SCREENING OF BRINJAL GENOTYPES TO IDENTIFY GENETIC RESOURCES WITH HIGHER YIELD AND YIELD ATTRIBUTES

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Abstract

The present study was conducted for morphological evaluation of 65 brinjal genotypes at the research field of Bangladesh Institute of Nuclear Agriculture (BINA), Mymensingh. Morphological characterization, performed as per the minimum descriptors as prescribed by IBPGR, revealed wide and significant variations for most of the traits investigated. In terms of individual fruit weight, the heaviest fruits were obtained from the genotype SM17 (251.78 g) followed by SM6 (221.56 g), whereas the lightest fruits were found in genotype SM58 (50.78 g). At 120 days of planting (DAP), the longest and shortest plants were recorded from the genotypes SM44 (73.67 cm) and SM24 (31.22 cm), respectively. Most importantly, the highest yield (58.34 t ha^{-1}) was recorded from the genotype SM28 followed by SM6 (56.95 t ha^{-1}). By contrast, the genotype SM46 yielded the lowest (8.36 t ha^{-1}). Among the 65 genotypes studied, 13 promising genotypes (SM1, SM5, SM6, SM7, SM11, SM16, SM17, SM21, SM28, SM33, SM42, SM54 and SM56) were selected based on yield and other quality attributes, namely colour, shape, size, texture and glossiness.

Key words: Brinjal, eggplant, genotype screening, yield, yield attributes.

Introduction

Brinjal (*Solanum melongena* L.) also known as eggplant or aubergine, is an important solanaceous vegetable crop grown widely in the central, south and south-east Asian countries, and in a number of African countries of the world (Kalloo, 1993; Alam *et al*., 2003; Kumar *et al*., 2003; Shaukat *et al*., 2009). Brinjal is believed to have been originated in India, as the people of this subcontinent were reported to grow brinjal since last 4000 years (Dunlop, 2006). It occupies a distinct place in the realm of vegetable crops globally. The current global production of brinjal is estimated as 54.08 million tons of which 93% is contributed by the Asian countries (FAO, 2020). In terms of production, China ranked the top (45% of world output) followed by India (24%) (FAO, 2020). Brinjal is one of the most nutritious and culturally important vegetables and is a good source of minerals and vitamins. It is also one of the most common, popular and principal vegetables grown both in summer and winter seasons in Bangladesh. To meet domestic demand Bangladesh produces substantial amounts brinjal every year. During 2019-20, 558 thousand metric tons of brinjal were produced from 53.44 thousand hectare of land (BBS, 2021).

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Numerous species of the genus *Solanum* are available in nature of which most of them are wild and few are cultivated like *S. melongena* L. and *S. tuberosum* L. There exist numerous cultivars with considerable morphological and genetic variability required for varietal improvement of brinjal. Different morphological studies are very much important for characterization and classification of germplasm (Agdagwa and Nadukwa, 2004; Sudre *et al*., 2010). The seeds of different varieties or cultivars of brinjal in our country are readily available and cheap and could be preserved by the farmers themselves thus reducing their cost of production. Many local varieties are well known among the farmers but their improvement is needed. So characterization of genotypes based on yield and yield attributes is helpful for identification of superior genotypes for breeding programme. For sustainable improvement of any vegetable crop, judicious and effective use of genotypes is a must for the advancement of agronomic characters coupled with resistant ability against biotic and abiotic stresses. So, keeping in the view the vast opportunity for improvement of brinjal, the present research was undertaken to perform morphological characterization of brinjal genotypes with desired yield and yield attributes.

Materials and methods

The experiment was conducted at the research field of Bangladesh Institute of Nuclear Agriculture (BINA), Mymensingh with 65 brinjal genoypes were collected from IPM Lab of Bangladesh Agricultural University (BAU), Mymensingh, Bangladesh Agriculture Research Institute (BARI), Gazipur and BINA, Myemensingh. The collected genotypes were assigned to accession numbers starting from SM1-SM65 (Table 1). The seeds were sown and seedlings of 35 days old were planted in the prepared land flowing randomized complete block design (RCBD) with three replications. One genotype represented one treatment and 5 plants of one genotype represented one replication. Plant to plant and row to row distances were 80 and 60 cm, respectively. The plot size was 6.0 × 5.6 m. Fifty centimeters drain was kept between two adjacent plots to facilitate drainage of excess water. Fertilizers were applied as per Fertilizer Recommendation Guide (BBS, 2011). Middle three plants in a row were selected for observations in each replication per genotype. Data were recorded on various yield attributers (e.g. plant height, number of primary branches, canopy area, individual fruit weight and number of fruits per plant) and yield. Statistical analyses of the reorded data were performed through descriptive statistics (percentage, mean, standard error of mean) and analysis of variance (ANOVA) was performed using computer package MStat C to find out the statistical significance of the treatments (genotypes). The mean separation was done least significance difference (LSD) test (Gomez and Gomez, 1984).

