GENETIC DIVERSITY, HERITABILITY AND GENETIC ADVANCE OF *SOLANUM MELONGENA* L. FROM THREE SECONDARY CENTERS OF DIVERSITY

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Abstract

Indo-Birmanian is considered as the domesticated region and primary center of eggplant diversity from where it spread to other secondary centers of diversity. In this study, the genetic diversity among 56 eggplant genotypes from three secondary centers of diversity (Bangladesh, Malaysia and Thailand) was assessed using 11 morphological traits. The experiment was laid in a complete randomized block design with three replications. A wide significant variation was observed for all the morphological traits, and highly significant differences among the three centers of diversity. High heritability and genetic advance was found for different traits *i.e.* fruit length, fruit diameter, fruit girth, fruit length to width ratio, average fruit weight, number of fruits per plant, fruit yield per plant, plant height and number of primary branches per plant. The selected best traits *i.e.* number of fruits per plant, average fruit weight and fruit yield per plant showed high heritability along with high genetic advance and less environmental influence but the high value of PCV and GCV. So these traits could be useful for selection criteria in the future breeding program. These results are relevant for evolutionary studies, breeding programs, and management of eggplant genetic resources.

Introduction

Eggplant (*Solanum melongena* L.) is an important vegetable crop belonging to the Solanaceae family. It is also known as brinjal, aubergine or guinea squash that are widely cultivated in the tropics, subtropics and temperate regions. The eggplant name is obtained from egg-shaped fruit of some cultivars (Akhter *et al*., 2012). It is a perennial crop but commercially cultivated as an annual vegetable crop for its immature, unripe fruits which are used in making various types of cooked curries. It has high nutritive value, high market demand and the most cost-effective and profitable among other vegetables. It is also known as the "king of vegetables" for its versatility use in Indian food (Dhaka *et al*., 2017). Some ayurvedic properties also appear in eggplant and it is helpful for diabetic patients (Fraikue, 2018). It acts as an excellent medicine for those who suffer from liver trouble (Akhter *et al*., 2012). In spite of the nutritional and economic importance of eggplant, there are limited studies on eggplant breeding program (Daunay, 2008). For addressing breeding challenges and improvement of eggplant, the use of wide and exotic germplasm has been extensively adopted (Muñoz-Falcon *et al*., 2009) and a significant reduction

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in genetic diversity of modern black eggplants cultivars was reported. However, this reduction can be overcome by incorporating black fruit traits from genetically distant materials into the genetic background of elite cultivars thereby increasing the genetic base of this cultivar (Rodriguez-Burruezo *et al.*, 2008). Assessment of relationship and diversity of the cultivated genotype helps in the understanding crop evolution, establishment of conservation strategies and utilization of genetic resources. The evolution and domestication of eggplant has been studied using molecular, morphological and historical analyses.

Eggplant was generally believed to be domesticated in Southeast Asia from *Solanum incanum* L. the wild relative of commercial cultivar. This hypothesis was supported by molecular, morphological and fertility of F_1 hybrids crossed with *Solanum melongena* (Muñoz-Falcòn *et al.*, 2009). Although it is unknown how *S. incanum* reached in the Indo-Birmanian center of diversity which is naturally distributed in the Middle East and Africa. It has been speculated that the dispersal can be intentionally or unintentionally through oceanic current from Africa to India (Lester and Hasan, 1991). As in the case of tomato, domestication outside the area where is the wild ancestor are naturally distributed resulted in an important genetic constriction (Daunay, 2008). Dispersal of the eggplant from Indo-Birmanian region which is considered as the primary center of diversity to other regions resulted in the crop diversification due to micro-evolutionary forces such as artificial and natural selection, gene flow, recombination, and mutation has led to the accumulations of genetic variability in numerous secondary centers of diversity (Hurtado *et al.*, 2012). Therefore, assessment of genetic diversity of distant geographically centers of diversity will assist in understanding the structure of eggplant genetic variability, crop improvement and conservation of genetic resources. Similar studies have been performed on several crops such as sorghum (Strelchenko *et al.*, 2010), oil palm (Myint *et al.,* 2019) and rice (Sarif *et al.,* 2020).

Morphological characterization has proven useful in studying the relationship and diversity of different varieties of eggplant. Characterization using agronomic traits is essential in crop improvement breeding programs. The morphological characterization for eggplant has been define by the European Eggplant Genetic Resources Network (EGGNET) (Vander Weerden and Barendse, 2006) which have been validated and used in characterization of eggplant breeding materials in numerous studies (Muñoz-Falcòn *et al.,* 2009; Rodriguez-Burruezo *et al.,* 2008; Sulaiman *et al.*, 2020). Morphological diversity is the first issue of description and discrimination of genetic resources (Smith and Smith, 1989; Shrestha, 2013). Low genetic diversity was reported, among the dark purple to black color eggplant fruits (Muñoz-Falcòn *et al.,* 2009; Boyaci *et al.,* 2015). Hence, creation of variation through mutation, hybridization and approaches of biotechnology is a high-priced and time dependent method (Boyaci *et al.*, 2015). So, it is necessary to characterize collected germplasm (populations) to identify lines suited for new variety development (Boyaci *et al.,* 2015). Genetic diversity studies based on quantitative traits are of interest to plant breeders as such traits can be rapidly and easily scored using low cost methods (Myint *et al.*, 2019). For this method, no sophisticated equipment is required and the data can be easily recorded without specific biochemical or molecular techniques.

