yield and were identified as yield attributing characters. Thus, selection can be effective upon these characters for the genetic improvement of brinjal yield.

Path co-efficient analysis

Table 6 shows the partitioning of genotypic correlations into direct and indirect effects of significant features of brinjal. Path analysis showed that the highest positive direct effect was number of fruits plant^{-1} (1.421) and the lowest positive direct effect was fruit length (0.083). Days to 50% flowering, days to first harvesting, no. of primary branches plant^{-1}, no. of secondary branches plant^{-1}, leaf blade width, individual fruit weight, fruit length, fruit diameter, no of fruits plant^{-1} and percent of BSFB infestation showed positive direct effect on fruit yield plant^{-1} indicating that direct selection based on these traits may be effective in evolving high yielding varieties. The residual effect of path co-efficient analysis was 0.1033 which reported that the traits under study contributed 89.67% of the fruit yield plant^{-1}. It can be said that there were some other traits that contributed 10.33% to the yield plant^{-1} that were not included in the present study.

Table 4. Genotypic and Phenotypic correlation co-efficient among different pairs of yield and yield contributing characters for 20 genotypes of brinjal

Traits	Symbol	DFF	DFPF	DFH	DLH	PH	NPBP	NSBP	LBL	LBW	FW	FL	FD	NFPP	BFSBI
DFPF	rg	0.984**													
	rp	0.913**													
DFH	rg	0.907**	0.868**												
	rp	0.854**	0.748**												
DLH	rg	0.389^{NS}	0.354^{NS}	0.505*											
	rp	0.345**	0.288*	0.413**											
PH	rg	0.736**	0.712**	0.800**	0.580**										
	rp	0.611**	0.555**	0.683**	0.496**										
NPBP	rg	0.296^{NS}	0.328^{NS}	0.236^{NS}	0.536*	0.673**									
	rp	0.210^{NS}	0.172^{NS}	0.128^{NS}	0.359**	0.358**									
NSBP	rg	0.093^{NS}	-0.175^{NS}	0.237^{NS}	0.651**	0.480*	0.654**								
	rp	0.060^{NS}	-0.023^{NS}	0.091^{NS}	0.312*	0.267*	0.328*								
LBL	rg	0.509*	0.375^{NS}	0.492*	0.877**	0.721**	0.832**	0.884**							
	rp	0.285*	0.176^{NS}	0.309*	0.565**	0.504**	0.376**	0.434**							
LBW	rg	0.561*	0.399^{NS}	0.566**	0.845**	0.694**	0.656**	0.974**	0.956**						
	rp	0.344**	0.227^{NS}	0.353**	0.571**	0.496**	0.395**	0.490**	0.853**						
FW	rg	0.572**	0.478*	0.555*	0.518*	0.385^{NS}	0.349^{NS}	0.533*	0.593**	0.607**					
	rp	0.489**	0.447**	0.462**	0.444**	0.312*	0.243^{NS}	0.288*	0.389**	0.462**					
FL	rg	0.031^{NS}	-0.053^{NS}	0.260^{NS}	0.354^{NS}	0.139^{NS}	-0.164 NS	0.061^{NS}	0.041^{NS}	0.096^{NS}	-0.388^{NS}				
	rp	0.03^{NS}	-0.041^{NS}	0.216^{NS}	0.319*	0.130^{NS}	-0.077 NS	0.017^{NS}	0.041^{NS}	0.097^{NS}	-0.325*				
FD	rg	0.189^{NS}	0.220^{NS}	-0.003^{NS}	0.197^{NS}	-0.054^{NS}	0.203^{NS}	0.046^{NS}	0.329^{NS}	0.246 NS	0.751**	-0.748**			
	rp	0.179^{NS}	0.204^{NS}	-0.002^{NS}	0.180^{NS}	-0.042^{NS}	0.116^{NS}	0.107^{NS}	0.205^{NS}	0.194^{NS}	0.720**	-0.696**			
NFPP	rg	-0.370^{NS}	-0.407^{NS}	-0.458*	0.262^{NS}	-0.046^{NS}	0.143^{NS}	0.637**	0.384NS	0.349^{NS}	-0.290^{NS}	0.155^{NS}	-0.044^{NS}		
		-0.373**	-0.377**	-0.421**	0.242^{NS}	0.017^{NS}	0.041^{NS}	0.240^{NS}	0.283*	0.283*	-0.240^{NS}	0.135^{NS}	-0.042^{NS}		

