



ISSN: 2455-9377

Morpho-genetic variability, character association and diversity studies for yield attributing traits of mungbean [*Vigna radiata* (L.) Wilczek]

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ABSTRACT

Crop improvement requires an understanding of genetic diversity and the relationships between different variables that affect seed yield. The goal of this study was to characterize twenty-two mungbean genotypes in order to estimate genetic variability, heritability, genetic advancement, and genetic diversity as well as the correlation coefficient for nine variables and the degree to which they are associated with yield. The experiment was conducted during Kharif-1 season of 2023 following a randomized complete block design with three replications. Data on key yield-attributing morphological traits viz., days to first flowering, days to maturity, plant height, number of branches plant⁻¹, number of pods plant⁻¹, pod length, number of seeds pod⁻¹, 100-seed weight and yield plant⁻¹ were recorded. Based on yield and traits attributed to yield, the genotypes BMX 11140, BMX 1148, BMX 11170, BMX 11111 and BARI Mung-6 were selected as promising genotypes. The highest differences between genotypic and phenotypic coefficients of variation were observed for number of branches plant⁻¹, number of pods plant⁻¹, yield plant⁻¹, pod length and days to first flowering. High heritability coupled with high genetic advance as percentage of mean was recorded for the traits yield plant⁻¹, number of pods plant⁻¹ and 100-seed weight. Yield plant⁻¹ showed a significant positive correlation with number of pods plant⁻¹ (0.783**) and number of seeds pod⁻¹ (0.738**). The traits number of pods plant⁻¹, 100-seed weight, number of seeds pod⁻¹, number of branches plant⁻¹, pod length, plant height, and days to maturity exerted positive direct effect on yield plant⁻¹ whereas days to first flowering showed negative effects. Principal component analysis revealed that the first three components explained 71.66% of the total variation among the genotypes. Cluster analysis grouped twenty-two genotypes into four distinct clusters where cluster III indicated the highest yield plant⁻¹. The maximum inter cluster distance was observed between clusters III and II (2.33). Thus, the promising genotypes viz., BMX 11140, BMX 1148, BMX 11170, BMX 11111 and BARI Mung-6 isolated from this study can be used for developing high-yielding mungbean variety.

KEYWORDS: Mungbean, Yield-traits, Correlation and path-coefficient, Principal component analysis, Cluster analysis

Received: March 09, 2025

Revised: May 01, 2025

Accepted: May 05, 2025

Published: May 19, 2025

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INTRODUCTION

Under the Leguminosae family, mungbean (*Vigna radiata* L. Wilczek) is a significant herbaceous, annual, self-pollinating legume pulse crop. Mungbean is primarily grown for its tasty flavor and high protein content in the seeds. It is readily digested, with 22-28% of seed protein, 1-1.5% fat, and 60-65% carbohydrates, as well as different vitamins, minerals and various antioxidants that are necessary for human health to work effectively (Dahiya *et al.*, 2015; Sandhu & Singh, 2021). Mungbean is widely grown in both upland and low-land ecosystems in South Asia, Southeast Asia and Australia (Nair & Schreinemachers, 2020). In Bangladesh, among pulses,

mungbean ranks fifth in acreage, second in production and first in market price (BBS, 2023). They are unparalleled in their innate capacity to flourish in adverse environments. Moreover, it requires minimum input of water and fertilizer and can grow in harsh environmental conditions over a broad range of temperate and tropical climates (Tantasawat *et al.*, 2015). As a legume crop, mungbean has also the ability to improve the physical and chemical and properties of soil through biological nitrogen fixation from the atmosphere (Graham & Vance, 2003; Jat *et al.*, 2012; Nair & Schreinemachers, 2020; Singh *et al.*, 2022; Zhao *et al.*, 2022). Easy assimilability, short duration of cropping and the ease with which it could be grown as mixture with other crops makes it superior than other legumes (Islam *et al.*, 2020).

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Maintaining food and nutritional security for the populace has proven to be challenging due to unrestrained population expansion and fast urbanization, despite the assistance of cutting-edge agricultural science technologies (Lipton, 2001; Thirtle *et al.*, 2003). The necessity to investigate alternative minor or lesser-known crops is growing in light of the anticipated increase in the world's population. In this case, mungbean is a unique gift presented by nature to mankind, which has the potency to make up the gap of protein shortage in view of its three-fold amount of protein as much as cereals (Ghosh *et al.*, 2019). Mungbean is a prominent and essential pulse crop in Bangladesh but its productivity remains low as compared to other mungbean producing countries due to several constraints, such as low yield, poor crop management practices, variable growth habits, pod shattering, lodging, late or indeterminate maturity, vulnerability to diseases and pests, and importantly the grain quality (Ullah *et al.*, 2020).

A complex quantitative characteristic of crop plants, yield is influenced by a variety of physio-morphological plant traits. Yield contributing characters are inter-related with each other and exhibit multiple patterns of relationship, which is highly affected by the environmental conditions (Jahan *et al.*, 2020). Because of the complicated nature of yield regulated by polygenes, empirical selection for genotypes with high yield is challenging. Mungbean improvement programs have been limited due to low genetic diversity among the mungbean gene pool (Yimram *et al.*, 2009; Kumar *et al.*, 2011; Nair & Schreinemachers, 2020). To provide food security for the populace and eradicate all factors limiting mungbean yield, productivity must be raised (Jahan *et al.*, 2020). In light of this, there is a pressing need to boost mungbean productivity, but it is hampered by the state of agriculture and the availability of enough land. It needs a large-scale, methodical investigation to produce promising or enhanced cultivars. Identifying appropriate genotypes as parental sources would help plant breeders create a diverse population for selection and the creation of better mungbean cultivars. A significant barrier to mungbean cultivation is the lack of short-duration and high-yielding cultivars and lack of synchronized maturity.

Phenotypic diversity evaluation, through characterizing morphological and agronomical traits, plays a crucial role in the selection of appropriate parents for genetic improvement and future breeding programs (Abna *et al.*, 2012; Basnet *et al.*, 2014; Van Haeften *et al.*, 2023). In crop improvement programs, the selection of superior genotypes entirely depends on the variability of genotypes (Sarker *et al.*, 2001). The extent of genetic erraticism and the extent of heritability of desirable traits determine the success of the improvement of crop breeding (Hasan-Ud-Daula & Sarker, 2020). In light of these considerations, the current study was carried out to achieve the following objectives: (i) to characterize twenty-two mungbean genotypes based on yield and yield attributing traits; (ii) to study the relationship, genetic variability, heritability and genetic advances among the yield and yield contributing traits of mungbean; (iii) to identify superior diverse genotypes for future plant breeding program.

