ASSESSMENT OF GENETIC VARIABILITY AND CHARACTER ASSOCIATION IN MUNGBEAN *(Vigna radiata* **L.)** GENOTYPES

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CERTIFICATE

This is to certify that the thesis entitled **ASSESSMENT OF GENETIC VARIABILITY AND CHARACTER ASSOCIATION IN MUNGBEAN** *(Vigna radiata L.)* **GENOTYPES** submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE IN GENETICS AND PLANT BREEDING,** embodies the result of a piece of bonafide research work carried out by **SADIA SHARMIN, Registration No.14-05809**, under my supervision and guidance. No part of this thesis has been submitted for any other degree or diploma.

I further certify that any help or sources of information as has been availed of during the course of this work has been duly acknowledged & style of the thesis have been approved and recommended for submission.

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ABSTRACT

The purpose of this study was to examine the genetic variability and correlation between several yield contributing features in mungbean *(Vigna radiata* L.). Randomized Complete Block Design (RCBD) was used with three replications. Based on 14 genotypes from different Agricultural Research Institute, the study examined nine quantitative features during Kharif I season from March to June, 2020 at the Sher-e-Bangla Agricultural University's research farm. The analysis of variance showed significant variation among all the genotypes in all the traits studied. The phenotypic variances were greater than the genotypic variances with little differences in all traits. High estimated Phenotypic coefficient of variance and genotypic coefficient of variance were observed for Number of branches /plant followed by 19.671& 18.309, Weight of 1000 seeds (g)25.339 & 25.254 and yield/plant (g) 31.296 & 31.049 respectively. High heritability coupled with high genetic advance as percent of mean were observed for plant height (cm) followed by 96.073 & 21.421, Number of leaves/plant 95.977& 31.950, Number of branches /plant 86.636 &35.107, Number of pods/plant 99.335 &55.623, pods length/plant (cm) 98.389 & 29.455, Number of seeds/pod 92.371 &33.375, Weight of 1000 seeds (g) 99.331 &51.848 and yield/plant (g)98.427 &63.456 respectively which indicated the effect of additive genes. In the correlation co-efficient analysis yield/plant had highly significant positive relation with Number of leaves/plant followed by 0.697&0.662, Number of branches/plant 0.872&0.799, Number of pods/plant 0.658&0.653, Number of pods cluster/plant 0.656&0.405, pods length/plant (cm) 0.736&0.722, no of seeds/pod 0.878&0.843 and Weight of 1000 seeds (g) 0.541&0.537 in both genotypic and phenotypic level which indicates these character can be considered during future Mungbean improvement program. Path analysis revealed that Number of seeds/pod 0.689, Number of leaves/plant 0.338, Number of branches/plant 0.196, Number of pods/plant 0.435 and Weight of 1000 seeds (g) 0.016 showed positive direct effect on yield/plant. This suggesting that selection of these qualities, the chance of simultaneous improvement of Mungbean could increase as well. Based on the results of this study the genotypes were grouped into four clusters by diversity (D^2) analysis where cluster IV comprised 6 genotypes, cluster I had 4 genotypes and cluster II and III had 2 genotypes in each. The maximum inter-genotypic distance was observed between G_1 and G_6 (1.288). Genetic diversity in Mungbean can be explained 89.82% by the first four components, according to principal component analysis. G_1 (BARI 1), G_2 (BARI 2), G_6 (BARI 6), G_7 (BARI 7) and G_{10} (BINA 5) were shown to have potential for further hybridization in breeding programs, based on group distance and other agronomic performance measures.

LISTS OF CONTENTS

LISTS OF CONTENTS(CONT'D)

LISTS OF CONTENTS(CONT'D)

LISTS OF CONTENTS(CONT'D)

LISTS OF CONTENTS(CONT'D)

LIST OF TABLES

LIST OF FIGURES

LIST OF APPENDICES

LIST OF ABBREVIATIONS

FULL NAME	ABBREVIATIONS
Analysis of variance	ANOVA
Agro-Ecological Zone	AEZ
Bangladesh Agricultural Research Institute	BARI
Bangladesh Bureau of Statistics	BBS
Bangladesh Institute Nuclear Agriculture	BINA
Bangladesh Metrological Department, Agargaon	BMD
Bangabandhu Sheikh Mujibur Rahman Agricultural University	BSMRAU
Cluster Analysis	CA
Centimeter	cm
Degrees of Freedom	DF
Duncan's Multiple Range Test	DMRT
Deoxyribonucleic acid	DNA
And others	*et al.*
Etcetera	etc.
Gram	g
Genetic Advance	GA
Genotypic Coefficient of Variation	GCV
Harvest Index	HI
Journal	J
Kilogram	Kg
Least Significant Differences	LSD
Mega Bases	Mb
Mean sum of squares	MS
Mean sum of square for error	MSE
Mean sum of square for genotypes	MSG
Percentage	%
Principal Component Analysis	PCA
Principal Coordinate Analysis	PCO
Phenotypic Coefficient of Variation	PCV
Pulse Research Centre	PRC
Random Amplified Polymorphic DNA	RAPD
Randomized Complete Block Design	RCBD

LIST OF ABBREVIATIONS(CONT'D)

FULL NAME	ABBREVIATIONS
Recombinant Inbred lines	RILs
Sher-e-Bangla Agricultural University	SAU
Science	Sci
Standard Error of mean	SE
Soil Resource and Development Institute, Dhaka	SRDI
Tonnes per hectare	t/ha
Unweighted Pair Group Method with Arithmetic mean	UPGMA
Variety	var.
Weight	Wt.

CHAPTER I

Introduction

Mungbean (*Vigna radiata* L.) is a very common and important pulse crop belongs to the family Leguminoseae sub family papilionaceae, grown principally for its protein rich edible seeds (Bangar *et al*. 2018). Mungbean belongs to the genus *Vigna* in the tribe Phaseoleae, which contain seven subgenera including the African subgenus *Vigna* and the Asian subgenus *Ceratotropis* (Gupta *et al*. 2014). The subgenus *Ceratotropis* of the Fabaceae family contain 23 species. Mungbean is a grain legume originating from south Asia (Noble, 2018). The crop is vital to smallholder farmers in Asia with an annual production of 3.5–4.0 million tons (Noble, 2018).

In Bangladesh it is one of the most important pulse crops because of its easy digestibility and high protein percentage (Azam *et al*. 2018). It is mainly grown for its high protein and consume as 'Dal' along with cereals in south asian countries also consider it as a vital ingredient for human diet. Its seeds are also consumed as sprouts in many countries (Singh *et al*. 2014). Dry seeds contain 27% protein (Day, 2013). Mungbean is a very good source of protein, amino acids, carbohydrates, antioxidant and fibers (Bangar *et al*. 2018). One cup (202 g) boiled mungbean contain 212 calories, 14.2 g protein, carbohydrate 38.7 g, fiber 15.4 g, fat 0.8 g. It also contains manganese, magnesium, vitamin B1, phosphorus, zinc, vitamin B2, B3, B5, B6 and selenium.

In Bangladesh, the total production is 0.377 million tons on 0.371 million hectares with an average productivity of 1000 kg/ha (BBS, 2017). During 2017, the total area covered by mungbean cultivation was 0.32 million hectares with an average production of 663 kg/ha (Krishi diary, 2017). Its ranks 3rd position in among the pulse crops in our country (Azam1 *et al*. 2018). Singh *et al*. (2014) stated that mungbean production (90%) is mainly located in asia; India is the largest producer with more than 50% of world production but also consumes almost its entire production. China produces large amounts of mungbean which is 19% of its legume production. The main exporter of mungbean is Thailand and its production increased by 22% per year (Heuze *et al*. 2015). Over the last three decades, the global mungbean consumption has increased by 60%

with a corresponding growth in production area up to 6 million hectares, concentrated mainly in south, east, and southeast asia (Kim *et al.* 2015).

Mungbean is a tropic/sub tropic crop and requires optimum temperature (30-35°C) for growth and yield (Singh *et al.* 2014). It is a photo-period insensitive crop. It is well-adapted to low water and soil fertility. Mungbean has good effect on environment as it can fix atmospheric nitrogen with association of particular soil bacteria and root nodules which are available for use by the plants. Therefore, mungbean can be fixed about 86 kg/ha atmospheric nitrogen (Morris *et al.* 1986). It is used in crop rotation practices (Somta and Srinives, 2007; Lavanya *et al.* 2008). It has short growth duration (55–70 days from sowing to maturity), delivers economic farming systems and environmental benefits. (Noble, 2018).

Although mungbean is a nutritious crop, overall production is low due to abiotic and biotic stresses, low level of crop management by farmers and the shortage of suitable varieties for varying geographical conditions (Singh *et al.* 2015). The present yield is not high enough to meet the demand of consumers and farmers because of its low yield potential, small seed size and susceptibility to disease (Srivastava and Singh, 2013). More food is required for it's over growing population in Bangladesh. To meet up the high demand of food farmers are growing more cereal crops in decreasing agricultural land. So at present the cultivation of pulse has gone to marginal land because farmers are not interested to use their fertile land in pulse cultivation.

Mungbean is a self-pollinated diploid species with a chromosome number of 2n = 22 with an estimated genome size of 579 mega bases (Mb) (Singh *et al.* 2014). As an orphan crop of subsistence agriculture with limited genetic information available, for most of its cultivated history mungbean improvement has relied on traditional plant breeding methodologies (Fernandez *et al.* 1988; Humphry *et al.* 2002). In fact investment in the development of new mungbean varieties has been increasingly low, which result in a narrow genetic base of the crop leaving the crop vulnerable to many abiotic and biotic stresses.

The relatively small genome size makes it a valuable model for advancing the understanding of diversity and evolution of legume genomes. The domestication of mungbean is considered to have taken place approximately 3500 years ago (kim *et al.* 2015). The domestication process has arised in significant genetic bottlenecks in the

cultivated mungbean genome (Lakhanpaul *et al*. 2000). Previous studies on genetic diversity of cultivated and wild mungbean germplasm, using both morphological and molecular markers, have highlighted low levels of genetic diversity in cultivated mungbean compared to the broader diversity found in wild mungbean (Santalla et al., 1998; Saravanakimar *et al*. 2004; Sangiri *et al*. 2007).

However genetic variability is essential for a successful breeding program of any crop species and a critical survey of genetic variability is necessary before initiating an improvement program aiming to develop high yielding varieties. The correlation co-efficient between yield components usually show a complex chain of interacting relationship. Path co-efficient analysis the components of correlation co-efficient into direct and indirect effects and visualize the relationship in more meaningful way. Multivariate statistics help the researcher to summarize data and reduce the number of variables (Anderson, 1972). The multivariate techniques, such as cluster analysis, vector analysis and principal component analysis may be an efficient tool in the quantitative estimation of genetic variation. To select germplasm in a more systemic and effective way, study of genetic diversity in genetic resources is a critical factor for breeders is necessary to better understand the evolutionary and genetic relationships among accessions (Lavanya *et al*. 2008). Multivariate technique also plays an important role in choice of divergent parents for hybridization to exploit maximum heterosis.

Considerably less improvement has been done in mungbean than its field demand. It is necessary to find genetically diverse parents for hybridization.

Aim and Objective

To generate information on the variability, degree of genetic diversity and co-efficient of direct and indirect association among yield contributing characters this study was undertaken with the following Objectives:

i. To estimate the nature and magnitude of genetic variations among the mungbean genotypes in respect of different yield and yield contributing characters;

ii. To estimate the extent of correlation between pairs of characters at genotypic and phenotypic level;

iii. To assess the direct and indirect effect of different characters on yield of mungbean and

iv. To identify the diversified parents among the genotypes for the utilization in future hybridization program.

CHAPTER II

Review of Literature

In spite of the best efforts for improving the mungbean varieties, the yield of its remains low. Several studies have been done to understand their performances which mainly include the contribution of various yield components towards yield. The yield components depend on some agromorphophysiological traits. To understand the agromorphophysiological basis of yield difference among the genotypes of mungbean, it is essential to quantify the components of growth, and the variation, if any, may be used crop improvement (Hassan *et al.*, 1995 and Hakim *et al.* 2008).

Planning for a breeding program, a thorough knowledge about variability, genetic parameter, correlation co-efficient, path co-efficient, and multivariate analysis of yield contributing characters are important. To get a better insight of ancillary characters under selection, correlation and path co-efficient analysis are the tools, which are being effectively used for determining the rate of various yield components in different crops, leading to the selection of superior genotypes.

Researches have been done over the several decades on variability, genetic parameter, correlation co-efficient, path co-efficient and multivariate analysis in mungbean is insufficient. The available important literature and their findings which are related to the present study are exhibited in the following sections:

2.1 Variability of mungbean genotypes

Genetic variability is the difference in individual genotypes (and thus traits) within a population, and the rate at which a certain genotype can change in response to environmental or genetic factors (King *et al.* 2006). A high genetic variability makes a healthy population. A higher variability means that the population is more able to respond to a change their environment and become more resistant to disease, climate change and competition from invading species and so on. Several scientists evaluated few experiment on mungbean and their findings are given below-

The genetic improvement in mungbean depends on the nature and amount of variability present in the population. The trait, yield, is highly influenced by environmental factors

which indicates the need to have clear understanding on existed amount of variability in the breeding material for the yield contributing traits including yield.

Sabatina *et al*. (2021) conducted an experiment on 30 genotypes of advanced breeding lines of greengram were evaluated to know the variability parameters for yield and yield contributing traits for their exploitation in the breeding programs. The analysis of variance was significant for yield and yield contributing traits revealing the existence of sufficient variability for their exploitation. The mean range of the traits was huge for most of the traits indicating use of simple selection, while exploiting genetic variability of the material.

Kumar *et al*. (2020) conducted a study on the genetic variability parameters for seed yield and its component traits in mungbean. Significant differences were observed among genotypes for all 11 characters studied. The high degree of genetic variability was observed for seed yield/plant, Number of pods/plant, harvest index, biological yield/plant and plant height; therefore, form the basis of selection for mungbean improvement program. Besides quantitative traits, all these varieties were also found early in flowering and maturity, which are considered as the most desirable traits for crop cultivation in an arid environment.