Traits	Symbol	DFF	DFPF	DFH	DLH	PH	NPBP	NSBP	LBL	LBW	FW	FL	FD	NFPP	BFSBI
BFSBI	rg	0.278^{NS}	0.204^{NS}	0.483*	0.709**	0.590**	0.777**	0.514*	0.829**	0.746**	0.280^{NS}	0.378^{NS}	-0.068^{NS}	-0.010^{NS}	
	rp	0.288*	0.196^{NS}	0.403**	0.553**	0.436**	0.404**	0.227^{NS}	0.462**	0.485**	0.194^{NS}	0.322*	-0.088^{NS}	-0.039^{NS}	
YPP	rg	-0.048^{NS}	-0.103^{NS}	-0.182^{NS}	0.495*	0.170^{NS}	0.366^{NS}	0.885**	0.714**	0.674**	0.249^{NS}	-0.182^{NS}	0.416^{NS}	0.798**	0.147^{NS}
	rp	-0.121^{NS}	-0.135^{NS}	-0.205^{NS}	0.454**	0.163^{NS}	0.134^{NS}	0.291*	0.462**	0.479**	0.238^{NS}	-0.166^{NS}	0.370**	0.787**	0.058^{NS}

*(5% level of significance), ** (1% level of significance), NS (Non- significant), rg - Genotypic correlation, rp- Phenotypic correlation DFPF- Days to first flowering, DFPF- Days to 50% flowering, DFH- Days to first harvesting, DLH- Days to last harvesting, PH- Plant height (cm), NPBP- No. of primary branches plant^{-1}, NSBP- No. of secondary branches plant^{-1}, LBL- Leaf blade length (cm), LBW- Leaf blade width (cm), FL- Fruit length (cm), FD- Fruit diameter (cm), FW- Individual fruit weight (g), NFPP- No. of fruits plant^{-1}, BSFB- Percent of BSFB infestation, YPP- Yield plant^{-1} (kg)

Table 5. Path coefficient analysis showing direct and indirect effects of different characters on yield plant^{-1} of brinjal

Characters	DFF	DFPF	DFH	DLH	PH	NPBP	NSBP	LBL	LBW	FW	FL	FD	NFPP	BFSBI	r
DFF	-1.209	0.900	0.952	-0.160	-0.375	0.165	0.010	-0.469	0.321	0.237	0.003	0.069	-0.526	0.035	-0.048^{NS}
DFPF	-1.190	0.915	0.910	-0.145	-0.362	0.183	-0.018	-0.345	0.228	0.198	-0.004	0.081	-0.578	0.026	-0.103^{NS}
DFH	-1.097	0.794	1.049	-0.207	-0.407	0.131	0.024	-0.453	0.323	0.230	0.022	-0.001	-0.651	0.061	-0.182^{NS}
DLH	-0.471	0.324	0.529	-0.411	-0.295	0.299	0.066	-0.808	0.483	0.215	0.030	0.072	0.372	0.090	0.495*
PH	-0.890	0.651	0.839	-0.238	-0.509	0.375	0.049	-0.664	0.397	0.160	0.012	-0.020	-0.066	0.075	0.170^{NS}
NPBP	-0.358	0.300	0.247	-0.220	-0.343	0.557	0.067	-0.766	0.375	0.145	-0.014	0.074	0.203	0.098	0.366^{NS}
NSBP	-0.113	-0.160	0.248	-0.267	-0.244	0.364	0.102	-0.814	0.557	0.221	0.005	0.017	0.906	0.065	0.885**
LBL	-0.615	0.343	0.516	-0.360	-0.367	0.463	0.090	-0.921	0.546	0.246	0.003	0.121	0.546	0.105	0.714**
LBW	-0.679	0.365	0.594	-0.347	-0.353	0.365	0.100	-0.881	0.571	0.252	0.008	0.090	0.495	0.094	0.674**
FW	-0.692	0.437	0.582	-0.213	-0.196	0.194	0.054	-0.547	0.347	0.414	-0.032	0.276	-0.412	0.035	0.249^{NS}
FL	-0.038	-0.048	0.273	-0.146	-0.071	-0.091	0.006	-0.038	0.055	-0.161	0.083	-0.275	0.220	0.048	-0.182^{NS}
FD	-0.229	0.202	-0.003	-0.081	0.028	0.113	0.005	-0.303	0.141	0.311	-0.062	0.367	-0.063	-0.009	0.416^{NS}
NFPP	0.448	-0.372	-0.480	-0.108	0.024	0.080	0.065	-0.354	0.199	-0.120	0.013	-0.016	1.421	-0.001	0.798**
BFSBI	-0.336	0.186	0.507	-0.291	-0.301	0.433	0.053	-0.764	0.426	0.116	0.031	-0.025	-0.014	0.127	0.147^{NS}