MATERIALS AND METHODS

Experimental Site and Season

The experiment was conducted at the Farm Research Laboratory of the Department of Genetics and Plant Breeding, Bangladesh Agricultural University, Mymensingh. The experiment was carried out during Kharif-I season started from 28th March, 2023 to 21st June, 2023.

Climate and Soil

The experiment was conducted during summer season. The land of the experimental area was medium high land belonging to the Old Brahmaputra alluvium, Agro-Ecological Zone-9. The soil of the experimental area was texturally silt having a sub-tropical climate and the pH value of the soil ranging from 6.5 to 6.7. The weather report of the experimental area is presented in Figure 1.

Plant Materials and Sources

The experiment was conducted by using twenty-two mungbean genotypes out of which five cultivated variety (i.e., Binamoog-5, Binamoog-8, Binamoog-9, BARI Mung-6, and Regalona) were collected from Bangladesh Agricultural Research Institute (BARI), Bangladesh Institute of Nuclear Agriculture (BINA), Tottori University, Japan and rest of the seventeen advanced lines (i.e., BMX 11107, BMX 1131, BMX 1137, BMX 1141, BMX 1148, BMX 11106, BMX 11108, BMX 11111, BMX 11116, BMX 11122, BMX 11140, BMX 11153, BMX 11154, BMX 11157, BMX 11159, BMX 11170, BMX 11176) were collected from Asian Vegetable Research and Development Center (AVRDC).

Design and Layout of the Experiment

Three replications of the experiment were carried out using a randomized complete block design (RCBD). The unit plot size was measured as 5 m² (2.8 m × 1.8 m). Thirty centimeters separated each row. Two experimental units were spaced 60 cm apart.

Fertilizer Application

Manures and fertilizers were applied following standard recommendations. At the time of land preparation, a whole

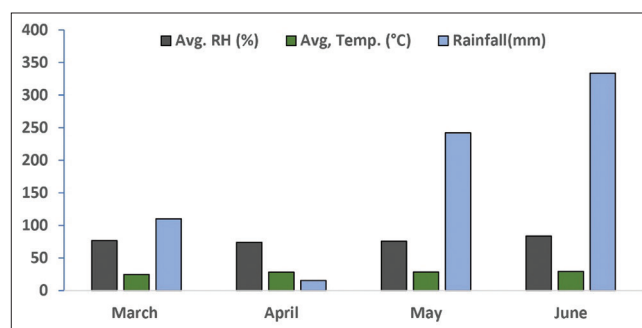


Figure 1: Monthly average relative humidity (RH), temperature (□), and rainfall (mm) data of the growing region from the period March 2023 to June 2023. (Source: Weather station, BAU Campus)

amount of well-decomposed cow dung, triple super phosphate (TSP), muriate of potash (MoP) and half-amount of urea was applied to the field. The rate of manures and fertilizers used in the experimental plot was cow dung at 2500 kg ha⁻¹, nitrogen (N) at 20.7 kg ha⁻¹ (from 45 kg ha⁻¹ of urea), phosphorus (P₂O₅) at 36.8 kg ha⁻¹ (from 80 kg ha⁻¹ of TSP), and potassium (K₂O) at 24 kg ha⁻¹ (from 40 kg ha⁻¹ of MoP). Half of the nitrogen was top-dressed 25-30 days after sowing.

Seed Sowing and Intercultural Operation

Line sowing was operated keeping five lines in each plot maintaining equal distance from line to line on 28th March, 2023 at early morning. After germination, seedlings were frequently watered. Thinning was done after 10 days of germination. First weeding was done at 15 days of sowing and second weeding was done at 25 days of sowing. Irrigation was applied two times - at seedling establishment and mid-vegetative stage. The schedule was adjusted based on soil moisture status and synchronized with rainfall, as the crop was grown during the summer. Other intercultural operations were performed as needed.

Harvesting and Processing

Mungbean pods were ready to harvest after 60 days of sowing. First harvesting was done on 8th June. Only matured and black colored pods were harvested. Regular harvesting were done keeping 1-2 days interval. Final harvesting was done on 21st June. After picking, pods were sun dried for 1-2 days. When the pods were properly dried then threshing was done carefully by hand. Then the seeds were collected from pods and sun dried and data were recorded.

Data Collection

Data on nine quantitative traits such as days to first flowering (DFF); days to maturity (DM); plant height (PH); number of branches plant⁻¹ (NBP); number of pods plant⁻¹ (NPP); pod length (PL); number of seeds pod⁻¹ (SPP); hundred seed weight (HSW); yield plant⁻¹ (YP) were recorded from five randomly selected plants of each genotype in each replication. Mean of the five plants for each character were used for statistical analysis.

Statistical Analysis

The collected data were compiled and analyzed using R software (version 3.4.1). The analysis encompassed one-way ANOVA to evaluate variations among genotypes. To differentiate the means, the Tukey's test was used at a 5% probability level. In order to identify quantitative variation patterns with the eigenvectors and eigenvalues, Minitab 19 statistical software was used for principal component analysis (PCA).

Estimation of Genetic Parameters

Following the procedures described by Johnson *et al.* (1955) and Allard (1960), genetic parameters such as genetic variance,

broad-sense heritability (h^2b), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), genetic advance (GA), and genetic advance as a percentage of the mean (GA%) were computed. According to the standards put forth by Deshmukh *et al.* (1986), the phenotypic coefficient of variation and genotypic coefficient of variation estimates were classified as low (<10%), moderate (10%-20%), and high (>20%). Similarly, Johnson *et al.* (1955) defined GA% as low (<10%), moderate (10%-20%), and high (>20%), and broad-sense heritability (h^2b) as low (0%-30%), medium (31%-60%), and high (>60%).

Estimation of Correlation Co-efficient, Path-Coefficient and Cluster Analysis

The phenotypic and genotypic correlation coefficient was estimated using the formula suggested by Miller *et al.* (1958) and path analysis was performed following formula provided by Dewey and Lu (1959), cluster analysis was performed using Ward's method (Ward, 1963).