Gayachran *et al*. (2020) conducted a study on 1,232 mungbean accessions where wide range of variation was recorded for days to flowering, days to maturity, pod length, Number of seeds/pod and 100-seed weight. Relatively high phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV) was noted for 100-seed weight, flowering period, seed length and seed breadth.

Marawar *et al*. (2020) studied with thirty diverse mungbean (*Vigna radiata* L. Wilczek) genotypes for ten characters for the estimation of genetic variability parameters. The higher values of GCV and PCV recorded for almost all the characters studied.

Joseph *et al*. (2020) carried out a study on the genetic variability yield and yield related traits among the 64 recombinant inbred lines (RILs) Analysis of variance expressed significant differences among the RILs, indicating the presence of genetic variability for almost all the traits studied except for days to 50 per cent flowering. Presence of minimum difference between phenotypic co-efficient of variation (PCV) and genotypic

co-efficient of variation (GCV) for all the traits indicated that the phenotypes were true to the genotypes and the expression of these traits had low environmental influence.

Asari *et al.* (2019) conducted an experiment on 44 mungbean [*Vigna radiata* (L.) Wilczek] genotypes to assess the genetic variability parameters for yield and yield contributing characters. The genotypes differed significantly for all twelve characters were studied. High GCV and PCV were recorded for primary branches/plant, Number of pod, Number of seeds/plant and Number of pod clusters/plant.

Azam *et al.* (2018) conducted an experiment to estimate the extent of genetic variability and relation between yield and related characters. Twenty-eight mungbean varieties were grown to estimate the extent of genetic variability and association between yield and yield related traits. Analysis of variance expressed that all the traits showed highly significant difference among genotypes except seeds/pod. Number of pod, plant height and 100 seed weight showed high genotypic co-efficient of variation (GCV) and phenotypic co-efficient of variation (PCV).

Dhole and Reddy (2018) conducted a study to assess the amount of genetic variation present among 17 mutants developed through electron beam and gamma rays. The genotypic co-efficient of variation (GCV) was estimated by standard methods. Highest GCV was observed for seed yield/plant followed by pods/cluster and clusters/plant.

Genotypic and phenotypic variation for yield and yield contributing traits were studied by Ahmad *et al.*, (2014) in 14 genotypes of mungbean (*Vigna radiata* L.). Analysis of variance for parameters expressed the significant variations for all variables under consideration. Genotypic and phenotypic variances were observed high for Number of pods/plant and days to maturity. Genotype 8010 produced maximum number of pods/cluster and number of pods/plant. Maximum plant height was noted for genotype 8003 while genotype 98002 took maximum days to flowering and days to maturity. Similarly, maximum 100-seed weight and seed yield/plant were observed in genotypes 8004 and 8002, respectively. Existing variation may helpful for selection and further hybridization breeding program.

Degefa *et al.* (2014) showed that being highly self-pollinated crop, natural variability for yield and yield related traits was very narrow in mungbean making selection ineffective.

Niharika *et al.* (2014) estimated PCV, GCV for eight quantitative traits in 20 mungbean and one blackgram genotypes of intra-and inter-specific origin. The genotypes differed significantly for all the characters studied. Higher GCV and PCV values were gained for yield/plant, 100-seed weight and pods/plant.

Narasimhulu *et al.* (2013) studied genetic variability and character association in forty mungbean genotypes for different quantitative characters during rabi, 2012. Highest GCV and PCV were found for Number of branches/plant, Number of pods/plant, biological yield/plant and harvest index, respectively.

Fetemeh *et al.* (2012) evaluated an experiment to study genetic diversity of 20 genotypes of mungbean. They reported that among the 20 genotypes, the highest variation was observed for seed yield followed by 1000 seed weight and plant height. Moderate variation was observed for pods/plant and Number of pods clusters/plant. Low variability was found for number of fruiting branches/plant, pod length, and Number of seeds/pod.

Zaid *et al.* (2012) tested 20 Mungbean (*Vigna radiata* L. Wilezek) genotypes for genetic variability among different yield contributing traits i.e., plant height, pods/plant, pod length, seeds/pod, biological yield, and grain yield. Maximum plant height was recorded for genotype NFM5-63-19 cm; maximum Number of pods/plant was noted for genotype NFM5-63-19, while; genotype NFM-12-8 and NFM-6-5 found with a maximum pod length. Similarly, the maximum Number of seeds/pod, biological yield and grain yield was noted in genotype NFM-6-5, NFM-12-6 and NM98 respectively.

Tabasum *et al.* (2010) conducted an experiment on 10 mungbean genotypes to assess variability associated with seed yield. Primary and secondary branches, pods cluster/plant and pod length expressed lesser variability while clusters/plant, 100 seed weight and harvest index exhibited intermediate range of variability. Sufficient genetic variability was recorded for plant height, Number of pod, total plant weight and seed yield. The present findings could be useful for selection criteria for high seed yield in the mungbean breeding.

Rahim *et al.* (2010) evaluated Genotypic and phenotypic variance for yield and yield contributing characters in 26 mungbean genotypes. Significant variations among the genotypes were recorded for all the characters.

8

Khan *et al.* (2005), Srivastava and Singh (2012) and Gadakh *et al.* (2013) showed that significant differences were observed among various genotypes through genetic variability between yield and yield components in mungbean.

2.2 Heritability, genetic advance and genetic advance in percentage of mean

Heritability measures the fraction of phenotype variability that can be attributed to genetic variation. Estimates of heritability use statistical analysis to identify the causes of differences between individuals. Improvement in the mean genotypic value of selected plants over the parental population is known as genetic advance. It helps to know the causes of genetic gain under selection. So it is important to measure these genetic parameters to select more diverse genotype. There are few experiments on mungbean and their findings are given below-

Gayachran *et al.* (2020) conducted a study on 1,232 mungbean accessions where broad sense heritability (h^2) analysis showed days to 50% flowering, flowering period, days to 80% maturity, 100-seed weight and seed-dimension-related traits were highly suitable for mungbean breeding programs.

Marawar *et al.* (2020) carried out an investigation with thirty diverse mungbean (*Vigna radiata* L. Wilczek) genotypes for heritability and genetic advance analysis. High estimates of heritability in broad sense was noted for plant height, grain yield/plant, days to 50 % plant flowering, 100 seed weight, plant stand at harvest, Number of pods/plant, Number of seeds/pod, days to maturity and Number of branches/plant. High genetic advance observed for plant stand at harvest plant height, days to 50 % flowering, Number of pods /plant.

Joseph *et al.* (2020) determined the heritability analysis for yield and yield related traits among the 64 recombinant inbred lines (RILs). The RILs significantly differed for all the characters studied. Heritability estimates in broad sense and genetic advance were high for all the characters except for test weight indicating that estimates expressed the presence of additive gene action in the expression of all the traits of interest except test weight.

Asari *et al.* (2019) conducted an experiment on 44 mungbean [*Vigna radiata* (L.) Wilczek] genotypes. High heritability along with high genetic advance as percent of mean was noted for plant height, primary branches/plant, pod clusters/plant, Number of pods/plant and seed yield indicating preponderance of additive gene action. Therefore, more emphasis should be given on these characters while selection for high yielding mungbean cultivar.

Azam *et al.* (2018) stated that broad sense heritability with moderate genetic advance as percent of mean was recorded for 100 seed weight, days to flower and pods/plant suggesting preponderance of additive gene action for these characters and selection of such traits might be effective for the improvement of grain yield.

Dhole and Reddy (2018) studied to assess heritability present among 17 mutants. Heritability was highest for seeds/pod (0.92), followed by pod length (0.89), branches/plant (0.88), 100 seed weight (0.88). Highest GA as per cent of mean was observed for seed yield/ plant.

To utilize mungbean gene pool effectively, studies on heritability and genetic advance were conducted by Raturi *et al.* (2015) under rain-fed conditions during kharif 2009, 2010 and 2011. The data of ten quantitative characters was noted. The Number of pods/plant and seed yield were recorded with significantly higher heritability (>60%) with more than 30% genetic advance. The present study suggests that seed yield and Number of pods/plant are greatly influenced by the additive gene effect and greater proposition of variations are heritable for these characters.

Degefa *et al.* (2014) conducted a study to assess the magnitude of heritability in broad sense and genetic advance among thirteen mungbean accessions for growth and grain yield characters. The combined results for heritability showed that the high estimates of heritability and genetic advance were recorded for seeds/plant and seed yield indicating that these characters were under the control of additive genetic effects. High genetic advance expected as percent of mean with high heritability was observed for Number of primary branches at Hirna, Number of seeds/plant at Rare and Number of secondary branches, pods/plant and 100 seed weight for combined analysis. The findings from this study could be useful for establishing selection criteria for high seed yield in the mungbean breeding.

Ahmad *et al.* (2014) in 14 genotypes of mungbean (*Vigna radiata* L.) studied that high heritability with high genetic advance as percentage of mean for Number of pods/plant exhibited the additive gene effect for these characters. Genotypic and phenotypic variances were observed high for Number of pods/plant and days to maturity. Heritability was high for 100 seed weight and lowest for seed yields/plant.

Niharika *et al.* (2014) studied heritability and genetic advance for eight quantitative traits in 20 mungbean and one blackgram genotypes of intra-and inter-specific origin. High values of estimated heritability were observed for plant height, pod length and 100 seed weight. High expected genetic advance as percent of mean coupled with high heritability was recorded for 100 seed weight.

Narasimhulu *et al.* (2013) studied high heritability with high genetic advance as per cent of mean was recorded for plant height, pods/plant, pods/cluster, biological yield/plant, harvest index and seed yield/plant suggesting that these characters were controlled by additive gene action. Direct selection may be exercised for improvement of these traits.

Zaid *et al.* (2012) tested 20 mungbean (*Vigna radiata* L. Wilezek) genotypes to know the heritability among different yield contributing traits. The high heritability was recorded for pod length (99%) and plant height (70%), while pods/plant (29%) and seeds/pod (17%) had shown low heritability.

Tabasum *et al.* (2010) conducted an experiment on 10 mungbean genotypes. Moderate to high heritability estimates were found for all characters.

Rahim *et al.* (2010) evaluated heritability and genetic advance for yield and yield contributing characters in 26 mungbean genotypes. High heritability (broad) coupled with high genetic advance in percent of mean was noted for plant height, Number of pods/plant, Number of seeds/pod, 1000 grain weight and grain yield/plant indicating these characters would be best for phenotypic selection.

2.3   Multivariate analysis

For a successful plant breeding program, genetic divergence is very much essential to classify the experimental material, based on the extent of similarity, into close and divergent types. Genetic improvement in any crop mainly depends upon the amount of

genetic variability present in the population. Mahalanobis (1936) developed a statistic known as D² form of a generalized distance, which considers the variation produced by any character statistic to measure the distance between two populations. Mahalanobis also pointed out that D² would be remaining constant when samples were drawn from two different populations irrespective of the size of the representative sample. This indicates that D² provided a measure of actual magnitude of divergence between two individuals under comparison.

Mungbean or green gram (*Vigna radiata* L. Wilczek) is an important pulse crop of southeast asia. This is one of the most liked pulses in bangladesh because of its good palatability, nutritional quality and easy digestibility which grown in subsistence farming systems. The crop species has evolved in a diverse range of agro climatic conditions and therefore the local germplasm has rich genetic diversity. However, this diversity has not been explored to identify useful traits and germplasm to utilize in crop development program.

Therefore, Gayachran *et al.* (2020) conducted a study on 1,232 mungbean accessions using 8 quantitative, 18 qualitative traits and 4 seed morphometric traits to understand genetic diversity of the crop and identify trait-specific germplasm. Agglomerative hierarchical clustering analysis based on morphological quantitative traits showed that the diversity in the mungbean germplasm has no significant relationship with respect to their geographical origin. Principal component analysis (PCA) revealed that first five principal components (PCs) explained 91.4% of total variation. The maximum variance was explained by PC1 (44.61%) followed by PC2 (21.15%). Plotting of observations in two-dimensional space corresponding to PC1 and PC2 revealed wide distribution of accessions, and certain accessions were observed associated with variables. The agro-morphological variability and its genetic nature revealed from this study may prove very useful in future breeding programs.

Pavithra *et al.* (2020) conducted an experiment to evaluate thirty-one mungbean genotypes (including four checks) collected from the different parts of India. The genotypes were sown in an incomplete augmented bock design with four checks varieties. viz. 'Kamdev', 'OBBGG-52', 'IPM-02-14' and 'IPM-02-3'. All the mungbean genotypes were evaluated for different phenotypic characters and their tolerance to powdery mildew disease at two cropping seasons as well as at two different

locations in Odisha. Seven molecular markers viz., VrCSSTS1, VrCSSTS2, VrCSSSR3, CEDG191, MB-SSR238, CEDG166, and CEDG282 were analyzed also. SSR marker such as VrCSSSR and VrCSSTS linked with powdery mildew resistance gene were tested in different genotypes with known powdery mildew reaction and the results showed a consistent association of the marker in all the powdery mildew resistant genotypes and absent in all the powdery mildew susceptible genotypes. The results confirmed the validation of these markers with the powdery mildew resistance gene in different genetic backgrounds. Similarly, CEDG191, CEDG166, CEDG282 markers, considered to be linked to powdery mildew resistance, amplified the respective marker fragment of 100 to 300 bp in mungbean genotypes.

Dhole and Reddy (2018) conducted a study to assess the amount of genetic variation present among 17 mutants developed through electron beam and gamma rays. A cluster analysis segregated 17 mutants into six clusters. Considerable genetic variability was present in mutants which can be used in mungbean improvement.

Gupta *et al.* (2014) carried out an experiment in a randomized block design with three replications. Principal component analysis revealed that the first three main PCAs amounted 78.80% of the total variation among genotypes for different characters. Out of total principal components, PC1 accounts for maximum variability in the data with respect to succeeding other components. Number of branches/plant (28.62%), Number of clusters/plant (23.55%) and seed yield (15.58%) showed maximum percent contribution towards total genetic divergence on pooled basis. Cluster analysis exhibited that genotypes fall into seven different clusters and inter and intra cluster distance showed genetic diversity between different genotypes. The maximum number of genotypes 8 was found in cluster II followed by cluster III comprising of 6 genotypes. Genotypes RMG-1138 and IPM02-03 representing the mono genotypic cluster signifies that it can be the most diverse variety and it would be the appropriate genotype for hybridization with ones present in other clusters to tailor the agriculturally important characters and ultimately to boost the seed yield in mungbean under rain fed conditions.