Heritability is defined as the proportion of the total variation in a given phenotypes within a population that is attributable to genetic variance. The genetic makeup of a plant and the surrounding environment regulate the phenotypic expression of the plant trait (Pujer *et al.*, 2017). Consequently, the magnitude of variability available in some main profitable characters and their heritability together with genetic advances will be fruitful to the breeders for selecting effectively and constructing sound breeding programs. Knowledge regarding heritability assists plant breeders to forecast the nature of the progeny, to create a proper selection and to evaluate the expansion of genetic advancement through selection (Khatun *et al.*, 2010). Development of superior yielding genotypes not only depends on yield trait but also influenced by many other characters because

yield is a complex character. The interrelation between yield and yield attributing traits can be determined by correlation coefficient which provides information on nature, extent and selection direction. Knowledge on genetic parameters is also important for improvement in crops. The objective of this research was to identify and classify variations among eggplant accessions from three different centres of diversity. These results will be relevant for evolutionary studies, breeding programs, management and conservation of eggplant genetic resources.

Materials and Methods

Experiment location, design and plant materials

`This experiment was done from mid-July to mid-December, 2018 at Ladang 15, Faculty of Pertanian in Universiti Putra Malaysia. This place located geographically between 2°59`north latitude to 101°43`east latitude, with 55 m altitude. The randomized complete block design (RCBD) along with three replications was followed. Fifty-six eggplant genotypes seed (Table 1) collected from Bangladesh, Malaysia and Thailand were used in this study.

Eggplant genotypes, seedlings, transplantation and their management

Seeds were placed on a tray for germination which filled with peat moss soil. Each tray containing 104 holes and 1-2 seeds were sown per hole. Twenty one days old seedlings were transferred from tray to polybag and kept in net house until transplanting in the field. The polybags were filled with soil and peat moss at 2:1 ratio. Forty-five days old seedlings were transplanted in the field. Just one seedling was transplanted in each hole. Seedlings were transplanted at a distance of 60 cm from plant to plant and 80 cm from row to row. Ten seedlings were transplanted per accession per replication. All recommended cultural practices were followed as per package of practices to raise a healthy crop.

Data collection

Data were collected from randomly selected three plants of each genotype in every replication for plant height, primary branches per plant, fruit length, fruit diameter, fruit girth, fruit length to width ratio, days to first flowering, days to 50 percent flowering, individual fruit weight, number of fruits per plant and average yield per plant. All of these traits were measured from all accessions at each of replications, as shown in Table 2. Fruits were harvested at proper maturity stage. Maturity stage was determined by firmness and external glossiness of fruits. All data were taken according to eggplant descriptor of International Board for Plant Genetic Resources (IBPGR, Italy).

Data analyses

All the morphological traits were subjected to analysis of variance (ANOVA) using SAS 9.4 software. Least significant difference (LSD) was used for mean comparison at 5% level of significance. REML (Restricted Maximum Likelihood) of proc varcomp in SAS 9.4 was used to estimate variance components. Proc corr of SAS command was used to determine simple phenotypic correlation analysis. NTSYS-PC software (version 2.1) was used for clustering (UPGMA) and principal component analysis (PCA) to analyze diversity.

The different genetic parameters such as phenotypic coefficient of variation, genotypic coefficient of variation, broad-sense heritability and genetic advance as a percentage of the mean (GAM), were estimated using the formula given by Myint *et al.* (2019) and Pujer *et al.* (2017).

Table 1. List of selected eggplant genotypes.

Sl.No.	Accession code	Source code	Collection country
1	BB1	China 3	Bangladesh
2	BB3	MuktaJhuri	Bangladesh
3	BB4	MuktaKeshi	Bangladesh
4	BB5	Chinese Macra	Bangladesh
5	BB6	BARI Eggplant 2	Bangladesh
6	BB7	Tal Begun	Bangladesh
7	BB8	Pahuja seed co.	Bangladesh
8	BB9	Pahuja seed co.	Bangladesh
9	BB10	Laskar seed	Bangladesh
10	BB11	Singhnath	Bangladesh
11	BB12	BARI Eggplant1	Bangladesh
12	BB13	BARI Eggplant4	Bangladesh
13	BB14	BARI Eggplant5	Bangladesh
14	BB15	BARI Eggplant6	Bangladesh
15	BB16	BARI Eggplant7	Bangladesh
16	BB17	BARI Eggplant8	Bangladesh
17	BB18	BARI Eggplant9	Bangladesh
18	BB19	BARI Eggplant10	Bangladesh
19	BB20	220	Bangladesh
20	BB21	217	Bangladesh
21	BB22	253	Bangladesh
22	BB23	222	Bangladesh
23	BB24	275	Bangladesh
24	BB26	288	Bangladesh
25	BB27	291	Bangladesh
26	BB28	311	Bangladesh
27	BB30	330	Bangladesh
28	BB31	338	Bangladesh
29	BB32	317	Bangladesh
30	BB33	346	Bangladesh
31	BB34	350	Bangladesh
32	BB35	262	Bangladesh
33	BB36	357	Bangladesh
34	BM3	214, Mini eggplant	Malaysia
35	BM4	311, Round purple	Malaysia
36	BM5	330,White eggplant	Malaysia
37	BM6	418, Purple king	Malaysia
38	BM7	428, Nyonya eggplant	Malaysia
39	BM8	313, Little Nyonya	Malaysia
40	BM9	312, Super Naga	Malaysia
41	BM10	MTe2	Malaysia
42	BT1	636/2559	Thailand
43	BT2	01387/2552	Thailand
44	BT3	1845/2338	Thailand
45	BT4	00558/2551	Thailand
46	BT5	Parquy	Thailand
47	BT6	969/2560	Thailand
48	BT7	01451/2551	Thailand
49	BT8	914/2558	Thailand
50	BT9	01450/2551	Thailand
51	BT10	01166/2551	Thailand
52	BT11	762/2556	Thailand
53	BT13	1745/2560	Thailand
54	BT15	548/2558	Thailand
55	BT16	01200/2553	Thailand
56	BT17	548/2556	Thailand

Note: BB: Brinjal Bangladesh, BM: Brinjal Malaysia, BT: Brinjal Thailand.

