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Research Paper

Morphological assessment of segregating population of interspecific hybrids developed from brinjal and its wild relatives

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Abstract

The eggplant is third most important vegetable crop of *Solanaceae* family after potato and tomato which is susceptible to number of insect and disease specially fruit and shoot borer (FSB). In the present investigation eleven eggplant accessions consisting of six hybrids, two wild and three cultivated, were evaluated for seven agromorphological characters in order to access the genetic variation. The estimated biometrical data revealed that most of the accessions were significantly different at both 5% and 1% levels, after 90 days of plantation except for the character of the number of leaves/plant and number of branches/plant. High heritability values were not observed in any of the characters on 30 and 60 DAP. The traits such as plant height (PH), number of branches/plant (NBPP), number of fruits/plant (NFPP), canopy size (CSPP), and number of infected fruit/plant (NIFPP) on 90 DAP has given better performance specifically, phenotypic and genotypic coefficients, variance components, broad-sense heritability and its components. The result from this study revealed that 11 eggplant accessions had ample genetic variation in agro-morphological characters when these were cultivated in an open field.

Keyword: Eggplant, Fruit and shoot borer (FSB), Heritability, Genetic parameter

INTRODUCTION

Eggplant is an important source of vitamins A and C, minerals, fiber in addition to phytochemicals and antioxidant compounds as flavonoid which have medicinal properties (Gebhardt and Thomas 2002; Piao et al. 2014). Asia, Africa, and the Mediterranean region are considered the main regions of eggplant production worldwide (Mutlu et al. 2008). Different pest and disease species that attack eggplant cause economic loss partly depends on the growth stage of the plant. Injury to the older leaves at a late stage in crop development for example, will not influence the final yield. Wild relatives of the crop are likely to play a significant role in securing food security of 21st century (Dempewolf et al. 2014). This is due to their potential uses in plant breeding to produce crop varieties which withstand adverse impacts of climate change, increasing scarcity of nutrients, water and other inputs, and new pest and diseases (Hopkins and Maxted 2010). In this respect, identification of wild relatives with interest for crop improvement and conservation of genetic variation are key areas to address food security in the future. Brinjal (*Solanum melongena*) is related to a large number of wild species that are a source of variation for breeding programmes, in particular for traits related to adaptation to climate change. This has necessitated eggplant breeders to search resistance for genes in wild *Solanum* species that are taxonomically related and compatible with cultivated brinjal. The brinjal is related to a large number of wild species that are a source of variation for breeding programmes, in particular for traits related to resistance to eggplant fruit and shoot borer. However, wild species remain largely unexploited for FSB resistant eggplant breeding.

Eggplant (*Solanum melongena* L.) is the most popular vegetable crop in respect of total acreage (50,415 ha) and production (504,817 ton) in Bangladesh with an average yield of 10.0 tons per hectare (BBS 2020), which is very low as compared to that in other tropical countries. Very few studies was focusing on eggplant landraces simultaneously to integrate their FSB resistant gene in the cultivated varieties by distant hybridization methods and comparing plant performance between segregated populations to give insight in production of insecticides free eggplant.

The research questions for this study is to find out the level of variation in segregated eggplant populations

Table 1 List of eggplant accessions used in this study

and the commercial eggplant accessions. Apart from that, the relationship between the aspect of phenotypic characterization and conditions was also the main key research question in this study.

MATERIALS AND METHODS

Plant materials

The plant materials for the present study comprised of 11 brinjal accessions with five parents (two cultivated and three were wild relatives of brinjal) and six were segregating populations of hybrids created previous year in the field laboratory of the Deptartment of Botany, Rajshahi University, as indicated in table 1. The parents' seeds were collected from private seed companies, the Bangladesh Agriculture Research Institute (BARI), and different parts of Bangladesh. Wild species were collected from Srilanka (*S. insanum*) and Khagrasori district (*S. incanum*) of Bangladesh.

No.	Genotype Code	Accession name	Country of origin	Fruit type	Collection source
1.	P1-1	Akshita (Cultivated)	Bangladesh	Oblong	Local market
2.	P1-2	China begun (Cultivated)	China	Oblong	Local market
3.	P2-1	Srilanka (Wild)	Srilanka	Round	Srilanka
4.	P2-2	CHT-1 (Wild)	Bangladesh	Round	Khagrachori
5.	P2-3	CHT-2 (Wild)	Bangladesh	Round	Khagrachori
6.	SP-1	$AKS \times SL$	Hybrid	Oblong	Field laboratory
7.	SP-2	$CHT-1 \times SL$	Hybrid	Round	Field laboratory
8.	SP-3	$CHT-2 \times SL$	Hybrid	Round	Field laboratory
9.	SP-4	$SGO \times SL$	Hybrid	Oblong	Field laboratory
10.	SP-5	$SPL \times SL$	Hybrid	Oblong	Field laboratory
11.	SP-6	CHINA × SL	Hybrid	Oblong	Field laboratory

Here, AKS = Akshita, CHT = Chittagong, SL = Srilanka, SGO = Super Green Oblong, SPL = Super Pink Long

Experimental layout and field preparation

Accessions of hybrids and parents were evaluated in the experiment field (open field condition) of the Department of Botany, University of Rajshahi, Bangladesh. The experimental field was $16 \text{ m} \times 12 \text{ m}$ in size, including a 0.5 m boundary. The experiments were laid out under a Randomized Complete Block Design (RCBD) with three replications from November 2022 to December 2022. The field was divided into 3 equal blocks, and each block was divided into 16 lines, and the line to line distance was

1 m. The block to block distance was 1 m. Seedlings of each variety were planted 0.5 m apart in a single row 4.5 m long. Therefore, the total number of plants per row was 10.