Divyaramakrishnan and Savithramma (2014) investigated to determine variability among 374 mungbean genotypes through Principal Component Analysis (PCA), cluster analysis and the relationship existing between yield and other characters through Pearson's correlation analysis. According to principal component analysis, 4 principal

components (PC) had Eigen values more than unity and accounted for 65.76% of the total variance among 12 traits. Amongst first four PCs, PC1 was accounted high proportion of total variance (30.53%) and the remaining three principal components viz., PC2, PC3 and PC4 revealed 16.05, 10.05 and 9.13% of total variance respectively. 374 accessions were grouped into 8 clusters through hierarchical cluster analysis method. Cluster I composed of 218 accessions and it has maximum number of genotypes, whereas Cluster II and Cluster III consisted of 55 and 85 accessions respectively. Based on the cluster analysis results it was recommended that crosses could be made between the varieties of Cluster VI and VIII, Cluster V and VIII, Cluster III and VIII and Cluster V and VIII.

Basnet *et al.* (2014) conducted an experiment to evaluate the collected Nepalese/ local and exotic mungbean genotypes based on eight qualitative traits. The genotypes were classified into 6 clusters according to Unweighted Pair Group Method with Arithmetic mean (UPGMA) hierarchical techniques. Cluster analysis grouped genotypes together with greater genetic similarity; the clusters did not necessarily include all genotypes from the same origin. Some cluster consisted only of the local or the exotic varieties while in others, both categories were grouped under the same cluster. This was primarily due to similarity in the different genotypes for the qualitative traits recorded. Although Principal Component Analysis (PCA) did not form robust group as outlined by the cluster analysis, it supported the groups formed in the dendogram. In general, the clusters formed displayed the closeness of the local and exotic genotypes among themselves than for the mixed population consisting of both varieties. Principal component analysis showed that five Principal Components (PCs) together accounted for 92.30% of the total phenotypic variability observed in the genotypes. The first three PCs had almost 78% of the total variation with individual share of 40.60%, 22.30% and 14.70% respectively.

Dutta *et al.* (2012) studied the DNA polymorphism in indian mungbean cultivars by using random amplified polymorphic DNA (RAPD) markers. A total of 60 random primers were used in the study and 33 of them generated reproducible RAPD patterns. Amplification of genomic DNA of most popular 24 indian mungbean cultivars with these RAPD primers yielded 249 fragments that could be scored, of which 224 were polymorphic, with an average of 7.0 polymorphic fragments per primer. Number of amplified fragments with random primers ranged from 2 (OPI 9) to 17 (OPD 7).

Percentage polymorphism ranged from 33% (OPX 5) to a maximum of 100% (OPX 4, OPX 6, OPX 13, OPX 15, OPX 19, OPD 5, OPD 7, OPD 20, OPI 4, OPI 6, OPI 13, OPI 14, OPI 18 and OPF1), with an average of 90%. The Jaccard's similarity indices based on RAPD profiles were subjected to UPGMA cluster analysis and genotypes grouped in two major groups. Sixteen out of 24 released cultivars grouped to cluster I. This indicated the narrow genetic base in the indian mungbean cultivars used in the study.

Rahim *et al.* (2010) evaluated genetic divergence for yield and its contributing characters in 26 Mungbean genotypes. Twenty-six genotypes were segregated into 3 clusters. Maximum number of genotypes (12) was into cluster II. The maximum range of variability was noted for Number of pods/plant (12.22-20.55) among all the characters in 3 clusters. Crosses involving cluster I and III may exhibit high heterosis for yield as well as earliness of mungbean.

Singh *et al.* (2009) carried out a genetic divergence study consisting of 80 germplasm collections of mungbean for 12 quantitative characters by using Mahalanobis's D^2 statistics and grouped them into 11 non distinct overlapping clusters. The study revealed that no parallelism was observed between genetic and geographic diversity.

Manish *et al.* (2009) studied on 33 genotypes of French bean and grouped into 6 clusters based on their diversity. As inter cluster distance was the maximum between cluster IV and cluster V and served as potential parents for hybridization.

Chauhan (2008) showed that 210 true breeding lines of urdbean and were grouped into nine clusters based on their diversity. As inter cluster distance was the maximum between cluster II and cluster III serve as potential parents for hybridization.

Valarmathi *et al.* (2007) estimated genetic divergence in 60 cowpea genotypes using Mahalanobois's D^2 statistics and grouped them into 12 clusters and reported the maximum genetic diversity by days to maturity.

Umadevi (2007) evaluated 60 blackgram genotypes and grouped into four clusters based on their diversity. Inter cluster distance was the maximum between cluster I and IV which serve as potential parents for hybridization.

Shanthi *et al*. (2006) studied genetic divergence in 60 urdbean genotypes and were grouped into 17 clusters by Mahalanobis's D^2 statistics. Inter cluster distance was the maximum between cluster II and XVII.

Rangarao *et al.* (2006) performed multivariate analysis among 60 genotypes of mungbean and grouped them in top eight clusters. From pooled data he reported that the 20 characters viz. days to maturity, 100-seed weight, Number of pods/plant and dry matter contributed through 80% of total divergence.

2.4   Correlation co-efficient

Correlation co-efficient measures the mutual relationship between various plant characters and determines the component characters on which selection can be done for genetic improvement in yield. Among the types of correlation, genotypic correlation is more stable and is of paramount importance for a plant breeder to bring about genetic improvement in one character by selecting the other character of a pair, if that is genetically correlated in desirable direction. This type of correlation may be either due to pleiotropic action of genes or due to linkage or more likely both but the pleiotropic effect is considered to be more important which refers to manifold effect of gene (Falconer, 1960). Correlation co-efficient measures the association between any two characters. These, however, may not give the information about the direct and indirect effect of one variable on the other.

Dhunde *et al.* (2021) undertaken an investigation among twelve quantitative traits and to know the direct and indirect effects of various yield contributing characters on grain yield by correlation analysis in thirty five mungbean genotypes The results of the study revealed that, grain yield/plant expressed highly significant and positive correlation at both genotypic and phenotypic levels with Number of branches/plant, Number of pods/cluster, Number of clusters /plant, Number of pods/plant and hundred seed weight.

Ahmad and Belwal (2020) conducted a study using 112 diverse genotypes of mungbean, along with five high yielding checks. Observations were noted on fifteen morphological characters of plant, pod and seed. The genotype differed significantly for all the characters studied. Correlation analysis revealed that seed yield showed positive significant correlation with Number of pods/plant, pods diameter, pods length,

100 seed weight, Number of clusters, Number of leaves, seed diameter, plant height, seed length, pod wall thickness, Number of branches and seed density.

Marawar *et al.* (2020) carried out an investigation with thirty diverse mungbean (*Vigna radiata* L. Wilczek) genotypes for ten characters with three replications for the estimation of correlation. The yields/plant were highly significant with positively correlated with plant stand at harvest, plant height, Number of branches/plant, Number of pods/plant, 100 seed weight, Number of seeds/pod.

Joseph *et al.* (2020) carried out a study to determine correlation co-efficients analysis for yield and yield related traits among the 64 recombinant inbred lines (RILs). Seed yield/plant showed significant positive correlation with pod yield/plant followed by Number of pods/plant, Number of clusters/plant and threshing percentage.

Dhole and Reddy (2018) conducted a study to assess the correlation present among 17 mutants. Seed yield/plant showed significant positive correlation with clusters/plant, pods/cluster and seeds/pod.

Kritika and Yadav (2017) studied that the biological yield/ plot was positive and its correlation with seed yield/plot was positively significant.

To utilize mungbean gene pool effectively, studies on correlation were conducted by Raturi *et al.* (2015) under rain-fed conditions during kharif 2009, 2010 and 2011. The correlation studies showed highly significant and positive association of all the quantitative characters with seed yield except with that of days to 50% flowering.

Hemavathy *et al.* (2015) undertaken an investigation to evaluate thirteen diverse mungbean (*Vigna radiata* (L.) Wilkeezek) genotypes for the estimation of correlation co-efficient for nine quantitative traits. This analysis indicated that, Number of clusters/plant, Numberof pods/plant, 100 seed weight and Number of seeds/pod had positive correlation with seed yield. The present findings could be suggested that on the basis of genetic parameter correlation, Number of pods/cluster, Number of pods/plant, Number of seeds/pod and 100 seed weight should be given topmost priority while formulating a selection strategy for improvement of yield in mungbean.

Niharika *et al.* (2014) conducted a study of correlation co-efficient analysis for eight quantitative traits in 20 mungbean and one blackgram genotypes. Yield/plant was recorded to exhibit highly significant positive correlation with pods/plant, 100 seed

weight and pod length. Yield/plant exhibited significant and negative correlation with days to initial and 50% flowering which suggesting that breeding for early flowering may be progressed with caution so that yield is not hampered while utilizing diverse germplasm.

Srivastava and Singh (2012) conducted and experiment on mungbean. The estimation of correlation expressed that seed yield had positive and significant correlation with Number of pods/plant, 100 seed weight, days to first picking maturity, primary branches/plant and Number of pods/cluster.

Zaid *et al.* (2012) tested 20 mungbean (*Vigna radiata* L. Wilezek) genotypes for correlation among different yield contributing traits i.e., plant height, pods/plant, pods length, seeds/pod, biological yield, and grain yield. Based on genotypic correlation analysis characters like plant height, pods plant, pod length and on phenotypic basis grain yield and seeds/pod could be the best criteria in any breeding program for increasing yield in mungbean genotypes under agro-climatic conditions of Peshawar.

Rahim *et al.* (2010) evaluated correlation for yield and its contributing characters in 26 mungbean genotypes. The Number of pods/plant, panicle length and Number of seeds/pod are positively correlated with grain yield.

Makeen *et al.* (2007) evaluated an experiment in Uttar Pradesh, India on twenty diverse mungbean genotypes to estimate correlation co-efficient for 10 quantitative characters. They observed higher genotypic and phenotypic co-efficients of variation for seed yield and Number of pods/plant. They also showed that pods/plant and plant height had significant positive correlation with seed yield.

Sirohi and Kumar (2006) performed an experiment on 19 diverse genotypes of mungbean (*Vigna radiata* L.) to know the correlation analysis for yield and yield components. The genotypic correlation was dominant to the phenotypic correlation. Significant and positive correlations were exhibited in case of the Number of clusters /plant and Number of productive pods/plant with seed yield /plant.

2.5   Path co-efficient

Path co-efficient analysis permits the separation of direct and indirect effect through the other related characters by partitioning the correlation co-efficients. The review of

the work done utilizing path coefficient analysis in mungbean is presented below. The method of path co-efficient analysis provides an effective means of finding out direct and indirect causes of association of various component characters. This technique was originally developed by Wright (1921) and it was first used for plant selection by Dewey and Lu (1959). To use this technique, it requires cause and effect situation among the variables. In any crop, grain yield has been associated with a number of yield contributing characters and these characters themselves are inter related.

Dhunde *et al.* (2021) undertaken an investigation to know the direct and indirect effects of various yield contributing characters on grain yield by path analysis in thirty-five mungbean genotypes. Path analysis showed that, Number of branches /plant, pod length, plant height, Number of pods/cluster and Number of pods/plant recorded the highest direct effect at in desirable direction. Their association with grain yield was also significant and positive indicating perfect association. Therefore, direct selection would help in isolating high yielding genotypes from highly segregating population.

Dash *et al.* (2021) conducted an experiment comprised of 230 mungbean germplasm to assess the path analysis. Path analysis revealed that pod Number /plant is desirable contributing trait next to seed Number /pod and 100 seed weight towards seed yield. For genetic improvement in the seed yield, direct selection of genotypes based on component traits exhibiting positive correlation and higher positive direct effect will be effective and fruitful in mungbean under cold stress in the winter season.

Ahmad and Belwal (2020) conducted an experiment using 112 diverse genotypes of mungbean, Path analysis indicated that Number of pod/plant and 100 seed weight exerted a high magnitude of positive direct effect, pod length showed moderate effect while Number of cluster and seed density exerted positive but low magnitude of direct effect on seed yield.

Marawar *et al.* (2020) carried out an investigation with thirty diverse mungbean (*Vigna radiata* L. Wilczek) genotypes for the estimation of path co-efficient analysis. Path co-efficient analysis indicated high direct effect on days to 50% flowering, Number of branches/plant, Number of pods/plant.

Joseph *et al.* (2020) carried out a study to determine the path coefficient analysis for yield and yield related traits among the 64 recombinant inbred lines (RILs). Among the traits studied, pod yield /plant exerted very high positive direct effect followed by the

Number of pods/plant, threshing percentage and Number of clusters/plant towards seed yield/plant.

Kritika and Yadav (2017) revealed that, path co-efficient analysis indicated Number of pods/plant, Number of seeds/pod, biological yield/plot and harvest index had the maximum direct contribution on seed yield and these characters should be given importance while formulating selection criteria for seed yield. Harvest index exerted positive indirect effects via Number pods/plant. Number of seeds/pod exerted the highest negative indirect effect on seed yield/plot. Plant height and Number of branches /plant recorded high positive indirect effect on seed yield via Number of pods/plants.

To utilize mungbean gene pool effectively, studies on path co-efficient were conducted by Raturi *et al.* (2015) under rain-fed conditions during kharif 2009, 2010 and 2011. The data of ten quantitative characters was noted. The Number of pods/plant had the maximum direct effect followed by plant height and 1000 seed weight suggesting their direct contribution towards seed yield.

Degefa *et al.* (2014) studied 30 genotypes of mungbean for path analysis to know that at genotypic level, maximum positive direct effect was exerted on seed yield/plot by Number of primary branches, plant height and pods/plant. This indicated that the high yielding mungbean could be obtained by selecting pods/plants, plant height and primary branches. In addition, positive indirect effect through all characters except 100 seed weight and days to flowering was also observed on seed yield/plot. So, direct and indirect selection through these characters should be effective.

Alom *et al.* (2014) showed that pods/plant contributed the maximum positive direct effects on seed yield. Plant height, pod length and 100 seed weight had also positive direct effect on seed yield. Thus selection based on pods/plant, days to first flowering, plant height and 100 seed weight might be effective for improving seed yield in mungbean.

