J Bangladesh Agril Univ 23(2): 99–112, 2025 https://doi.org/10.3329/jbau.v23i2.82563

ISSN 1810-3030 (Print) 2408-8684 (Online)

Journal of Bangladesh Agricultural University

Journal home page: http://baures.bau.edu.bd/jbau

Research Article

Genetic Variability, Character Association and Diversity Analysis in Bitter Gourd (*Momordica Charantia* L.) for Growth and Yield Attributing Traits in Bangladesh

Tuhin Hasan[1], Md. Golam Rabbani[1]✉, Md. Mokter Hossain[1], Nayan Chandra Howlader[1], Md. Mahfuzul Hasan[1], Faisal Ahmed Shourov[3], Shuvro Sarker[1] and Md. Al Amin[2]

[1]Department of Horticulture, Faculty of Agriculture, Bangladesh Agricultural University, Mymensingh- 2202, Bangladesh

[2]Department of Genetics and Plant Breeding, Faculty of Agriculture, Bangladesh Agricultural University, Mymensingh- 2202, Bangladesh

[3]Department of Genetics and Plant Breeding, Faculty of Agriculture, Hajee Mohammad Danesh Science and Technology University, Dinajpur- 5200, Bangladesh

ARTICLE INFO

Article history
Received: 28 January 2025
Accepted: 22 June 2025
Published: 30 June 2025

Keywords
Bitter gourd,
Genetic advance,
Genotypic correlation,
Phenotypic correlation,
Momordica charantia,
Morphological variability

Correspondence
Md. Golam Rabbani
✉: drmgrabbani@gmail.com

ABSTRACT

The goals of this study are to assess the field performance, character association, variability, and genetic diversity of 50 bitter gourd (*Momordica charantia* L.) accessions collected from various locations of Bangladesh. To evaluate the morphological and qualitative characteristics, as well as to assess the genotypic and phenotypic variability and correlation, the study employed a randomized complete block design (RCBD) with three replications. MC022 exhibited the highest yield (2.50 kg/plant), MC080 in number of fruits per plant (35.67), and MC079 in average fruit weight (101.69 g) among all accessions. Numbers of flowers per plant (99.14), petiole (97.84), vine length (97.81), and yield per plant (94.08) exhibited high heritability with genotypic and phenotypic coefficients of variation. The maximum phenotypic variance (4676.60) and genotypic variance (4574.40) were both recorded at vine length. The average fruit weight was significantly positively correlated with the yield per plant at both the genotypic (r = 0.873**) and phenotypic (r = 0.861**) levels. Cluster I contained the most accessions (14). No limitations were detected. It can be concluded that bitter gourd accessions exhibit a diverse array of qualitative and morphological traits. In addition, the yield of different bitter gourd accessions was correlated with an assortment of yield-contributing attributes. The genotypic coefficient of variation was less than the phenotypic coefficient of variation in all of the traits. Fruit length, average fruit weight, number of fruits per plant, and yield per plant were found to have higher values and lower differences between phenotypic and genotypic co-efficient of variation, indicating a high potential for selecting superior accessions.

Introduction

Bitter gourd (*Momordica charantia* L.) is a paramount widely consumed vegetable in Bangladesh, designated under the Cucurbitaceae family, and the plant is believed to have originated in India, with China serving as a subsidiary center of diversification (Abbas et al., 2024). It draws in both tropical and subtropical climates and gets grown solely for its highly bitter fruit. Momordica is a large genus, with *M. charantia* L. being the most extensively grown species. The species is acknowledged for its high degree of cross-pollination due to its monoecious nature, and its somatic chromosome number is 2n=2x=22 (Jat et al., 2024). Additional noted species within the genus include *M. dioca*, *M. cochin chinenesis*, *M. balsamina*, and *M. trosa*, and the plant makes simple, alternate leaves, and each possesses separate male and female yellow flowers (Batool et al., 2022).

Bitter gourd is noteworthy for its high nutritional value compared to other cucurbits, especially within terms of iron and vitamin C content. Each 100g portion of the edible fruit contains 83.2g of water, 2.1g of protein, 1g of fat, 1.4g of minerals, 1.7g of fiber, 10.6g of carbohydrate, and various vitamins and minerals, making it an excellent nutrition item (Barua et al., 2020). Also, it has medicinal qualities and is used for curing afflictions such as blood diseases, rheumatism, diabetes, and asthma. Its berry juice is known to have hypoglycemic activity and has been shown to inhibit,

Cite This Article
Hasan, T., Rabbani, M.G., Hossain, M.M., Howlader, N.C., Hasan, M.M., Shourov, F.A., Sarker, S. and Amin, M.A. 2025. Genetic Variability, Character Association and Diversity Analysis in Bitter Gourd (*Momordica Charantia* L.) for Growth and Yield Attributing Traits in Bangladesh. *Journal of Bangladesh Agricultural University,* 23(2): 99-112. https://doi.org/10.3329/jbau.v23i2.82563

and the proliferation of HL60 human leukemia cells, which would assist in preventing cancer (Patel et al., 2020; Sultana et al. 2025).

The crop prefers sandy alluvial soil in medium-high and medium-low lands and is raised commercially throughout Bangladesh. Fortunately, its yield remains modest, with a production of 65 metric tons on 29 acres of land and an average yield of 2274.66 kg/acre in 2021-2022 (Hoque et al., 2022). The low yield is partly attributed to the paucity of high-yielding varieties. Improving the growing capacity of cucurbit crops, such as bitter gourd, is critical for addressing nutritional deficiencies in Bangladesh. Moreover, bitter gourd cultivation accounts for 2.61% of winter vegetables and 4.74% of summer vegetables produced in the country (Tejaswini et al., 2024; Al Masum et al. 2025). While its nutritional and medicinal benefits make it a valuable crop, systematic research for boosting its yield potential has been lacking.

Gene diversity is essential for breeding programs since it provides the foundation for crop enhancement and variety development, as a result, it assists in discovering diverse genotypes for hybridization to enhance traits like disease resistance and yield (Cui et al., 2022; Karim et l., 2024; Ahsan et al. 2025; Ali et al. 2025). Knowledge of genetic diversity allows breeders to select progenitors for new breeding populations. Multivariate analysis, especially Mahalanobis D2 statistics, is a valuable tool for measuring genetic diversity and divergence among biological populations. This method has been used to quantify variation among commodities such as pumpkins, cucumbers, and snake gourds.

Bitter gourd is imported into Bangladesh due to supply gaps during off-seasons, lower production costs in neighboring countries like India, and consumer preference for specific varieties. Imports also help maintain a stable supply, prevent shortages during poor harvests or unfavorable weather conditions, and streamline the import process through trade agreements and regional market integration (Islam et al., 2022).

Despite the abundance of bitter gourd landraces in Bangladesh, no explicitly advised or released varieties exist. A number of indigenous cultivars have been collected under the “Collection, Evaluation, Conservation, and Utilization of Land Races and Wild Relatives of Some Important Vegetables and Fruits in Bangladesh” initiative at the Bangladesh Agricultural University, but systematic evaluation of their potential has not been conducted. Therefore, comprehending the genetic architecture of bitter gourd was crucial. The present study sought to evaluate 50 accessions of bitter gourd for yield and yield-contributing characters, estimate their interrelationships, and assess direct and indirect effects on yield using path coefficient analysis.

Materials and Methods

Experimental site and their setup

The experiment took place in the field and laboratory as part of the research effort "Collection, Morpho-molecular Characterization, Bitter gourd *(Momordica charantia* L.) Germplasm" at Bangladesh Agricultural University, Mymensingh, located at 24°75' N latitude and 90°50' E longitude, with a rise of 18 meters above sea level. The experimental site was medium height land assigned to the Old Brahmaputra Flood Plain Alluvial Tract (UNDP, 1988). The soil texture was silty loam with a pH 6.7. The trial's location was subtropical in nature. This research study occurred from February to June 2023. This period is characterized by no or mild rainfall, as well as low to normal temperatures.