The experimental plot was thoroughly prepared by repeated ploughing using a power tiller and for several times with a power tiller followed by laddering until a good tilth was obtained up to a depth of 6-7 inches. All the weeds and stubble were collected and removed from the land. The clods were broken into friable soil and the surface was leveled. The soil was treated with insecticides (Furadan 5G @ 25 kg/ha) at the time of final land preparation to protect young plants from the attack of soil insects such as cutworm and mole cricket. Finally, irrigation and drainage channels were prepared around the plot. The land was prepared 10 days before the seedlings were planted.

Methods of for data collection

The following data were collected to justifying the present investigation:

1. **Plant height (PH):** The plant heights of all the interspecific hybrids of six brinjal varieties and there five parents were measured in centimeter at 30, 60 and 90 DAP.

2. The canopy size (CS): Canopy size of randomly selected three plant were taken in cm² three times at 30, 60 and 90 DAP.

3. Number of leaf (NL): The number of leaf of selected three plants was noted three times at 30, 60 and 90 DAP.

4. Number of branch (NB): The no. of branches/plant in all interspecific hybrids of six brinjal varieties and there five parents were similar trend of no. of branches/ plant like plant height three times at 30, 60 and 90 DAP.

5. Number of fruit per plant: Similar way that were noted for number of branch/plant three times at 30, 60 and 90 DAP.

6. Number of infected fruit per plant: The infected fruit were counted in every plant at 90 DAP.

Statistical analysis of data

The analysis of variance for different parameters was performed and means were compared by Duncan Multiple Ranged Test (DMRT) at 5% level of significance. After that genetic parameters were studied. All the statistical procedure was operated by using the online software OPSTAT.

RESULTS

The mean values of the respective characters of individual accessions were calculated. The test of significance among the mean values was calculated by DMRT. Components of variation in all the characters were also done.

Results obtained at 30 days after plantation (DAP)

Plant height (PH): The plant height ranged from 2.22 cm (F1-6) to 4.60 cm (CHT-1) at 30 DAT. The highest was observed in CHT-1 (4.60 cm) and it was followed by F1-1 (4.0 cm), F1-3 (3.80 cm), CHT-2 (3.74 cm) and the lowest height was observed in F1-6 (2.22 cm) (**table 2a**). The result of genetic parameters such as phenotypic variance (1.05) was greater than genotypic variance (0.51). The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation were 22.47 and 5.74, respectively. Broad sense heritability (h²b), genetic advance (GA) and GA as % of mean were 48.92, 99.56, and 3111.31, respectively (**table 2b**).

The canopy size (CS): The highest canopy was observed in Akshita (97.49) and it was followed by China (61.40), F1-1 (54.20), F1-6 (46.00), F1-5 (45.40), and the lowest was observed in F1-4 (26.80) (table 2a). The genetic parameters phenotypic variance (576.16) is higher than genotypic variance (382.75). GCV and PCV were 290.12 and 355.95, respectively. The values for broad sense heritability (h2b), genetic advancement (GA), and GA as a percentage of mean were 66.43, 3145.16, and 6916.58, respectively (table 2b).

Number of leaf (NL): The highest number of leaves was observed in CHT-1 (5.2) and it was followed by Sri Lanka (4.8), China (4.4), F1-2 (4.6), F1-3 (4.4), F1-6 (4.4) and the lowest was observed in F1-4 (3.8), CHT-2 (3.8) (table 2a). The genetic parameters phenotypic variance (0.82) is higher than genotypic variance (0.01). GCV and PCV were 5.20 and 43.50, respectively. Broad sense heritability (h2b), genetic advance (GA), and GA as a percentage of mean was all 1.42, 185.76, and 4257.19 (table 2b).

Number of branch (NB): The highest number of branches was observed in F1-4 (4.40) and it was followed by F1-6 (3.60), F1-3 (3.40), F1-5 (3.20), F1-2 (2.80), F1-1 (2.40) and the lowest was observed in Akshita (0.60) (table 2a). The genetic parameters phenotypic variance and genotypic variance were 1.14

and 1.190, respectively. The GCV and PCV were 68.26 and 88.18, respectively. Broad sense heritability (h2b), genetic progress (GA), and GA as a percentage of mean were 59.92, 277.26, and 11295.98, respectively (**table 2b**).

Accessions	PH at 30 DAP	Canopy size at 30 DAP	No. of leaf at 30 DAP	No of branch at 30 DAP
	Mean±SE	Mean±SE	Mean±SE	Mean±SE
1.Akshita	2.360±0.186a	97.400±10.505a	4.2±0.74ab	0.600±0.245e
2.China	2.260±0.216a	61.400±5.653b	4.4±1.2ab	1.200±0.200de
3.Srilanka	2.560±0.319a	36.200±7.248cd	4.8±0.74ab	1.800±0.374cde
4.CHT-1	4.600±0.430a	29.400±2.522d	5.2±1.46a	1.800±0.374cde
5.CHT-2	3.740±0.487a	30.400±2.713d	3.8±0.74b	1.800±0.374cde
6.SP-1	4.000±0.032a	54.200±7.539bc	4.4±0.48ab	2.400±0.510bcd
7.SP-2	3.280±0.208a	43.800±9.583bcd	4.6±0.48ab	2.800±0.374bcd
8. SP-3	3.800±0.122a	29.200±2.596d	4.4±0.48ab	3.400±0.510ab
9. SP-4	3.320±0.583a	26.800±2.596d	3.8±0.74b	4.400±0.510a
10. SP-5	3.060±0.209a	45.400±3.501bcd	4.0±0.63ab	3.200±0.374ab
11. SP-6	2.220±0.271a	46.000±3.536bcd	4.4±0.48ab	3.600±0.400ab
C.V.	22.957	30.584	30.584	35.644
MS	5.79**	10.89**	1.07ns	8.47**