Table1. List of brinjal genotypes along with sources used in the experiment (information provided in the parentheses indicate original source of the genotypes)

Sl. No.	Accession No.	Local name	Sources of collection
1.	SM1	Zhumki	IPM Lab, BAU, Mymensingh (Nandina, Jamalpur)
2.	SM2	ISD-006	IPM Lab, BAU, Mymensingh (BARI, Joydebpur, Gazipur)
3.	SM3	Laffa-M	IPM Lab, BAU, Mymensingh (Marichar Char, Mymensingh)
4.	SM4	Laffa-G	IPM Lab, BAU, Mymensingh (Gaffargoan, Mymensingh)
5.	SM5	Laffa-B	IPM Lab, BAU, Mymensingh (Rupgonj, Narayangonj)
6.	SM6	Laffa-S	IPM Lab, BAU, Mymensingh (Sherpur)
7.	SM7	Volanath-M	IPM Lab, BAU, Mymensingh (Marichar Char, Mymensingh)
8.	SM8	Thamba	IPM Lab, BAU, Mymensingh (Marichar Char, Mymensingh)
9.	SM9	Dohazari Red	IPM Lab, BAU, Mymensingh (Dohazari, Chittagong)
10.	SM10	Dohazari-G	IPM Lab, BAU, Mymensingh (Dohazari, Chittagong)
11.	SM11	Borka	IPM Lab, BAU, Mymensingh (Notun Bazar, Mymensingh)
12.	SM12	Khatkhatia-B	IPM Lab, BAU, Mymensingh(Bhurungamari, Kurigram)
13.	SM13	Khatkhatia	IPM Lab, BAU, Mymensingh (BAU, Mymensingh)
14.	SM14	Kaikka-N	IPM Lab, BAU, Mymensingh (Nandina, Jamalpur)
15.	SM15	Kaikka-G	IPM Lab, BAU, Mymensingh (Gaffargoan, ymensingh)
16.	SM16	Islampuri-BADC	IPM Lab, BAU, Mymensingh (BADC, Mymensingh)
17.	SM17	Jessore-L	IPM Lab, BAU, Mymensingh (Manirampur, Jessore)
18.	SM18	Dharala	IPM Lab, BAU, Mymensingh (Betila, Manikgonj)
19.	SM19	Uttara	IPM Lab, BAU, Mymensingh (BARI, Joydebpur, Gazipur)
20.	SM20	Kazla	IPM Lab, BAU, Mymensingh (BARI, Joydebpur, Gazipur)
21.	SM21	BL-118	IPM lab, BAU, Mymensingh (BARI, Joydebpur, Gazipur)
22.	SM22	Dundhul	IPM Lab, BAU, Mymensingh (Gaffargoan, Mymensingh)
23.	SM23	EG-190	IPM Lab, BAU, Mymensingh (AVRDC, Taiwan)
24.	SM24	China oblong	IPM Lab, BAU, Mymensingh (Paba, Rajshahi)
25.	SM25	Ishurdi-WS	IPM Lab, BAU, Mymensingh (Ishurdi, Pabna)
26.	SM26	Ishurdi-BS	IPM Lab, BAU, Mymensingh (Ishurdi, Pabna)
27.	SM27	Putabegun	IPM Lab, BAU, Mymensingh (Chittagong)
28.	SM28	Longla Long	IPM Lab, BAU, Mymensingh (Longla Moulvibazar)
29.	SM29	Shingnath-S	IPM Lab, BAU, Mymensingh (BAU, Mymensingh)
30.	SM30	Longla Talbegun	IPM lab, BAU, Mymensingh (Longla Moulvibazar)
31.	SM31	Islampuri	IPM Lab, BAU, Mymensingh (Islampur, Jamalpur)
32.	SM32	Thapara	IPM Lab, BAU, Mymensingh (Gabtoli, Bogra)
33.	SM33	Menter	IPM Lab, BAU, Mymensingh (Gabtoli, Bogra)
34.	SM34	Salta	IPM lab, BAU, Mymensingh (Burirhut, Rangpur)
35.	SM35	Iribegun	IPM Lab, BAU, Mymensingh (Betila Manikgonj)
36.	SM36	Eye-red	IPM Lab, BAU, Mymensingh (Betila Manikgonj)
37.	SM37	Deembegun	IPM lab, BAU, Mymensingh (BAU, Mymensingh)
38.	SM38	Comilla-L	IPM Lab, BAU, Mymensingh (Comilla)
39.	SM39	Chega	IPM Lab, BAU, Mymensingh (Jessore)

Table 1. (Continued)