Garje *et al.* (2014) reported that Number of pod/plant had the maximum direct effect on seed yield followed by Number of cluster/plant and Number of secondary branches/plant.

Gadakh *et al.* (2013) evaluated fifty diverse mungbean (*Vigna radiata* L. Wilczek) genotypes for the estimation of path co-efficient analysis. Maximum direct effect of

harvest index, biological yield / plant and Number of primary branches/plant on seed yield was recorded.

Srivastava and Singh (2012) indicated that Number of pods/plant, Number of seeds/pod, Number of clusters/plant had maximum direct contribution on seed yield.

According to Reddy *et al.* (2011), days to flowering, days to maturity, Number of pods/plant, shoot dry matter/plant and 100 seed weight had positive direct effects on seed yield.

Rahim *et al.* (2010) evaluated path co-efficient for yield and its contributing characters in 26 Mungbean genotypes. Based on path co-efficient parameter, the Number of pods/plant and Number of seeds/pod are the important traits.

Haritha and Reddy (2002) examined 50 genotypes of mungbean for path co-efficient analysis and clusters/plant exhibited maximum direct effect followed by pods/cluster on grain yield.

CHAPTER III

MATERIALS AND METHODS

The investigation was undertaken on mungbean (*Vigna radiata* L.) at the experimental farm of the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka during the period from March 2020 to June 2020 to study the genetic variability, heritability, genetic advance, character association, path co-efficient analysis, genetic divergence, nutrient and chlorophyll content. Details pertaining to materials used and methodology employed in the investigation are presented in this chapter.

3.1 Location of experimental site

The experimental field was located at 90º22′ E longitude and 23º41′ N latitude at an altitude of 8.6 meters above the sea level. The experimental field belongs to the Agro-ecological zone of the Modhupur Tract, AEZ-28. The experimental site was shown in the map of AEZ of Bangladesh in Appendix I.

3.2 Characteristics of soil

The experimental site of the soil was clay loam in texture and belongs to Tejgaon soil series characterized by shallow red brown terrace soils. Soil pH ranged from 5.47 to 5.63 whereas organic matter was 0.82%. Experimental area was flat having available irrigation and drainage system and above flood level. Soil samples from 0-15 cm depths were collected from experimental field and analyzed. The analysis was done by Soil Resource and Development Institute (SRDI) Dhaka. Physicochemical properties of the soil were presented in Appendix II.

3.3 Climate

The experimental site is situated in subtropical climatic region that is characterized by high temperature along with high relative humidity and heavy rainfall in Kharif I (March/April-May/June) season. Mungbean can be cultivated throughout the year. During the studying period, the crop received total rainfall of 26.50 mm. At that time,

the average maximum and minimum temperatures were 29.42°C and 20.36°C respectively (Appendix III). Details of the meteorological data in respect of temperature, rainfall, relative humidity, total sunshine and soil temperature during the period of experiment were collected from the Abhawa Bhaban (Bangladesh Metrological Department), Agargaon presented in Appendix III. During this period the humidity was low, the temperature was average with plenty of sunshine.

3.4 Genetic materials used in the experiment

The present study was performed with 14 genotypes of mungbean. The genotypes were collected from Pulse Research Centre of Bangladesh Agricultural Research Institute (BARI), Gazipur, BSMRAU, BINA, Lalmonirhat and Barisal. The name and source of these genotypes are presented in Table 1.

Table 1. Sources of 14 genotypes of mungbean

Serial number	Local name	Mark	Source
1	BARI 1	G_1	Pulse Research Centre , BARI
2	BARI 2	G_2	Pulse Research Centre , BARI
3	BARI 3	G_3	Pulse Research Centre , BARI
4	BARI 4	G_4	Pulse Research Centre , BARI
5	BARI 5	G_5	Pulse Research Centre , BARI
6	BARI 6	G_6	Pulse Research Centre , BARI
7	BARI 7	G_7	Pulse Research Centre , BARI
8	BARI 8	G_8	Pulse Research Centre , BARI
9	BU MUNG 1	G_9	Department of Agronomy, BSMRAU
10	BINA 5	G_{10}	Plant Breeding Division , BINA
11	BINA 8	G_{11}	Plant Breeding Division , BINA
12	BINA 9	G_{12}	Plant Breeding Division , BINA
13	CHAITA MUNG	G_{13}	Lalmonirhat
14	SONA MUNG	G_{14}	Barishal

3.5 Design and layout of the experiment

The experiment was laid out in randomized complete block design (RCBD) with three replications. Then it was sub-divided into three blocks where 14 genotypes were

randomly assigned. The plot size was 2.5m with single line. Row to row distance was 30 cm and plant to plant distance was 10 cm.

3.6 Preparation of the experimental field

The experimental plot was prepared by ploughing. Weeds and stubbles were removed. Manures and fertilizers were applied as per the recommended dose before the final land preparation. The final land preparation was done on 16 March, 2020. Preparation of the experimental field are presented in figure 1 and some of the growing plants of different genotypes are presented in figure 2.

Figure 1. Preparation of the experimental field

Figure 2. Plant height of different mungbean genotypes

3.7   Manures and fertilizers

Due to its ability of nitrogen fixation from the atmosphere, mungbean requires less nitrogen application. But for initial establishment of plant up to the stage of nodule formation a starter dose of 20-40-20 NPK respectively was applied. In this study fertilizer was applied as per the recommendation of Bangladesh Agricultural Research Institute (BARI). The following doses of fertilizers and manures were applied to the plot for mungbean cultivation in table 2. Urea, TSP and MP were applied at the time of final land preparation. Cow dung was applied two weeks before sowing during the land preparation.

Table 2. Doses of manures and fertilizers used in the present study

Serial number	Name of fertilizers and manures	Rate(kg/ha)
1	Urea	50
2	TSP	75
3	MP	35
4	Cowdung	10000

3.8 Sowing of seeds and intercultural operation

The seeds of 14 mungbean genotypes were sown in the field on 18th march, 2020. Intercultural practices were done uniformly for all the genotypes. Thinning was done 25 days after sowing and wedding was done twice, one was the first during thinning and the second one was after about two months of sowing.

3.9 Harvesting

Harvesting of mungbean pods was done after maturity stage. Different genotypes matured at different times. Mature pods were harvested when fruits turned to brown in color. The pods were allowed to ripe and then seeds were collected and different genotypes with different replications were collected separately. Harvesting was completed on 23 June, 2020.

3.10 Recording of Experimental Data

Data on the following characters were recorded on individual plant basis from 10 randomly selected plants per genotypes in each replicate. The data were recorded in the field condition and the other characters were recorded in the field laboratory after harvest.

3.10.1 Plant height

Plant height of each plant was measured at mature stage in cm using meter scale and mean was calculated.

3.10.2 Number of leaves/plant

Each plants leaf was counted and recorded.

3.10.3 Number of branches/plant

The total Number of branches arisen from the main stem of a plant was counted as the Number of branches/plant.

3.10.4 Number of pod

Total number of pod of each plant was counted and considered as the Number of pods/plant.

3.10.5 Number of pods cluster/plant

The total number of pods cluster in individual plants was recorded.

3.10.6 Pod length

This measurement was taken in cm from the bottom to the tip of a pod without beak.

3.10.7 Number of seeds/pod

Total number of seed in each pod within the individual plants was counted.

3.10.8 Weight of 1000 seed (gm)

Weight in grams of randomly counted thousand seeds of each entry was recorded.

3.10.9 Yield/plant (gm)

Seed weight/plant was measured from the randomly selected plants and then average was designated as seed yield/plant in gm.

3.11 Statistical analysis

The mean values of ten randomly selected plants used for recording observations were computed for each of fourteen traits for each genotype in each replication and were subjected to statistical analysis. Univariate analysis of the individual character was done for all characters under study using the mean values (Singh and Chaudhury, 1985) and was estimated using Statistix 10 computer program. Duncan's Multiple Range Test (DMRT) was performed for all the characters to test the differences between the means of the genotypes. Mean, range and co-efficient of variation (CV %) were also estimated using Statistix 10. Multivariate analysis was done by computer using GENSTAT 5.13

and Microsoft Excel 2016 software through four techniques viz., Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO) and Cluster Analysis (CA).

3.11.1 Analysis of variance:

The analysis of variance for different characters was carried out utilizing mean data in order to assess the genetic variability among populations as given by Cochran and Cox (1957). The level of significance was tested at 5% and 1% using F- test. The model of ANOVA used is presented below:

Table 3: ANOVA

Sources of variation	Degrees of freedom (D.F.)	Mean sum of squares (MS)	Expected MS
Replication	(r-1)	Mr	$p\,\sigma_r^2 + \sigma_e^2$
Population	(p-1)	Mp	$r\,\sigma_p^2 + \sigma_e^2$
Error	(p-1) (r-1)	Me	σ_e^2
Total	(rp-1)		

Where, p = number of treatments (population)

      r = number of replications

      σ_r^2 = variance due to replications

      σ_p^2 = variance due to treatments (population)

      σ_e^2 = variance due to error

To test significance of the difference between any two-adjusted genotypic mean, the standard error of mean was computed using the formula:

$$S.E = \sqrt{\frac{2Me}{r}}\ \left(1 + \frac{rqu}{q+1}\right)$$

Where, S. E = Standard error of mean

      Me = Mean sum of square for error (Intra block)

      r = Number of replications

      q = Number of population in each sub-block

      u = Weightage factor computed

3.11.2 Estimation of least significant differences (lsd):

Least Significant Differences were estimated according to the formula of Gomez and Gomez(1984).

$$lsd_\alpha = t_\alpha \sqrt{\frac{s^2}{r}}$$

Here, α = Level of significance, t= tabulated t value with concerned df at same level of significance, s^2 = Error Mean Sum of Square and r = Number of replication.

3.12 Study of variability parameters:

Estimation of the variability among the populations for traits related to yield/plant in *Vigna radiata* were narrated below:

3.12.1 Estimation of Genotypic variance and phenotypic variance:

To estimate phenotypic and genotypic components of variance, Johnson *et al.* (1955) suggested a formula which is mentioned below:

a. Genotypic variance, $\sigma_g^2 = \frac{MSG-MSE}{r}$

Where,

MSG = Mean sum of square for genotypes

MSE = Mean sum of square for error, and

 r = Number of replication

 b. Phenotypic variance, $\sigma_p^2 = \sigma_g^2 + \sigma_e^2$

Where,

σ_p^2= Phenotypic variance

σ_g^2= Genotypic variance

σ_e^2 = Environmental variance = Mean square of error

3.12.2 Estimation of genotypic and phenotypic co-efficient of variation:

To compute genotypic co-efficient of variation (GCV) and phenotypic co-efficient of variation (PCV) for all the characters, following formula was given by Burton, 1952:

$$GCV = \frac{\sigma_g \times 100}{\bar{x}}$$

$$PCV = \frac{\sigma_p \times 100}{\bar{x}}$$

GCV = Genotypic co-efficient of variation

PCV = Phenotypic co-efficient of variation

σ_g= Genotypic standard deviation

σ_p= Phenotypic standard deviation

$\bar{x}$ = Population mean

Sivasubramanian and Madhavamenon (1973) categorized phenotypic coefficient of variation (PCV) and genotypic co-effcient of variation (GCV) as

Low (0-10%),

Moderate (10-20%) and

High (>20%)

3.13 Estimation of heritability in broad sense:

Singh and Chaudhary (1985) suggested a formula to estimate broad sense heritability which is given below:

$$h_b^2(\%) = \frac{\delta_g^2}{\delta_p^2} \times 100$$

Where, h_b^2=Heritability in broad sense

σ_g^2= Genotypic variance

σ_p^2= Phenotypic variance

Robinson *et al.* (1966) suggested the following categories for heritability estimates in cultivated plants:

Categories: Low: 0-30%

Moderate: 30-60%

High: >60%

3.13.1 Estimation of genetic advance:

Allard (1960) suggested the following formula which was used to estimate the expected genetic advance for different characters under selection:

$$GA = \frac{\sigma_g^2}{\sigma_p^2} \cdot K \cdot \sigma_p$$

Where,

GA = Genetic advance

σ_g^2 = Genotypic variance

σ_p^2 = Phenotypic variance

σ_p = Phenotypic standard deviation

K= Standard selection differential which is 2.06 at 5% selection intensity.

Categories: Low (<10%)

Moderate (10-20%)

High (>20%)

3.13.2 Estimation of genetic advance in percentage of mean:

Following formula was given by Comstock and Robinson (1952) to compute genetic advance in percentage of mean:

$$GA \text{ in percent of mean} = \frac{GA}{Grand\ mean} \times 100$$

Johnson *et al.* (1955) suggested that genetic advance in percent of mean was categorized into following groups:

Categories:

Less than 10% - Low

10-20% - Moderate

More than 20% - High

3.14 Multivariate analysis

The genetic diversity among the genotypes was assessed by Mahalanobis's (1936) general distance (D^2) statistic and its auxiliary analyses. The parent's selection in hybridization program based on Mahalanobis's D^2 statistic is more reliable as requisite knowledge of parents in respect of a mass of characteristics is available prior to crossing. Rao (1952) suggested that the quantification of genetic diversity through biometrical procedures had made it possible to choose genetically diverse parents for a hybridization program. Multivariate analysis viz. Principal Component Analysis (PCA) and Cluster Analysis (CA), which quantify the differences among several quantitative traits, are efficient method of evaluating genetic diversity. These are as follows:

3.14.1 Principal component analysis (PCA)

Principal Component Analysis, one of the multivariate techniques, is used to examine the inter-relationships among several characters and can be done from the sum of squares and products matrix for the characters. Thus, PCA finds linear combinations of a set variate that maximize the variation contained within them, thereby displaying most of the original variability in a smaller number of dimensions. Therefore, Principles components were computed from the correlation matrix and genotypes scores obtained for first components (which has the property of accounting for the maximum variance) and succeeding components with latent roots greater than unity. Contribution of the different morphological characters towards divergence is discussed from the latent vectors of the first two principal components.