RESULTS

Mean Performance Analysis

The analysis of variance (ANOVA) results showed highly significant ($P \leq .001$) variation for all the traits studied (Table 1). The mean performance of nine quantitative traits of mungbean is presented in Table 2. Among the studied genotypes, the minimum number of days to first flowering was recorded in the genotype BMX 11116 (31.72 days), in contrast, the maximum number of days to first flowering was required for the genotype BMX 11107 (43.13 days) (Table 2). The minimum number of days to maturity was recorded in the genotype Binamoog-8 (52.65 days), whereas, the maximum number of days to maturity was recorded for the genotype BMX 107 (67.68 days). The minimum plant height was observed in the variety Regalona (38.75 cm). On the other hand, maximum plant height was recorded in the variety Binamoog-5 (59.00 cm). The highest number of branches plant⁻¹ was found in BMX 1148 (4.00). In contrast, the lowest number of branches plant⁻¹ was observed in the variety Binamoog-8 (1.88). The maximum number of pods plant⁻¹ was recorded in BMX 11170 (43.00). In addition, the minimum number of pods was found in BMX 1137 (15.88). The maximum pod length was observed in the variety Regalona (9.10 cm), and the minimum length of the pods was found in BMX 11159 (6.04 cm). The maximum number of seeds pod⁻¹ was recorded in BMX 11111 (11.03). The minimum number of seeds pod⁻¹ was found in BMX 11107 (8.57). Regalona had the highest hundred seed weight (6.40 g) whereas the lowest hundred seed weight was found in BMX 11159 (2.17 g). The maximum seed yield plant⁻¹ was recorded in BMX 11140 (17.91 g), followed by BMX 1148 (16.46 g), BMX 11170 (15.75 g), BMX 11111 (16.67 g) and BARI Mung-6 (15.51 g). The minimum seed yield plant⁻¹ was recorded in BMX 11107 (5.18 g).

Table 1: Analysis of variance (mean square) for yield and yield attributing traits

Source of variation	Df	DFF	DM	PH (cm)	NBP	NPP	PL (cm)	NSP	HSW (g)	YP (g)
Replication	2	1.06	0.01	5.50	0.02	1.15	0.01	0.18	0.10	0.96
Genotypes	21	27.14***	52.91***	128.98***	1.14***	224.68***	1.87 ***	1.59***	3.02***	45.29***
Error	42	1.44	0.23	13.38	0.16	10.18	0.10	0.06	0.05	1.03

*, ** and *** indicate significant at 5%, 1% and 0.1% level of probability, respectively. Here, DFF=Days to first flowering, DM=Days to maturity, PH=Plant height (cm), NBP=Number of branches plant⁻¹, NPP=Number of pods plant⁻¹, PL=Pod length (cm), NSP=Number of seeds pod⁻¹, HSW=Hundred seed weight (g), YP=Yield plant⁻¹ (g)

Table 2: Mean performance for nine different morphological traits of mungbean genotypes grown at BAU farm during Kharif-1 season of 2023

Genotype	DFF	DM	PH	NBP	NPP	PL	NSP	HSW	YP
BMX 1148	34.49 ^{gh}	63.11 ^c	50.75 ^{c-e}	4.00 ^a	36.00 ^{bc}	7.03 ^{e-h}	10.68 ^{a-c}	4.29 ^{de}	16.46 ^{ab}
BMX 11159	39.56 ^{cd}	61.40 ^d	56.63 ^{a-c}	3.38 ^{a-d}	36.13 ^{bc}	6.04 ^k	9.72 ^{g-i}	2.17 ^k	7.80 ^{hi}
Binamoog-9	33.83 ^{gh}	63.08 ^c	38.88 ^g	2.00 ^{hi}	21.50 ^{g-j}	7.56 ^d	9.55 ^{h-j}	4.75 ^c	8.64 ^{f-h}
Binamoog-8	34.63 ^{gh}	52.65 ^o	39.63 ^g	1.88 ⁱ	22.63 ^{g-i}	7.70 ^{cd}	10.00 ^{a-g}	3.80 ^{f-h}	7.80 ^{hi}
BMX 11176	35.12 ^g	54.82 ^m	42.13 ^{fg}	3.88 ^a	19.63 ^{h-k}	6.84 ^{g-i}	8.58 ⁿ	3.39 ^{ij}	5.71 ^j
BMX 11154	35.67 ^{fg}	56.17 ^{kl}	50.75 ^{c-e}	3.00 ^{c-f}	19.63 ^{h-k}	6.86 ^{f-i}	8.95 ^{l-n}	3.19 ^j	5.66 ^j
BMX 1141	40.40 ^{bc}	60.57 ^{ef}	55.88 ^{a-d}	3.38 ^{a-d}	20.63 ^{g-k}	7.44 ^{de}	9.13 ^{kl}	4.04 ^{ef}	7.61 ^{hi}
BMX 1131	40.07 ^{bc}	59.95 ^{fg}	50.00 ^{de}	3.38 ^{a-d}	22.68 ^{g-i}	7.63 ^{cd}	8.62 ^{mn}	4.27 ^{de}	8.55 ^{f-h}
BMX 11106	41.71 ^{ab}	67.66 ^a	40.75 ^{fg}	3.63 ^{a-c}	25.75 ^{fg}	6.82 ^{g-j}	9.23 ^{j-l}	3.32 ^{ij}	7.81 ^{hi}
BMX 11111	35.68 ^{fg}	57.84 ^h	46.63 ^{ef}	2.88 ^{d-g}	41.13 ^{ab}	6.46 ^{i-k}	11.03 ^a	3.51 ^{h-j}	15.67 ^b
BMX 11122	32.93 ^{hi}	61.06 ^{de}	58.88 ^a	3.88 ^a	29.25 ^{d-f}	7.01 ^{e-h}	8.99 ^{lm}	3.81 ^{f-h}	10.01 ^{e-g}
BMX 11116	31.72 ⁱ	53.44 ⁿ	57.88 ^{ab}	3.13 ^{b-e}	19.88 ^{h-k}	7.46 ^{de}	9.13 ^{kl}	4.43 ^{cd}	8.16 ^{hi}
BMX 1137	38.93 ^{c-e}	59.64 ^g	49.88 ^{de}	3.38 ^{a-d}	15.88 ^k	7.38 ^{d-f}	9.12 ^{kl}	5.97 ^b	8.49 ^{gh}
BMX 11157	38.89 ^{c-e}	65.83 ^b	50.63 ^{c-e}	3.00 ^{c-f}	28.88 ^{ef}	6.74 ^{h-j}	9.90 ^{f-h}	4.19 ^{de}	11.93 ^{cd}
BMX 11140	39.63 ^{cd}	61.85 ^d	50.75 ^{c-e}	3.50 ^{a-d}	39.88 ^{ab}	7.45 ^{de}	10.35 ^{c-e}	4.25 ^{de}	17.91 ^a
BMX 11108	39.98 ^{bc}	56.04 ⁱ	51.88 ^{b-e}	2.50 ^{e-i}	34.25 ^{cd}	6.31 ^{jk}	9.50 ^{i-k}	3.48 ^{h-j}	11.31 ^{de}
BMX 11153	37.25 ^{ef}	57.18 ^{h-j}	52.13 ^{b-e}	3.75 ^{ab}	22.86 ^{gh}	9.00 ^a	9.81 ^{f-i}	6.20 ^{ab}	13.55 ^c
BMX 11170	35.29 ^{fg}	57.55 ^{hi}	41.50 ^{fg}	2.63 ^{e-h}	43.00 ^a	7.29 ^{d-g}	10.41 ^{b-d}	3.43 ^{ij}	15.75 ^b
BARI Mung-6	35.80 ^{fg}	56.95 ^{i-k}	52.13 ^{b-e}	2.38 ^{f-i}	32.63 ^{c-e}	8.10 ^{bc}	10.80 ^{ab}	4.43 ^{cd}	15.51 ^b
Regalona	35.63 ^{fg}	56.75 ^{i-l}	38.75 ^g	2.29 ^{g-i}	16.50 ^{jk}	9.10 ^a	9.70 ^{g-i}	6.40 ^a	10.18 ^{ef}
Binamoog-5	37.81 ^{de}	57.67 ^{hi}	59.00 ^a	3.63 ^{a-c}	17.50 ^{i-k}	8.39 ^b	10.16 ^{d-f}	3.94 ^{e-g}	6.73 ^{ij}
BMX 11107	43.13 ^a	67.68 ^a	52.38 ^{b-e}	3.00 ^{c-f}	17.63 ^{h-k}	6.69 ^{h-j}	8.57 ⁿ	3.61 ^{g-i}	5.18 ^j
Maximum	43.13	67.68	59.00	4.00	43.00	9.10	11.03	6.40	17.91
Minimum	31.72	52.65	38.75	1.88	15.88	6.04	8.57	2.17	5.18
SD	0.98	0.39	2.99	0.33	2.61	0.26	0.20	0.17	0.83
Tukey's value	1.98	0.79	6.03	0.67	5.26	0.52	0.40	0.35	1.67
CV	3.23	0.80	7.40	13.01	12.02	4.34	2.50	5.19	9.84