In this investigation, fifty bitter gourd accessions were assessed, with seeds received from diverse regions of Bangladesh through the CVFB project. The collected accessions of bitter gourd (MC) are categorized by their locations. From Jamalpur, Bangladesh, accessions include MC01, MC02, MC03, MC04, MC05, MC06, MC07, MC11, MC12, MC13, MC16, and MC17. Accessions from Mymensingh, Bangladesh, include MC19, MC21, MC22, MC42, MC43, MC47, MC61, MC62, MC78, MC79, MC80, MC81, MC84, MC86, MC88, MC89, MC90, MC92, MC95, and MC96. Tangail, Bangladesh, contributed accessions MC52, MC53, MC54, MC55, MC56, MC57, MC58, MC59, and MC60. Comilla accessions include MC101, MC103, MC104, MC105, MC107, and MC108. Additionally, MC63 was collected from Pabna, and MC139 from Patuakhali, Bangladesh.

Variability, character association, and diversity were measured among these accessions, which were denoted as experimental treatments, in the experiment, and each accession represented a treatment, and three plants per accession made up a replication in a Randomized Complete Block Design (RCBD) with three replications. Therefore, the experimental area extended 48 m × 20 m and is divided into three blocks. The 50 treatments were randomly distributed across plots within each block.

Collecting data

Data on these variables can be obtained from the examined plants during the experiment. The specifications of data recording are given below on an individual plant basis:

Quantitative characters

The vine length was measured in centimeters from the base to the tip of the growing point using a measuring scale at intervals of 30, 45, 60, and 75 days after sowing (DAS), as well as at the final harvest (Rahman et al. 2024).

To determine the days to the first male flowering, each accession was closely observed, and the number of days from sowing to the opening of the first male flower was recorded. Likewise, for the first female flowering, observations were made for the emergence and opening of the first female flower, and the number of days was noted.

For fruit measurements, three randomly selected fruits from each accession were measured for length at the time of harvest using a measuring scale. The diameter of three green fruits was measured at the broadest part using slide calipers, and the measurements were expressed in centimeters.

The weight of three randomly selected fruits was measured using a digital balance at the horticultural maturity stage for each accession, and the average weight in grams was calculated. The total number of fruits from selected plants of each accession was recorded, and the mean was determined (Howlader et al., 2024).

The fruit yield per plant was calculated using the formula (Hasan et al., 2024; Nikson et al. 2024):

Fruit yield = Number of fruits × Average fruit weight

Qualitative characters

Additionally, various qualitative traits of fruits at horticultural maturity were noted, including the predominant fruit skin color, the shape of the stem end, and the shape of the blossom end, using a measuring scale.

Statistical analysis

The data were subjected to statistical investigation using STATISTIX version 10 software. The F test was used to do analyses of variance (ANOVA) on all of the variables. In their study, a group researchers used the LSD test to discern the statistical significance of the disparity between the means at the 5% and 1% levels of probability (Howlader et al. 2025).

Estimation of genotypic and phenotypic variances

Genotypic and phenotypic variance estimated according to the formula given by Johnson er al. (1955).

Genotypic variance ($\sigma^2 g$) = $\frac{GMS-EMS}{r}$

Where, GMS = Genotypic mean sum of square, EMS = Error mean sum of square, r = number of replications

Phenotypic variance (σ^2_{ph}) = $\sigma^2 g$ + EMS

Where, $\sigma^2 g$ = Genotypic variance, EMS = Error mean sum of square, $\sigma^2 e$ = Error variance

Estimation of genotypic and phenotypic co-efficient of variation

Genotypic and phenotypic co-efficient of variation were calculated by the formula suggested by Genotypic co-efficient of variation

$$(\%GCV) = \sqrt{\frac{\sigma 2g}{x}} \times 100$$

Where, $\sigma^2 g$ = Genotypic variance, x = Population Mean

Similarly, the phenotypic co-efficient of variation was calculated from the following formula.

$$\text{Phenotypic co-efficient variation (PCV)} = \sqrt{\frac{\sigma 2ph}{x}} \times 100$$

Where, σ^2_{ph} = Phenotypic variance, x = Population Mean

$$\text{Genotypic correlation } (r_{pxy}) = \frac{\sigma pxy}{\sqrt{\sigma 2\ px, \sigma 2\ py}}$$

Where, σ_{gxy}= Genotypic co-variance between the traits x and y, σ^2_{px}= Genotypic variance of the trait x, σ^2_{py}= Genotypic variance of the trait y

$$\text{Phenotypic correlation } (r_{pxy}) = \frac{\sigma pxy}{\sqrt{\sigma 2\ px, \sigma 2\ py}}$$

Where, σ_{gxy} = Phenotypic co-variance between the traits x and y, σ^2_{px} = Phenotypic variance of the trait x, σ^2_{py} = Phenotypic variance of the trait y

Estimation of heritability

Broad sense heritability was estimated by the following formula, suggested by Johnson, et al. (1955).

$$h^2_b\% = \frac{\sigma 2\ g}{\sigma 2\ ph} \times 100$$

Where, h^2_b =Heritability in broad sense, σ^2_g =Genotypic variance, σ^2_{ph} =Phenotypic variance

Estimation of genetic advance

The expected genetic advance for different characters under selection was estimated using the formula suggested by Lush (2024) and Johnson, et al (2021).

$$GA = K \frac{\sigma 2g}{\sigma 2ph} \times \sigma 2ph$$

Where, K=Selection intensity, the value which is 2.06 at 5% selection intensity

Results

Variability and field performance of 50 bitter gourd

Vine length

The vine length at 75 DAS varied substantially among the accessions, with a mean value of 253.93 cm and a range of 116.67 to 458.67 cm. The longest vine (458.67 cm) was observed in MC101 at 75 DAS, while the shortest vine (116.67 cm) was discovered in MC58 (Table 2). The differences between genotypic (4574.40) and phenotypic (4676.60) variances, as well as the very small difference between genotypic (26.64%) and phenotypic (26.93%) coefficient of variation, indicated a small environmental effect on vine length at 75 DAS. Additionally, the heritability (97.81), genetic advance (137.80), and genetic advance percentage (54.27) were determined (Table 1).

Petiole length

Petiole length varied substantially among the accessions and ranged from 5.15 cm to 8.30 cm, with a mean value of 6.81 cm (Table 2). The lowest value of petiole length was recorded for MC89 (5.15) which was statistically near to MC56 (8.30), which was highest. There was a very small difference between genotypic (1.52) and phenotypic (1.56) variances, as well as the differences between genotypic (18.14%) and phenotypic (18.34%) coefficients of variations. It also found that the heritability (97.84), genetic advance (2.52), and genetic advance% (36.97%) (Table 1).

Flowering characteristics

Number of male flowers

The number of male flowers among bitter gourd accessions showed significant variation, ranging from 8.33 to 105.00, with a mean of 31.33 (Table 2). MC42 had the highest number of male flowers (105.00), while MC90 had the fewest (8.33). Phenotypic variance (539.25) exceeded genotypic variance (397.33), with heritability at 73.68%. The genetic advance was 35.25, and genetic advance% was 112.52 (Table 1).

Number of female flowers

The number of female flowers among the bitter gourd accessions varied significantly, ranging from 6.67 to 34.33 with an average of 18.40. MC81 had the highest number of flowers (34.33), while MC512 had the lowest (6.67). Genotypic and phenotypic variances differed slightly, with heritability at 67.92% and genetic advance at 10.45 (Table 1).

Days to first male flower

Days to the first male flower, as observed, varied significantly among the accessions and ranged from 70.33 to 73.33 with a mean value of 75.64 (Table 3). It took the shortest time (70.33 days) to flower, which was statistically similar to MC108 (73.33 days) and MC59 (73.33 days), while MC105 took the maximum time for flowering (83.67 days), which was statistically similar to MC98 (82.33). There were slightly higher differences between genotypic (5.72) and phenotypic (13.83) variances, as well as minor differences between genotypic (3.16%) and phenotypic (4.92%) coefficients of variation. It also demonstrated that the heritability (41.35) and the difference between genetic advance (3.17) and genetic advance% (4.19%) were very small (Table 1).