Residual: 0.1033, r indicates genotypic correlation coefficient with NS (Non- significant), 5% (*) and 1% (**) level of significance

DFPF- Days to first flowering, DFPF- Days to 50% flowering, DFH- Days to first harvesting, DLH- Days to last harvesting, PH- Plant height (cm), NPBP- No. of primary branches plant^{-1}, NSBP- No. of secondary branches plant^{-1}, LBL- Leaf blade length (cm), LBW- Leaf blade width (cm), FL- Fruit length (cm), FD- Fruit diameter (cm), FW- Individual fruit weight (g), NFPP- No. of fruits plant^{-1}, BSFB- Percent of BSFB infestation, YPP- Yield plant^{-1} (kg)

Genetic diversity of twenty brinjal genotypes

A two-dimensional scatter diagram utilizing component score 1 as the X-axis and component score 2 as the Y-axis was constructed based on the values of principal component scores 2 and 1 obtained from the principal component analysis. This diagram is shown in Figure 1. There was clearly a five-group distribution of genotypes positions in the scatter diagram, indicating that there was a high degree of genotypic diversity.

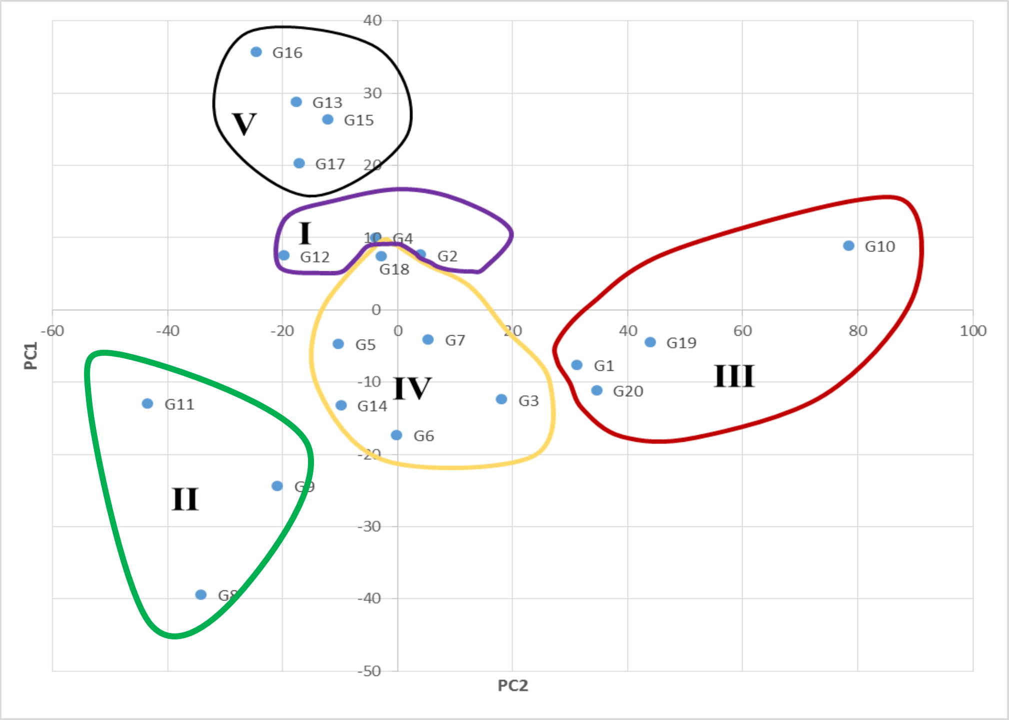

Figure 1. Scattered distribution of twenty brinjal genotypes on principal component score superimposed with clustering

According to PCA, D^2 and Cluster analysis, the genotypes were grouped into five different clusters. Cluster I, II, III, IV and V composed of three, three, four, six and four genotypes respectively (Table 6).