Sl. No.	Accession No.	Local name	Sources of collection
40.	SM40	BARI Begun-1 (Uttara)	BARI, Joydebpur, Gazipur
41.	SM41	BARI Begun-4 (Kazla)	BARI, Joydebpur, Gazipur
42.	SM42	BARI Begun-5 (Nayantara)	BARI, Joydebpur, Gazipur
43.	SM43	BARI Begun-6 (Ishurdi local)	BARI, Joydebpur, Gazipur
44.	SM44	BARI Begun-7 (Singnath)	BARI, Joydebpur, Gazipur
45.	SM45	BARI Begun-9 (Dohazari)	BARI, Joydebpur, Gazipur
46.	SM46	BARI Begun-10 (Bholanath)	BARI, Joydebpur, Gazipur
47.	SM47	BAU Begun-1	BINA, BAU campus, Mymensingh
48.	SM48	Indian-1	BINA, BAU campus, Mymensingh
49.	SM49	Pahuza-1	BINA, BAU Campus, Mymensingh
50.	SM50	Pahuza-2	BINA, BAU Campus, Mymensingh
51.	SM51	Magura Local	BINA, BAU Campus, Mymensingh
52.	SM52	Long Lived High Plant	BINA, BAU Campus, Mymensingh
53.	SM53	Purple Long	BINA, BAU Campus, Mymensingh
54.	SM54	Kansant Local	BINA, BAU Campus, Mymensingh
55.	SM55	Laffa-BAU	IPM Lab, BAU, Mymensingh (BAU, Mymensingh)
56.	SM56	Katabegun-WS	IPM Lab, BAU, Mymensingh (Paba, Rajshahi)
57.	SM57	Marich Begun-S	IPM Lab, BAU, Mymensingh (Sherpur)
58.	SM58	Marich Begun-E	IPM Lab, BAU, Mymensingh (Sherpur)
59.	SM59	Natore Local (Long)	BINA, BAU Campus, Mymensingh
60.	SM60	Apple Begun	BINA, BAU Campus, Mymensingh
61.	SM61	Natore Local (Round)	BINA, BAU Campus, Mymensingh
62.	SM62	China Round	BINA, BAU Campus, Mymensingh
63.	S M63	BAU Begun-2	BINA, BAU Campus, Mymensingh
64.	SM64	Kansat-1	BINA, BAU Campus, Mymensingh
65.	SM65	Kansat-2	BINA, BAU Campus, Mymensingh

Results and discussion

Plant height

Plant height widely varied among the collected 65 brinjal genotypes during the entire period of investigation (Table 2). Plant height gradually increased over time. Plant heights ranged from 4.44-19.44, 24.11-56.22, 31.44-69.67 and 31.22-73.67 cm at the 40. 70, 100 and 120 DAP, respectively (Table 2). At the 120th DAP, the longest and shortest plants were recorded from the genotypes SM44 (73.67 cm) and SM24 (31.22 cm), respectively (Table 2). Other comparatively taller genotypes included SM15, SM16, SM21, SM25, SM36, SM49 and SM62. The genotype SM24 was found to be the shortest (31.22 cm) followed by SM30 (38.44 cm) at the same day of observation. The observed variation was possibly attributed to the genetic factor. Similar trend was also observed by Kumar *et al.* (2011), Ahmed *et al.* (2014).

Number of primary branches plant^{-1}

Branching is an important character of brinjal plants since fruiting and yield depend greatly on profuse benching. Number of primary branches plant^{-1} varied significantly among the genotypes at all the days of investigations (40, 70, 100 and 120 days after transplanting). Number of primary branches plant^{-1} increased with the advancement of plant growth. At the 40th DAP, plants of some genotypes had zero (SM7, SM16, SM17, SM61 and SM62) to 3.11 primary branches (Table 2). Number of primary branches pant^{-1} ranged from 0-3.11, 0.11-8.33, 3.56-12.22 and 4.11-12.22 at the 40, 70, 100 and 120 DAP, respectively. The highest number of primary branches plant^{-1} were recorded in the genotype SM42 (12.22) followed by SM58 (9.33), SM51 (9.11) and SM6 (9.00) (Table 2). The least number of primary branches plant^{-1} was recorded in the plants of the genotype S10 (4.11) followed by SM9 (4.44); SM45, SM62 & SM64 (4.67); SM47 & SM55 (4.89). The rest of the genotypes had moderate branching (Table 2). The variation was very wide and was due to difference in genetic constituents.