Different letters in the same column indicated statistically significant differences at 5% level of probability following Tukey's test. Here, DFF=Days to first flowering, DM=Days to maturity, PH=Plant height (cm), NBP=Number of branches plant⁻¹, NPP=Number of pods plant⁻¹, PL=Pod length (cm), NSP=Number of seeds pod⁻¹, HSW=Hundred seed weight (g), YP=Yield plant⁻¹ (g), SD=Standard deviation and CV=Co-efficient of variation.

Genetic Parameters Analysis

The characters which showed very high genotypic variance (σ^2_G) and phenotypic variance (σ^2_P) were number of pods plant⁻¹ (71.50 and 81.68, respectively), followed by plant height (38.53 and 51.91, respectively), days to maturity (17.56 and 17.79, respectively) and yield plant⁻¹ (14.76 and 15.78, respectively) (Table 3). Co-efficient of variation studies indicated that the values of phenotypic coefficient of variation were higher than those of the genotypic coefficient of variation for all the traits. The high phenotypic coefficient of variation and genotypic coefficient of variation were recorded for the traits number of branches plant⁻¹ (22.52 and 18.37%, respectively), number of pods plant⁻¹ (34.06 and 31.87%, respectively), hundred seed weight (24.68 and 24.13%, respectively) and yield plant⁻¹ (34.60 and 37.33%, respectively), whereas low phenotypic coefficient of variation and genotypic coefficient of variation were recorded for days to first flowering (8.51 and 7.87, respectively), days to maturity (7.09 and 7.04%, respectively), and number of seeds

pod⁻¹ (7.84 and 7.43%, respectively) (Table 3). In general, high broad-sense heritability (>60%) was recorded for all studied traits. Importantly, high heritability (>60%) coupled with high genetic advance as percentage of mean (>20%) was recorded for the traits plant height (22.38%), number of branches plant⁻¹ (30.89%), number of pods plant⁻¹ (61.42%), hundred seed weight (48.59%) and yield plant⁻¹ (74.36%).

Phenotypic Correlation Co-efficient

Days to first flowering exhibited a significant positive correlation with days to maturity (0.54**) (Table 4). Days to maturity showed significant positive correlation with number of branches plant⁻¹ (0.24*) whereas it showed a significant negative correlation with pod length (-0.31*). Plant height showed a significant positive correlation with number of branches plant⁻¹ (0.45**). Number of pods plant⁻¹ showed a significant positive correlation with number of seeds pod⁻¹ (0.60**) and yield plant⁻¹ (0.78**), whereas it showed a

Table 3: Genetic parameters of different traits of twenty-two mungbean genotypes

Characters	Phenotypic variance (σ^2_p)	Genotypic variance (σ^2_g)	PCV (%)	GCV (%)	Heritability in a broad sense (%)	GA	GA (%)
DFF	10.08	8.57	8.51	7.87	85.59	5.58	14.99
DM	17.79	17.56	7.09	7.04	98.71	8.58	14.42
PH	51.91	38.53	14.57	14.57	74.23	11.02	22.28
NBP	0.49	0.33	22.52	18.37	66.59	0.96	30.89
NPP	81.68	71.50	34.06	31.87	87.54	16.30	61.42
PL	0.69	0.59	11.34	10.47	85.34	1.46	19.93
NSP	0.57	0.51	7.84	7.43	89.84	1.40	14.50
HSW	1.04	0.99	24.68	24.13	95.58	2.01	48.59
YP	15.78	14.76	38.60	37.33	93.50	7.65	74.36