Table 2. List of eleven quantitative characters of eggplants.

Traits	Method of evaluation
Fruit Length (FL, cm)	The average length of 10 marketable fruits per Plant from top to bottom was taken
Fruit Diameter (FD, cm)	Measured along the middle part of 10 harvestable fruit per plant by Caliper and finally, the average value was converted into cm
Fruit Length to Width Ratio (FLWR, ratio)	The value of fruit diameter was divided by the value of fruit length of individual
Fruit Length to Width Ratio (FLWR)	The value of fruit diameter was divided by the value of fruit length of individual plant
Fruit Girth (FG, cm)	Measured along the middle part of 10 harvestable fruit per plant by measuring tape and finally, the average value was taken
Fruit Length to Width Ratio (FLWR, ratio)	The value of fruit diameter was divided by the value of fruit length of individual
Average Fruit Weight (FW, g)	The average weight of 10 harvestable fruit per plant was taken
Number of Fruits per plant (NF, no)	Total number of fruits harvested from individual plant
Average Yield per plant (YPP, g)	Total fruits harvested from each selected plant in each replication & each harvest was weighted and summed up
Days to first flowering (DF, days)	Days from transplanting to the first flowering of every plant of each accession was recorded
Days to fifty percent flowering (DFF, days)	Days from transplanting to the first flowering of fifty percent plant of every genotype were recorded
Plant Height (PH, cm)	Length of the main stem from the ground to tip of the stem was measured at 90 Days after Transplanting (DAS)
Number of Primary Branches (PB, no)	Number of primary branches of the selected plant was recorded at 90 DAS

These traits include the following formulas:

a) Phenotypic Coefficient of Variation (PCV)

$$\text{PCV (\%)} = \frac{\sqrt{\sigma^2 p}}{\bar{X}} \times 100$$

Here, phenotypic variance i.e. $\sigma^2 p$ and X is the mean of a specific trait

b) Genotypic Coefficient of Variation (GCV),

$$\text{GCV (\%)} = \frac{\sqrt{\sigma^2 g}}{\bar{X}} \times 100$$

Here, $\sigma^2 g$ is genotypic variance and X is expressed as a mean of a specific trait.

PCV and GCV were grouped into as low (0-10%), medium (10-20%) and high (> 20%) by Sivasubramanian and Menon (1973).

c) Heritability in broad sense ($H_b{}^2$),

$$H_b{}^2 = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

The heritability value was grouped into three categories i.e. low (0 to 30%), moderate heritability from (30 to 60%) and high means ($\geq 60\%$) as given by Burton and De vane (1953).

d) Genetic Advance of Mean (GAM),

$$GAM\ (\%) = H_b^2 \times \frac{\sqrt{\sigma^2 p}}{\bar{x}} \times k$$

Where k is constant (2.06 at 5% selection intensity), x is the mean of a specific trait. It is divided into low (i.e. 0 to 10%) moderate from (10 to 20%) and high value (≥ 20%) (Johnson *et al.,* 1955).

Results and Discussion

Morphological traits

All quantitative characters of this research showed a highly significant difference (P ≤ 0.01) among the accessions, countries, and accessions within countries (Table 3a-b) except days to first flowering. This result indicates that a significant amount of genetic variation present among accessions, countries, and accessions within countries. The trait days to first flowering showed no significant effect among countries. There was no significant difference in genetic variation among replication except the traits days to fifty percent flowering, number of primary branches per plant and plant height. The mean performance of 56 accessions for different quantitative traits is presented in (Table 5).The yield per plant ranged from 127.18 (BB9) to 1545.83 g (BB6). The number of fruits per plant ranged from 0.89 to 47 which were recorded by BB32 and BT15 accessions respectively (Table 5). The accession BT6 recorded the lowest fruit weight (7.52 g) while the accession BB15 gave the highest fruit weight (261.20 g). The average weight of fruit in this study was to be 108.29g.

Table 3a. Mean Squares of Analysis of Variance among 56 accessions of eggplant.

SOV	df	FL	FD	FG	FW	FLWR	YPP
Replications (R)	2	1ns	0.04ns	0.41ns	88.08ns	7.94ns	978.43ns
Accessions (A)	55	70.88**	7.61**	78.19**	11768.5**	139.08**	414451**
Countries (C)	(2)	711.83**	10.87**	109.58**	81393.40**	84.64**	767384.3**
[A/C]	(53)	46.7**	7.49**	77**	9141.13**	141.13**	401132**
Error	110	0.92	0.1	1.13	79.22	5.85	2786.81
$\sigma^2 a$		23.32	2.5	25.69	3896.4	44.41	137232
$\sigma^2 e$		0.92	0.1	1.11	79.22	5.85	2754.5

*Significant at 0.05, **Highly significant at 0.01 and ns= non-significant, SOV: Sources of Variation, FL: Fruit Length, FD: Fruit Diameter, FG: Fruit Girth, FLWR: Fruit Length to Width Ratio, FW: Average Fruit Weight, YPP: Yield Per Plant, df= degrees of freedom, σ2a= accession variance, σ2e = error variance, [A/C] = Accession within Countries,