Table 6. Distribution of twenty brinjal genotypes in five different clusters

Clusters	No. of genotypes	Name of genotypes
I	3	G2, G4, G12
II	3	G8, G9, G11
III	4	G1, G10, G19, G20
IV	6	G3, G5, G6, G7, G14, G18
V	4	G13, G15, G16, G17

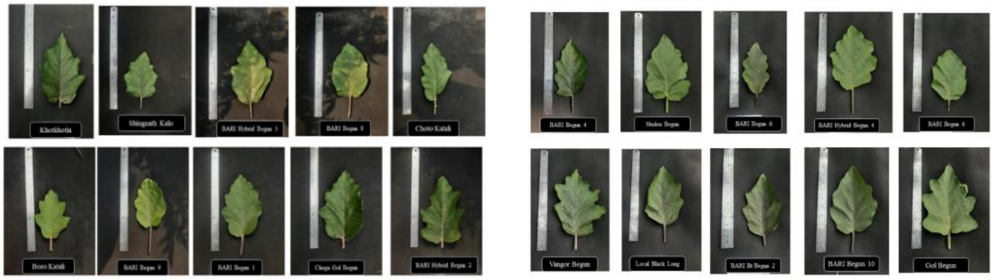

Plate 1. Leaves from twenty genotypes of brinjal

Plate 2. Flowers from twenty genotypes of brinjal

Plate 3. Fruits shapes of twenty brinjal genoty

Plate 4. BSFB infected fruits from sixteen genotypes of brinjal

Table 7. Cluster mean for fifteen characters of twenty genotypes of brinjal

Characters	Clusters				
	I	II	III	IV	V
Days to first flowering	104.78	116.44	96.16	106.77	108.08
Days to 50% flowering	111.22	119.00	104.91	113.83	113.91
Days to first harvesting	129.33	141.67	124.33	129.28	136.25
Days to last harvesting	194.78	201.00	176.92	204.33	210.00
Plant height (cm)	74.99	83.71	61.30	75.02	83.46
No. of primary branches plant^{-1}	9.03	8.31	6.76	8.74	9.07
No. of secondary branches plant^{-1}	15.55	18.48	12.69	17.13	16.75
Leaf blade length (cm)	19.64	18.76	14.83	18.99	18.98
Leaf blade width (cm)	13.43	13.94	9.18	13.32	13.86
Individual fruit weight (g)	68.45	103.91	40.82	70.13	56.78
Fruit length (cm)	11.68	11.22	13.78	12.38	19.40
Fruit diameter (cm)	5.15	5.59	3.02	4.97	2.60
Number of fruits plant^{-1}	10.44	3.67	9.41	13.45	10.78
Percent of BSFB infestation	47.23	34.50	5.23	23.72	59.54
Yield plant-1 (kg)	0.55	0.38	0.30	0.71	0.48