3.14.2 Cluster analysis (CA)

Cluster Analysis divides the genotypes of a data set into some Number of mutually exclusive groups. Clustering was done using non-hierarchical classification. In GENSTAT, the algorithm is used to search for optimal values of chosen criterion proceeds as follows. Starting from some initial classification of the genotypes into required number of groups, the algorithm repeatedly transferred genotypes from one group to another so long as such transfer improved the value of the criterion. When no further transfer can be found to improve the criterion, the algorithm switches to a second stage which examines the effect of swooping two genotypes of different classes and so on.

3.14.3 Calculation of D^2 values

The Mahalanobis's distance (D^2) values were calculated from transformed uncorrelated means of characters according to Rao (1952), and Singh and Chaudhury (1977). The D^2 values were estimated for all possible combinations between genotypes. In simpler form D^2 statistic is defined by the formula

$$D^2 = \sum_i^x d_i^2 = \sum_i^x \left(Y_i^j - Y_j^k\right) \qquad (j \neq k)$$

Where,

Y = Uncorrelated variable (character) which varies from i = 1 to x

x = Number of characters.

Superscript j and k to Y = A pair of any two genotypes.

3.14.4 Computation of average intra-cluster distances

Average intra-cluster distances were calculated by the following formula as suggested by Singh *et al.* (1985).

Average intra-cluster distance $= \frac{\sum d_i^2}{n}$

Where, D_i^2 = the sum of distances between all possible combinations (n) of genotypes included in a cluster

n = Number of all possible combinations between the populations in cluster.

3.14.5 Computation of average inter-cluster distances

Average inter-cluster distances were calculated by the following formula as suggested by Singh *et. al.* (1985)

Average inter-cluster distance$= \dfrac{\sum D_{ij}^2}{n_i \times n_j}$

Where,

$\sum D_{ij}^2 =$ the sum of distances between all possible combinations of the populations in cluster i and j

n_i = number of populations in cluster i.

n_j = number of populations in cluster j.

3.14.6 Cluster diagram

Using the values of intra and inter-cluster distances (D $= \sqrt{D^2}$), a cluster diagram was drawn as suggested by Singh and Chuadhury (1985). It gives a brief idea of the pattern of diversity among the genotypes included in a cluster.

3.15 Selection of varieties for future hybridization program

Divergence analysis is usually performed to identify the diverse genotypes for hybridization purposes. The genotypes grouped together are less divergent among themselves than those, which fall into different clusters. Clusters separated by largest statistical distance (D^2) express the maximum divergence among the genotypes included into these different clusters. Variety (s) or line(s) were selected for efficient hybridization program according to Singh and Chaudhury (1985). According to them the following points should be considered while selecting genotypes for hybridization program.

3.16 Correlation co-efficient analysis:

To determine the level of relationship of characters with yield and furthermore among the yield parts, the correlation coefficients were computed. Both genotypic and phenotypic correlation co-efficients between two characters were determined by utilizing the variance and covariance components as suggested by Al-Jibouri *et al.* (1958).

$$r_{gxy} = \frac{Cov_{gxy}}{\sqrt{\sigma_{gx}^2} \cdot \sqrt{\sigma_{gy}^2}}$$

$$r_{pxy} = \frac{Cov_{pxy}}{\sqrt{\sigma_{px}^2} \cdot \sqrt{\sigma_{py}^2}}$$

Where,

$r_g(xy), r_p(xy)$ the genotypic and phenotypic correlation co-efficients of x and y, respectively.

Cov_{gxy}, Cov_{pxy} are the genotypic and phenotypic covariance of x and y, respectively.

σ_{gx}^2= Genotypic variance of the trait x and σ_{gy}^2 = Genotypic variance of the trait y.

σ_{px}^2= Phenotypic variance of the trait x and σ_{py}^2= Phenotypic variance of the trait y.

The calculated value of 'r' was compared with table 'r' value with n-2 degrees of freedom at 5% and 1% level of significance, where, n refers to number of pairs of observation. Thus, the data obtained from various experimental objectives were subjected to pertinent statistical analysis to draw meaningful inference towards the genetic divergence of mustard populations.

3.17 Path co-efficient analysis:

According to the procedure employed by Dewey and Lu (1959) also quoted in Singh and Chaudhary (1985) and Dabholkar (1992), Path coefficient analysis was done utilizing simple correlation values. In path analysis, correlation coefficient is partitioned into direct and indirect independent variables on the dependent variable.

$$r_{yx1} = P_{yx1} + P_{yx2}r_{x1x2} + P_{yx3}r_{x1x3}$$

$$r_{yx2} = P_{yx1}r_{x1x2} + P_{yx2} + P_{yx3}r_{x2x3}$$

$$r_{yx3} = P_{yx1}r_{x1x3} + P_{yx2}r_{x2x3} + P_{yx3}$$

In order to estimate direct & indirect effect of the correlated characters, say x1, x2 and x3 yield y, a set of simultaneous equations (three equations in this example) is required to be formulated as shown below:

Where, r's denote simple correlation coefficient and P's denote path coefficient (unknown).

P's in the above equations may be conveniently solved by arranging them in matrix from. Total correlation, say between x1 and y is thus partitioned as follows:

P_{yx1} = the direct effect of x1 on y.

$P_{yx2}r_{x1x2}$ = the indirect effect of x1 via x2 on y.

$P_{yx3}r_{x1x3}$ = the indirect effect of x1 via x3 on y.

After calculating the direct and indirect effect of the characters, residual effect (R) was calculated by using the formula given below (Singh and Chaudhary, 1985):

$$P_{RY}^2 = 1 - \sum P_{iy} \cdot r_{iy}$$

Where,

$$P_{RY}^2 = (R^2)$$

Hence, residual effect, $R = (P_{RY}^2)^{1/2}$

P_{iy}= Direct effect of the character on yield

r_{iy}=Correlation of the character with yield

Categories:

Negligible (0.00 to 0.09);

Low (0.10 to 0.19);

Moderate (0.20 to 0.29);

High (0.30 to 1.0);

Very High (>1.00)

CHAPTER 4

RESULTS AND DISCUSSIONS

4.1 Genetic variability for mungbean genotypes

The analysis of variance investigated that there was highly significant variation among the genotypes. The subsequent sections show the mean, minimum, maximum, mean sum of squares, variance components, genotypic and phenotypic co-efficient of variance, heritability, genetic advance, and genetic advance in percent of mean for all genotypes, as well as the least significant difference (LSD).

Table 4. Mean sum of square from the ANOVA of 14 mungbean genotypes in respect of nine characters

Characters	Mean sum of square			Co-efficient of variation (%)
	Genotype (g-1)=13	Replication (r-1)=2	Error (g-1) (r-1)=26	
Plant height (cm)	72.131**	1.071	0.970	2.140
Number of leaves/plant	9.637**	0.081	0.133	3.240
Number of branches/plant	1.139**	0.056	0.056	7.190
Number of pod	36.900**	0.048	0.082	2.220
Number of pods cluster/plant	1.094*	0.755	0.466	12.220
Pod length (cm)	4.815**	0.044	0.026	1.840
Number of seeds/pod	9.570**	0.667	0.256	4.840
Weight of 1000 seed (gm)	216.419**	0.024	0.485	2.070
Yield/plant (gm)	5.50**	0.02	0.03	4.06

**, indicates 1% level of significance

*, indicates 5% level of significance

4.1.1   Plant height (cm)

Highly significant differences were observed among the genotypes for plant height (cm) (Table 4). According to values the maximum plant height (cm) was produced by the line G_4 (56.233) and the second maximum height was produced by G_3 (53.967). Whereas minimum plant height was produced by the line G_{13} (40.927) (Table 5).

The genotypic variance (23.720) was negligibly lower than the phenotypic variance (24.690) for plant height in mungbean genotypes suggesting less influence of environment (Table 6). Genotypes co-efficient of variation (10.609) was also lower than phenotypic co-efficient of variation (10.824) (Table 6). The lower range of variation between genotypic and phenotypic variance for plant height indicated that the genotypes represented dominantly and differently even when grown under the same environment. Highest phenotypic and genotypic variances and genotypic and phenotypic co-efficient of variations for plant height were also observed by Makeen *et al* (2007), Abrahim *et al*. (2007). Rao *et al*. (2006). Vikas *et al*. (1998) and Reddy *etal*. (2003) in their study.

4.1.2   Number of leaves/plant

The analysis of variance for this character showed highly significant differences among the genotypes (Table 4). The genotype G_{10} gave the highest value of Number of leaves/plant (13.660) and the second highest value was G_6 (13.220) (Table 5). The lowest Number of leaves/plant was observed in G_1 (7.553) (Table 5).

Phenotypic variance (3.301) was serial numberightly higher than genotypic variance (3.168). Low difference seen in phenotypic co-efficient of variation (16.160) and genotypic co-efficient of variation (15.831) (Table 6) indicating negligible environmental effect upon the expression of Number of leaves/plant.

4.1.3 Number of branches/plant

Highly significant variation for Number of branches/plant was observed among the genotypes. The genotype G_{11} produced the highest Number of branches/plant (4.440) (Table 5). The genotype G_{13} produces the lowest Number of branches /plant (2.440) (Table 5).

Phenotypic variance (0.417) is negligibly higher than genotypic variance (0.361) while phenotypic co-efficient of variation (19.671) serial numberightly higher than genotypic co-efficient of variation (18.309) indicating minor environmental effect on them (Table 6). Kumar *et al* (2003) found significant differences for Number of primary branches/plant.

4.1.4 Number of pod

The analysis of variance for this character showed highly significant differences among the genotypes (Table 4). The genotype G_8 gave the highest value of Number of pod (18.527) which was statistically similar with G_7 (18.330) and G_6 (18.327) and significantly superior to all other lines (Table 5). The lowest Number of pod was observed in G_1 (8.567) (Table 5).

Phenotypic variance (12.355) was relatively higher than genotypic variance (12.273) and phenotypic co-efficient of variation (27.182) and genotypic co-efficient of variation (27.092) indicating serial numberightly environmental influence of the expression of this characters (Table 6). High heritability coupled with high genetic advance was observed for Number of pod by Reddy *et al*. (2003), Venkateswarlu *et al* (2001). Vikas *et al* (1998) and Rahman (1982).

4.1.5 Number of pods cluster/plant

Highly significant variation for Number of pods cluster/plant was observed among the genotypes (Table 4). The genotypes G_{10} (7.033) gave the highest mean value of Number of pods cluster/plant which was significantly superior to all other varieties. The lowest value was observed in G_1 and G_9 (4.667) (Table 5).

Phenotypic variance (0.675) was serial numberightly higher than genotypic variance (0.209) (Table 6) that indicates high environmental effect on them. Phenotypic co-efficient of variation (14.716) was higher than genotypes co-efficient of variation (8.194) which indicating a moderate influence of environment of expression of this characters.

Table 5. Mean performance of nine characters of 14 genotypes of mungbean

Genotypes	Plant height (cm)	Number of leaves/plant	Number of branches /plant	Number of pod	Number of pods cluster/plant	Pod length(cm)	Number of seeds/pod	Weight of 1000 seed (g)	Yield/plant (gm)
G_1	49.300 c	7.553 j	2.777 fg	8.567 g	4.667 d	7.300 f	8.667 hi	27.66f	2.62 h
G_2	48.833 c	8.440 i	2.553 g	8.767 g	5.133 cd	7.367 f	8.333 i	27.333 f	2.52 hi
G_3	53.967 b	10.440 g	3.440 cde	12.913 d	5.600 bcd	8.633 de	9.667 fg	28.333 f	3.84 g
G_4	56.233 a	11.667 ef	3.550 cd	10.303 f	5.533 bcd	8.867 d	10.333 ef	31.000 d	3.94 fg
G_5	45.300 d	12.440 cd	2.660 g	11.417 e	5.333 bcd	10.333 a	11.333 d	40.333 c	4.14 ef
G_6	44.033 de	13.220 ab	3.773 bc	18.327 a	5.667 bcd	10.567 a	12.333 bc	51.667 a	4.85 d
G_7	42.943 ef	12.997 bc	3.773 bc	18.330 a	5.767 bcd	10.333 a	9.333 gh	50.000 b	5.25 c
G_8	41.383 fg	9.773 h	3.440 cde	18.527 a	5.833 bc	8.433 e	10.333 ef	31.667 d	4.95 d
G_9	42.403 efg	10.773 g	3.220 de	11.310 e	4.667 d	9.433 bc	11.000 de	29.667 e	4.34 e
G_{10}	49.187 c	13.660 a	4.110 ab	11.407 e	7.033 a	9.700 b	13.667 a	39.333 c	6.06 a
G_{11}	41.233 g	12.220 de	4.440 a	15.813 b	5.333 bcd	9.300 c	13.000 ab	30.667 de	6.06 a
G_{12}	45.257 d	12.333 d	3.107 ef	14.000 c	6.300 ab	8.400 e	11.667 cd	31.000 d	5.55 b
G_{13}	40.927 g	10.440 g	2.440 g	10.360 f	5.633 bcd	6.467 g	8.333 i	26.000 g	2.22 j
G_{14}	41.703 fg	11.440 f	2.660 g	11.000 e	5.667 bcd	7.567 f	8.333 i	25.667 g	2.32 ij
$lsd_{0.05}$	1.653	0.612	0.396	0.481	1.145	0.271	0.850	1.169	0.29
Mean	45.907	11.243	3.282	12.931	5.583	8.764	10.452	33.595	4.19
Std Error	0.804	0.2976	0.1927	0.2341	0.5572	0.132	0.4134	0.5688	0.14
Stdv	4.852	1.773	0.632	3.429	0.824	1.243	1.797	8.302	1.32
Minimum	40.927	7.553	2.44	8.567	4.6667	6.467	8.333	25.667	2.22
Maximum	56.233	13.66	4.44	18.527	7.0333	10.567	13.667	51.667	6.06

4.1.6 Pod length (cm)

Highly significant variation was found for pod length (cm) among the genotypes selected for the study (Table 4). The highest pod length was observed in G_6 (10.567). Second highest was observed by G_5 and G_7 (10.333). The lowest pod length was G_{13} (6.467) (Table 5).

Phenotypic variance (1.662) and genotypic variance (1.596) differs serial numberightly for this trait indicating little differences on environment. Genotypic co-efficient of variation (14.415) and phenotypic co-efficient of variation (14.533) indicating high variability present on this character (Table 6). Pod length showed high genotypic co-efficient of variation by Das *et al.* (1998).