Estimation of genetic variations

The phenotypic variances ($\sigma^2 p$) for all characters were greater than the genotypic variances ($\sigma^2 g$) (Table 4). Similarly, the PCV (Phenotypic Coefficient of Variation) was also higher than the GCV (Genotypic Coefficient of Variation). The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) estimation ranged from 8.55-113.98% and 7.91-110.85 % respectively. The highest PCV was observedfor trait fruit length to width ratio (113.98%) and followed by number of fruits per plant (111.43%) and fruit yield per plant (68.19%). Similarly, the maximum GCV was observed for traits number of fruits per plant (110.85%) and followed by the trait fruit length to width ratio (107.14%) and fruit yield per plant (67.51%). The PCV and GCV

were lowest for days to fifty percent flowering which was 8.55% and 7.91% respectively (Table 4).

Table 3b. Mean squares of analysis of variance among 56 accessions of eggplant.

SOV	df	PB	DF	DFF	NF	PH
Replications (R)	2	1.79**	16.79ns	34.47**	0.05ns	76.06*
Accessions (A)	55	4.95**	144.91**	127.60**	253.63**	615.71**
Countries (C)	(2)	7.23**	13.66ns	123.93**	1195.74**	2027.92**
[A/C]	(53)	4.86**	149.86**	127.74**	218.07**	562.42**
Error	110	0.16	6.15	6.74	0.9	16.7
$\sigma^2 a$		1.6	46.25	40.29	84.25	199.67
$\sigma^2 e$		0.16	6.15	6.75	0.89	16.7

*Significant at 0.05, **Highly significant at 0.01 and ns= non-significant, SOV: Sources of Variation, PB: number of Primary Branches Per Plant, DF: Days to first Flowering, DFF: Days to Fifty Percent of Flowering, NF: Number of fruits per plant, PH: Plant Height, df= degrees of freedom, σ2a= accession variance, σ2e = error variance, [A/C] = Accession within Countries.

Table 4. Estimated value of genetic parameters of different accessions of eggplant.

Traits	$\sigma^2 g$ (%)	$\sigma^2 p$ (%)	H_b^2 (%)	PCV (%)	GCV (%)	GAM (%)
FL	23.32	24.24	96.20	37.88	37.14	75.05
FD	2.50	2.60	96.23	52.21	51.22	103.49
FG	25.69	26.81	95.84	52.24	51.15	103.15
FW	3896.07	3975.26	98.01	58.50	57.92	118.11
FLWR	44.41	50.26	88.37	113.98	107.14	207.48
YPP	137230.6	140013.7	98.03	68.19	67.51	137.71
PB	1.60	1.75	91.10	23.65	22.58	44.39
DF	46.25	52.40	88.27	9.68	9.09	17.59
DFF	40.22	47.12	85.66	8.55	7.91	15.08
NF	84.24	85.14	98.96	111.43	110.85	227.16
PH	199.70	216.41	92.28	19.60	18.83	37.26

PCV: Phenotypic coefficient of Variation, GCV: Genotypic Coefficient of Variation, GAM: Genetic Advance of Mean, σ2p= Phenotypic Variance, σ2g= Genotypic Variance, Hb2= Heritability, FL: Fruit Length, FD: Fruit Diameter, FG: Fruit Girth, FLWR: Fruit Length to Width Ratio, FW: Average Fruit Weight, YPP: Yield Per Plant, PB: number of Primary Branches per Plant, DF: Days to first Flowering, DFF: Days to Fifty Percent of Flowering, NF: Number of fruits per plant, PH: Plant Height.

Heritability and genetic advance

Estimation of heritability (H_b^2) and genetic advance are presented in Table 4. Heritability and GAM values ranged between 85.66-98.96% and 15.08-227.16% respectively. Estimates of heritability were high (> 60.00%) for all the traits. The estimates of GAM were also high for most of the traits except the traits days to first flowering and days to fifty percent flowering. These two traits showed moderate value of GAM. PCV and GCV are also important tools for the selection of

Table 5. Mean performance of 56 eggplant accessions concerning quantitative characters.