Canopy area

Highly significant variations were observed among the collected genotypes in terms of canopy area during the entire period of investigation. Irrespective of the genotypes, canopy area trended to increase as the time after planting advanced. However, the rates of increase were higher until the 100th DAP, and reduced afterwards. Canopy areas ranged from 83.04 (SM64) to 575.10 (SM16); 718.97 (SM62) to 2704.94 (SM26); 1384.39 (SM30) to 4205.42 (SM20); and 1529.18 (SM62) to 4264.82 (SM20) cm^2 at the 40, 70, 100 and 120 DAP, respectively (Table 2). At the 120th DAP, the genotype with the largest canopy area was SM20 (4264.82 cm^2) followed by SM42 (4006.99 cm^2), SM33 (3913.31 cm^2) and SM46 (3840.57 cm^2) (Table 2). On the contrary, the genotype with the smallest canopy was SM62 (1529.18 cm^2) followed by SM53 (1832.10 cm^2) and S24 (1695.86 cm^2). The rest of the genotypes had moderate canopy area at the 120 days after transplanting. Similar trends of canopy area for the collected genotypes were also manifested at the 40, 70 and 100 DAP (Table 2).

Individual fruit weight

There were marked variation in fruit weight among the collected 65 brinjal genotypes. Individual fruit weight ranged from 50.78 (SM58) to 251.78 g (SM17). The heaviest fruit was obtained from the genotype SM17 (251.78g) followed by SM6 (221.56g) and SM47 (194.78 g), whereas the lightest fruits were obtained from the genotype SM58 (50.78 g) followed by SM57 (67.00 g) and SM23 (86.78 g) (Table 3).

Fruit length

Fruit length and diameter significantly differed among the genotypes. Length of fruit ranged from 6.78 (SM60) to 30.40 cm (SM45). The longest fruit was harvested from the genotype SM45 (30.40 cm) followed by SM44 (27.24 cm) and SM50 (19.22 cm), while the

shortest was recorded in the genotype SM60 (6.78 cm) followed by SM24 (7.04 cm) and SM39 (7.26 cm) (Table 3). Variation of fruit length has also been reported by Gavade and Ghadge (2015), Vandana *et al.* (2014), Kumer *et al.* (2011).

Fruit diameter

Significant variation was also observed among the genotypes in case of fruit diameter. Similar to fruit length, fruit diameter also varied among the genotypes. Fruit breadth ranged from 2.50 (SM13) to 8.66 cm (SM29). The widest fruit was obtained from the genotype SM29 (8.66 cm) followed by SM45 (8.40 cm) and SM56 (8.38 cm). By contrast, the narrowest fruits were obtained from the genotype SM13 (2.50 cm) followed by SM49 (2.52 cm) and SM53 (2.52 cm). Considering both length and diameter, the genotype SM45 had the largest fruit (Table 3). This result is supported by Ahmed *et al.* (2014), Begum *et al*. (2013) and Kumer *et al.* (2011).

Length of fruit peduncle

Fruit peduncle length varied significantly among the collected genotypes. The fruit of genotype SM27 had the longest peduncle (11.42 cm) followed by SM46 (9.66 cm) and SM44 (9.42 cm). On the other hand the fruits of the genotype SM16 had the shortest peduncle (2.52 cm) followed by SM16 (2.71 cm) and SM34 2.76 cm) (Table 3).

Number of fruits plant^{-1}

Total number of fruits plant^{-1} varied significantly among the genotypes. Number of fruits plant^{-1}ranged from 4.33 to 18.89. The maximum number of fruits were harvested from the genotype SM25 (18.89 plant^{-1}), which was closely followed by the genotypes SM51 (18.56 plant^{-1}), SM28 (17.78 plant^{-1}) and SM40 (17.67 plant^{-1}). In contrast, the lowest number of fruits were recorded in genotype SM46 (4.33 plant^{-1}) followed by the genotypes SM43 (5.00 plant^{-1}), SM35 (5.67 plant^{-1}) and SM59 (5.89 plant^{-1}) (Table 3).

Weight of fruits plant^{-1}

Total weight of fruits per plant differed significantly amongst the collected brinjal genotypes. Average weight of brinjal fruits per plant was in the range from 401.33 to 2800.33 g. The highest amount of fruits was obtained from the genotype SM28 (2800.33 g), which was closely followed by the genotypes SM6 (2733.44 g) and SM7 (2595.56 g). On the other hand, the lowest amount of fruits were harvested from the genotype SM46 which yielded only 401.33 g fruit per plant and was followed closely by the genotypes SM64 (715.22 g per plant) and SM58 (852.78 g per plant) (Table 3). Ahmed *et al.* (2014) found a result as high as 5320 g plant^{-1}. Lower yield per plant for some genotype may be because of non-favourable environment.