From the clustering mean values, it was observed that cluster I produced the highest mean values for leaf blade length (19.64 cm) in comparison with other five clusters (Table 9). On the other hand, cluster II produced the highest mean values for days to first flowering (116.44 days), days to 50% flowering (119 days), days to first harvesting (141.67 days), plant height (83.71 cm), no. of secondary branches plant-1 (18.48), leaf blade width (13.94 cm), individual fruit weight (103.91 g) and fruit diameter (5.59 cm) (Table 9). Cluster III produced the second highest mean value for fruit length (13.78 cm). Cluster IV had the highest mean values for number of fruits plant-1 (13.45) and yield plant-1 (0.71 kg). Cluster V had the highest mean values for the number of primary branches plant-1 (9.07), fruit length (19.4 cm), and percentage of BSFB infestation (59.54) (Table 7).

Table 8. Average intra (bold) and inter cluster distances (D^2) for twenty brinjal genotypes

Cluster	I	II	III	IV	V
I	0.819				
II	71.42	0.855			
III	14.44	72.24	1.918		
IV	7.95	64.79	11.94	0.957	
V	24.37	95.69	30.1	31.72	0.604

Results showed the maximum inter cluster distance was recorded between cluster II and V (95.69), followed by between II and III (72.24), and II and I (71.42). So, genotypes from these clusters if involved in hybridization might produce a wide range of segregating populations, as genetic variation was very distinct among these groups. The lowest inter cluster distance was found between the cluster I and IV (7.95) followed by III and IV (11.94), I and IV (14.44) representing a close relationship among these clusters. The intra cluster divergence varied from 1.918 from cluster III which comprised of four cultivars of diverse origin to 0.604 from cluster V which comprised four genotypes. Higher inter cluster distances indicated greater genetic variation among the genotypes of different clusters (Table 8).

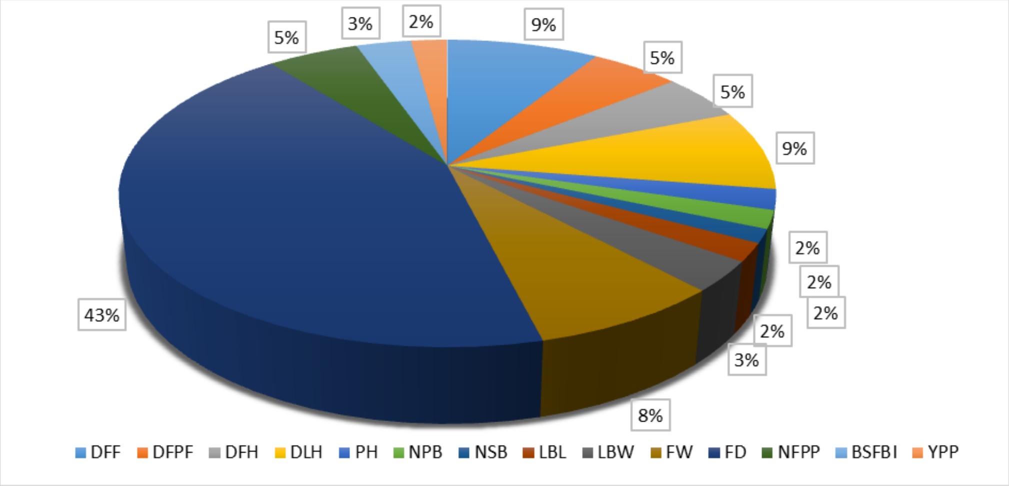

Figure 2. Relative contribution of fifteen characters of twenty brinjal genotypes towards divergence

The relative contribution of fifteen quantitative traits to genetic divergence among the twenty germplasms of brinjal is presented in Figure 2. Among the all characters, the maximum contribution towards divergence was made by fruit diameter (36.4%) followed by fruit length (16%) (Figure 2).