Days to first female flower

The analysis of variance revealed substantial variability among the 50 bitter gourd accessions, with flowering days ranging from 68.67 to 84.00 and a mean of 75.89 (Table 3). MC61 exhibited the earliest flowering, while MC90 was the latest. Heritability was 71.75%, with a genetic advance of 5.94 and genetic advance% of 7.82 (Table 1).

Table 1. Estimation of genetic parameters of bitter gourd for morphological traits

Characters	GVR (d2g)	PVR (d2p)	GCV (%)	PCV (%)	H^2	GA	GA (%)	CV (%)	Mean ± SE	Range
Vine length (cm)	4574.4	4676.6	26.64	26.93	97.81	137.8	54.27	3.980	253.93±9.60	116.67-458.67
No. of male flower	397.33	539.25	63.63	74.13	73.68	35.25	112.52	38.03	31.330±2.98	8.33-105.00
No. of female flower	37.860	55.74	33.44	40.58	67.92	10.45	56.78	22.98	18.400±0.94	6.67-35.00
Days first male flower	5.7200	13.83	3.160	4.920	41.35	3.170	4.19	3.760	75.640±0.41	70.33-83.67
Days to first female flower	11.570	16.13	4.480	5.290	71.75	5.94	7.82	2.810	75.890±0.51	68.67-84.00
Petiole length (cm)	1.5200	1.560	18.14	18.34	97.84	2.52	36.97	2.700	6.8100±0.18	4.13-9.47
Length of fruit (cm)	8.0100	9.850	25.35	28.12	81.28	5.26	47.08	12.17	11.160±0.42	5.09-16.53
Breadth of fruit (cm)	1.0300	1.110	20.54	21.31	92.95	2.02	40.8	5.660	4.9400±0.15	3.06-7.10
No. of fruits/plant	46.750	56.84	27.16	29.95	82.24	12.77	50.74	12.62	25.170±1.00	7.00-35.67
Average fruit weight (g)	466.64	537.8	63.76	68.45	86.77	41.45	122.35	24.90	33.880±3.13	8.87-101.69
Yield/plant (kg)	0.3000	0.320	64.84	66.85	94.08	1.100	129.56	16.27	0.8500±0.08	0.16-2.50

Here, GVR: genotypic variance, PVR: phenotypic variance, PCV: phenotypic coefficient of variation, GCV: genotypic coefficient of variation, H^2= heritability, GA= genetic advance, CV: coefficient of variation

Table 2. Variability and field performance of 50 bitter gourd accessions

Accessions No.	Vine length (cm)	Petiole length (cm)	No. of male flowers
MC01	262.67	4.13	36
MC02	190.67	5.27	28
MC03	256.33	6.3	21.33
MC04	293	4.31	15.67
MC05	217.67	4.27	38
MC06	255.67	5.26	23
MC07	280.33	5.3	28
MC11	339.67	6.15	20
MC12	293	7.18	28.67
MC13	197.33	6.23	46.67
MC16	325.67	7.25	31.33
MC17	201.33	8.2	9.67
MC19	264.67	8.19	32
MC21	349	7.3	80.33
MC22	343.33	6.28	78
MC42	292.33	8.28	105
MC43	242.33	5.23	15.33
MC47	213	7.25	24
MC52	124.67	6.25	18.67
MC53	323.67	5.25	28
MC54	279.67	6.2	26
MC55	271.67	7.24	34.33
MC56	234	8.3	25.33
MC57	302	8.28	26
MC58	116.67	6.28	9.33
MC59	270	5.21	24
MC60	275.33	8.21	20.33
MC61	334	6.24	16.33
MC62	190.33	7.25	17
MC63	230	7.23	31.33
MC78	266	8.15	32.67
MC79	330.33	7.26	71.33
MC80	273.67	7.31	62.67
MC81	242	6.61	73.33
MC84	184.67	8.29	22.67
MC86	211.33	7.12	24.33
MC88	206	6.09	20
MC89	166	5.15	15.33
MC90	200.33	7.21	8.33
MC92	170.67	6.28	18
MC95	388	8.28	24.33
MC96	331	7.29	13.33
MC98	184.67	8.23	20.67
MC101	458.67	7.25	20.33
MC103	283	8.16	21
MC104	231.33	6.17	12.33
MC105	183	9.47	59.33
MC107	152.67	7.26	21.67
MC108	213	6.21	21.67
MC139	250	8.15	65.33
LSD0.05	16.34	0.3	19.26
LSD0.01	21.6	0.39	25.46
LS	**	**	**

Here, LS= Level of Significance and, ** = 1% Level of significance

Table 3. Variability and field performance of 50 bitter gourd accessions

Accessions No.	No. of female flowers	Days to first male flower	Days to first female flower	Length of fruit (cm)	Breadth of fruit (cm)
MC01	16	79.33	78.67	7.42	4.05
MC02	14.33	74.33	78.67	13.04	6.12
MC03	24	70.33	74	8.08	5.14
MC04	20.33	77.33	76	8.08	5.1
MC05	24	78	82.33	12.52	6.1
MC06	23	74.33	78	8.76	5.09
MC07	18.33	77.67	73.67	14.36	5.73
MC11	12.67	72.33	72.33	12.69	5.02
MC12	22.33	74.33	71	11.07	4.08
MC13	27	76	78	11.08	4.05
MC16	18.33	78	78.67	9.08	5.09
MC17	34.33	73	74.33	12.38	5.12
MC19	15.33	74.67	72	7.75	6.11
MC21	24.67	74	73	16.35	6.76
MC22	25.67	72	74.33	14.37	3.06
MC42	21	78.67	70.33	10.58	4.12
MC43	19.33	79.67	80.67	9.71	4.04
MC47	22	76.33	70.67	13.68	5.03
MC52	6.67	80	77	14.68	4.12
MC53	21.67	73.67	77.33	9.75	6.1
MC54	18	78.33	75.67	9.05	4.12
MC55	18.67	75	75	8.08	4.43
MC56	20	75.67	76.67	9.08	4.07
MC57	9.67	73.67	80	11.72	3.08
MC58	11	74	74	11.41	5.13
MC59	14.67	73.33	76.33	13.14	6.09
MC60	10	73.67	72.33	13.85	6.04
MC61	21	75.33	68.67	12.53	5.02
MC62	13.33	71.67	79	11.16	4.05
MC63	17	77.67	82	11.22	4.07
MC78	13	74.33	78.33	11.08	3.73
MC79	23	73	74.67	11.69	4.08
MC80	35	74.67	75.33	5.09	5.1
MC81	34.33	74	74	8.53	3.08
MC84	15.33	74	72.67	8.2	6.07
MC86	16.67	72.33	72.67	6.54	6.07
MC88	15.33	74	79.67	5.88	5.08
MC89	13.33	75.33	80.67	6.49	4.05
MC90	13.67	82	84	8.81	4.08
MC92	12.33	76	71	8.19	5.08
MC95	13.33	73.67	70.67	13.86	4.1
MC96	23	74	71.67	16.53	6.1
MC98	11.67	82.33	75.67	14.52	7.1
MC101	19	74.67	75	11.7	6.05
MC103	18	79.33	72.67	13.75	4.04
MC104	11.67	73.33	76.33	10.4	4.41
MC105	8.33	83.67	78.33	15.39	7.05
MC107	14	78.33	80	15.73	6.09
MC108	13.33	73.33	81	15.39	5.02
MC139	31.33	77.33	79.33	13.69	4.48
LSD0.05	6.84	4.6	3.45	2.2	0.45
LSD0.01	9.04	6.09	4.56	2.9	0.6
LS	**	**	**	**	**

Here, LS = Level of Significance and, ** = 1% Level of significance

Fruits characteristics

Length of fruit

It was observed that length of fruit varied considerably, rising from 5.88 cm to 16.53 cm with a mean value of 11.16. The minimal length of fruit (5.88 cm) was recorded in MC88, and the maximum length of fruit (16.53 cm) was recorded in MC96, which differed significantly from the other accessions. There were very differences between genotypic (8.01) and phenotypic (9.85) variances. Furthermore, the phenotypic (28.12%) coefficient of variation was higher than the genotypic (25.35%) coefficient of variation (Table 3). It also demonstrated that the heritability (81.28) genetic advance (5.26) was very small compared to the genetic advance% (47.08%) (Table 1).