Yield of brinjal

Yield is the most important parameter in respect of crop improvement. Yield of brinjal varied markedly and significantly among the collected 65 genotypes, and which ranged from 8.36 to 58.34 t ha^{-1}. The highest yield of 58.34 t ha-^{1} was recorded from the genotype SM28 that was closely followed by the genotypes SM6 (56.95 t ha^{-1}) and SM7 (54.07 t ha^{-1}). By contrast, the lowest yielding genotype was SM46 that yielded only 8.36 t ha^{-1} and was closely followed by the genotypes SM64 (14.90 t ha^{-1}) and SM58 (17.77 t ha^{-1}). This result is in support of Kumer *et al.* (2014) and Sanas *et al*. (2014). Lower yield were found of some genotypes due to may be genetical and environmental effect. As per BBS (2020), average yield of rabi brinjal is 12.25 t ha^{-1}. The average yield of BARI released varieties ranges from 45-55 t ha^{-1} (Krishi Projukti Hatboi, 2020). Among the 65 genotypes, 13 promising genotypes (SM1, SM5, SM6, SM7, SM11, SM16, SM17, SM21, SM28, SM33, SM42, SM54 and SM56) were selected based on yield (equal or higher than BARI released varieties) and other quality attributes, namely cooler, shape, size, texture and glossiness (Fig. 1).

Fig. 1. Selected 13 high yielding brinjal genotypes.

Table 2. Variation in plant height, number of primary branches plant^{-1} and canopy area among 65 brinjal genotypes at different days after planting (DAP)

Genotypes	Plant height (cm) at different DAP				Number of primary branch plant^{-1} at different DAP				Canopy area (cm^2) at different DAP			
	40	70	100	120	40	70	100	120	40	70	100	120
SM1	14.56	40.11	57.78	56.33	0.44	3.56	5.22	5.33	508.24	1676.06	2562.33	2642.66
SM2	8.56	27.00	47.22	50.00	0.83	3.28	5.89	6.17	335.98	1264.20	3281.83	3416.15
SM3	8.56	30.44	44.33	47.56	0.11	3.00	5.11	5.44	367.29	1795.73	3069.09	3279.47
SM4	11.06	32.56	49.44	51.89	0.56	6.56	6.22	6.44	597.04	2081.56	3237.69	3361.72
SM5	12.67	37.67	53.22	55.78	0.22	3.33	4.56	5.11	362.15	1837.08	3064.20	3234.20
SM6	11.56	39.78	55.11	57.33	0.78	5.56	8.89	9.00	547.36	1954.91	3416.06	3576.72
SM7	12.67	40.89	53.89	57.11	0.00	5.00	7.22	7.44	592.15	2206.98	3100.92	3200.18
SM8	9.00	25.56	40.56	42.89	0.33	3.22	6.56	6.89	456.87	1789.45	3093.68	3284.79
SM9	7.44	26.44	34.56	44.89	0.56	3.56	4.33	4.44	312.52	2187.88	3329.62	3438.13
SM10	11.22	35.67	41.00	46.67	0.22	3.44	3.56	4.11	312.69	1824.17	2578.46	2634.72
SM11	15.22	26.56	34.89	46.78	0.56	3.33	4.78	6.44	411.34	1087.31	2203.58	3038.12
SM12	11.67	34.67	50.56	52.67	0.11	5.00	5.89	6.11	299.74	1146.89	1744.62	2015.71
SM13	17.11	36.89	48.22	53.56	0.78	5.44	6.78	7.00	435.42	1973.32	2749.51	3037.08
SM14	8.00	27.44	40.89	46.33	0.22	4.00	4.56	4.89	323.46	1225.99	1917.06	2040.65
SM15	11.11	33.00	50.89	72.22	0.11	3.89	5.22	6.56	418.84	1319.50	1915.92	3510.00
SM16	19.44	53.56	69.56	70.89	0.00	2.56	4.44	4.67	575.10	2210.47	3419.20	3491.68
SM17	11.11	31.33	45.89	49.89	0.00	0.11	4.00	5.22	370.35	1664.55	2851.03	3083.40
SM18	23.44	37.00	46.00	56.33	0.22	3.33	4.67	6.44	428.52	1301.71	2177.59	3829.23
SM19	12.78	27.11	36.89	42.33	0.44	6.44	8.33	8.33	387.09	2257.05	3539.48	3773.75
SM20	13.89	30.11	48.11	49.44	1.33	6.33	6.00	6.33	336.33	2168.17	4205.42	4264.82
SM21	15.78	43.22	59.33	63.00	1.22	6.22	7.11	7.22	480.07	2190.41	2971.66	3164.77
SM22	11.89	29.33	43.78	48.78	0.89	4.11	6.11	6.22	249.50	1991.37	2627.40	2762.24
SM23	12.78	27.56	37.11	43.56	0.11	4.56	5.89	5.78	283.82	1241.09	1783.78	2036.38
SM24	10.11	25.22	29.33	31.22	0.11	2.33	3.67	4.44	193.99	1177.15	1656.78	1695.86
SM25	12.78	38.89	52.56	63.11	0.22	3.78	4.78	6.11	526.47	1552.91	2673.54	2554.39
SM26	14.78	30.78	40.11	43.22	0.22	6.33	7.22	7.22	446.49	2704.94	3948.64	3950.99
SM27	19.44	42.89	55.33	57.89	1.56	4.11	5.44	5.67	426.26	2088.80	2803.06	2893.34
SM28	14.67	36.22	47.78	48.44	0.22	4.22	6.67	7.11	338.25	1718.63	2429.31	2476.06
SM29	13.67	33.22	44.22	45.00	0.89	5.44	5.89	6.00	421.24	1421.98	1987.10	1993.90
SM30	13.67	24.56	31.44	38.44	0.78	3.33	4.67	6.78	318.45	769.82	1384.39	1975.84
SM31	11.44	32.00	42.44	47.11	0.22	4.56	5.89	6.22	584.22	2336.68	2959.27	3071.79
SM32	10.78	32.89	51.67	55.22	0.78	3.33	5.00	5.67	188.40	1676.06	2562.33	2642.66
$LSD_{0.05}$	6.07	10.54	10.65	10.77	1.31	2.53	2.28	2.19	257.15	704.64	1161.61	1180.83
$LSD_{0.01}$	7.98	13.85	13.99	14.15	1.72	3.32	3.00	2.87	337.97	926.10	1526.69	1551.94
Level of sig.	**	**	**	**	**	**	**	**	**	**	**	**