CONCLUSION

Among all the genotypes, maximum (1.10 kg) yield plant^{-1} was found in G5 due to better performances in important yield contributing characters such as number of secondary branches and number of fruits plant^{-1}. The phenotypic co-efficient of variation was higher than the genotypic co-efficient of variation for all characters. High heritability associated with high genetic advance and high genetic advance in percentage of mean was found in plant height, individual fruit weight and percent of BSFB infestation which indicated that additive gene expression on this character, suggesting the high possibility of selecting the genotypes for this trait. Considering cluster distances, genetic parameters and based on the objectives, the genotypes G10 (Choto Katali) and G20 (BARI Bt Begun 2) from cluster III, G11 (BARI Hybrid Begun 2) and G8 (BARI Begun 6) from cluster II, G5 (BARI Hybrid Begun 4) along with G18 (Local Black Long) from cluster IV might be used in future breeding program.

ACKNOWLEDGEMENTS

The work was supported by the special research grant (Biological Science) of Ministry of Science & Technology, Ministry of Science and Technology, Government of the People’s Republic of Bangladesh (Grant No. BS 1).

REFERENCES

Baral, K., Roy, B.C., Rahim, K.M.B., Chatterjee, H., Mondal, P., Mondal, D., Ghosh, D. and Talekar, N.S. (2006). Socio-economic parameters of pesticide use and assessment of impact of an IPM strategy for the control of eggplant fruit and shoot borer in West Bengal, India. *Tech. Bull*., 37. AVRDC publication number 06–673. AVRDC – The World Vegetable Center. Shanhua, Taiwan, pp. 36.

Barik, S., Reddy, A.C., Ponnam, N., Kumari, M., Acharya G.C., Reddy, L.D.C., Petikam, S. and Sahu, G.S. (2020). Breeding for bacterial wilt resistance in eggplant (*Solanum melongena* L.): *Progress and prospects Crop Protection*. **137**: 0261–2194.

BBS, (2022). Yearbook of Agricultural Statistics (2021), Bangladesh Bureau of Statistics, Ministry of Planning, Govt. of the People's Republic of Bangladesh. Dhaka. p.281–336.

Dadmal, S.M., Nemade, S.B. and Akhare, M.D. (2004). Field screening of brinjal cultivar for resistance to *Leucinodes orbonalis* Guen. Pest Manage. *Hort. Ecosys.* **10**: 145–150.

De Candolle, A. (1886). Origin of Cultivated Plants. 2nd edition. Reprinted in 1959. New York.

FAOSTAT (2020). "Eggplant production in 2019, Crops/Regions/World list/Production Quantity (pick lists)". UN Food and Agriculture Organization, Corporate Statistical Database. Retrieved 2021.

Fraikue FB. (2016). Unveiling the potential utility of eggplant: a review, Conference Proceedings of INCEDI., 883–895.

Harish, D.K., Agasimani, A.K., Imamsaheb, S.J. and Patil, S.S. (2011). Growth and yield parameters in brinjal as influenced by organic nutrient management and plant protection conditions. *Res. J. Agric. Sci.* **2**: 221–225.

Mahalanobis, P.C. (1936). On the generalized distance in statistics. *Proc. Natl. Inst. Sci. India.* **2**:49–55.

Mishra, H.P. (2008). New promising insecticides for the management of brinjal shoot and fruit borer, *Leucinodes orbonalis* Guenee. *Pest Manage. Hort. Ecosys.* **14**:140–147.

Saha, S., Haq, M. E., Parveen, S., Firoz Mahmud, F., Chowdhury, S. R. and Harun–Ur–Rashid, M. (2019). Variability, correlation and path coefficient analysis: principal tools to explore genotypes of Brinjal (*Solanum melongena* L.). *Asian J. Biotech. Gen. Engineering*. **2**(3): 1–9.

Subbarathnam, G.V. and Butani, D.K. (1982). Chemical control of Insect pest complex of brinjal. *Entomon*. **7**: 97–100.