Breadth of fruits

Fruit breadth varied significantly, ranging from 3.06 cm in MC22 to 7.10 cm in MC98, with an average of 4.94 cm (Table 3). Genotypic and phenotypic variances were closely matched, as were their coefficients of variation. Heritability (92.95) and genetic advance (2.20) were modest, with a genetic advance percentage of 40.80% (Table 1).

Number of fruits per plant

The number of fruits per plant had a very high significant range value of 7.00 to 35.67 with a mean value of 25.17. The maximum number of fruits in MC080 was 35.67, whereas the minimum number in the MC101 variety was 7.00 (Figure 1).

There were very close differences between genotypic (46.75) and phenotypic (56.84) variances, as well as the differences between genotypic (27.16%) and phenotypic (29.95%) coefficients of variations; the genetic advance (12.77) was higher than the genetic advance% (50.74%) (Table 1).

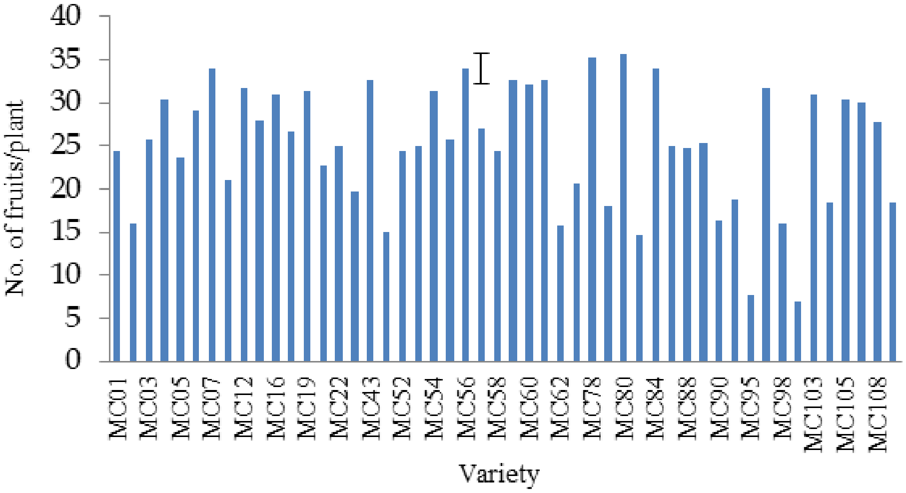

Figure 1. Effect of accessions on numbers of fruits/plant of bitter gourd accessions. Vertical bar represents LSD result 1% significant

Average fruit weight per plant

For this character, a significant difference was observed among the 50 accessions of bitter gourd, ranging from 8.87 g to 101.69 g, with a mean value of 33.88. It is one of the most important yields, contributing character. The highest value was obtained from MC 079, which was 101.69 g per plant. And the lowest value was obtained from MC 084, which was 8.87 g per plant (Figure 2).

The phenotypic (537.80) variance was higher than the genotypic (466.64) variance. The phenotypic (68.45%) coefficient of variation is also higher than the genotypic (63.76%). It also found that heritability (86.77) and genetic advance (41.45) were very smaller compared to genetic advance% (122.35%) (Table 1).

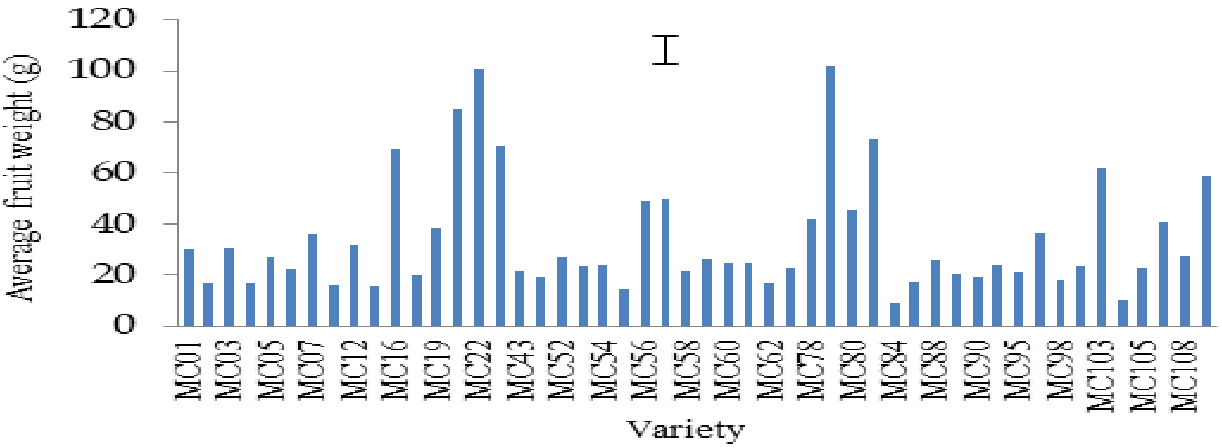

Figure 2. Effect of accessions on average weight of fruit/plant (g) of bitter gourd accessions. Vertical bar represents the LSD result 1% significant

Yield per plant

The highest yield of fruits per plant found at MC22 was 2.50 kg/plant, and the lowest was 0.16 kg/plant at MC101 (Figure 3). The phenotypic (0.32) variance was very close to the genotypic (0.30) variance. The phenotypic (66.85%) coefficient of variation is also higher than the genotypic (64.84%) coefficient of variation (Table 3). It also found that the heritability (86.77) and genetic advance (1.10) were very smaller compared to the genetic advance% (129.56%) (Table 1).

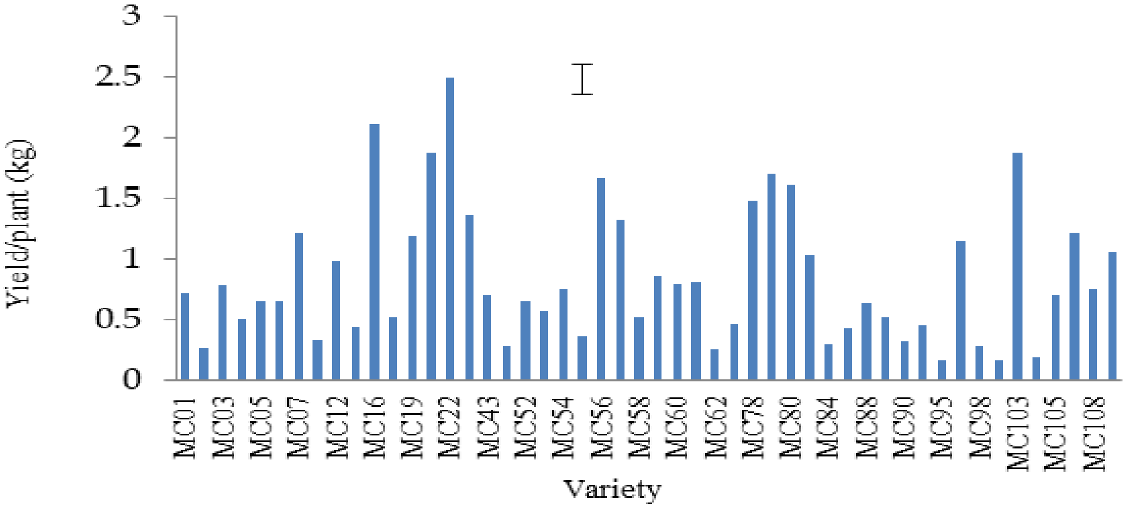

Figure 3. Effect of accessions on yield/plant (kg) of bitter gourd germplasm. Vertical bar represents the LSD result 1% significant

Qualitative Characters

A wide range of variability was observed in fruit color among 50 bitter gourd accessions and Fruit skin color varied from dark green to green and pale green color (Table 4). A wide spectrum of variability is also found in the shape of the stem end and the shape of the blossom end of fruit. Stem end and blossom end were recorded either as pointed or rounded.