The second and the s	Table 2a.	The mean,	standard errors,	C.V. and	d Mean sq	uare of p	olant heig	ht, canop	oy size an	d number	of leaf a	at 30 D	DAP.
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Means with the same letter(s) in a column are not significantly different according to DMRT at 5% level

Table 2b. Genetic parameters of plant height, canopy size and number of leaf at 30 DAP.

Component of variation	PH at 30 DAP	Canopy size at 30 DAP	No. of leaf at 30 DAP	No of branch at 30 DAP
Genotypic Variance ($\sigma^2 g$)	0.51 (l)	382.75 (h)	0.01 (1)	1.14 (l)
Phenotypic Variance ($\sigma^2 p$)	1.05 (1)	576.16 (h)	0.82 (1)	1.90 (1)
Genotypic coefficient of variation (GCV)	22.47 (m)	290.12 (h)	5.20 (1)	68.26 (h)
Phenotypic coefficient of variation (PCV)	5.74 (1)	355.95 (h)	43.50 (m)	88.18 (h)
Heritability (h ² b)	48.92 (m)	66.43 (h)	1.42 (l)	59.92 (h)
Genetic Advance (GA)	99.56 (h)	3145.16 (h)	185.76 (h)	277.26 (h)
GA as % of mean	3111.31 (h)	6916.58 (h)	4257.19 (h)	11295.98 (h)

Results obtained at 60 days after plantation (DAP)

Plant height (cm) (PH): The plant height ranged from 10.4 cm (F1-6) to 19.0 cm (CHT-2) at 60 DAPS. The highest was observed at 19.0 cm (CHT-2) and it was followed by F1-2 (18.4 cm), CHT-1 (16.6 cm), China (16.4 cm), Akshita (16.0 cm), F1-3 (15.2 cm), F1-1 (14.2 cm) and the lowest height was observed in F1-6 (10.4 cm) (**table 3a**). Phenotypic variance was (13.17) it was higher than genotypic variance (5.04). GCV and PCV were 57.75 and 93.38, respectively. Broad sense heritability (h²b), genetic advance (GA) and GA as % of mean were 38.25, 715.41, and 4734.97, respectively (**table 3b**).

The canopy size (cm²) (CS): The highest canopy was observed in CHT-2 (430.6 cm²) and it was followed by F1-1 (416.6 cm²), F1-2 (367.6 cm²), F1-6 (364.0 cm²), Akshita (352.0 cm²), and the lowest was observed in F1-5 (211.2 cm²) (table 3a). Here, phenotypic variance was (10546.55) it was higher than genotypic variance (4172.96). The GCV and PCV were 360.32 and 572.83, respectively. Broad sense heritability (h2b), genetic progress (GA), and GA as a percentage of mean were 39.56, 20595.27, and 6407.98, respectively (table 3b).

Number of leaf (NL): The analysis of variance reveals that the number of leaves of different accessions has no significant difference at both the 5% and 1% level of significance (**table 3a**). The highest number of leaves was found in CHT-1 (10.2), followed by Akshita (10.0), F1-6 (9.4), F1-5 (9.2), China (9.2), Sri Lanka (8.6), and F1-(6.6) (**table 3a**). The genetic parameters phenotypic variance (4.29) was higher than genotypic variance (0.34). GCV and PCV were 19.97 and 70.17, respectively. Broad sense heritability (h2b), genetic progress (GA), and GA as a percentage of mean were 8.10, 429.34, and 4919.53, respectively (**table 3b**).

Number of branch (NB): The highest number of branches was observed in Akshita (5.8), CHT-1 (5.8) and CHT-2 (5.8) and it was followed by Srilanka (5.4), F1-1 (5.4), F1-6 (5.4), F1-2 (5.0), F1-5 (5.0) and the lowest was observed in F1-3 and F1-4 (4.6) (**table 3a**). The genetic parameters phenotypic variance and genotypic variance were 0.73 and 0.05, respectively. The GCV and PCV were 10.59 and 37.31, respectively. Broad sense heritability (h2b), genetic progress (GA), and GA as a percentage of mean were 8.06, 177.66, and 3369.46, respectively (**table 3b**).