** = Significant at 1% level of probability

Table 2 (Contd.)

Genotypes	Plant height (cm) at different DAP				Number of primary branch plant $^{-1}$ at different DAP				Canopy area (cm^2) at different DAP			
	40	70	100	120	40	70	100	120	40	70	100	120
SM33	9.22	37.33	47.44	50.22	1.22	5.56	6.11	6.22	364.50	2398.96	3562.59	3913.31
SM34	10.39	28.00	50.89	54.22	0.33	2.22	4.56	4.78	316.49	1338.43	2655.74	2753.34
SM35	8.00	27.33	44.56	47.56	0.22	3.33	4.78	5.11	399.26	2055.48	3507.21	3542.44
SM36	17.44	43.33	61.33	68.22	0.22	5.22	6.56	7.00	591.45	2215.27	3595.91	3733.11
SM37	13.67	29.89	47.00	50.22	0.67	4.00	5.11	5.33	475.45	2217.19	2930.84	3070.05
SM38	20.22	39.00	51.33	52.56	0.44	3.56	4.56	5.22	219.28	1844.92	2499.27	2581.95
SM39	16.00	32.67	44.89	48.89	0.67	3.33	4.44	5.11	446.84	1940.78	2723.86	2869.52
SM40	15.11	34.89	46.89	49.78	0.89	6.11	5.44	5.78	361.01	2163.02	3054.79	3167.13
SM41	11.33	36.89	51.00	55.44	0.89	5.56	8.00	8.11	305.71	1690.54	2621.55	2757.62
SM42	13.33	38.22	51.44	56.00	1.22	8.33	12.22	12.22	346.10	2250.59	3872.93	4006.99
SM43	7.67	22.56	56.44	59.44	0.33	3.33	5.89	6.11	350.90	1658.97	3018.59	3266.91
SM44	13.67	56.22	69.67	73.67	1.56	5.89	6.33	6.78	480.77	2146.19	2727.96	2893.16
SM45	14.11	54.00	65.11	66.67	0.22	3.00	4.33	4.67	223.20	1698.22	2818.85	2988.58
SM46	15.22	34.11	47.22	57.89	1.44	4.33	5.33	5.89	366.51	2580.56	3651.30	3840.57
SM47	12.00	30.11	47.22	49.56	0.44	3.56	4.56	4.89	404.19	1638.90	3136.43	3254.18
SM48	11.11	38.44	54.67	58.33	1.00	6.33	7.00	7.11	400.22	1855.74	2561.98	2904.94
SM49	14.78	45.33	60.78	65.33	1.33	5.89	7.33	7.56	446.12	2034.46	3102.58	3436.03
SM50	15.33	33.11	48.44	52.11	3.11	6.33	6.89	6.89	443.35	1730.14	2945.76	2993.38
SM51	13.67	38.00	52.44	56.00	2.11	8.67	9.11	9.11	439.86	2063.16	2903.63	3006.38
SM52	14.89	40.22	61.33	72.00	1.00	4.33	5.11	5.78	763.20	2102.23	3393.47	3823.04
SM53	10.44	34.33	47.11	49.00	1.78	7.11	7.67	7.78	142.09	1221.63	1689.76	1832.10
SM54	18.56	39.00	53.56	55.78	1.44	5.11	5.67	6.11	568.34	1936.33	2863.68	3032.19
SM55	12.33	27.00	44.11	45.44	0.00	2.22	4.11	4.89	506.41	2041.35	2799.92	2913.05
SM56	12.33	33.00	47.00	52.44	1.44	4.44	6.22	6.22	597.30	1892.20	2587.19	3003.23
SM57	8.50	27.89	38.56	55.11	1.89	2.56	4.67	6.33	228.70	1458.09	2672.84	4316.72
SM58	12.00	30.00	53.67	53.67	1.44	8.89	9.22	9.33	437.51	2727.35	3877.81	3875.63
SM59	7.11	24.11	40.56	45.78	0.33	3.56	5.78	6.22	186.53	960.84	1945.23	2594.34
SM60	6.67	24.33	37.56	49.44	0.00	3.22	4.56	5.56	145.18	1328.13	2629.14	2664.64
SM61	6.89	30.00	48.44	55.22	0.56	3.89	4.78	5.11	111.08	1277.80	1954.13	1966.16
SM62	8.83	32.78	61.11	61.67	0.00	1.89	4.00	4.67	88.15	718.97	1429.57	1529.18
SM63	4.44	30.00	47.89	53.56	0.67	4.22	5.00	5.44	200.09	946.62	2915.23	3049.29
SM64	5.22	28.67	47.11	46.89	0.11	3.00	3.78	4.67	83.04	1020.85	2397.56	2489.84
SM65	9.56	30.78	46.78	49.67	0.89	4.78	5.56	5.89	197.91	1653.82	3323.34	3822.08
$LSD_{0.05}$	6.07	10.54	10.65	10.77	1.31	2.53	2.28	2.19	257.15	704.64	1161.61	1180.83
$LSD_{0.01}$	7.98	13.85	13.99	14.15	1.72	3.32	3.00	2.87	337.97	926.10	1526.69	1551.94
Level of sig.	**	**	**	**	**	**	**	**	**	**	**	**