Here, DFF=Days to first flowering, DM=Days to maturity, PH=Plant height (cm), NBP=Number of branches plant⁻¹, NPP=Number of pods plant⁻¹, PL=Pod length (cm), NSP=Number of seeds pod⁻¹, HSW=Hundred seed weight (g), YP=Yield plant⁻¹ (g), PCV=Phenotypic coefficient of variation, GCV=Genotypic coefficient of variation, GA=Genetic advance, GA (%)=Genetic advance as percentage of mean

Table 4: Phenotypic correlation co-efficient of yield and yield contributing traits

	DFF	DM	PH	NBP	NPP	PL	NSP	HSW
DM	0.54**							
PH	0.10	0.02						
NBP	0.19	0.24*	0.45**					
NPP	-0.05	0.09	0.02	0.06				
PL	-0.24	-0.31*	-0.10	-0.15	-0.39**			
NSP	-0.22	-0.11	-0.10	-0.20	0.60**	0.14		
HSW	-0.16	-0.12	-0.13	-0.09	-0.41**	0.76**	0.04	
YP	-0.16	0.01	-0.04	0.02	0.78**	0.10	0.74**	0.19

*, ** and *** indicate significant at 5%, 1% and 0.1% level of probability, respectively. Here, DFF=Days to first flowering, DM=Days to maturity, PH=Plant height (cm), NBP=Number of branches plant⁻¹, NPP=Number of pods plant⁻¹, PL=Pod length (cm), NSP=Number of seeds pod⁻¹, HSW=Hundred seed weight (g), YP=Yield plant⁻¹ (g)

significant negative correlation with pod length (-0.39**) and hundred seed weight (-0.41**). Pod length showed significant positive correlation with hundred seed weight (0.76**) and number of seeds pod⁻¹ showed a significant positive correlation with yield plant⁻¹ (0.74**). Importantly, yield plant⁻¹ showed a strong and significant positive correlation with number of pods plant⁻¹ (0.783**) and number of seeds pod⁻¹ (0.738**).

Phenotypic Path-coefficients

At the phenotypic level, there were notable positive direct effects on yield plant⁻¹ from number of pods plant⁻¹ (0.8946) and hundred seed weight (0.5342) (Table 5). Additionally, number of seeds pod⁻¹ (0.1937), number of branches plant⁻¹ (0.0471), pod length (0.0279), plant height (0.0153) and days to maturity (0.0151) exerted a moderate positive direct effect on yield plant⁻¹. Conversely, days to first flowering (-0.0043) demonstrated negative direct effects on yield plant⁻¹. The residual effect was 0.0532.

Principal Component Analysis

Principal component analysis (PCA) was conducted on morphological traits of twenty-two mungbean genotypes to explore their variability and relationships. The analysis revealed three principal components (PCs) that collectively explained 71.66% of the total variance (Table 6). PC1 was

the most significant, explaining 29.15% of the variance, followed by PC2 (27.05%) and PC3 (15.46%). Loadings on PC1 indicated strong associations with number of seeds pod⁻¹, yield plant⁻¹, number of pods plant⁻¹, pod length and hundred seed weight. PC2 showed positive correlations with number of pods plant⁻¹, days to maturity, days to first flowering, number of branches plant⁻¹, yield plant⁻¹ and plant height. PC3 showed positive correlations with number of branches plant⁻¹, plant height, hundred seed weight, pod length, yield plant⁻¹, days to maturity, days to first flowering and number of seeds pod⁻¹. The eigenvalues confirmed the importance of PC1 in capturing the most variation, followed by PC2 and PC3.

Biplot Analysis

The biplot analysis indicates positive correlations between number of pods plant⁻¹, number of seeds pod⁻¹, hundred seed weight, pod length, number of branches plant⁻¹, days to maturity with yield plant⁻¹, evidenced by their close positioning in the plot and the formation of small angles (Figure 2). Additionally, yield plant⁻¹ demonstrates negative correlations with days to first flowering and plant height, as they diverge and form a large angle, indicating a negative correlation.

Cluster Analysis

The twenty-two mungbean genotypes were grouped into four distinct clusters under this study based on Euclidean distance following Ward's method (Table 7 & Figure 3). On the basis of D²-values, the genotypes were grouped into four clusters. The distribution pattern revealed that cluster I was the largest one containing eight genotypes while cluster II and IV included minimum number of genotypes (four genotypes per cluster). Cluster III contained six genotypes.

Intra- and -Inter Cluster Distances

According to Figure 4, cluster III had the largest intra-cluster distance, measuring 1.94. Cluster I, which included the most genotypes (eight), had the lowest intra-cluster distances (1.68), whereas cluster II and IV had intra-cluster distances of 1.86 and 1.72, respectively (Figure 4). We found that the inter-cluster distance ranged from 1.99 to 2.33. In contrast to the minimum

Table 5: Direct (diagonally bold figures) and indirect effect of different characters on yield plant⁻¹ at phenotypic level

	DFF	DM	PH	NBP	NPP	PL	NSP	HSW	YP correlation coefficient
DFF	-0.0043	0.0081	0.0016	0.0089	-0.0436	-0.0066	-0.0431	-0.0841	-0.16
DM	-0.0023	0.0151	0.0004	0.0115	0.0797	-0.0085	-0.0208	-0.0648	0.01
PH	-0.0004	0.0004	0.0153	0.0212	0.0158	-0.0027	-0.0192	-0.0696	-0.04
NBP	-0.0008	0.0037	0.0069	0.0471	0.0554	-0.0042	-0.0378	-0.0502	0.02
NPP	0.0002	0.0014	0.0003	0.0029	0.8946	-0.0109	0.1152	-0.2204	0.78**
PL	0.0010	-0.0046	-0.0015	-0.0070	-0.3503	0.0279	0.0278	0.4082	0.10
NSP	0.0010	-0.0016	-0.0015	-0.0092	0.5323	0.0040	0.1937	0.0195	0.74**
HSW	0.0007	-0.0018	-0.0020	-0.0044	-0.3690	0.0213	0.0071	0.5342	0.19