4.1.7 Number of seeds/pod

The analysis of variance for Number of seeds/pod showed highly significant variation among the genotypes (Table 4). The maximum Number of seeds/pod was recorded in G_{10} (13.667). The second maximum number was G_{10} (13.000) (Table 5). On the other hand, the variety G_2, G_{13} and G_{14} (8.333) found the minimum Number of seeds/pod.

The environmental influence was little for this trait, which could be realized from the difference between genotypic variance 3.104 and phenotypic variance 3.361 and also the difference between genotypic co-efficient of variation 16.857 and phenotypic co-efficient of variation 17.540 (Table 6). High genotypic and phenotypic co-efficient of variation indicated high variation in the trait for all the genotypes. Pandey *et al.* (2002) was observed highest Number of seeds/pod.

4.1.8 Weight of 1000 seed (gm)

The analysis of variance for weight of 1000 seed (gm) showed highly significant variation among the genotypes (Table 4). The maximum weight of 1000 seed (gm) was recorded in G_6 (51.667) (Table 5). On the other hand, genotype G_{14} found the minimum number of weight of 1000 seed (gm) (25.667).

Phenotypic variance was 72.463 and genotypic variance was 71.978 with little differences in genotypic co-efficient of variation 25.254 and phenotypic co-efficient of variation 25.339 indicating negligible environmental effect (Table 6). Sandhu *et al.* (1979) was found similar result.

4.1.9 Yield/plant (gm)

Significant difference was observed for yield/plant (gm) among the genotypes under this study (Table 4). The significant varietal differences indicated that there was wide range of variation among the genotypes for yield/plant with the mean values ranging from 2.22 gm to 6.06 gm (Table 5). The highest yield/plant was recorded in G_{10} and G_{11} (6.06 gm). The lowest value was found in G_{13} (2.22) (Table 5).

The phenotypic variance (1.85) was negligibly lower than genotypic variance (1.82) indicating minor environmental influence on this trait (Table 6) and genotypic co-efficient variation (32.22) to that of phenotypic co-efficient of variation (32.48) was low which indicated low environmental influence on yield/plant (Table 6).

4.2 Heritability, genetic advance and genetic advance in percentage of mean

The estimate of heritability, genetic advance and genetic advance in percentage of mean are presented in Table 6.

4.2.1 Plant height (cm)

Plant height showed high heritability (96.073%) and genetic advance (9.834) and moderate GA% (21.421%) (Table 6). High heritability and genetic advance showed the presence of additive gene action indicating fixable and heritable character with very low influence of environment. Due to its high heritability it can easily be improved by selection and can be used for future development of HYV. Low heritability and low genetic advance for plant height was reported by loganathan *et al* (2001).

4.2.2 Number of leaves/plant

Number of leaves/plant showed high heritability (95.977%) but low genetic advance (3.592) and high GA% (31.950%) (Table 6). High heritability and high genetic advance showed the presence of additive gene action indicating fixable and heritable character with very low influence of environment. Due to its high heritability it can easily be improved by selection and can be used for future development of HYV. Heritability estimate alone is not enough to produce a high genetic gain.

43

Table 6. Genetic parameters for nine yield and its related characters of mungbean

Serial number	Characters	Genotypic variance (δ^2_g)	Phenotypic variance (δ^2_p)	GCV	PCV	Heritability (h^2b)	GA	GA (%)
1	Plant height (cm)	23.720	24.690	10.609	10.824	96.073	9.834	21.421
2	Number of leaves/plant	3.168	3.301	15.831	16.160	95.977	3.592	31.950
3	Number of branches/plant	0.361	0.417	18.309	19.671	86.636	1.152	35.107
4	Number of pod	12.273	12.355	27.092	27.182	99.335	7.193	55.623
5	Number of pods cluster/plant	0.209	0.675	8.194	14.716	31.007	0.525	9.400
6	Pod length (cm)	1.596	1.622	14.415	14.533	98.389	2.582	29.455
7	Number of seeds/pod	3.104	3.361	16.857	17.540	92.371	3.488	33.375
8	Weight of 1000 seeds (gm)	71.978	72.463	25.254	25.339	99.331	17.418	51.848
9	Yield/plant (gm)	1.82	1.85	32.22	32.48	98.427	2.76	65.85

GCV= Genotypic co-efficient of variation, PCV= Phenotypic coefficient of variation,
GA= Genetic advance, GA (%) = Genetic advance in percent of mean,
δ^2_g= Genotypic variance, δ^2_p= Phenotypic variance.

4.2.3　Number of branches/plant

Number of branches/plant showed high heritability (86.636%) and low genetic advance (1.152) but high GA% (35.107%) (Table 6), which indicated the character was less influenced by environmental effects and presence of additive gene action. It can be considered for future improvement of HYV. Number of branches/plant was observed the highest heritability (91.7) by Shamsuzzaman and Shaikh (1982).

4.2.4　Number of pod

Number of pod showed high heritability (99.335%) and low genetic advance (7.193) but high GA% mean (55.623) (Table 6), which indicated the trait was less influenced by environmental effects and the presence of additive gene action. It can be considered for future improvement of hybrid variety.

4.2.5　Number of pods cluster/plant

Number of pods cluster/plant showed moderate heritability (31.007%) and low genetic advance (0.525) and low GA% (9.400) (Table 6). It revealed non-additive gene action involved in the maintenance of this trait and low heritability was seen due to influence of higher environmental effect rather than genotypes, so selection may not be rewarded.

4.2.6　Pod length (cm)

Pod length showed high heritability (98.389%) where genetic advance (2.582) was very low but GA% mean (29.455%) was high (Table 6) which indicated this character was less influenced by environmental effects and presence of additive gene action which can be used for future development of HYV. Length of pod were highly heritable was reported by Abrahim *et al* (2006) and Tiwari *et al* (1995). High heritability associated with high genetic advance over mean was observed for pods length by Das *et al* (1998).

4.2.7　Number of seeds/pod

Number of seeds/pod showed high heritability (92.371%) and low genetic advance (3.488) but high GA% mean (33.375) (Table 6), which indicated this character was moderate influenced by environmental effects. High heritability accompanied with high genetic advance in percentage of mean indicated that the heritability was due to additive gene effects and which can be used for the future development of HYV. High

heritability coupled with high genetic advance was observed for Number of seeds/pod reported by Rohman *et al* (2003) and Reddy *et al.* (2003).

4.2.8   Weight of 1000 seed (gm)

Thousand seed weight showed high heritability (99.331%) of this trait and medium genetic advance (17.418) but high GA% mean (51.848) (Table 6) which indicated this character was less influenced by environmental effects and possibility of predominance of additive gene action and therefore, this characters could be improved through selection process for the future development of HYV. High values for heritability and genetic advance were estimated for 1000-seed weight by Iserial numberam *et al* (1999), Sharma *et al* (1999) and Sandhu *et al.* (1979).

4.2.9   Yield/plant (gm)

Yield/plant showed high heritability (98.427%), low genetic advance (2.76) and high GA% mean (65.85) (Table 6), which indicating low influence of environment and apparent variability and the presence of additive gene action which can be used for future HYV variety. High heritability estimates coupled with high genetic advance were observed for yield/plant by Rao *et al* (2006). Rohman *et al* (2003), Reddy *et al.* (2003) and Sharma *et al.* (1999).

4.3   Diversity of mungbean genotypes

Genetic diversity has been evaluated using GENSTAT software. The analysis of genetic diversity includes many stages, i.e., distancing of the varieties, grouping and study of the inter cluster distance. More than one multivariate method has been showed and the results of numerous studies have been cleared (Bashar, 2002; Uddin, 2001; Juned *et at*., 1988 and Ario, 1987). Genetic diversity was analyzed using multivariate methods.

4.4   Multivariate Analysis

4.4.1   Principal component analysis

Principal components were computed from the correlation matrix and genotype scores obtained from first components and succeeding components with latent roots greater than the unity. Eigen values corresponding nine principal component axes and

percentage of total variation accounting for them obtained from the principal component analysis are presented in Table 7. Eigen values represents that the cumulative eigen values of four principal components accounted for 89.82% of the total variation among the varieties. The 1st principal component accounted for 57.45% of the total variation, the second, third and fourth components accounted for 14.09%, 10.03% and 8.25% of the total percent of variation, respectively (Table 7).

Table 7. Eigen values, percentage of variation and cumulative percentage in respect of nine axes in 14 genotypes of mungbean

Principal component axes	Eigen value	Percent variation	Cumulative % of percent variation
I	5.17	57.45	57.45
II	1.268	14.09	71.54
III	0.903	10.03	81.57
IV	0.742	8.25	89.82
V	0.517	5.74	95.56
VI	0.184	2.05	97.61
VII	0.117	1.3	98.91
VIII	0.067	0.74	99.65
IX	0.032	0.35	100

4.4.2 Principal coordinate analysis

Principal coordinate analysis (PCO) was performed on auxiliary principal component analysis. This analysis helps in estimating distances (D^2) for all combinations between pairs of varieties. The highest inter genotype distance was observed between the genotype G_1 and G_6 (1.288). The second highest value observed between the genotype G_2 and G_6 (1.270). The tenth highest pair distance was observed between genotype G_2 and G_{11} (1.150). The lowest distance was observed between the genotypes G_1 and G_2 (0.150). The second lowest observed between genotype G_{13} and G_{14} (0.185). The tenth lowest distance was observed between the genotype G_8 and G_{12} (0.394). The difference between the highest and the lowest inter-genotypic distance indicated the prevalence of variability among the 14 genotypes of mungbean (Table 8).

Table 8. Ten of each lower and higher inter genotypic distances (D^2) between pairs of mungbean genotypes

Highest 10 inter genotypic distances				Lowest 10 inter genotypic distances			
Serial number	Genotypes	Genotypes	Values	Serial number	Genotypes	Genotypes	Values
1	G_1	G_6	1.288	1	G_1	G_2	0.150
2	G_2	G_6	1.270	2	G_{13}	G_{14}	0.185
3	G_1	G_7	1.254	3	G_3	G_4	0.261
4	G_6	G_{13}	1.250	4	G_6	G_7	0.268
5	G_2	G_7	1.229	5	G_2	G_{13}	0.346
6	G_7	G_{13}	1.209	6	G_3	G_9	0.359
7	G_{10}	G_{13}	1.186	7	G_4	G_9	0.359
8	G_1	G_{10}	1.171	8	G_{11}	G_{12}	0.380
9	G_2	G_{10}	1.154	9	G_5	G_9	0.390
10	G_2	G_{11}	1.150	10	G_8	G_{12}	0.394

4.5 Non-hierarchical clustering

With the application of co-variance matrix for non-hierarchical clustering, 14 mungbean genotypes were grouped into four different clusters (Table 9). Cluster II and Cluster III consists of two genotype, which is smallest cluster. Cluster IV composed of six genotypes that was largest cluster. Finally, cluster I composed of four genotypes (Table 9). These results confirmed the clustering pattern of the genotypes obtained through principal component analysis. Cluster mean values of nine different characters of 14 mungbean genotypes are presented in Table 10. The clustering pattern obtained coincided with the apparent grouping patterns performed by PCA. It is clear from the above that the results obtained through PCA were supported by non-hierarchical clustering.

Table 9. Distribution of 14 mungbean genotypes into four different clusters

Cluster number	Number of genotypes	Percent (%)	Name of genotypes
I	4	28.57	G1 , G2 , G3 , G4
II	2	14.29	G6 , G7
III	2	14.29	G5 ,G10
IV	6	42.86	G8 , G9 , G11, G12, G13, G14

4.5.1 Cluster I

Cluster I had four genotypes namely G_1, G_2, G_3 and G_4 (Table 9). According to the cluster means (Table 10), cluster I (52.08 cm) had the highest cluster mean value for plant height. Second highest value was (28.58gm) for weight of 1000 seeds. The performance of different character of cluster II were arranged according to descending orders, Number of pods/plant (10.14), Number of leaves/plant (9.53), Number of seeds/pod (9.25), pod length (8.04cm), Number of pods cluster/plant (5.23), yield/plant (3.23gm) and Number of branches/plant (3.08) (Table 10). This indicates that, genotype of cluster I could be used for parent in future hybridization program.

4.5.2 Cluster II

Cluster II was composed of two genotype name G_6 and G_7 (Table 9). This is the smallest cluster. Cluster II had highest value weight of 1000 seed (50.84 gm). The performance of different character of cluster II were arranged according to descending order, plant height (43.49cm), Number of pods/plant (18.33), Number of leaves/plant (13.11), Number of seeds/pod (10.83), pod length (10.45 cm), Number of pod clusters/plant (5.72), yield/plant (5.05 g), Number of branches /plant (3.77) (Table 10). This indicates that, genotype of cluster II could be used as parent in future hybridization program.

4.5.3 Cluster III

Cluster III was composed of two genotype name G_5 and G_{10} (Table 9). Cluster III had the highest value for plant height (cm) (47.25 cm). Second highest value for weight of 1000 seed was (39.83 gm) and lowest value was (3.39) (Table 10).This indicates that genotype of cluster III could be used for parent in future hybridization program.

4.5.4 Cluster IV

Cluster IV was composed of six genotypes name G_8, G_9, G_{11}, G_{12}, G_{13} and G_{14} (Table 9). Cluster IV had highest value for plant height (42.15 cm). This cluster showed lowest values for Number of branches/plant (3.22) (Table 10).

Table 10. Cluster mean values of nine different characters of 14 mungbean genotypes

Characters	I	II	III	IV
Plant height (cm)	52.08	43.49	47.25	42.15
Number of leaves/plant	9.53	13.11	13.05	11.16
Number of branches /plant	3.08	3.77	3.39	3.22
Number of pod	10.14	18.33	11.41	13.5
Number of pods cluster/plant	5.23	5.72	6.18	5.57
Pod length(cm)	8.04	10.45	10.02	8.27
Number of seeds/pod	9.25	10.83	12.5	10.44
Weight of 1000 seed (gm)	28.58	50.84	39.83	29.11
Yield/plant (gm)	3.23	5.05	5.1	4.24

4.6 Selection of genotypes for future hybridization program

Selection of genetically divergent genotypes is an important step for hybridization program. So, the genotypes were to be selected on the basis of specific objectives. A higher heterosis could be produced from the crosses between genetically distant parents (Falconer, 1960; Moll *et al.* 1962; Ramanujam *et al.* 1974; Ghaderi *et al.* 1989; main and Bhal, 1989). Considering the magnitude of genetic distance and agronomic performance, the genotypes G_1, G_2, G_6 and G_7 from cluster I and cluster II would be suitable for efficient hybridization program.