Accession name	FL (cm)	FD (cm)	FG (cm)	FW (g)	FLWR (ratio)	YPP (g)	PB (no)	DF (days)	DFF (days)	NF (no)	PH (cm)
BB1	10.87	5.85	18.47	121.08	1.85	337.94	4.33	80.00	83.67	2.22	64.67
BB3	15.42	1.52	4.70	72.36	10.29	1395.10	6.89	69.00	78.00	20.33	86.22
BB4	12.63	3.32	10.84	130.72	3.80	343.12	6.11	81.00	84.33	1.67	76.44
BB5	14.18	6.28	19.96	224.27	2.26	859.75	6.89	74.33	77.33	4.45	87.00
BB6	12.17	3.60	11.65	154.21	3.40	1545.80	6.56	70.67	74.00	8.55	87.44
BB7	10.44	4.32	14.22	64.56	2.42	250.89	5.22	61.33	65.67	2.56	69.67
BB8	18.23	2.68	8.59	122.55	6.86	767.83	4.33	80.33	81.33	9.55	84.89
BB9	12.81	0.82	2.52	44.22	15.70	127.18	4.22	71.33	75.33	3.11	45.11
BB10	15.82	3.59	11.93	138.69	4.45	437.48	7.11	75.76	80.00	1.78	82.22
BB11	17.88	0.38	1.71	64.34	47.41	661.54	6.00	83.33	89.00	8.44	109.22
BB12	11.75	2.22	6.31	53.38	5.31	1418.30	7.67	63.33	74.00	27.67	86.56
BB13	14.30	1.78	5.74	79.83	8.07	918.81	6.56	68.67	75.67	12.00	68.28
BB14	8.82	3.50	11.15	54.22	2.54	166.58	5.22	59.33	64.00	2.33	77.89
BB15	11.93	6.51	20.50	261.20	1.84	1239.70	6.22	84.00	82.67	6.33	83.89
BB16	20.04	1.50	4.80	92.95	13.50	272.91	5.56	73.00	82.00	5.22	102.56
BB17	18.20	2.07	6.19	37.13	8.84	192.57	6.33	90.67	93.33	4.00	74.78
BB18	10.44	4.13	13.16	116.89	2.55	898.15	6.56	76.67	78.67	8.33	70.33
BB19	25.65	2.26	7.26	157.63	11.38	539.23	6.44	78.33	81.33	4.56	89.89
BB20	17.76	4.51	14.54	250.78	3.94	1240.30	6.56	71.67	78.00	13.11	85.22
BB21	10.45	2.53	7.98	82.11	4.17	244.70	4.44	65.33	71.67	3.11	46.72
BB22	17.58	4.96	16.23	234.32	3.54	1215.80	6.67	80.67	86.33	5.22	87.33
BB23	15.01	2.37	7.62	229.38	6.42	405.39	4.67	71.00	74.67	3.44	58.00
BB24	11.55	3.47	10.85	118.40	3.34	138.05	5.11	77.00	79.00	1.22	75.78
BB26	19.17	3.54	11.48	118.72	5.42	1043.20	6.56	67.33	72.67	10.00	91.11
BB27	14.03	5.05	16.48	140.28	2.77	172.50	4.22	87.00	90.00	1.33	65.00
BB28	14.17	3.62	11.52	158.24	3.94	267.44	6.56	77.67	81.67	1.22	77.94
BB30	10.04	3.81	12.43	89.89	2.64	744.29	3.89	79.67	86.33	7.11	57.83
BB31	10.87	5.59	17.81	149.29	1.98	455.13	5.22	67.00	74.33	2.67	75.22
BB32	10.80	5.75	18.79	129.35	1.88	168.73	3.89	73.33	78.33	0.89	66.44
BB33	14.36	0.76	2.26	64.15	20.04	295.12	5.11	77.00	80.00	3.55	99.89
BB34	15.72	2.03	6.54	105.10	7.80	223.14	5.22	71.33	74.00	3.55	73.94
BB35	9.93	1.81	5.81	58.76	5.51	184.49	3.22	78.33	84.33	4.78	71.55
BB36	13.34	4.41	13.87	168.89	3.04	799.23	5.78	79.00	83.67	5.89	81.17
BM3	13.78	1.69	5.81	97.19	8.25	558.68	4.45	75.67	80.67	9.89	76.66
BM4	13.86	3.86	12.22	175.93	3.63	759.79	5.11	62.00	71.67	6.33	85.67
BM5	17.67	2.38	7.45	139.75	7.49	1036.70	4.00	67.67	76.33	7.11	73.78
BM6	21.33	2.60	8.35	182.15	8.33	227.69	5.33	83.00	89.00	2.00	105.66
BM7	21.62	3.54	11.42	126.93	6.15	403.95	5.89	81.33	91.00	2.67	79.56
BM8	16.71	2.48	7.83	78.36	6.78	761.95	5.33	69.00	75.00	8.89	83.89
BM9	18.27	2.42	7.54	126.32	7.85	685.33	4.56	76.00	78.67	5.67	65.22
BM10	11.84	5.86	19.62	170.67	1.96	460.81	5.00	79.00	84.67	3.33	65.89
BT1	10.81	4.53	14.49	135.04	2.40	214.62	3.22	75.00	81.33	2.00	67.56
BT2	5.02	1.48	5.13	12.06	3.39	687.39	9.00	76.00	80.00	47.00	70.33
BT3	12.13	1.53	5.13	66.76	8.04	369.90	5.11	71.67	79.00	6.00	64.00
BT4	6.20	3.45	11.31	60.10	1.80	662.72	4.56	76.00	84.67	11.22	74.67
BT5	7.14	0.87	2.39	27.29	14.70	266.69	5.22	63.33	71.00	15.67	59.89

Table 5 contd.

Accession name	FL (cm)	FD (cm)	FG (cm)	FW (g)	FLWR (ratio)	YPP (g)	PB (no)	DF (days)	DFF (days)	NF (no)	PH (cm)
BT6	5.19	1.88	5.78	7.52	2.76	188.15	8.89	82.33	96.00	15.44	60.22
BT7	4.42	0.62	2.09	10.54	7.15	257.47	6.78	76.00	78.00	15.44	69.45
BT8	17.82	2.90	9.44	104.04	6.15	452.27	7.22	78.33	82.00	4.56	83.55
BT9	6.78	2.75	8.82	44.09	2.48	510.79	7.22	77.67	83.67	8.78	80.56
BT10	17.90	2.76	8.58	124.16	6.49	246.24	4.89	80.33	86.33	3.22	87.22
BT11	6.12	2.75	8.83	43.60	2.23	619.48	7.22	78.00	84.67	13.44	62.22
BT13	13.60	1.76	6.38	36.18	7.73	432.05	6.33	69.33	75.67	33.00	44.89
BT15	3.63	0.97	3.25	7.47	3.73	251.53	4.78	63.33	75.00	47.00	55.78
BT16	9.53	5.16	16.06	96.29	1.85	362.28	4.11	88.00	93.67	3.22	78.22
BT17	10.35	5.05	16.32	104.82	2.05	538.91	4.22	76.00	79.33	3.00	46.78
Mean	13.18	3.10	9.96	108.29	6.29	552.24	5.60	74.81	80.23	8.44	75.03
LSD	1.55	0.51	1.77	14.40	3.91	85.42	0.64	4.01	4.20	1.54	6.61