** = Significant at 1% level of probability

Table 3. Important yield attributes (fruit characters) of the 65 genotypes at commercial maturity

Genotypes	Fruit length (cm)	Fruit breadth (cm)	Peduncle length (cm)	Number of fruit plant^{-1}	Individual fruit wt. (g)	Wt. of fruits plant^{-1} (kg)
SM1	18.22	3.48	5.32	16.67	130.89	2.17
SM2	14.56	4.41	3.52	11.78	99.56	1.16
SM3	15.52	5.18	4.98	9.89	189.44	2.03
SM4	11.96	4.90	5.50	11.00	167.33	1.87
SM5	16.10	4.46	4.24	14.33	159.78	2.26
SM6	17.13	5.32	6.56	12.22	221.56	2.73
SM7	17.59	5.81	4.80	14.00	187.22	2.60
SM8	11.50	4.45	4.22	8.89	123.89	1.08
SM9	12.06	6.60	3.80	6.11	167.67	1.02
SM10	12.46	6.64	5.34	9.78	178.67	1.81
SM11	11.62	7.07	4.48	13.78	184.00	2.57
SM12	14.36	3.30	3.80	13.78	87.11	1.19
SM13	20.61	2.50	4.86	15.11	101.78	1.51
SM14	11.94	4.76	5.10	9.44	149.11	1.44
SM15	16.45	4.00	3.30	14.89	108.44	1.57
SM16	8.53	8.11	2.71	15.33	167.78	2.57
SM17	12.30	8.16	2.52	9.00	251.78	2.25
SM18	9.32	6.42	3.71	10.89	169.44	1.85
SM19	10.96	6.00	4.54	15.89	134.22	2.13
SM20	10.25	5.12	3.97	15.11	101.67	1.53
SM21	15.53	4.08	6.86	16.33	134.11	2.19
SM22	17.32	4.96	9.08	12.56	151.89	1.94
SM23	14.10	3.76	6.26	19.11	86.78	1.67
SM24	7.04	4.87	4.71	10.78	92.56	0.99
SM25	15.04	4.37	5.42	18.89	90.89	1.74
SM26	8.39	5.16	4.16	14.56	115.22	1.70
SM27	7.28	6.09	4.83	13.89	129.67	1.82
SM28	17.21	4.35	11.42	17.78	157.89	2.80
SM29	17.50	8.66	5.35	14.78	149.56	2.22
SM30	15.41	3.73	4.52	12.67	140.22	1.77
SM31	10.70	6.78	5.79	10.44	197.00	2.08
SM32	10.31	5.82	3.80	8.89	187.78	1.69
SM33	9.74	6.32	3.64	14.00	167.33	2.34
SM34	13.44	3.45	2.76	13.00	107.78	1.39
SM35	9.12	7.22	3.01	5.67	194.56	1.06
SM36	11.86	3.31	7.53	13.00	107.56	1.37
SM37	9.15	5.85	3.32	8.33	123.00	1.03
SM38	8.44	6.75	3.62	10.44	154.22	1.62
SM39	7.26	6.87	3.23	8.00	175.78	1.41
SM40	13.15	3.87	3.52	17.67	102.00	1.82
SM41	13.75	3.96	2.77	13.00	140.33	1.53
SM42	8.70	6.82	3.90	13.78	156.89	2.19
SM43	8.50	5.51	6.68	5.00	182.56	0.94

Table 3. (Contd.)