Table 4. Variability in different qualitative characters in respect of fruit color, shape of stem end and shape of blossom end of 50 bitter gourd germplasm

Accessions No.	Fruit color	Shape of stem end	Shape of blossom end
MC01	Light Green	Pointed	Rounded
MC02	Dark Green	Pointed	Rounded
MC03	Light Green	Rounded	Pointed
MC04	Green	Rounded	Pointed
MC05	Green	Rounded	Rounded
MC06	Light Green	Pointed	Pointed
MC07	Dark Green	Rounded	Pointed
MC11	Light Green	Rounded	Pointed
MC12	Green	Pointed	Rounded
MC13	Green	Rounded	Rounded
MC16	Light Green	Pointed	Pointed
MC17	Green	Pointed	Pointed
MC19	Dark Green	Rounded	Rounded
MC21	Light Green	Pointed	Rounded
MC22	Green	Rounded	Pointed
MC42	Light Green	Rounded	Rounded
MC43	Light Green	Pointed	Pointed
MC47	Dark Green	Rounded	Rounded
MC52	Green	Pointed	Rounded
MC53	Light Green	Pointed	Pointed
MC54	Dark Green	Rounded	Pointed
MC55	Light Green	Rounded	Rounded
MC56	Green	Rounded	Rounded
MC57	Light Green	Pointed	Pointed
MC58	Light Green	Rounded	Rounded
MC59	Dark Green	Pointed	Rounded
MC60	Green	Pointed	Rounded
MC61	Green	Rounded	Pointed
MC62	Light Green	Pointed	Pointed
MC63	Dark Green	Rounded	Rounded
MC78	Green	Pointed	Pointed
MC79	Dark Green	Pointed	Pointed
MC80	Light Green	Rounded	Rounded
MC81	Green	Pointed	Pointed
MC84	Green	Rounded	Pointed
MC86	Green	Rounded	Rounded
MC88	Dark Green	Pointed	Rounded
MC89	Green	Rounded	Pointed
MC90	Dark Green	Rounded	Pointed
MC92	Light Green	Rounded	Rounded
MC95	Green	Pointed	Pointed
MC96	Light Green	Pointed	Rounded
MC98	Dark Green	Rounded	Pointed
MC101	Green	Rounded	Rounded
MC103	Dark Green	Rounded	Pointed
MC104	Dark Green	Pointed	Pointed
MC105	Dark Green	Rounded	Rounded
MC107	Green	Rounded	Pointed
MC108	Green	Pointed	Rounded
MC139	Green	Rounded	Pointed

Genotypic correlation coefficient of yield and different yield-related characters

Vine length showed a significant positive correlation with average fruit weight (r = 0.386**) and yield per plant (r = 0.332*), while negatively correlating with days to the first male flower (r = -0.281*) and first female flower (r = -0.365**) (Table 5). This suggests longer vines lead to earlier flowering and higher yield. Days to first male flowering had a positive correlation with days to first female flowering (r = 0.340*), but negatively correlated with average fruit weight (r = -0.081) and yield per plant (r = -0.033), indicating delayed male flowering reduces yield.

Table 5. Coefficients of genotypic correlation among different yield components

Characters	Days to first male flower	Days to first female flower	Length of fruit (cm)	Breadth of fruit (cm)	No. of fruits/plant	Average fruit weight (g)	Yield/plant (kg)
Vine length (cm)	-0.281*	-0.365**	0.11	-0.057	-0.097	0.386**	0.332*
Day to first male flower		0.340*	0.137	0.098	0.073	-0.081	-0.033
Days to first female flower			-0.119	-0.143	-0.002	-0.142	-0.102
Length of fruit (cm)				0.257	-0.1	0.193	0.16
Breadth of fruit (cm)					0.101	-0.293*	-0.211
No. of fruits/plant						0.037	0.417**
Average fruit weight (g)							0.873**

Here, ** = 1% Level of significance

Days to first female flowering had a strong positive correlation with the node number of the first male flower (r = 0.514**), but negatively correlated with fruit length, average fruit weight, number of fruits per plant, and yield per plant (Table 5). Fruit length showed a positive correlation with yield per plant (r = 0.160), average fruit weight (r = 0.193), and fruit breadth, but a negative association with the number of fruits per plant (Table 5). The number of fruits per plant was highly correlated with yield per plant (r = 0.417**) and positively associated with average fruit weight. Average fruit weight had a very strong positive correlation with yield per plant (r = 0.873**), indicating that heavier fruits significantly boost yield (Table 5).

Path analysis in genotypic level

Vine length versus yield per plant

Vine length had a direct positive effect (0.412) on plant yield (Table 6). Vine length also shows positive effects to the node of first male flowering (0.0033), node of first female flowering (0.0199), length of fruit (0.0070), breadth of fruit (0.0008), average fruit weight (0.3162), yield per plant (0.332**), whereas a negative indirect effect on days to first male flower, days to first female flower, and number of fruits per plant.

Days to first male flowering versus yield per plant

Days to the first male flowering showed a positive direct effect (0.0031) on the plant's yield (Table 6). It also shows positive effects on days to first female flower (0.0161), length of fruit (0.0087), number of fruits per plant (0,0289), whereas negative indirect effects on plant height, days to first female flowering, node of first male flowering, node of first female flowering, and average fruit weight plant.

Days to first female flowering versus yield per plant

Days to the first female flowering showed a positive direct effect (0.0472) on the yield per plant (Table 6). It also showed a negative indirect effect on yield per plant through nodal position of first female flowering, days to first male flowering, and fruit length (Table 6).

Length of fruit versus yield per plant

The path analysis revealed that fruit length had a positive direct effect (0.0637) on yield per plant (Table 6). It showed a negative indirect effect on yield through days to first female flowering, breadth of fruit, and number of fruits per plant. Fruit length showed positive indirect effect on yield through plant height, days to first male flowering, average fruit weight, and yield per plant.

Breadth of fruit versus yield per plant

The path analysis revealed that fruit length had a negative direct effect (-0.0137) on yield per plant. Fruit breadth also shows a negative indirect effect on plant height, days to first female flowering, average fruit weight, and yield per plant. It showed a positive indirect effect on days to first male flowering, length of fruit, and number of fruits per plant (Table 6).

Table 6. Partitioning of direct and indirect effects morphological characters of 50 genotypes of genotypic level by path

Characters	Plant height (cm)	Days to first male flower	Days to first female flower	Length of fruit (cm)	Breadth of fruit (cm)	No. of fruits/ plant	Average fruit weight (g)	Yield/ plant (kg)
Vine length (cm)	0.0412	-0.0009	-0.0172	0.007	0.0008	-0.0384	0.3163	0.332*
Days to first male flower	-0.0116	0.0031	0.0161	0.0087	-0.0013	0.0289	-0.0664	-0.033
Days to first female flower	-0.015	0.0011	0.0472	-0.0076	0.0019	-0.0008	-0.1164	-0.102
Length of fruit (cm)	0.0045	0.0004	-0.0056	0.0637	-0.0035	-0.0396	0.1582	0.16
Breadth of fruit (cm)	-0.0023	0.0003	-0.0068	0.0164	-0.0136	0.04	-0.2401	-0.211
No. of fruits/plant	-0.004	0.0002	-0.0001	-0.0064	-0.0014	0.3962	0.0303	0.417**
Average fruit weight (g)	0.0159	-0.0003	-0.0067	0.0123	0.004	0.0147	0.8195	0.873**

Here, ** = 1% Level of significance

Number of fruits per plant versus yield per plant

The number of fruits per plant had a positive direct effect on yield (0.3962). Fruit numbers showed a positive indirect effect on yield through days to first male flowering and, and average fruit weight. It showed a negative indirect effect on yield through plant height, days to first female flowering, and fruit length.