Note: FL: Fruit Length, FD: Fruit Diameter, FG: Fruit Girth, FW: Average Fruit Weight, FLWR: Fruit Length to Width Ratio, YPP: Average Yield per Plant, PB: Number of Primary Branches per Plant, DF: Days to First Flowering, DFF: Days to Fifty percent of Flowering, NF: Number of Fruits per Plant, PH: Plant Height, LSD: Least Significant Difference

superior traits in breeding. All of the traits had high PCV and GCV except the traits days to first flowering and days to fifty percent of flowering. The highest GCV was recorded in the number of fruits per plant (110.85%) and the highest PCV was recorded from the trait fruit length to width ratio (113.98%). All traits assessed showed slightly higher PCV values compared to the corresponding GCV values. This means that there was little environmental influence on the expression of these traits.

Correlation coefficient

Simple correlation coefficients of phenotypic characters are shown in Table 6. Fruit yield per plant (YPP) is directly correlated with all the traits except days to the first flowering of the plant, days to fifty percent flowering of the plant and fruit length to width ratio. The correlation level of yield per plant with other traits ranged from 0.17 - 0.37. The highest correlation value (0.37) was observed from the correlation between average fruit weight and yield per plant. The second highest correlation (0.34) was between the numbers of primary branches per plant and yield per plant.

Table 6.Phenotypic correlation coefficient among different traits with yield per plant

Traits	rp with yield per plant (YPP)
FL	0.20**
FD	0.18*
FG	0.17*
FW	0.37**
FLWR	-0.04ns
PB	0.34**
DF	-0.13ns
DFF	-0.13ns
NF	0.26**
PH	0.33**

Note: *significant at 0.05. **significant at 0.01 and ns= non-significant, FL: Fruit Length, FD: Fruit Diameter, FG: Fruit Girth, FW: Average Fruit Weight, FLWR: Fruit Length to Width Ratio, YPP: Average Yield per Plant, PB: Number of Primary Branches per Plant, DF: Days to First Flowering, DFF: Days to Fifty percent of Flowering, NF: Number of Fruits per Plant, PH: Plant Height, rp= Phenotypic correlation.

Cluster analysis

The Euclidean distance was estimated by using standardized morphological data. An UPGMA (unweighted pair group method with arithmetic mean) dendrogram was constructed using the values of all morphological data for 56 eggplant genotypes. The genetic similarities varied from 0.92 to 7.97. Seven main groups were determined among 56 genotypes at a value of 4.45 dissimilarity coefficient (Fig. 1) based on multivariate analysis. The value 4.45 was chosen for the convenience of explanation. The maximum number of genotypes (36) was recorded for group I which consisted of 64.28 % of all genotypes in Table 7. Group II contained 5 genotypes (Table 7). Group III, IV, V, VI, and VII had 4, 4, 4, 2 and 1 accessions respectively (Table 7). The highest yield per plant (1350.6 g) was observed in cluster III (Table 8). The highest average fruit weight was observed in cluster IV (242.64 g), in combination with a moderate number of fruits per plant (7.28). Cluster VII was ranked third as it had moderate individual fruit weight (64.34 g) with a moderate number of fruits per plant (8.44). Cluster VI took place fourth position due to its highest number of fruits per plant (39.00) but the lowest number of average fruit weight (24.12 g). Cluster I and cluster II had the lowest yield per plant 459.12 g and 353.69 g respectively due to their low average fruit weight (Table 8). Group I had 459.12 g yield per plant due to its second-best average fruit weight (118.87 g) with the lowest number of fruits per plant (4.58). There was no obvious relation between the geographical area and grouping (Table 7). Genotypes from Bangladesh, Malaysia and Thailand clustered into the same group I due to their genetic reflection. The other accessions were also divided into groups based on their similarity in genetic variation mindless of their geographical area (Table 7).
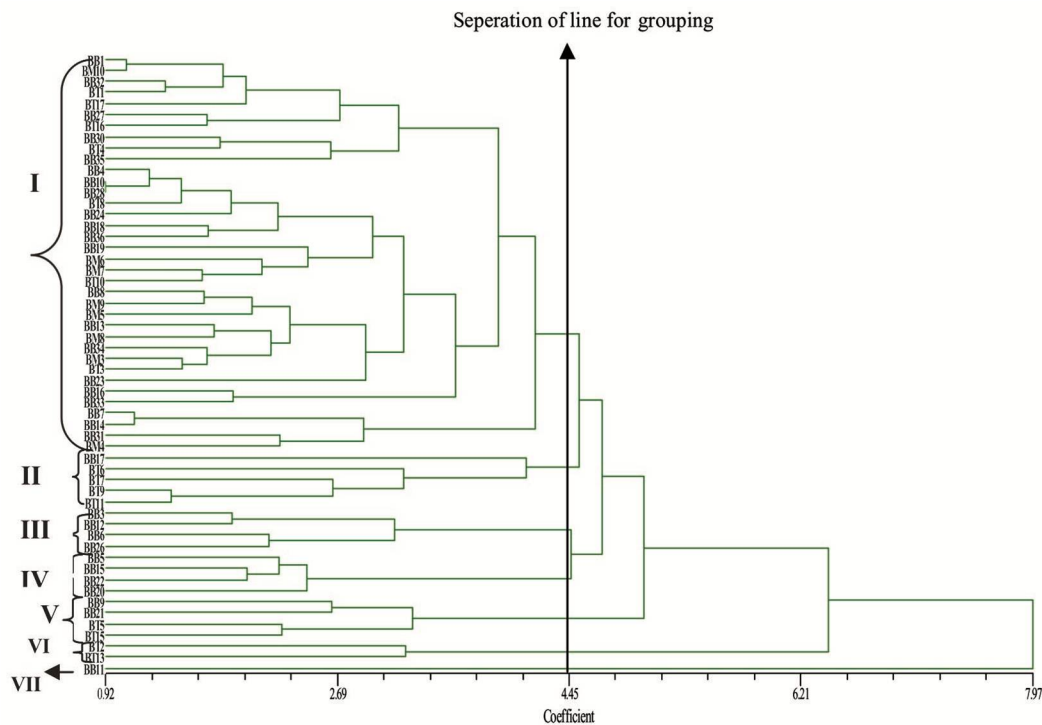