Genotypes	Fruit length (cm)	Fruit breadth (cm)	Peduncle length (cm)	Number of fruit plant^{-1}	Individual fruit wt. (g)	Wt. of fruits plant^{-1} (kg)
SM44	27.24	2.81	9.42	12.00	107.67	1.26
SM45	30.40	8.40	4.49	12.11	133.00	1.62
SM46	16.78	2.95	9.66	4.33	92.56	0.40
SM47	7.60	7.56	4.52	7.44	194.78	1.46
SM48	12.46	4.62	5.82	11.33	138.33	1.56
SM49	18.54	2.52	4.10	17.22	95.56	1.69
SM50	19.22	3.15	4.92	16.78	98.44	1.65
SM51	14.21	4.56	4.10	18.56	100.44	1.88
SM52	15.22	5.88	3.82	8.78	193.22	1.63
SM53	18.06	2.54	5.68	12.11	107.11	1.25
SM54	15.14	4.66	5.44	15.67	137.78	2.16
SM55	10.32	5.94	4.14	10.22	181.78	1.89
SM56	10.36	8.38	3.30	14.22	161.56	2.30
SM57	9.16	3.06	3.93	16.67	67.00	1.11
SM58	8.49	2.74	3.32	16.56	50.78	0.85
SM59	11.22	2.64	3.34	5.89	176.44	1.03
SM60	6.78	7.31	3.26	9.00	166.89	1.50
SM61	9.62	5.05	3.28	11.67	153.67	1.80
SM62	8.52	7.46	3.53	6.67	148.56	0.99
SM63	11.18	6.26	5.33	8.89	161.11	1.44
SM64	14.49	3.33	4.86	6.56	108.44	0.72
SM65	12.45	5.73	6.75	6.56	168.67	1.08
$LSD_{0.05}$	2.02	2.06	1.33	2.59	33.63	0.55
$LSD_{0.01}$	2.65	2.71	1.74	3.40	44.20	0.72
Level of sig.	**	**	**	**	**	**

** = Significant at 1% level of probability

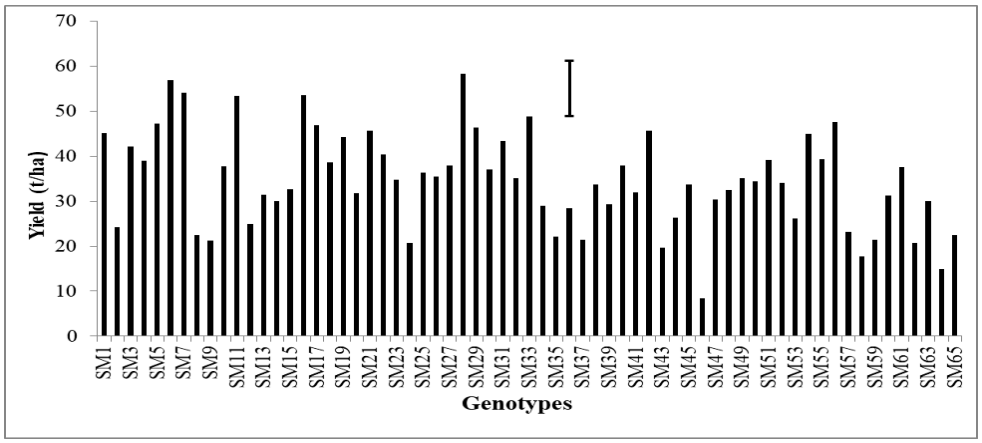

Fig. 1. Genotypic difference in yield of brinjal among the 65 genotypes at their commercial maturity. The vertical bar represents LSD at the 5% level of significance.

Conclusion

The genotypes of brinjal differed significantly for most of the yield attributing characters. Characterization plays a vital role to maintain genetic purity of a genotype. The highest yield of 58.34 t ha^{-1} was recorded from the genotype SM28 followed by SM6 (56.95 t ha^{-1}). The promising genotype(s) with desirable yield attributes and other horticultural characteristics can be utilized in crop breeding programme for development of superior genotypes with high yield and optimal quality. The outputs of the present research would be useful to the brinjal researchers in Bangladesh.

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