Parents/	PH at 60 DAP	Canopy size at 60 DAP	No. of leaf at 60 DAP	No of branch at 60 DAP
Trybrids	Mean±SE	Mean±SE	Mean±SE	Mean±SE
1.Akshita	16.000±1.095ab	352.000±18.407ab	10.000±0.894a	5.800±0.374a
2.China	16.400±1.364ab	322.800±66.446abc	9.200±1.772ab	5.200±0.374a
3.Srilanka	14.200±0.735bcd	259.600±51.269bc	8.600±0.600ab	5.400±0.245a
4.CHT-1	16.600±0.927ab	267.400±40.139bc	10.200±0.917a	5.800±0.374a
5.CHT-2	19.000±0.447a	430.600±31.644a	8.200±0.583ab	5.800±0.374a
6.SP-1	14.200±1.562bcd	416.600±17.134a	7.400±0.748ab	5.400±0.400a
7.SP-2	18.400±1.939a	367.600±35.125ab	8.800±1.158ab	5.000±0.316a
8. SP-3	15.200±1.020abc	320.800±18.348abc	6.600±0.400b	4.600±0.400a
9. SP-4	14.000±1.378bcd	222.800±30.689c	8.400±0.510ab	4.600±0.400a
10. SP-5	11.800±1.428cd	211.200±20.284c	9.200±0.860ab	5.000±0.316a
11. SP-6	10.400±0.812d	364.000±25.612ab	9.400±0.748ab	5.400±0.510a
C.V.	18.877	24.840	22.773	15.587
MS	4.09**	4.27**	1.44ns	1.43ns

Table 3a The me	ean standard errors	C V Mean s	quare of plant height	canony size and	number of leaf at 60 DAP
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Means with the same letter(s) in a column are not significantly different according to DMRT at 5% level

Component of variation	PH at 60 DAP	Canopy size at 60 DAP	No. of leaf at 60 DAP	No of branch at 60 DAP
Genotypic Variance ($\sigma^2 g$)	5.04	4172.963	0.3482	0.0592
Phenotypic Variance $(\sigma^2 p)$	13.175	10546.55	4.2982	0.7342
Genotypic coefficient of variation (GCV)	57.75587	360.3291	19.97446	10.59603
Phenotypic coefficient of variation (PCV)	93.38049	572.8386	70.17849	37.31552
Heritability (h ² b)	38.25427	39.56709	8.101066	8.063198
Genetic Advance (GA)	715.4112	20595.27	429.3409	177.6625
GA as % of mean	4734.972	6407.985	4919.531	3369.461

Table 3b. Genetic parameters of plant height, canopy size and number of leaf at 60 DAP.

Results obtained at 90 days after plantation (DAP)

Plant height (cm) (PH): The plant height varied significantly among the accessions at both a 5% and 1% level of significance. The plant height ranged from 24.2 cm (Srilanka) to 35.0 cm (F1-1) at 90 DAPS. The highest was observed at 35.0 cm (F1-1) and it was followed by F1-2 (29.2 cm), F1-2 (29.2), CHT-2 (28.2 cm), F1-4 (27.6), China (26.4 cm), Akshita (26.0 cm), F1-5 (26.0 cm) and the lowest height was observed in Sri Lanka (24.2 cm). The genetic parameters phenotypic variance (15.71) is higher than genotypic variance (6.87). The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were 49.95 and 75.52, respectively. Broad sense heritability (h2b), genetic progress (GA), and GA as a percentage of mean were 43.74, 808.70, and 2935.89, respectively (table 4b).

The canopy size (cm²) (CS): The highest canopy was observed in F1-4 (1018.0 cm²) and it was followed by F1-6 (994.0 cm²), F1-3 (980.0 cm²), F1-2 (834.0 cm²), F1-5 (774.4 cm²), Srilanka (684.6 cm²⁾ and the lowest was observed in Akshita (512.0 cm²) (table 4a). The genetic parameters phenotypic variance (47197.21) is higher than genotypic variance (32264.25). The GCV and PCV were 658.87 and 796.89, respectively. The values for broad sense heritability (h2b), genetic advancement (GA), and GA as a percentage of mean were 68.36, 43260, and 5820.75, respectively (**table 4b**).

Number of leaf (NL): The highest number of leaves was observed in F1-6 (17.8) and it was followed by F1-4 (16.8), F1-1 (16.8), China (16.8), Sri Lanka (16.6) and the lowest was observed in F1-3 (13.4) (table 4a). The genetic parameters phenotypic variance (5.54) is higher than genotypic variance (0.98). The GCV and PCV were 24.87 and 58.88, respectively. Broad sense heritability (h2b), genetic progress (GA), and GA as a percentage of mean were 17.84, 488.26, and 3055.10, respectively (table 4b).

Number of branch (NB): The highest number of branches was observed in F1-1 (8.6), F1-5 (8.6) and F1-4 (8.4) and it was followed by F1-3 (7.6), China (7.0), Srilanka (7.0), F1-6 (7.0), F1-2 (6.6) and the lowest was observed in CHT-1 (6.2) and CHT-2 (5.0) (table 4a). The genetic parameters phenotypic variance and genotypic variance were 2.75 and 0.90, respectively. The GCV and PCV were 35.69 and 62.22, respectively. Broad sense heritability (h2b), genetic progress (GA), and GA as a percentage of mean were 32.89, 355.0, and 4993.73, respectively (table 4b).