Fig 1. Cluster analysis of 56 eggplant genotypes based on quantitative traits.

Table 7. Eggplant accessions clusters according to the group of origin.

Group	Bangladesh	Malaysia	Thailand
I	BB1, BB32, BB27, BB30, BB35, BB4, BB10, BB28, BB24, BB18, BB36, BB19, BB8, BB13, BB34, BB23, BB16, BB33, BB14, BB31, BB7	BM10, BM6, BM7, BM9, BM5, BM8, BM3, BM4	BT1, BT17, BT16, BT4, BT8, BT10, BT3,
II	BB17		BT6, BT7, BT9, BT11
III	BB3, BB12, BB6, BB26,		
IV	BB5, BB15, BB22, BB20		
V	BB9, BB21		BT5, BT15
VI			BT2, BT13
VII	BB11		

Note: BB: Brinjal Bangladesh, BM: Brinjal Malaysia, BT: Brinjal Thailand.

Table 8. Clustering and means of their quantitative traits.

Cluster	FL	FD	FG	FW	FLWR	YPP	PB	DF	DFF	NF	PH
I	14.08	3.38	10.65	118.87	5.40	459.12	4.97	75.33	80.45	4.58	75.78
II	8.14	2.01	6.34	28.50	4.69	353.69	6.93	80.93	87.13	11.42	69.45
III	14.63	2.72	8.54	99.67	6.11	1350.60	6.25	67.58	74.67	16.64	87.83
IV	15.36	5.57	17.81	242.64	2.90	1138.92	6.42	77.67	81.08	7.28	85.86
V	8.51	1.30	4.03	40.27	9.57	222.52	4.58	65.83	73.25	17.22	51.88
VI	4.31	1.22	5.76	24.12	5.56	559.72	8.00	72.67	77.84	39.00	57.61
VII	17.88	0.38	1.71	64.34	47.41	661.54	6.00	83.33	89.00	8.44	109.22

Note: FL: Fruit Length, FD: Fruit Diameter, FG: Fruit Girth, FW: Fruit Weight, FLWR: Fruit Length to Width Ratio, YPP: Average Yield per Plant, PB: Number of Primary Branches per Plant, DF: Days to First Flowering, DFF: Days to Fifty percent of Flowering, NF: Number of Fruits per Plant, PH: Plant Height.

Principal component analysis (PCA)

The Principal Component analysis (PCA) revealed that the first four components comprised 84.59% of total variation (Table 9). The PC1, PC2, PC3 and PC4 showed 31.21, 52.94, 70.15 and 84.59% of the cumulative variation respectively, which were explained in the Table 9 (eigenvector and eigenvalue analysis). In case of first principal component analysis, the most contributing traits were DF (0.227), FL (0.234), FD (0.471), FG (0.47) and FW (0.458). But for PC2, the most important traits were FLWR (0.477), PH (0.462), FL (0.433) DFF (0.32) and DF (0.314).

This research showed huge variation for the studied traits. Such considerable variation pointed out the scope for improving the characters concerning high yield. Similar results were recorded by Yadav *et al.* (2016) who reported significant variation in yield and yield-related traits of forty eggplant genotypes. Analysis of genetic variation for quantitative characters is a precondition in plant breeding programs. From this study, it was found that all the traits showed a higher PCV value than the corresponding GCV value. Slightly greater PCV from GCV was also obtained by Mili *et al.* (2014) and Rad *et al.* (2015). It indicates that the environmental influence on any trait is controlled by the enormity of the gap between the phenotypic and genotypic coefficient of variation; low difference indicates more prevalence of genetic influence. In contrast, large difference reveals a large environmental effect. From the study, all of the traits revealed little

difference between them (PCV and GCV) indicated that the phenotypic expression of these traits had little environmental influence. It also indicates that the selection of these traits would hold effective for future hybridization. On the contrary, the high difference between PCV and GCV indicates the more environmental influence on the exposure of these traits. The high PCV and GCV was recorded for the traits FL, FD, FG, FW, FLWR, NF, YPP, and PB also recorded by the Pujer *et al.* (2017), Mili *et al.* (2014), and Rad *et al.* (2015). The lowest PCV and GCV were recorded for days to fifty percent flowering. This result is closely related with the findings of Vandana *et al.* (2014) and Mili *et al.* (2014).

Table 9. Eigenvectors and eigenvalues of the first four principal components of eleven traits.