Residual effect=0.0532

Here, DFF=Days to first flowering, DM=Days to maturity, PH=Plant height (cm), NBP=Number of branches plant⁻¹, NPP=Number of pods plant⁻¹, PL=Pod length (cm), NSP=Number of seeds pod⁻¹, HSW=Hundred seed weight (g), YP=Yield plant⁻¹ (g)

Table 6: Principal components (PCs) for yield and yield-related from PCA with Eigen vectors (loadings) of the first three PCs

Variable	PC1	PC2	PC3
DFF	-0.49	0.38	0.24
DM	-0.33	0.50	0.31
PH	-0.28	0.29	0.52
NBP	-0.37	0.33	0.64
NPP	0.65	0.73	-0.04
PL	0.28	-0.80	0.42
NSP	0.89	0.23	0.12
HSW	0.22	-0.73	0.51
YP	0.86	0.30	0.34
Eigen value	2.62	2.43	1.39
%Variation explained	29.15	27.05	15.46
Cumulative variance (%)	29.15	56.21	71.66

Here, DFF=Days to first flowering, DM=Days to maturity, PH=Plant height (cm), NBP=Number of branches plant⁻¹, NPP=Number of pods plant⁻¹, PL=Pod length (cm), NSP=Number of seeds pod⁻¹, HSW=Hundred seed weight (g), YP=Yield plant⁻¹ (g)

Table 7: Cluster pattern of twenty-two mungbean genotypes by Euclidean distance method

Cluster no.	Total no. of genotypes	Genotypes
I	8	Binamoog-5 BMX 1137 BMX 1141 BMX 1131 BMX 11176 BMX 11154 BMX 11122 BMX 11116
II	4	BMX 11106 BMX 11107 BMX 11159 BMX 11108
III	6	BARI Mung-6 BMX 11111 BMX 11170 BMX 11157 BMX 1148 BMX 11140
IV	4	Binamoog-9 Binamoog-8 BMX 11153 Regalona

distance between the genotypes of clusters IV and II (1.99), the greatest inter-cluster distance was recorded between clusters

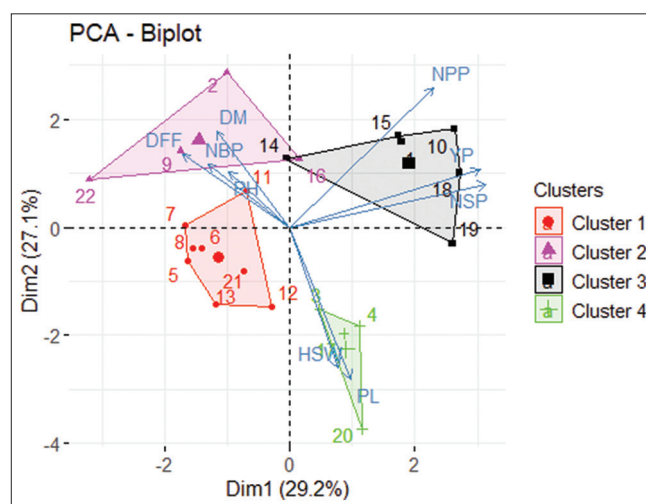


Figure 2: Biplot from principal component analysis of morphological traits. Here, DFF=Days to first flowering, DM=Days to maturity, PH=Plant height (cm), NBP=Number of branches plant⁻¹, NPP=Number of pods plant⁻¹, PL=Pod length (cm), NSP=Number of seeds pod⁻¹, HSW=Hundred seed weight (g), YP=Yield plant⁻¹ (g). 1=BMX 1148, 2=BMX 11159, 3=Binamoog-9, 4=Binamoog-8, 5=BMX 11176, 6=BMX 11154, 7=BMX 1141, 8=BMX 1131, 9=BMX 11106, 10=BMX 11111, 11=BMX 11122, 12=BMX 11116, 13=BMX 1137, 14=BMX 11157, 15=BMX 1140, 16=BMX 11108, 17=BMX 11153, 18=BMX 11170, 19=BARI Mung-6, 20=Regalona, 21=Binamoog-5, 22=BMX 11107

III and II (2.33), followed by clusters IV and I (2.15), III and I (2.12), clusters II and I (2.09), and clusters IV and III (2.08).

Cluster Mean Analysis

The mean value for days to first flowering was found the highest in cluster II (41.10), whereas the lowest value for days to first flowering was found in the cluster I (36.58) (Table 8). The highest mean value for days to maturity was observed in cluster II (63.20). Plant height was found to have the highest mean value in cluster I (53.05). The maximum mean value for number of branches plant⁻¹ was observed in cluster I (3.46). Number of pods plant⁻¹ was found to have the greatest mean value in cluster III (36.92), whereas the lowest was found in the cluster I (20.64). The mean value for pod length was found the highest in cluster IV (8.34). Number of seeds pod⁻¹ was found

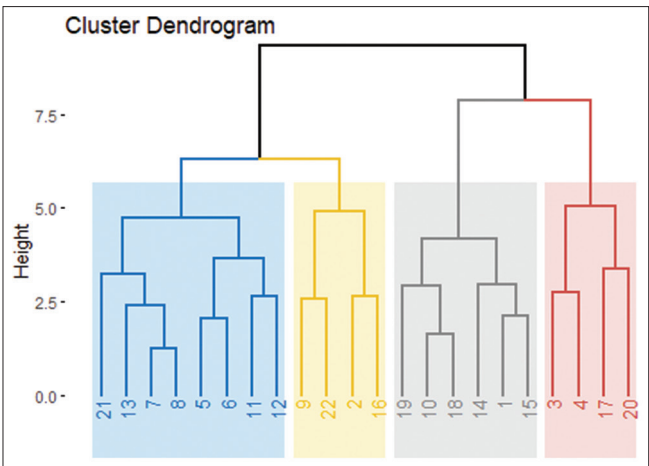


Figure 3: Hierarchical Ward's method dendrogram of twenty-two mungbean genotypes displaying various cluster groups. 1=BMX 1148, 2=BMX 11159, 3=Binamoog-9, 4=Binamoog-8, 5=BMX 11176, 6=BMX 11154, 7=BMX 1141, 8=BMX 1131, 9=BMX 11106, 10=BMX 11111, 11=BMX 11122, 12=BMX 11116, 13=BMX 1137, 14=BMX 11157, 15=BMX 1140, 16=BMX 11108, 17=BMX 11153, 18=BMX 11170, 19=BARI Mung-6, 20=Regalona, 21=Binamoog-5, 22=BMX 11107