Parents/ Hybrids	PH at 90 DAP	Canopy size at 90 DAP	No. of leaf at 90 DAP	No of branch at 90 DAP
	Mean±SE	Mean±SE	Mean±SE	Mean±SE
1.Akshita	26.000±1.140bc	512.000±31.369d	16.600±1.077abc	6.200±0.583bc
2.China	26.400±1.364bc	580.000±36.332d	16.800±1.241ab	7.000±0.837abcd
3.Srilanka	24.200±0.735c	684.600±26.574bcd	16.600±1.077abc	7.000±0.894abcd
4.CHT-1	25.800±0.374bc	557.800±35.593d	16.600±1.077abc	6.200±0.374de
5.CHT-2	28.200±2.905bc	634.200±40.175cd	15.800±0.663abc	5.000±0.316e
6.SP-1	35.000±1.000a	606.000±33.407cd	16.800±0.583ab	8.600±1.077a
7.SP-2	29.200±1.241b	834.000±66.000ab	14.000±0.707bc	6.600±0.510cde
8. SP-3	29.200±1.428b	980.000±64.420a	13.400±0.748c	7.600±0.510abcd
9. SP-4	27.600±0.927bc	1,018.000±52.28a	16.800±1.020ab	8.400±0.510abc
10. SP-5	26.000±1.304bc	774.400±73.673e	14.600±1.470bc	8.600±0.678ab
11. SP-6	25.400±1.166bc	994.400±97.356bc	17.800±0.800a	7.000±0.707abcde
C.V.	10.79	16.44	13.351	19.118
MS	4.88**	11.80**	2.08*	3.45**

Table 4a. The mean, standard errors, C.V., Mean square of plant height, canopy size and number of leaf, No. of branch at 90 DAP.

Means with the same letter(s) in a column are not significantly different according to DMRT at 5% level

Table 4b. Genetic parameters of plant height, canopy size and number of leaf at 90 DAP.

Component of variation	PH at 90 DAP	Canopy size at 90 DAP	No. of leaf at 90 DAP	No of branch at 90 DAP
Genotypic Variance ($\sigma^2 g$)	6.8728	32264.25	0.989	0.9056
Phenotypic Variance $(\sigma^2 p)$	15.7128	47197.21	5.542	2.7526
Genotypic coefficient of variation (GCV)	49.95073	658.8744	24.87626	35.6912
Phenotypic coefficient of variation (PCV)	75.52693	796.893	58.8871	62.22494
Heritability (h ² b)	43.74014	68.3605	17.84554	32.8998
Genetic Advance (GA)	808.706	43260.9	488.2613	355.009
GA as % of mean	2935.896	5820.754	3055.105	4993.733

Results obtained at 90 days after plantation (DAP) of the characters Number of fruit per plant, Number of infected fruit per plant, Number of fruit per plant.

Number of fruit per plant: The highest number of fruits per plant was observed in F1-5 (8.0) and it was followed by Srilanka (7.2), F1-3 (7.0), F1-6 (7.0), F1-4

(6.6), F1-2 (5.6) and the lowest height was observed in CHT-1 (1.6). The genetic parameters phenotypic variance is (5.62) is higher than genotypic variance (2.66). The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were 68.63 and 99.77, respectively. The values for broad sense heritability (h2b), genetic advancement (GA),

and GA as a percentage of mean were 47.32, 479.85, and 8486.21, respectively (**table 5b**).

Number of infected fruit per plant: The highest number of infected fruits per plant was observed in Akshita (2.6), China (2.4), both of which had no significant difference and it was followed by F1-4 (1.8), CHT-2 (1.2), F1-1 (1.2), F1-5 (1.2) and the lowest was observed in Srilanka (0.2), CHT-1 (0.4), F1-6 (0.4) and F1-3 (0.6). The genetic parameters phenotypic variance was (1.71), which was higher than genotypic variance (0.37). The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were 55.66 and 119.47, respectively. Table 4.19b shows that broad sense heritability (h2b), genetic advance (GA), and GA as a percentage of mean were 21.70, 258.78, and 21565.75, respectively.

Number of fruit per plant: The highest number of fruits per plant was observed in F1-5 (8.0) and was followed by Srilanka (7.2), F1-3 (7.0), F1-6 (7.0), F1-4 (6.6), F1-2 (5.6) and the lowest height was observed in CHT-1 (1.6). The genetic parameters phenotypic variance (5.62) is higher than genotypic variance (2.66). The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were 68.63 and 99.77, respectively. The values for broad sense heritability (h2b), genetic advancement (GA), and GA as a percentage of the mean were 47.32, 479.85, and 8486.21, respectively (**table 5b**).

Number of infected fruits per plant: The highest number of infected fruits per plant was observed in Akshita (2.6), China (2.4), both of which had no significant difference, and it was followed by F1-4 (1.8), CHT-2 (1.2), F1-1 (1.2), F1-5 (1.2), and the lowest was observed in Srilanka (0.2), CHT-1 (0.4), F1-6 (0.4) and F1-3 (0.6). The genetic parameters

phenotypic variance was (1.71), which was higher than genotypic variance (0.37). The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were 55.66 and 119.47, respectively. Table 4.19b shows that broad sense heritability (h2b), genetic advance (GA), and GA as a percentage of the mean were 21.70, 258.78, and 21565.75, respectively.

Varietal resistance study of against BFSB among Selected Cultivated Brinjals and hybrids plants.