Variable	PC1	PC2	PC3	PC4
Eigen value	3.43	2.39	1.89	1.59
Variation (%)	31.21	21.72	17.21	14.43
Cumulative (%)	31.21	52.94	70.15	84.59
FL	0.234	0.433	0.156	0.288
FD	0.471	-0.261	0.036	0.106
FG	0.47	-0.262	0.033	0.106
FW	0.458	0.043	0.226	-0.101
FLWR	-0.187	0.477	-0.016	-0.247
YPP	0.105	0.064	0.586	0.204
PB	-0.12	0.142	0.343	0.522
DF	0.227	0.314	-0.396	0.389
DFF	0.163	0.32	-0.402	0.438
NF	-0.36	-0.085	0.237	0.407
PH	0.153	0.462	0.294	-0.028

Note**:** FL: Fruit Length, FD: Fruit Diameter, FG: Fruit Girth, FW: Average Fruit Weight, FLWR: Fruit Length to Width Ratio, YPP: Average Yield per Plant, PB: Number of Primary Branches per Plant, DF: Days to First Flowering, DFF: Days to Fifty percent of Flowering, NF: Number of Fruits per Plant, PH: Plant Height, PC1: First Principal Component, PC2: Second Principal Component, PC3: Third Principal Component, PC4: Fourth Principal Component

All the variables have high heritability. Similar results reported by Jirankali *et al.* (2019) and Arunkumar *et al.* (2013). The GAM was also high for FL, FD, FG, FLWR, FW, NF, YPP, PH and PB that support to Jirankali *et al.* (2019) and Arunkumar *et al.* (2013). The moderate GAM was recorded for DF and DFF. Similar results found from the reporter Vandana *et al.* (2014) and Jirankali *et al.* (2019).

The selection for improvement of any character broad-sense heritability and GAM knowledge are important. The high heritability and high genetic advance percentage of the mean of the traits indicating, these characters mainly relied on genetic factors and can be acquired on the phenotypic perfection of these traits in crop improvement. So it is good for selection based on phenotypic traits to improve these specific characters. High heritability coupled with high GAM is also reported by Yadav *et al.* (2016), Mili *et al.* (2014) and Rad *et al.* (2015) in eggplant.

Correlation among different traits is very important for breeders because it helps to choose vital traits from the characters studied (Chattopadhyay *et al*., 2011). Most of the traits related to yield are controlled by genotype and environment interaction and hence it is easy to plant breeder to do selection based on correlation coefficient (Sohrabi *et al*., 2012). The traits days to the first

flowering of plants and days to fifty percent flowering showed a negative correlation with total fruit yield per plant. From here, we concluded that delay in first flowering and fifty percent flowering improved fruit yield per plant. Fruit diameter and average fruit weight not only showed positively correlated with fruit yield per plant but also these traits are highly and positively significant with each other. Similar results were found by Rad *et al.* (2015). So selection based on any traits which are positively and significantly inter-related traits is good to get a desired inter-related response with other traits.

The 56 genotypes grouped into seven clusters based on the characters of cluster analysis at a distant coefficient of 4.45 indicate diversity level among the genotypes. Group VII, which has one genotype may have different genes as contrasted to others for regulating the characters. The diversity analysis of quantitative characters indicated the most similar accessions such as BB8 and BB4, BB10 and BB33 and BB15 and BB20 based on the distant coefficient, meaning that crossing among these accessions will not be useful. As these accessions have more or less same genetic makeup. However, cross between BB1× BT2, BT10 × BB11 and BB36 × BT6 will be useful, as these accessions were being most dispersive. Genetic diversity among 35 genotypes based on D^2 statistics grouped into 10 clusters reported by Ravali *et al.* (2017). In this study, BB11 and BT2 for the individual group were distinguished from other accessions of other clusters that had a high genetic distance. Hybridization between the accessions of those clusters could be made following the findings of Tahir *et al.* (2013). The accessions of three different countries have the same genetic makeup and could be formed from the identical materials of breeding reported by Tahir *et al.* (2013). The accessions of the same group had genetic similarity and those were distributed randomly in several clusters had diverse though they had identical geographic regions reported by Balakrishna *et al.* (2017).

The PCA helps to explain how the similar genotypes group as compared to dissimilar genotypes. PCA can clarify the results of cluster analysis. The output of PCA supports the result of cluster analysis as for more precise and accurate data. Strong differences exist among the 56 genotypes in this research and these were also confirmed by PCA. Four principal components PC-1 to PC-4 were extracted from the original data analysis having eigen values more than one reported by Kaiser (1960). The principal components of first four attributed to 85% of the variation of whole variation which indicates that a strong correlation exists among all parameters studied. The value of first PC which subscribed 31.21% of the variation alone is most important. The trait fruit diameter (FD) contributed more to variation followed by fruit girth (FG), fruit weight (FW) and fruit length (FL) had the highest loading on PC1 which indicating significant importance of these components. Seventy entries of eggplant were studied by Sunseri *et al.* (2010) for determination of genetic diversity using PCA and denoted the first three components that attributed for 74% of the total variance which is more or less similar to these research findings (70.15 %).

Conclusions

This research exhibited the presence of genetic diversity among the 56 eggplant genotypes. This study also showed the significant economic traits which are important for the advancement of eggplant research. The aforementioned traits also showed a high genetic advance as a percentage of mean indicating all of these traits could be useful to select suitable accessions for a remarkable advancement in the breeding program. Based on yield performance, two groups, group III and group IV were indicated as proposed groups. Depending on the breeding objective, specific accessions would be identified from the core collection and would then be transplanted to the field, rather than maintaining the entire core collection in the field with the requirement to replant it every year. As a result, it will reduce maintenance costs in the field.

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