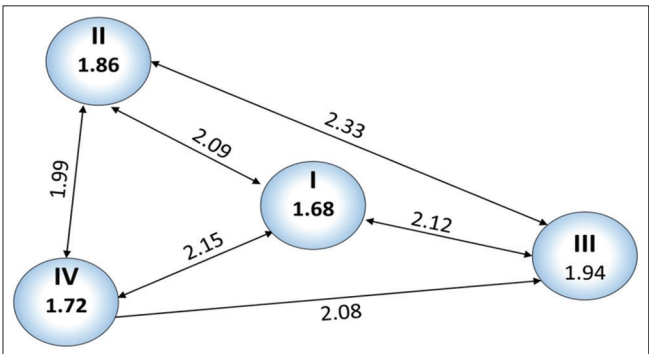


Figure 4: Cluster diagram showing average intra and inter cluster distance ($D = \sqrt{D^2}$ Values) of the mungbean genotypes. The values among the lines indicate inter cluster distance and values in the circle indicate intra cluster distance

Table 8: Cluster mean of nine quantitative traits of twenty-two mungbean genotypes

Characters	Clusters			
	I	II	III	IV
DFF	36.58	41.10	36.63	35.34
DM	57.92	63.20	60.52	57.42
PH	53.05	50.41	48.73	42.35
NBP	3.46	3.13	3.07	2.48
NPP	20.64	28.44	36.92	20.87
PL	7.38	6.47	7.18	8.34
NSP	9.09	9.26	10.53	9.77
HSW	4.13	3.15	4.02	5.29
YP	7.62	8.03	15.54	10.04

Here, DFF=Days to first flowering, DM=Days to maturity, PH=Plant height (cm), NBP=Number of branches plant⁻¹ (no.), NPP=Number of pods plant⁻¹ (no.), PL=Pod length (cm), NSP=Number of seeds pod⁻¹ (no.), HSW=Hundred seed weight (g), YP=Yield plant⁻¹ (g)

to have the highest mean value in cluster III (10.53). The maximum mean value for hundred seed weight was observed

in cluster IV (5.29). The mean value for yield plant⁻¹ was found the highest in cluster III (15.54), followed by cluster IV (10.04), II (8.03) and I (7.62).

DISCUSSION

This study revealed significant genetic variability among the 22 mungbean genotypes, indicating substantial potential for genetic improvement. The variations observed in days to first flowering and days to maturity suggest differences in flowering and maturity patterns, which are crucial for selecting genotypes suitable for specific agro-climatic conditions. BMX 11116 exhibited the earliest flowering, likely due to genetic factors favoring early reproductive transitions, while BMX 11107 had the longest duration to first flowering, possibly indicating a late-maturing trait beneficial for prolonged seed filling and yield stability. This variation in flowering time could have significant implications for crop management and the synchronization of planting schedules. When considering days to maturity, the study identified genotype Binamoog-8 demonstrating early maturity, with BMX 11107 requiring the longest time for the first mature pods to be harvested (Table 2). Plant architecture, as indicated by plant height and number of pods bearing branches plant⁻¹, also showed significant diversity among genotypes. Taller plants, such as Binamoog-5, BMX 11122, BMX 11116, BMX 11159, BMX 1141 may offer advantages in terms of light interception and overall productivity, while genotypes with more branches, like BMX 1148, BMX 11176, BMX 11122 could contribute to increased pod production and yield potential. The number of pods plant⁻¹ varied considerably, with BMX 11170 showcasing the highest number, while BMX 1137 had the lowest. Pod characteristics such as pod length and seeds pod⁻¹ are crucial factors influencing marketable yield and seed quality in various legume crops. Genotypes like Regalona and BMX 11153 exhibited longer pods, whereas BMX 11159 and BMX 11108 had shorter pods. On the other hand, genotypes like BMX 11111 and BARI Mung-6 exhibited maximum seeds pod⁻¹, whereas BMX 11107 and BMX 11176 had minimum seeds pod⁻¹ (Table 2). The study also evaluated hundred seed weight and yield plant⁻¹, providing insights into the genetic potential for seed production and overall crop productivity. Genotypes like Regalona demonstrated superior seed weight and BMX 11140 exhibited highest yield plant⁻¹, highlighting their suitability for commercial cultivation and potential contributions to food security and economic prosperity.

Genetic parameter analysis indicated high genotypic and phenotypic variances for number of pods plant⁻¹, plant height, days to maturity, and yield plant⁻¹, highlighting their importance in breeding programs. High broad-sense heritability coupled with high genetic advance was recorded for number of pods plant⁻¹, plant height, and yield plant⁻¹ (Table 3), suggesting that these traits are primarily controlled by additive gene action, making them suitable for direct selection. The higher phenotypic coefficient of variation compared to genotypic coefficient of variation across all traits emphasizes the role of environmental factors in influencing trait expression. This aligns with previous studies highlighting the pivotal role of environmental

conditions in modulating plant phenotypes (Bhardwaj *et al.*, 2023). However, the small phenotypic coefficient of variation-genotypic coefficient of variation differences for yield plant⁻¹ and number of pods plant⁻¹ suggested strong genetic control, making them reliable targets for selection (Table 3). Additionally, the assessment of genetic advance provides valuable insights into the potential for improvement through selection in breeding programs. From this study, traits with higher genetic advance, such as number of pods plant⁻¹, pod length, days to maturity, yield plant⁻¹ and days to first flowering indicate greater scope for improvement through breeding programs. Conversely, traits with lower genetic advance, like hundred seed weight and pod length, may present challenges for improvement through selection due to limited genetic variability. Lastly, traits like yield plant⁻¹ and number of pods plant⁻¹ showed the highest genetic advance as a percentage of the mean, suggesting substantial genetic variability and potential for improvement through selection.