Average fruit weight versus yield per plant

The average fruit weight had a positive direct effect (0.8195) on the yield per plant (Table 6). Average fruit weight showed a positive indirect effect on yield through plant height, node of the first male flower, fruit length, breadth of fruit, number of fruits per plant, and yield per plant, whereas it showed a negative indirect effect on yield via days to the first male flowering and days to the first female flowering.

Clustering of accessions

For hybridization, D2 clustering helps identify diversity among accessions, with those in the same cluster being less divergent. Based on D2 analysis, 50 bitter gourd accessions were grouped into six clusters (Table 7). Cluster I, the largest, contained 14 accessions (28%), while Cluster IV had the fewest with 3 accessions (6%). Cluster II included 13 accessions (26%), Cluster III had 4 (8%), Cluster V had 10 (20%), and Cluster VI comprised 6 accessions (12%) of the total studied genotypes.

Table 7. Name, percent and name of accession in different clusters

Cluster name	No. of varieties	Percent (%)	Name of accessions
I	14	28	MC01, MC04, MC05, MC06, MC13, MC43, MC53, MC54, MC55, MC63, MC88, MC89, MC90, MC92
II	13	26	MC02, MC03, MC12, MC17, MC19, MC47, MC58, MC59, MC60, MC62, MC84, MC86, MC104
III	4	8	MC07, MC21, MC61, MC96
IV	3	6	MC11, MC95, MC101
V	10	20	MC16, MC22, MC42, MC56, MC57, MC78, MC79, MC80, MC81, MC103
VI	6	12	MC52, MC98, MC105, MC107, MC108, MC139

Dendrogram

The dendrogram (Figure 4) grouped the studied bitter gourd accessions into six clusters. Cluster I had the most accessions, including MC01, MC04, MC05, and others. Cluster II included MC02, MC03, MC12, MC19, and more. Accessions MC07, MC21, MC61, and MC96 were in cluster III, while cluster IV contained MC11, MC95, and MC101. Cluster V comprised MC16, MC22, MC42, MC56, and others, and the final cluster VI included MC52, MC98, MC105, MC107, MC108, and MC139.

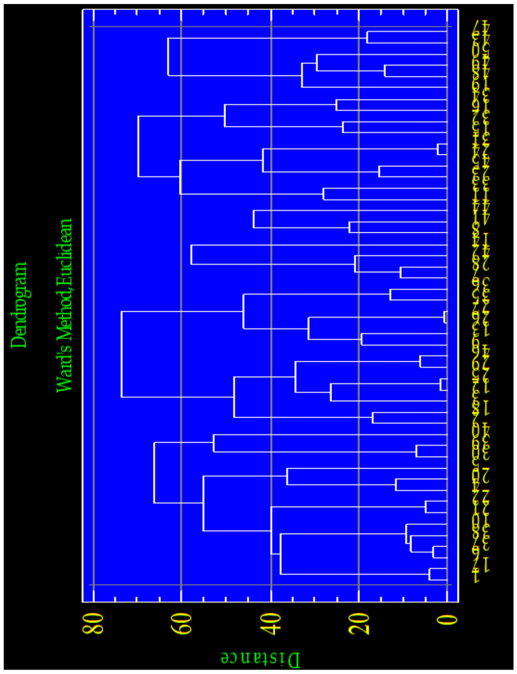

Figure 4. Dendrogram based on summarized data on differentiation among 50 accessions of bitter gourd according to Ward's method.

Discussion

The study of bitter gourd accessions revealed significant diversity in their morphological and qualitative traits, emphasizing the importance of genetic variation. The genotypic correlation coefficients were generally higher than phenotypic ones, highlighting stronger genetic relationships (Islam et al., 2015; Akhter et al., 2020). Correlation analysis, which shows how traits interact with yield, indicates that individual traits cumulatively affect yield, though they don't always explain cause-and-effect relationships (Zeba et al., 2022; Bashir et al. 2025; Mia et al. 2025).

In the present study, plant height had the highest genotypic (4574.40) and phenotypic (4676.60) variances, aligning with findings by Singh et al. (2017). High heritability (>60%) was observed for traits such as vine length, nodes per vine, fruit length, fruit weight, fruits per plant, and fruit yield per plant. The combination of high heritability with high genetic advance in traits like vine length, fruit length, and yield per plant suggests that effective selection can be made based on these traits (Talukdar et al., 2018). However, for traits like days to first female flowering, which showed high heritability but low genetic advance, non-additive gene effects are likely involved, making selection less profitable (Islam et al., 2009).

The results demonstrated that plant height, branch number, flower number, male flower number, average fruit weight, and yield per plant showed high genotypic and phenotypic coefficients of variation. Medium variation was observed in female flower numbers, fruit length, fruit breadth, and number of fruits per plant, while days to first male and female flowering showed low variation. Path analysis indicated that average fruit weight had the most significant positive direct effect on yield, whereas days to the first male flower had a minor direct effect (Gupta et al., 2015; Yesmin et al. 2025).

The study also involved clustering 50 bitter gourd accessions into six distinct groups using D2 statistics. Cluster I was the largest, containing 14 accessions (28% of the total), while Cluster IV had the fewest, with only three accessions (6%). Cluster II contained 13 accessions, Cluster III had four, Cluster V included 10, and Cluster VI comprised six accessions. Accessions within a cluster are generally less diverse, making this grouping useful for hybridization purposes (Cheema et al., 2011; Haque et al. 2025; Laboni et al. 2024).

MC01, MC04, MC05, and MC92 were among the accessions grouped in Cluster I, which had the largest number of accessions. Cluster IV, in contrast, had the fewest, including accessions MC11, MC95, and MC101. These major clusters indicated a high degree of homogeneity among accessions, suggesting clinal variation (Shankar et al., 2009; Hasan et al. 2025; Shumon et al. 2025).

Cluster analysis further revealed that the largest intra-cluster distance was found in Cluster III, followed by Cluster II and Cluster I, while Clusters IV and V had the shortest distances (Jatav et al., 2022). These results align with findings from Prasanth et al. (2020), who suggested that the selection of bitter gourd genotypes for better yield should focus on traits like fruit length, breadth, weight, and the number of fruits. Moreover, hybridization between accessions from Clusters I and II or I and III could result in improved fruit yield in the segregating population by emphasizing these traits.

In conclusion, the study's findings demonstrate that bitter gourd accessions exhibit significant genetic variability, particularly in traits like fruit length, weight, and vine length, which are critical for yield. The high heritability and genetic advance for certain traits suggest that effective selection for breeding programs is feasible, particularly by focusing on accessions from the most diverse clusters.

Conclusion

The findings of this study indicated that bitter gourd accessions exhibit a significant degree of variability. Furthermore, the yield of bitter gourd was correlated with a variety of yield-contributing characteristics. Based on the magnitude of the cluster mean and the yield attributing characteristics, it can be inferred that the vine length displayed the highest performance in MC101. The minimum time to flower was statistically similar to MC108, and MC61 exhibited early female flowering. The highest number of male flowers was observed in MC42, while the highest number of female flowers was discovered in MC81. MC79 had the highest number of flowers per plant (86.00), and MC 080 had the highest number of fruits. The maximum length of fruit was observed in MC96, while the maximum breadth of fruits (7.10) was recorded in MC98. The highest average weight of fruits per plant was discovered at MC 079. MC22 yielded the most crops per plant. Cluster I was the largest cluster, comprising 28.00% of the total investigated accessions with 14 accessions. Selection procedures should be applied for desired characteristics such as vine length at harvest, fruit length, average fruit weight, and number of fruits per plant to develop high-yielding varieties. Relatively higher value and lower differences between phenotypic co-efficient of variation and genotypic co-efficient of variation of different yield contributing characters like fruit length, average fruit weight, number of fruits per plant, and yield per plant were observed, which indicates high potentiality to select these characters in the future that are less affected by environmental influence.