There were 11 selected cultivated brinjal varieties and three wild species evaluated for BFSB resistance and the results on the degree of BFSB are presented in the table 6. The degree of BFSB infestation was found varied with types of hybrid accessions and both type of parents. It was observed that all the cultivated brinjal varieties were infested by BFSB. The % infestations among the cultivated brinjal varieties are ranged 3.33 to 48.62%. The variety of super pink long infestation rate was very high. The infestation was recorded in S. incanum and S. insanum. Among all the hybrid accessions maximum percent fruit infestation was found in F1-1 (AKS×SL) (5.18) and the minimum percent fruit infestation was found in F1-6 (China×SL) (2.89). On the other hand percent fruit infestation was the lowest among the wild Solanum sp. The infestation of brinjal fruits by FSB was fluctuating throughout the period understudy. At 65 DAT the highest fruit infestation percent was recorded on the variety of Super pink long (32.67%) followed by Akshita (31.16%) but significantly different from all other selected varieties. On the other hand, the lowest percent of BFSB infestation was show in the variety of Srilanka (1.24%). It was observed that the mean percent of highest fruit infestation was recorded on the variety Super pink long (48.62%) followed by Akshita (46.22%)

Table 5a. The mean, standard errors, C.V. of number of fruit/plant, number of infected fruit/plant and number of fruit borer/fruit at 90 DAPS.

Parents/Hybrids	NFPP at 90 DAP	NIFPP at 90 DAP	NFBPF at 90 DAP
	Mean±SE	Mean±SE	Mean±SE
1.Akshita	5.400±1.208bcd	2.600±0.927a	0.400±0.245b
2.China	4.200±0.374d	2.400±0.678a	2.400±1.913a
3.Srilanka	7.200±1.241ab	0.200±0.200b	2.200±1.020a
4.CHT-1	1.600±0.678e	0.400±0.400b	0.200±0.200b
5.CHT-2	5.000±0.949bcd	1.200±0.583ab	2.600±1.077a
6.SP-1	4.600±0.510cd	1.200±0.374ab	1.800±0.800a
7.SP-2	5.600±0.510abcd	1.200±0.374ab	1.600±0.678a
8. SP-3	7.000±0.707abc	0.600±0.400b	2.400±1.030a
9. SP-4	6.600±0.510abcd	1.800±0.490ab	1.800±0.800a
10. SP-5	8.000±0.707a	1.200±0.374ab	1.400±0.748a
11. SP-6	7.000±0.707abc	0.400±0.245b	1.400±0.600a
C.V.	30.454	96.498	91.516
MS	5.49**	2.38*	1.34ns

Table 5b. Genetic parameters of number of fruit/plant, number of infected fruit/plant and number of fruit borer/fruit at90 DAP.

Component of variation	NFPP at 90 DAP	NIFPP at 90 DAP	NFBPP at 90 DAP
Genotypic Variance ($\sigma^2 g$)	2.6638	0.3718	0.1582
Phenotypic Variance ($\sigma^2 p$)	5.6288	1.7128	2.4512
Genotypic coefficient of variation (GCV)	68.636	55.66267	30.92174
Phenotypic coefficient of variation (PCV)	99.77209	119.4711	121.7167
Heritability (h ² b)	47.32447	21.70715	6.453982
Genetic Advance (GA)	479.8569	258.789	416.1333
GA as % of mean	8486.215	21565.75	25150.91

Brinjal types	Percent BFSB infestation at different days after transplantation (DAP)							
5 51	65 DAP	75 DAP	85 DAP	95 DAP	105 DAP			
Akshita	31.16a	31.55a	35.50a	50.60a	82.29b	46.22a		
China begun	23.71b	29.50a	30.75b	46.71b	85.11a	43.15a		
S. incanum (Srilanka)	0.00	00.00	00.00	00.00	00.00	00.00		
S. insanum (CHT-1)	0.00	0.00	0.00	0.00	0.00	0.00		
S. insanum (CHT-2)	0.00	0.00	0.00	0.00	0.00	0.00		
SP-1 (AKS×SL)	3.67c	3.45b	3.66c	5.78c	9.36c	5.18b		
SP-2 (CHT-1×SL)	2.91c	3.01b	3.96c	4.69c	8.70c	4.65b		
SP-3 (SGO×SL)	2.43c	3.83b	3.51c	4.76c	7.43cd	4.39b		
SP-4 (CHT-2×SL)	2.75c	2.56c	2.15d	3.55cd	6.51d	3.50c		
SP-5 (SPL×SL)	1.32d	2.15c	2.99d	3.84cd	5.64de	3.18c		
SP-6 (China×SL)	1.21d	1.16cd	2.25d	3.14d	6.79d	2.89d		
CV (%)	25.64	22.48	27.55	32,32	30.89	33.78		

Table 6 Mean percent of fruit infestation by BFSB on six hybrid Brinjal, 3 wild *Solanum* sp. and 2 cultivated varieties at different ages in the field.

Means with the same letter(s) within a column are not significantly different according to DMRT at 5% level

DISCUSSION

In the present investigation, six hybrid accessions (segregating populations) were obtained from brinjal of cultivated and wild species, with two cultivated parents and three wild species used for the assessment of their morphological and disease incidence. To assess the whole accessions, some quantitative traits such as plant height, number of branches/plant, number of leaves/plant, canopy size/plant, on different age groups such as 30, 60, and 90 days after plantation (DAP), and number of fruits/plant, number of infected fruit/plant, and number of fruit borer/infected fruit were recorded on 90 DAP. Thus, data on the percentage of brinjal fruit and shoot borer infestation (BFSB) were also recoded and analyzed. The mean quantitative traits were evaluated using biometrical tools such as analysis of variance (ANOVA), standard error (SE), coefficient of variability percentage

(CV%), Duncan multiple range test (DMRT), and genetic parameter study.