The correlation analysis among various phenotypic traits of mungbean genotypes revealed intricate relationships that offer valuable insights into the plant's growth and development (Zhao *et al.*, 2022). Yield plant⁻¹ exhibited a strong positive correlation with number of pods plant⁻¹ and number of seeds pod⁻¹, emphasizing the importance of these traits in yield enhancement (Table 4). days to first flowering showed a significant positive correlation with days to maturity but had a negative association with number of pods plant⁻¹ and number of seeds pod⁻¹, suggesting that early flowering genotypes tend to have a reduced pod number (Table 4). Number of branches plant⁻¹ was positively correlated with plant height and number of pods plant⁻¹, indicating that bushier plants may contribute to increased pod production. However, pod length had a significant negative correlation with number of pods plant⁻¹ but a strong positive correlation with hundred seed weight, demonstrating a trade-off between pod quantity and seed size. Additionally, hundred seed weight showed a significant negative correlation with number of pods plant⁻¹, further reinforcing the inverse relationship between pod number and seed size.

The path-coefficient analysis discussed in this study aligns with the principles of quantitative genetics, offering insights into the direct and indirect effects of various traits on crop yield. Studies by Gravois and Helms (1992) provide a foundational understanding regarding the decomposition of phenotypic correlations into genotypic and environmental components, which is crucial for interpreting path coefficients accurately. Path coefficients elucidate the contributions of traits to yield plant⁻¹. Notably, number of pods plant⁻¹ emerge as the most influential factor positively impacting yield, emphasizing the critical role of maximizing pod production in enhancing overall productivity (Table 5). This finding is consistent with previous studies (Noor *et al.*, 2003; Freitas *et al.*, 2016), highlighting the significance of pod-related traits in determining yield in legume crops. Additionally, traits such as hundred seed weight and number of seeds pod⁻¹ exhibit significant positive direct effects on yield, underscoring their importance in determining crop productivity and quality. The residual factor, with a value of 0.0532, indicates the amount of unexplained variation in yield

plant⁻¹ that was not accounted for by the characters included in the study.

Principal component analysis (PCA) is a powerful statistical technique used to uncover patterns in data by reducing the dimensionality of the dataset while retaining most of the original variability. The results revealed several insights into the relationships between these traits and the contribution of each variable to the principal components (PCs). The Eigenvalues associated with each principal component indicate the amount of variance explained by that component. Principal component analysis (PCA) identified three principal components explaining 71.66% of total variation, with PC1 contributing the most (29.15%), followed by PC2 with 27.05%. Traits like number of seeds pod⁻¹, yield plant⁻¹, number of pods plant⁻¹, and pod length had high loadings on PC1, reinforcing their role in yield determination (Table 6). These results indicate that PC1 and PC2 are particularly important for capturing the major patterns of variation in the data, while PC3 also contributes significantly to explaining additional aspects of variability. Therefore, the information provided by these principal components can effectively summarize the multidimensional nature of the dataset, facilitating data interpretation and visualization in subsequent analyses (Jolliffe & Cadima, 2016). Similar to our results, Agbeleye *et al.* (2020) also reported three PCs accounted for 70.48% of total variation in a study with 20 mungbean genotypes. The biplot analysis conducted in this study offers valuable insights into the relationships between agronomic traits and yield plant⁻¹, aligning with principles of multivariate analysis in plant breeding (Gabriel, 1971). Positive correlations between number of pods plant⁻¹, number of seeds pod⁻¹, hundred seed weight and pod length with yield plant⁻¹ resonate with studies emphasizing the importance of these traits in determining crop productivity (Figure 2).

Any effective plant breeding effort must start with appropriate parent selection. Higher genetic gains via selection are predicted for parents with greater genetic variety. Genetic divergence analysis was used in this work to ascertain the genotypes' genetic relationships and choose the best genotypes for a future breeding effort. Four clusters were formed from the genotypes based on the D²-value (Table 7 & Figure 3). Cluster I had the greatest number of genotypes (8), according to the distribution pattern, while clusters II and IV had the fewest number of genotypes (4 each), indicating that there is greater diversity among the genotypes in cluster I than in clusters II and IV, which are more closely related. These results were parallel with the results of (Singh *et al.*, 2013; Singh & Bains, 2014; Mehandi *et al.*, 2015). The analysis of intra- and inter-cluster distances, as shown in Figure 4, further supported these findings. The maximum inter-cluster distance was observed between clusters II and III (2.33), followed by clusters I and IV (2.15), suggesting that genotypes from these clusters are highly divergent. This indicates that hybridization between genotypes from these clusters may result in heterotic progeny with broad genetic variability in the subsequent generations. While cluster I contained the highest number of genotypes, its intra-cluster distance was not the largest. Instead, Cluster III exhibited the highest intra-cluster distance, signifying considerable genetic variation

within this group. This suggests that genotypes within Cluster III hold strong potential for trait enhancement and breeding improvement in mungbean cultivars. The intra-cluster distances ranged from 1.68 to 1.94, demonstrating that genotypes within the same cluster share close genetic relationships. This insight is particularly valuable for plant breeders in selecting parental lines for crossing programs, ensuring the combination of diverse genetic backgrounds to enhance yield potential and overall genetic improvement. Hybridization between distantly related genotypes is expected to introduce novel variations, contributing to the development of superior high-yielding varieties with enhanced adaptability and resilience.

CONCLUSION

This study highlighted substantial genetic variation among mungbean genotypes. Traits such as plant height, number of branches plant⁻¹, number of pods plant⁻¹, 100 seed weight and yield plant⁻¹, exhibited high heritability and genetic advance, making them promising for selection in breeding programs. Yield plant⁻¹ showed significant positive correlations with number of pods plant⁻¹, 100 seed weight, number of seeds pod⁻¹, number of branches plant⁻¹, pod length, plant height, and days to maturity, while days to first flowering negatively affected yield. Principal component analysis accounted for 71.66% of the total variation, and cluster analysis grouped the 22 genotypes into four clusters, with Cluster III showing the highest diversity. The high-yielding genotypes BMX 11140, BMX 1148, BMX 11170, BMX 11111, and BARI Mung-6 were identified as potential candidates for further breeding. To confirm the stability of high-yielding genotypes, multi-location trials are recommended for varietal development.

ACKNOWLEDGEMENT

The authors gratefully acknowledge the financial support (grant no.: 2023/32/UGC) provided by University Grants Commission of Bangladesh.

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