4.7 Correlation co-efficient analysis

Yield is a complex character and associated with several yield contributing characters. Selection for yield may not be effective unless other yield components influencing it directly or indirectly are taken into consideration. When selection pressure is exercise for improvement of any character highly associated with yield, it simultaneouserial numbery affects a number of other correlated traits. Hence knowledge regarding association of characters with yield among themselves provides guidelines to the plant breeder for making improvement through selection. Genotypic and phenotypic correlations between pairs of characters are presented in Table 11. The genotypic correlation co-efficient were higher than the corresponding phenotypic correlation co-efficient in most of the cases indicating the association is largely due genetic reason. The results are discussed character wise as follows-

Table 11. Genotypic (rg) and phenotypic (rp) correlation co-efficient among different pairs of yield and yield contributing characters for 14 genotypes of mungbean

Characters		Plant height (cm)	Number of leaves/plant	Number of branches /plant	Number of pod	Number of pods cluster/plant	Pod length (cm)	Number of seeds/pod	Weight of 1000 seed (gm)
Number of leaves/plant	r_g	**-0.163^{NS}**							
	r_p	**-0.156^{NS}**							
Number of branches /plant	r_g	**0.045^{NS}**	0.595**						
	r_p	**0.056^{NS}**	0.543**						
No of pod	r_g	-0.438**	0.488**	0.627**					
	r_p	-0.431**	0.476**	0.567**					
Number of pods cluster/plant	r_g	**0.047^{NS}**	0.843**	0.523**	0.382*				
	r_p	**0.038^{NS}**	0.453**	**0.265^{NS}**	0.235^{NS}				
Pod length (cm)	r_g	**-0.021^{NS}**	0.746**	0.655**	0.569**	**0.260^{NS}**			
	r_p	**-0.018^{NS}**	0.727**	0.612**	0.564**	**0.167^{NS}**			
No of seeds/pod	r_g	**-0.049^{NS}**	0.704**	0.761**	0.394**	0.586**	0.709**		
	r_p	**-0.026^{NS}**	0.663**	0.699**	0.372*	0.353*	0.668**		
Weight of 1000 seed (gm)	r_g	**-0.123^{NS}**	0.676**	0.481**	0.634**	0.400**	0.835**	0.457**	
	r_p	**-0.121^{NS}**	0.657**	0.445**	0.631**	**0.228^{NS}**	0.827**	0.436**	
Yield/plant (gm)	r_g	**-0.116^{NS}**	0.697**	0.872**	0.658**	0.656**	0.736**	0.878**	0.541**
	r_p	**-0.108^{NS}**	0.662**	0.799**	0.653**	0.405**	0.722**	0.843**	0.537**

* and ** indicate significant at 5% and 1% level of probability and NS indicates non-significant respectability. r_g= genotypic correlation co-efficient, r_p= phenotypic correlation co-efficient

4.7.1 Plant height (cm)

Plant height showed non-significant positive correlation with Number of branches/plant (0.045 and 0.056) and Number of pods cluster/plant (0.047 and 0.038) and significant negative correlation with Number of pods/plant (-0.438 and -0.431) for both genotypic and phenotypic level. Non-significant negative phenotypic and genotypic correlation was also observed with Number of leaves/plant (-0.163 and -0.156), pod length (-0.021 and -0.018), Number of seeds/pod (-0.049 and -0.026), weight of 1000 seed (-0.123 and -0.121) and yield/plant (-0.116 and -0.108) (Table 11). This result indicated that plant height could increase the Number of branches/plant, pod length and Number of pods/plant.

4.7.2 Number of leaves/plant

Number of leaves/plant showed highly significant positive correlation with Number of branches /plant (0.595 and 0.543), no of pods/plant (0.488 and 0.476), Number of pods clusters/plant (0.843 and 0.453), pod length (cm) (0.746 and 0.727), Number of seeds/pod (0.704 and 0.663), weight of 1000 seed (0.676 and 0.657) and yield/plant (0.697 and 0.662) (Table 11).

4.7.3 Number of branches/plant

Number of branches/plant showed highly significant positive correlation with no of pods/plant (0.627 and 0.567), pod length/plant (0.655 and 0.612), Number of seeds/pod (0.761 and 0.699), weight of 1000 seed (0.481 and 0.445) and yield/plant (0.872 and 0.799) (Table 11). Number of branches/plant showed genotypic positive significant correlation (0.523) and phonotypic positive non-significant correlation (0.265) with Number of pods cluster/plant.

4.7.4 Number of pod

Number of pod showed highly significant positive correlation with pod length (0.569 and 0.564), Number of seeds/pod (0.394 and 0.372), weight of 1000 seed (0.634 and 0.631) and yield/plant (g) (0.658 and 0.653) (Table 11). No of pod showed genotypic positive significant correlation (0.382) and phonotypic positive non-significant correlation (0.235) with Number of pods cluster/plant.

4.7.5 Number of pods cluster/plant

Number of pods cluster/plant showed highly significant positive correlation with Number of seeds/pod (0.586 and 0.353) and yield/plant (g) (0.656 and 0.405) (Table 11) at both genotypic and phenotypic level, which indicated that Number of pods cluster/plant would increase Number of seeds/pod and yield/plant. It also showed non-significant positive correlation with pods length (0.260 and 0.167) both genotypic and phenotypic level (Table 11). Number of pods cluster/plant showed genotypic positive significant correlation (0.400) and phenotypic positive non-significant correlation (0.228) with weight of 1000 seed.

4.7.6 Pod length (cm)

Pod length showed highly significant positive correlation with Number of seeds/pod (0.709 and 0.668), weight of 1000 seed (0.835 and 0.827) and yield/plant (0.736 and 0.722) at both genotypic and phenotypic level (Table 11), which indicated that increasing the pod length would increase the Number of seeds/pod, weight of 1000 seed and yield/plant.

4.7.7 Number of seeds/pod

Number of seeds/pod showed highly significant positive correlation with weight of 1000 seed (0.457 and 0.436) and yield/plant (0.878 and 0.843) at both genotypic and phenotypic level (Table 11), which indicated that increasing Number of seeds/pod would increase weight of 1000 seed and yield/plant.

4.7.8 Weight of 1000 seed (gm)

Thousand seed weight showed significant positive correlation with yield/plant (0.541 and 0.537) at both genotypic and phenotypic level (Table 11), which indicated that increasing thousand seed weight would increase the yield/plant.

4.8 Path co-efficient analysis

Association of character determined by correlation co-efficient may not provide an exact picture of the relative importance of direct and indirect influence of each of yield components. In order to find out a clear picture of the interrelationship between yield/plant and other yield attributes, path analysis was done. Direct and indirect effects

were worked out using path analysis at genotypic level which also measured the relative importance of each component. Estimation of direct and indirect effect of path co-efficient analysis for mungbean was done and represented in Table 12.

4.8.1 Plant height (cm)

Plant height showed positive direct effect (0.160) on yield/plant (Table 12). It showed positive indirect effect on yield/plant via Number of branches/plant (0.009) and pod length (0.007). This trait showed negative indirect effect via Number of leaves/plant (-0.055), Number of pod (-0.190), Number of pods cluster/plant (-0.011), Number of seeds/pod (-0.034) and weight of 1000 seed (-0.002) which finally produce a non-significant negative correlation with yield/plant (-0.116). In such situations, the indirect causal factors are to be considered simultaneouserial numbery for selection.

4.8.2 Number of leaves/plant

Number of leaves/plant showed positive direct effect (0.338) on yield/plant (Table 12). It showed positive indirect effect on yield/plant via Number of branches/plant (0.116), no of pods/plant (0.212), Number of seeds/pod (0.485) and weight of 1000 seed (0.011) and also showed negative indirect effect via plant height (-0.026), Number of pods cluster/plant (-0.193) and pod length (cm) (-0.247). It has significant positive correlation with yield (0.697) (Table 12). Positive direct effects and positive correlations indicated that direct selection for yield/plant will be effective.

4.8.3 Number of branches/plant

Number of branches/plant showed positive direct effect (0.196) on yield/plant (Table 12). It showed positive indirect effect on yield/plant via plant height (cm) (0.007), Number of leaves/plant (0.201), Number of pod (0.273), Number of seeds/pod (0.524) and weight of 1000 seed (0.008). This trait showed negative indirect effect via Number of pods cluster/plant (-0.120) and pod length (-0.217). It has positive and significant correlation with yield/plant (0.872) (Table 12). Positive direct effects and positive correlations indicated that direct selection for yield/plant.

4.8.4 Number of pod

Number of pod showed positive direct effect (0.435) on yield/plant (Table 12). It showed positive indirect effect on yield/plant via Number of leaves/plant (0.165), Number of branches /plant (0.123), Number of seeds/pod (0.271) and weight of 1000 seed (0.010). This trait showed negative indirect effect with plant height (-0.070), Number of pods cluster/plant (-0.088) and pod length (-0.188). It showed positive significant correlation with yield/plant (0.658). Positive direct effects and positive correlations indicated the direct selection for yield/plant.

4.8.5 Number of pods cluster/plant

Number of pods cluster/plant showed negative direct effect (-0.229) on yield/plant (Table 12) and showed positive indirect effect on yield/plant via plant height (0.008), Number of leaves/plant (0.285), Number of branches /plant (0.102), Number of pod (0.166), Number of seeds/pod (0.403) and weight of 1000 seed (0.006). This trait showed negative indirect effect via pod length (-0.086). It showed positive and significant genotypic correlation with yield (0.656). Negative direct effect with positive significant correlation indicating dropping the selection based on this character.

4.8.6 Pod length (cm)

Pod length showed negative direct effect (-0.331) on yield/plant (Table 12). It showed positive indirect effect on yield/plant through Number of leaves/plant (0.252), Number of branches /plant (0.128), Number of pod (0.248), Number of seeds/pod (0.488) and weight of 1000 seed (0.013). This trait showed negative indirect effect via plant height (-0.003) and Number of pods cluster/plant (-0.060).It showed significant positive correlation with yield/plant (0.736). Negative direct effect with positive significant correlation indicating dropping the selection based on this character.

Table 12. Path analysis showing direct and indirect effects of different characters on fruit yield of 14 mungbean genotypes

Trait	Plant height	Number of leaves/plant	Number of branches /plant	Number of pods/plant	Number of pods cluster/plant	Pod length	Number of seeds/pod	Weight of 1000 seed	Genotypic correlation with yield/plant
Plant height (cm)	**0.160**	-0.055	0.009	-0.190	-0.011	0.007	-0.034	-0.002	-0.116^{NS}
Number of leaves/plant	-0.026	**0.338**	0.116	0.212	-0.193	-0.247	0.485	0.011	0.697**
Number of branches /plant	0.007	0.201	**0.196**	0.273	-0.120	-0.217	0.524	0.008	0.872**
Number of pod	-0.070	0.165	0.123	**0.435**	-0.088	-0.188	0.271	0.010	0.658**
Number of pods cluster/plant	0.008	0.285	0.102	0.166	**-0.229**	-0.086	0.403	0.006	0.656**
Pod length (cm)	-0.003	0.252	0.128	0.248	-0.060	**-0.331**	0.488	0.013	0.736**
Number of seeds/pod	-0.008	0.238	0.149	0.171	-0.134	-0.235	**0.689**	0.007	0.878**
Weight of 1000 seed (gm)	-0.020	0.229	0.094	0.276	-0.092	-0.276	0.314	**0.016**	0.541**

Residual effect: 0.106, * and ** indicate significant at 5% and 1% level of probability respectability

4.8.7   Number of seeds/pod

Number of seeds/pod showed positive direct effect (0.689) on yield/plant (Table 12). It showed positive indirect effect on yield/plant via Number of leaves/plant (0.238), Number of branches /plant (0.149), Number of pods/plant (0.171), Number of seeds/pod(0.689) and weight of 1000 seed (0.007) and showed negative indirect effect via plant height (-0.008), Number of pods cluster/plant (-0.134) and pod length (-0.235cm) (Table 12). It showed positive and significant correlation with yield/plant (0.878). Positive direct effects and positive correlations indicated that direct selection for yield/plant through this trait will be effective.

4.8.8   Weight of 1000 seed (gm)

Weight of 1000 seed showed positive direct effect (0.016) on yield/plant (Table 12). It showed positive indirect effect on yield/plant via Number of leaves/plant (0.229), Number of branches /plant (0.094), Number of pods/plant (0.276) and Number of seeds/pod (0.314) and showed negative indirect effect on yield/plant height (-0.020), Number of pods cluster/plant (-0.092) and pod length (-0.276). It showed positive significant correlation with yield (0.541). Positive direct effects and positive correlations indicated that direct selection for yield/plant through this trait will be effective.

4.8.9   Residual effect

The residual effect (R) of path co-efficient analysis was noted as 0.10 which indicated that the characters under study contributed 90% to the seed yield/plant. There are some other factors which contribute 10% to the yield/plant. But those factors were not utilized in the present study which could have considerable effect on yield/plant.

4.9 Nutrient component analysis

Nutrient component analysis is one of the important features of mungbean. So its production focuses on to grow a high yielding variety with high nutrient content percentage. Best quality determined by increasing percentage of nutrient content. On the other hand, chlorophyll absorbs the light energy required to convert carbon dioxide and water into glucose. Leaves with more chlorophyll are better able to absorb the light required for photosynthesis, so chlorophyll content can indicate the good vegetative production of crops. K%, P% and Chlorophyll Content (mg/g) in 14 mungbean genotypes are presented in Table 13.