According to Allard (1960), the segregating population can be divided into four categories based on average response and variability: high average response and high variability, high average response and low variability, low average response and high variability, and low average response and low variability. Selection is more important in the high average response and high variability groups than in the low average response and low variability groups because they are more likely to produce transgressive segregants than other groups. Low average response and high variability can result in more transgressive segregants, which may perform poorly.

Tables 2b, 3b, 4b, and 5b present heritability (h2b) and genetic parameters such as genotypic coefficient variation (GCV) and phenotypic coefficient variation (PCV) along with genetic advance (GA) with respective indicators viz. low, moderate, and high for the 7 traits. Heritability is a physical appearance dimension (phenotypic traits) or total variance that is passed down from parents. For the majority of the vield component traits, we found a wider range of low to high broad-sense heritability. Yield and yield traits such as canopy size (68.36%) had high heritability values (>60%). Plant height (43.74%), number of fruits/plant (47.32%), and number of branches/plant (32.89%) all have moderate heritability values (30-60%). Meanwhile, the number of leaves/plant (17.84%), number of infected fruit/plant (21.70%), and number of fruit borer/fruit (6.45%) were estimated to have low broad-sense heritability. These are the parameters primarily controlled by additive genes and are recommended for effective selection decisions, especially those that can result in a significant increase in fruit yield and FSB resistant eggplant genotypes. The findings agreed with previous research by Pathania et al. (2002), Chung et al. (2003), and Kumar et al. (2013). At 90 DAP, the vegetative and yield component traits produced high GCV (>20%), with the highest lead by plant height (49.95%), canopy size/plant (658.87%), number of leaves/plant (24.87%), number of branches/plant (35.69%), NFPP (68.63%), NIFPP (55.66), and NFBPP (30.92%). Aside from that, the range for PCV values found high in all yield component traits in NLPP was similar to the range observed in CSPP, with 58.88% to 796.89%. CSPP (796.89%) had the highest PCV, followed by NFBPP (121.71%), NIFPP (119.47%), NFPP (99.77%), PH (75.52%), NBPP (62.22%), and NLPP (58.88% at 90 DAP). Individual parameters are not as effective as a higher genotypic coefficient of variation combined with high heritability and genetic advance (Ayele 2011, Shabanimofrad et al. 2013). As a result, with the previous indicators as the primary criteria, traits such as plant height (PH), canopy size/plant (CSPP), number of fruits per plant (NFPP), and number of infected fruit/plant were chosen (NIFPP). These traits had higher genotypic coefficients of variation and heritability values. As a result, an important perspective on developing one trait that will positively influence other traits is presented.

To characterize the projected GCV and PCV values, the proposed index of 0-10% for low, 10-20% for moderate, and 20% for high variation was used. Closer PCV and GCV values were estimated in most of the traits in our experiment, which may have been less influenced by the environment, indicating the reliability of selection based on these traits. The selection procedure takes into account trait differences based on the degree of heredity. Concern for both heritability and genetic advancement is more effective than the unique use of heritability. We discovered that the phenotype variance values for all traits were greater than the genotype variance, indicating that the environment influences trait expression. Low to moderate heritability and genetic advanced values will inhibit trait improvement due to the strong influence of the environment on genetic effects. As a result, selecting higher values of GCV, PCV, hBS, and GA is the only way to achieve effective selection, implying that the influence of additive genes is more stable than the influence of the environment.

Evaluation of BFSB occurrence in relation to plant age and growing season

The field was monitored weekly for BFSB infestation for up to 18 weeks after the brinjal seedlings were transplanted. The brinjal plant was destroyed by BFSB soon after it was transplanted. The pest can attack the plant at any stage of development and in any part of the plant. Separate eggs were laid on the ventral surface of leaves, flowering buds, and, on rare occasions, early fruits. Caterpillars drilled into petioles, midribs of leaves, early shoots, and forage in young plants, then withered and dropped off. In some cases, the developing point was removed, and the plant will no longer grow and develop. The shoot infestation was noticed in the fourth week of transplanting and increased to a slightly higher level the following week. The BFSB infestation on the shoot then rapidly increased until the 15th week, when the infestation rate began to decline. The BFSB infestation shifted from shoots to fruits, resulting in a steady decrease in the trend of shoot infestation. Plant age, on the other hand, had a significant effect on fruit infestation, which began in the sixth week after seedling transplanting. The fruit infestation then showed a clear upward trend. The fruit infestation reached a peak in the 16th week after transplantation. It is clear that older plants suffered far more from the BFSB attack and caused far more damage to the brinjal plants, particularly the fruits. However, the level of infestation at various ages of the plant may vary depending on location, temperature, variety, and other factors. The management strategy should be chosen based on the level of BFSB infestation. The caterpillar drills into flower buds and fruits later in the development of the brijal plant, rendering them unusable (Lal and Ahmed 1965). Because the insect behaves as a shoot borer in the early stages and a fruit borer later on, a higher frequency of shoot infestation would typically result in a higher frequency of fruit invasion. Panda et al. (1971) reported a comparative invasion pattern in brinjal varieties, which is consistent with the findings of this study.

According to several authors, the infestation of BFSB is age dependent. According to Hossain et al. (2002), plant age had a significant effect on the incidence of brinjal shoot and fruit borer. They found the most BFSB infestation at 70 days after transplanting, which was statistically different from the infestation at 40 days. They also stated that the rate of infestation

Kobir et al. 2023

gradually increased with plant age and then began to decrease 100 days after transplanting. According to Naik et al. (2008), the initial infestation of BFSB occurred 51 days after transplanting, and the infestation gradually increased shoot damage. The peak incidence of BFSB occurred 74 days after transplantation. The maximum shoot damage in the current study was found in the 15th week, whereas Sharma and Chhibber (1999) found the maximum shoot damage at 29 days after brinjal transplanting.