Declarations

CRediT authorship contribution statement

Tuhin Hasan: Investigation, Methodology and Conceptualization. Md. Golam Rabbani: Conceptualization, Supervision, Project administration, Fund acquisition, Resources and Validation. Md. Mokter Hossain: Supervision and Validation. Nayan Chandra Howlader: Formal Statistical analysis, Data curation, writing – original draft and Software. Md. Mahfuzul Hasan: Writing – original draft and Software. Faisal Ahmed Shourov and Shuvro Sarkar: Writing – review & editing. Md. Al Amin: Methodology. All authors have read and agreed to the published version of the manuscript.

Conflicts of Interest

The authors declare they have no conflicts of interest.

Acknowledgements

The authors would like to express their gratitude to the concerned authority, the Ministry of Science and Technology, Government of the People's Republic of Bangladesh, and the project authority, CVBF, Department of Horticulture, Bangladesh Agricultural University, Mymensingh, for their financial and technical assistance in conducting the research work.

References

Abbas, M., Shabbir, M. A., Haq, S. M. A. U., Wahab, H. A., Hassan, S. A., Adeeba, F., ... & Aadil, R. M. (2024). Harnessing the potential of bitter gourd seeds for food and nutrition-A comprehensive review. *Applied Food Research*, 100508. https://doaj.org/article/937e2885370d475fa1a0f27fa074ec71

Akter, S., Jahan, I., Hossain, M. A., & Hossain, M. A. (2020). Variability for agromorphological traits, genetic parameters, correlation and path coefficient analyses in Lentil (Lens culinaris Medik.). Research in Plant Biology, 10, 1-7. DOI: https://doi.org/10.25081/ripb.2020.v10.6237

Ahsan, S. M., Injamum-Ul-Hoque, M., Howlader, N. C., Rahman, M. M., Rahman, M. M., Haque, M. A., & Choi, H. W. (2025). Haploid Production in Cannabis sativa: Recent Updates, Prospects, and Perspectives. *Biology*, *14*(6), 701. DOI: https://doi.org/10.3390/biology14060701

Al Masum, Md. A., Islam, Md. T., Hossain, Md. I., Das, K. R., Ahmad, M., Hasan, Md. M., & Howlader, N.C. (2025). Efficacy of spinosad for the management of mustard & wheat aphid species. *Bulgarian Journal of Crop Science*, 62(2) 96-103. DOI: https://doi.org/10.61308/ABXL3507

Ali, M. S., Masum, M. A. A., Nazmul, S., Das, K. R., Howlader, N. C., & Hasan, M. M. (2025). Investigation of Coccinia Grandis Leaf Extract and Its Efficacy Against Stored Grain Pests. *SVU-International Journal of Agricultural Sciences*, 7(1), 71-82. doi: https://doi.org/10.21608/svuijas.2025.334693.1410

Bashir, M. U. H. A., Haque, T., Howlader, N. C., Rashid, M. A. M. and Sarker, S. (2025). Molybdenum and Methods of Application in Relation to Growth and Yield of Cabbage (Brassica Oleacea Var Capitata L.). *Journal of Agricultural Sciences and Engineering*, 7(1), 19-31. doi: http://doi.org/10.48309/jase.2025.503480.1069

Barua, R., Talukder, M. E. U., Islam, M. S., Yesmin, F., Chakma, K., Kabir, M. G., & Bhuiyan, R. H. (2020). Nutritional analysis and phytochemical evaluation of Bitter Gourd (Momordica Charantia) from Bangladesh. *Asian Journal of Agriculture and Food Sciences (ISSN: 2321–1571)*, *8*(02). https://doi.org/10.24203/ajafs.v8i2.6094

Batool, F., Adeel, S., Iqbal, N., Azeem, M., & Hussaan, M. (2022). Sustainable natural coloring potential of bitter gourd (Momordica charantia L.) residues for cotton dyeing: innovative approach towards textile industry. *Environmental Science and Pollution Research*, *29*(23), 34974-34983. https://doi.org/10.1007/s11356-021-17803-w

Bojarian, M., Asadi-Gharneh, H. A., & Golabadi, M. (2019). Factor analysis, stepwise regression and path coefficient analyses of yield, yield-associated traits, and fruit quality in tomato. International Journal of Vegetable Science, 25(6), 542-553. DOI: https://doi.org/10.1080/19315260.2018.1551260

Cheema, K. L., Iqbal, M., Niaz, S., & Shafique, M. (2011). Assessment of variability of muskmelon. International journal of vegetable science, 17(4), 322-332. DOI: https://doi.org/10.1080/19315260.2011.554969

Cui, J., Zhou, Y., Zhong, J., Feng, C., Hong, Y., Hu, K., & Cao, Y. (2022). Genetic diversity among a collection of bitter gourd (Momordica charantia L.) cultivars. *Genetic Resources and Crop Evolution*, *69*(2), 729-735. https://link.springer.com/article/10.1007/s10722-021-01258-6

Gupta, N., Bhardwaj, M. L., Singh, S. P., & Sood, S. (2015). Correlation and path analysis of yield and yield components in some genetic stocks of bitter gourd (*Momordica charantia* L.). *SABRAO Journal of Breeding and Genetics*, 47(4), 475-481. https://sabraojournal.org/wp-content/uploads/2018/01/SABRAO-J-Breed-Genet-47-4-475-481-Gupta.pdf

Hasan, M. M., Hossain, M. M., Haque, T., Basunia, A. K., & Howlader, N. C. (2025). Morpho-biochemical Evaluation of Three Sugar Apple (Annona squamosa L.) Genotypes. *International Journal of Horticultural Science and Technology*, *12*(2), 189-198.

Hasan, M., Ahmed, K. S., Howlader, N.C, Hasan, M. M., Puja, M. S., Farhana, M. S., & Nikson, M. H. (2025). Optimization of Angoumois Grain Moth (Sitotroga cerealella Olivier) Infestation in Stored Grains as Influenced by Some Botanical Powders. *Turkish Journal of Agriculture - Food Science and Technology*, *13*(2), 321–326. https://doi.org/10.24925/turjaf.v13i2.321-326.7143

Haque, M. T., Howlader, N. C., Miah, M. H., Roy, T. K., Antu, U. B., Hasan, T., ... & Akther, S. (2025). Response of Integrated Pest Management Framework to Insect Pest Infestations of Tomato. *Iraqi Journal of Industrial Research*, *12*(1), 118-133. DOI: https://doi.org/10.53523/ijoirVol12I1ID552

Hoque, F., Kamruzzaman, M., Rana, M. J., Hassan, M. K., & Hassan, J. (2022). Yield gap in bitter gourd production: A perspective of farm-specific efficiency in Narsingdi district in Bangladesh. *Social Sciences & Humanities Open*, *6*(1), 100335. 10.1016/j.ssaho.2022.100335

Howlader, N. C., Hossain, M. M., Rabbani, M. G., Basunia, A. K., Hasan, M. M., & Saima, U. EFFECT OF IRRIGATION INTERVALS ON THE GROWTH, YIELD AND FRUIT QUALITY OF LEMON (CITRUS LIMON L.). (2024). Plant Physiology and Soil Chemistry, 04(01), 20-25. DOI: http://doi.org/10.26480/ppsc.01.2024.20.