In addition, among 11 accessions, hybrid accessions performed well for the rest of the yield component traits, but not the best, because yield is a complex trait influenced by many other traits.

REFERENCES

- Allard R.W. 1960. Principles of plant breeding. 1st Edn., John Wiley and Sons Inc., New York.
- Ayele A.G. 2011. Heritability and Genetic Advance in Recombinant Inbred Lines for Drought Tolerance and Other Related Traits in Sorghum (*Sorghum Bicolor*). Continental Journal of Agricultural Science 5(1): 1-9.
- BBS 2020. Statistical Yearbook Bangladesh. 34th edition. Bangladesh Bureau of Statistics. Ministry of Planning, Government of the People's Republic of Bangladesh, Dhaka, Bangladesh. 145pp.
- Caguiat X., D. Hautea 2014. Genetic Diversity Analysis of Eggplant (Solanum Melongena L.) and Related Wild Species in the Philippines Using Morphological and Ssr Markers. SABRAO Journal of Breeding and Genetics 46(2): 183-201.
- Chung W., S. Jeong, J. Oh, P. Hwang 2003. *Genetic* Analysis of F1 Generation in Eggplant. Retrieved from

Dempewolf H, R.J. Eastwood, L. Guarino, C. Khoury, J.V. Müller, J. Toll 2014. Adapting agriculture to climate change: a global initiative to collect, conserve, and use crop wild relatives. Agrocecol Sust Food Syst 38:369–377.

https://doi.org/10.1080/21683565.870629

- Gebhardt S.E., R.G. Thomas 2002. Nutritive value of foods. Home Garden Bulletin (USDA) 72: 80–81.
- Hopkins J., N Maxted 2010. Crop Wild Relatives: Plant genetic conservation for food security.
- Hossain M.M., M. Shajahan, M.A. Salam 2002. Screening of some brinjal varieties and lines against brinjal shoot and fruit borer, L. orbonalis Guenee. Pak. J. Biol. Sci. 5(10): 1032-1040.
- Kumar N, C.R. Muthukrishnan, I. Irulappan 1979. Correlation studies and path analysis in the segregating generations of tomato (*Lycopersicon esculentum* Mill.) South Indian Hort. 27: 44-48.
- Kumar SR, T. Arumugam, C. An, V. Premalakshmi 2013. Genetic variability for quantitative and qualitative characters in Brinjal (*Solanum melongena* L.). Afr. J. Agric. Res., 8: 4956– 4959.
- Lal B.S., S.Q. Ahmed 1965. The biology and control ofbrinjal shoot and fruit borer L. orbonalis. J Eco Ent58: 448-451. Available at https://doi.org/10.1093/jee/58.3.448
- Mutlu N., F.H. Boyaci, M. GCmen, K. Abak 2008. Development of SRAP, SRAP-RGA, RAPD and SCAR markers linked with a Fusarium wilt resistance gene in eggplant. Theor Appl Genet

- Naik V., B. Chinna, P. Rao, Arjuna, P.V. Krishnayya, M.S.V. Chalam 2009. Seasonal Incidence and Management of *Bemisia tabaci* Gennadius and *Amrasca biguttula biguttula* Ishida of Brinjal. Annals of Plant Protection Sciences, 17 (1): 9-13.
- Naujeer H.B. 2009. Morphological diversity in eggplant (*Solanum melongena* L.), their related species and wild types conserved at the National gene bank in Mauritius.
- Panda N, A. Mahapatra, M. Sahool 1971. Field evaluationof some brinjal varieties for resistance to shoot and fruit borer. Indian J Agric Sci 41: 597-601. Available at http://agris.fao.org/agrissearch/search.do?recordID=US201302293473
- Pathania N.K., D.R. Rajeev Katoch, C.K. Chaudhary 2002. Genetic Variability and Association Studies in Eggplant. Paper presented at the International Conference on Vegetables, Bangalore, India.
- Piao Xiang-Min, Jong-Wook Chung, Gi-An Lee, Jung-Ro Lee, Gyu-Taek Cho, Ho-Sun Lee, Kyung-Ho Ma, Jing Guo1, Hong Sig Kim3, Sok-Young Lee 2014. Variation in Antioxidant Activity and Flavonoid Aglycones in Eggplant (*Solanum melongena* L.) Germplasm. Plant Breed. Biotech. 2 (4): 396-403.
- San José, R., M.C. Sánchez-Mata, M. Cámara, J. Prohens 2014. Eggplant fruit composition as affected by the cultivation environment and genetic constitution. Journal of the Science of Food and Agriculture 94(13): 2774-2784.
- Shabanimofrad M., M. Rafii, P.M. Wahab, A. Biabani,M. Latif 2013. Phenotypic, Genotypic andGenetic Divergence Found in 48 Newly

Collected Malaysian Accessions of *Jatropha Curcas* L. Industrial Crops and Products 42: 543-551. Sharma A.K., R.C. Chhibber 1999. Effect of exposure periods and insecticides on *Leucinodes orbonalis* in brinjal. Indian Journal of Entomology 61(3): 242-251.