Howlader, N. C., Bulbul, M. T. A., Islam, M. Z., Arafat, E., Rana, M. S., & Hasan, M. Z. (2025). Assessing rice genotypes based on agro-morphological characterization and diversity analysis in southern Bangladesh. *Discover Plants*, *2*(1), 1-19. DOI: https://doi.org/10.1007/s44372-025-00253-w

Islam, M. N., Rabbani, M., Malek, M. A., Khalifa, M. S., Rahman, Z., Orpa, N. N., & Mannan, M. A. (2024). Improving Bitter Gourd Growth and Yield in Different Soil Environments by Combining Biochar and Inorganic Fertilizer. *Turkish Journal of Agriculture-Food Science and Technology*, *12*(8), 1318-1326. https://doi.org/10.24925/turjaf.v12i8.1318-1326.6723

Islam, M. R., Hossain, M. S., Bhuiyan, M. S. R., Husna, A., & Syed, M. A. (2009). Genetic variability and path-coefficient analysis of bitter gourd (Momordica charantia L.). Int. J. Sustainable Agric, 1(3), 53-57. https://www.idosi.org/ijsa/1(3)09/1.pdf

Islam, M. S., Haque, M. M., Bhuiyan, M. S. R., & Hossain, M. S. (2015). Estimation of genotypic and phenotypic coefficients variation of yield and its contributing characters of Brassica rapa L. *American-Eurasian Journal of Agricultural & Environmental Sciences*, 15(10), 2029-2034. DOI: https://doi.org/10.5829/idosi.aejaes.2015.15.10.12702

Jat, G. S., Behera, T. K., Singh, A. K., Bana, R. S., Singh, D., Godara, S., ... & Tomar, B. S. (2024). Antioxidant activities, dietary nutrients, and yield potential of bitter gourd (Momordica charantia L.) lines in diverse growing environments. *Frontiers in Nutrition*, *11*, 1393476. https://doi.org/10.3389/fnut.2024.1393476

Jatav, V., Singh, D. K., Singh, N. K., & Panchbhaiya, A. (2022). Principal component analysis in bitter gourd (Momordica charantia L.). Bangladesh Journal of Botany, 51(1), 1-7. DOI: https://doi.org/10.3329/bjb.v51i1.58813

Johnson, H. W., Robinson, H. F., & Comstock, R. E. (1955). Estimates of genetic and environmental variability in soybeans. http://dx.doi.org/10.2134/agronj1955.00021962004700070009x

Karim, F., Hossain, S. M. M., Hasan, M. M., Howlader, N. C., & Bhuiyan, M. M. A. (2024). Biological control of foot and root rot disease of pea by using formulated product of Trichoderma. *Journal of Agricultural Sciences (Belgrade)*, *69*(2).

Rahman, M. T., Hasan, M. A., Hasan, M. M., Howlader, N. C., & Tusar, M. R. S. (2024). Impact of supplemental irrigation and organic manure on growth and yield performance of rice variety BRRI dhan103 under terminal drought condition in Aman season. *Bulg J Crop Sci*, *61*(5), 21-31. DOI: https://doi.org/10.61308/UQNM4090

Mia, S., Howlader, N.C., Tanvir, M., Bulbul, A., & Hasan, R. (2025). Comparative impacts of organic and inorganic fertilizers on the emergence and early growth of BARI Tomato-7 (Solanum lycopersicum L.). *Plant Physiology and Soil Chemistry*, 5(1), 1-3. https://doi.org/10.26480/ppsc.01.2025.01.03

Nikson, M. H., Ahmeda, K. S., Howlader, N. C., Hasanb, M. M., Hasanc, M. R., Tanvir, M., ... & Ahmedc, M. Ecofriendly Management Of Maize Weevil (Sitophilus Zeamais) As Influenced By Different Spices Powder. (2024). Malysian Journal of Halal Research, 7(2), 74-78. DOI: http://doi.org/10.26480/mjhr.02.2024.74.78

Laboni, S. H., Chowdhury, A. K. M. M. B., Bahadur, M. M., Islam, M. R., Hasan, M. M., & Howlader, N. C. (2024). Effect of Different Fertilizer Combinations and Gibberellic Acid (GA3) on Yield Attributing Traits of Mustard: Fertilizer Combinations and GA3 on Yield Attributes of Mustard. *Journal of the Bangladesh Agricultural University*, *22*(2), 185-192. DOI: https://doi.org/10.3329/jbau.v22i2.74552

Patel, A. R., Patel, M. V., Mori, C. V., Kumar, M., & Patel, S. (2020). Effect of integrated nutrient management on growth and quality of bitter gourd (Momordica charantia L.). *Int. J. Chem. Stud*, *8*(3), 2575-2578. 10.22271/chemi.2020.v8.i3ak.9599

Prasanth, K., Sadashiva, A. T., Pitchaimuthu, M., & Varalakshmi, B. (2020). Genetic diversity, variability and correlation studies in bitter gourd (Momordica charantia L.). Indian Journal of Plant Genetic Resources, 33(02), 179-186. DOI: https://doi.org/10.5958/0976-1926.2020.00026.1

Saranyadevi, G., Lakshmanan, V., & Rohini, N. (2017). Performance evaluation and correlation analysis in mithipagal genotypes (Momordica charantia var. muricata). Electronic Journal of Plant Breeding, 8(2), 652-659. DOI: 10.5958/0975-928X.2017.00099.0

Shankar, R., Bagle, B. G., & More, T. A. (2009). Diversity analysis of bitter gourd (Momordica charantia L.) germplasm from tribal belts of India. The Asian and Australasian Journal of Plant Science and Biotechnology, 3(1), 21-25. http://www.ijat-aatsea.com/pdf/May_v7_n3_11/29%20IJAT2010_74FJ-R.pdf

Singh, V., Rana, D. K., & Shah, K. N. (2017). Genetic variability, heritability and genetic advance in some strains of bitter gourd (Momordica charantia L.) under subtropical conditions of Garhwal Himalaya. Plant Archives, 17(1), 564-568. https://plantarchives.org/PDF%2017-1/564-568%20(3584).pdf

Shumon, M. S. I., Howlader, N. C., Jewel, Z. A., Miah, M. H., Khan, S., Islam, M. N., ... & Islam, M. Z. (2025). Diversity Analysis of Rice Genotypes Collected from Six Southern Districts of Bangladesh Based on Agro-Morphological Traits. *Journal of Agroforestry and Environment*, *18*(1), 52-65. DOI: https://doi.org/10.55706/jae1807

Sultana, A., Hossain, S. M. M., Hasan, M. M., Howlader, N. C., Paul, S., Yesmin, M. S., & Hossain, A. (2025). Bio-control management of foot and root rot disease of lentil as impacted by different formulations of Trichoderma product. *Journal of Oasis Agriculture and Sustainable Development*, *7*(2), 1-12. DOI: https://doi.org/10.56027/JOASD.102025

Talukder, Z. H., Khan, M. H., Das, A. K., & Uddin, N. (2018). Assessment of genetic variability, heritability and genetic advance in bitter gourd (Momordica charantia L) for yield and yield contributing traits in Bangladesh. Scholar journal of applied sciences and research, 1(6), 9-18. https://www.innovationinfo.org/articles/SJASR/SJASR-6-161.pdf

Tejaswini, R., Kandpal, K., Swamy, T. S., Kumar, T. L., Dhange, P. R., Gunaga, C. M., & Ashika, S. (2024). Combining Ability and Heterosis for Yield and Yield Attributing Traits in Bitter Gourd. *Journal of Advances in Biology & Biotechnology*, *27*(9), 63-70. https://doi.org/10.9734/jabb/2024/v27i91274

UNDP, 1988: Land Resources Appraisal of Bangladesh for Agricultural Development. Report 2: Agro-ecological regions of Bangladesh.

Yadagiri, J., Gupta, N. K., Tembhre, D., & Verma, S. (2017). Genetic variability, correlation studies and path coefficient analysis in bitter gourd (Momordica charantia L.). Journal of Pharmacognosy and Phytochemistry, 6(2), 63-66. https://www.phytojournal.com/archives/2017/vol6issue2/PartA/6-5-144-541.pdf

Yesmin, M. S., Sikdera, M. S. I., Hossaina, M. S., Hasanb, M. M., & Howlader, N. C. (2023). Effect of organic seed priming on yield and yield attributing traits of chickpea (Cicer arietinum L.) in drought prone area. *Agriculture Extension in Developing Countries*, *1*(1), 38-42. DOI: http://doi.org/10.26480/aedc.01.2023.38.42

Zeba, N., Rasal-Monir, M., Modak, S., Sarker, A., & Rahaman, M. A. (2022). Genetic Variability, Correlation Co-efficient and Path Analysis in Soybean (Glycine max L. Merr.) Genotypes. Asian Journal of Advances in Agricultural Research, 19(2), 46-55. DOI: https://doi.org/10.9734/ajaar/2022/v19i2372