Table 13. K%, P% and Chlorophyll Content (mg/g) in 14 mungbean genotypes

Serial number	Genotypes	K Content %	P Content %	Chlorophyll Content (mg/g)
1	G_1	2.61 g	0.10 bcd	0.26 abcd
2	G_2	2.72 c	0.11 abcd	0.29 a
3	G_3	2.31 m	0.10 bcd	0.18 g
4	G_4	2.38 j	0.114 abcd	0.20 efg
5	G_5	2.33 l	0.113 abcd	0.21 defg
6	G_6	2.35 k	0.061 d	0.22 cdefg
7	G_7	2.47 i	0.113 abcd	0.29 a
8	G_8	2.38 j	0.065 cd	0.19 fg
9	G_9	2.59 h	0.142 ab	0.23 bcdefg
10	G_{10}	2.65 f	0.12 abc	0.28 ab
11	G_{11}	2.69 e	0.16 a	0.25 abcde
12	G_{12}	2.74 b	0.14 ab	0.27 abc
13	G_{13}	2.71 d	0.15 ab	0.20 efg
14	G_{14}	2.83 a	0.117 abcd	0.24 abcdef
	$LSD_{0.05}$	0.004	0.058	0.054

4.9.1 (%) K Content

In the present investigation, (%) K content in the genotypes of mungbean ranged from 2.31% to 2.83%. The highest value was found in G_{14} (2.83) and the lowest value was found in G_3 (2.31) (Table 13). So, G_{14} genotype can be used for future breeding program to development variety high K content variety.
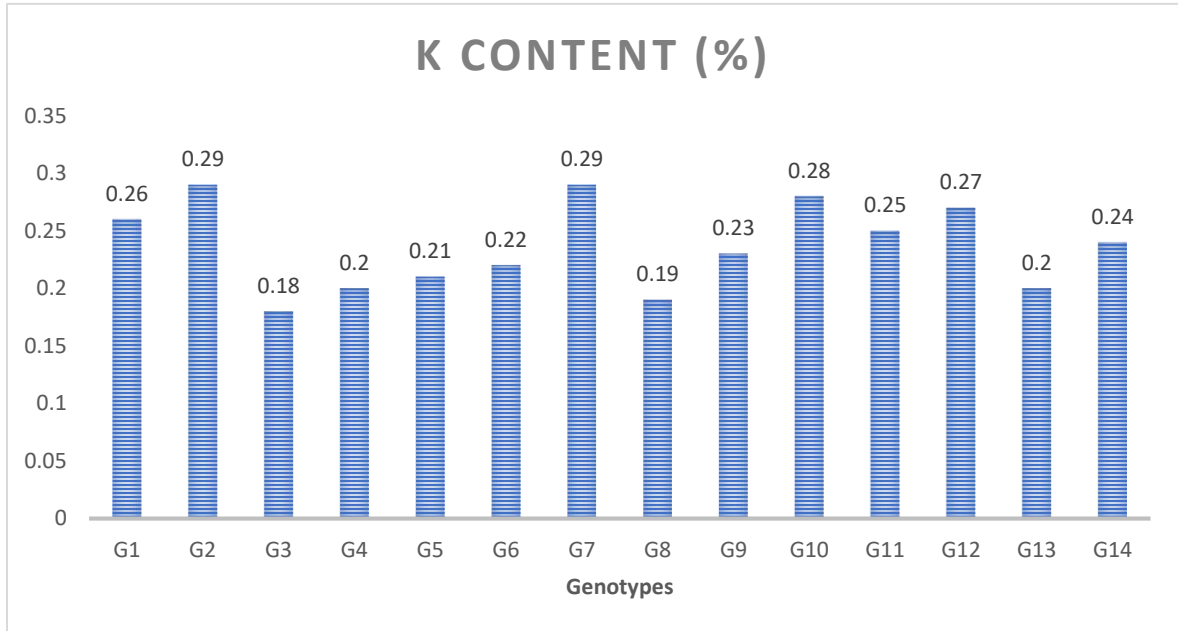

Figure 3: (%) K content in 14 genotypes of mungbean

4.9.2   (%) P Content

Genotypes G_{11} (0.16%) was observed to have highest amount of P content. The second highest amount is G_{13} (0.15%). The lowest value was found in G_6 (0.061%) (Table 13). So G_{11} genotype can be used for future development variety containing high P content percentage.
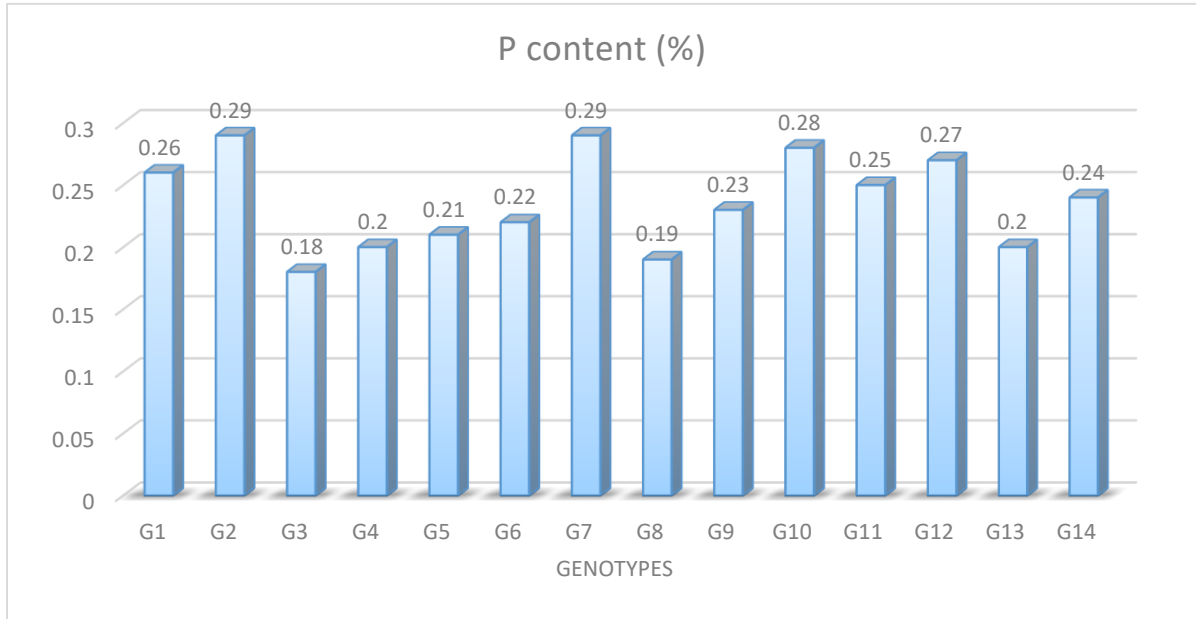
Figure 4: (%) P content in 14 genotypes of mungbean

4.9.3 Chlorophyll content (mg/g)

Chlorophyll content (mg/g) ranged from 0.18 mg/g to 0.29 mg/g. Genotypes G_2 and G_7 was observed to have highest amount of chlorophyll content (0.29) and the lowest value was found in G_3 (0.18) (Table 13). So G_2 and G_7 genotype can be used for future development variety containing high chlorophyll content percentage.
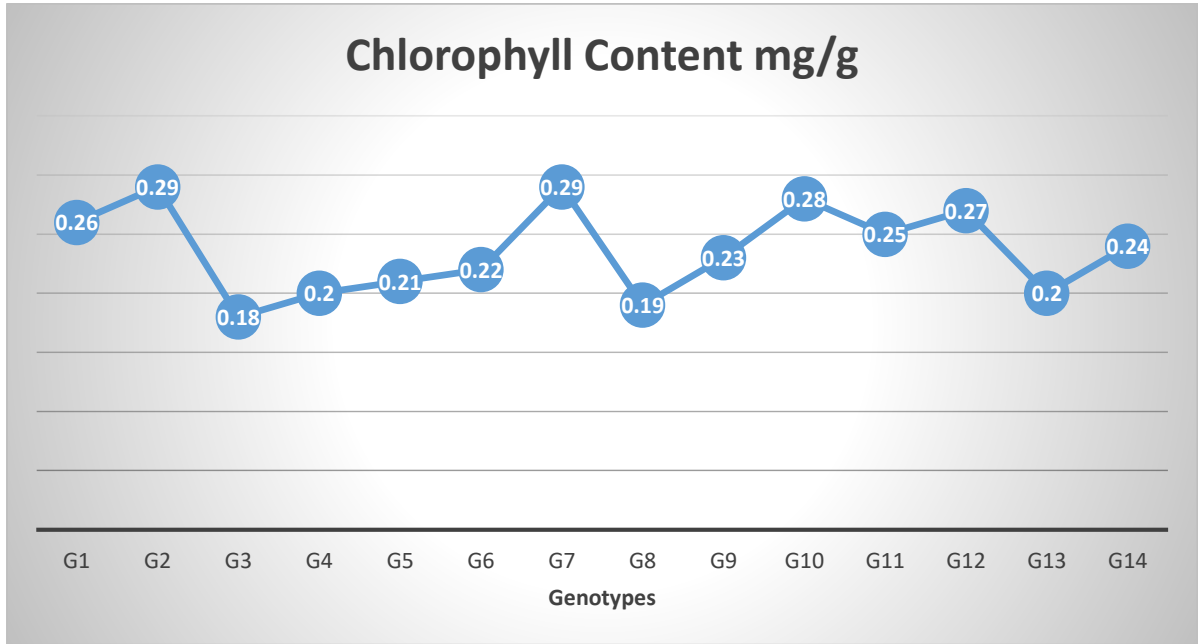

Figure 5: Chlorophyll content (mg/g) in 14 genotypes of mungbean

CHAPTER V

SUMMARY AND CONCLUSIONS

The experiment was conducted beside the Genetics and plant breeding field in Sher-e-Bangla Agricultural University, Dhaka, during March 2020 to June 2020. The aim of the study was to select the genotypes for hybridization program, identify the characters contributing to genetic diversity, assess the magnitude of genetic divergence in genotypes and determine the variability in respect of yield and some yield contributing characters, the degrees of association among the characters and their direct and indirect effects of 14 genotypes of mungbean. The experiment was performed with Randomized Complete Block Design (RCBD) with three replications. Data on various yield attributing characters such as, plant height (cm), Number of leaves/plant, Number of branches /plant, Number of pods/plant, Number of pods cluster/plant, pods length/plant (cm), Number of seeds/pod, weight of 1000 seeds (g) and yield/plant (g) were recorded. The salient findings of the present study have been summarized on the basis of the characters studied.

The analysis of variance showed significant differences among the genotypes for all the characters. The maximum plant height (56.233cm) was produced by the line G_4 whereas minimum plant height (40.927cm) was produced by the line G_{13}. The genotype G_{10} (13.660) gave the highest value of Number of leaves/plant and the lowest Number of leaves/plant was observed in G_1 (7.553). The genotype G_{11} (4.440) produced the maximum Number of branches /plant whereas G_{13} (2.440) produces the minimum Number of branches /plant. G_8 (18.527) gave the highest value of Number of pods/plant and the lowest Number of pods/plant was observed in G_1 (8.567). The genotypes G_{10} (7.033) gave the highest mean value of Number of pods cluster/plant and the lowest value was observed in G_1 (4.667). The highest pod length was observed in G_6 (10.567cm) and the least pod length genotype was G_{13} (6.467). The maximum number required for Number of seeds/pod was recorded in G_{10} (13.667) on the other hand, the variety G_2, G_{13} and G_{14} (8.333) required the minimum Number of seeds/pod. The maximum weight of 1000 seeds was recorded in

G_6 (51.667gm) whereas the variety G_{14} (0.733) required the minimum number of weight of 1000 seed. The highest yield/plant (gm) was recorded in G_{10} and G_{11} (6.06).

Phenotypic variance was always higher than genotypic variance for all the characters. The genotypic coefficient of variance for all the characters studied were lesser than the phenotypic coefficient of variance indicating the masking effect of the environment. High performance of Phenotypic coefficient of variance and genotypic coefficient of variance were observed for Number of branches /plant, weight of 1000 seeds (gm) and yield/plant (gm) indicating the existence of wide range of genetic variability in the germplasm for these traits.

High heritability coupled with high genetic advance as percent of mean were observed for plant height (cm), Number of leaves/plant, Number of branches /plant, Number of pod, pod length (cm), Number of seeds/pod, weight of 1000 seeds (g) and yield/plant (g) indicating the predominance of additive gene action and hence direct phenotypic selection is useful for these traits. Investigation on character association indicating that yield/plant had highest significant positive correlation with Number of leaves/plant, Number of branches /plant, Number of pod, Number of pods cluster/plant, pod length (cm), no of seeds/pod, weight of 1000 seed (g) in both genotypic and phenotypic level indicating the importance of these traits in selection for increasing yield and were identified as yield attributing characters. Thus selection can be relied upon these characters for the genetic improvement of yield of mungbean. Path analysis revealed that Number of seeds/pod, plant height (cm), Number of leaves/plant, Number of branches /plant, Number of pod and weight of 1000 seeds (g) showed positive direct effect on yield/plant indicating that direct selection based on these traits may be helpful in evolving high yielding genotypes of mungbean. On the other hand, Number of pods cluster/plant and pod length (cm) showed negative direct effects on yield/plant.

From the results of multivariate analysis, the presence of considerable genetic divergence among the 14 genotypes was revealed. First four principle component axes with Eigen values greater than 1 contributed 89.82% of the variability. All the genotypes were grouped

into four clusters. Cluster I, cluster II, cluster III and cluster IV contain four, two, two and six genotypes each. The clustering pattern of the genotypes collected from the same area was grouped into different clusters. The maximum inter-genotypic distance was observed between G_1 and G_6 (1.288) followed by the distances between genotypes G_2 and G_6 (1.270) and G_1 and G_7 (1.254). It was found that the genotypes G_1 and G_2 comes from Cluster I and the G_6 and G_7 genotypes come from cluster II. It is suggested that the genotypes selected from the more diversified cluster I and cluster II could be used as parents for future breeding programs. In respect of cluster mean performance of different clusters revealed that cluster II is important for maximum value of Number of leaves/plant, Number of branches /plant, Number of pods/plant, pods length/plant (cm) and weight of 1000 seeds (g). Cluster III is important for highest Number of pods cluster/plant, Number of seeds/pod and yield/plant (g) and cluster I is important for highest plant height. Considering the magnitude of genetic distance, magnitude of cluster means and agronomic performance the genotype G_1 and G_2 from cluster I; G_6 and G_7 from cluster II; G_{10} from cluster III may be exploited for the development of heterotic hybrids in future breeding programs.

CHAPTER 6

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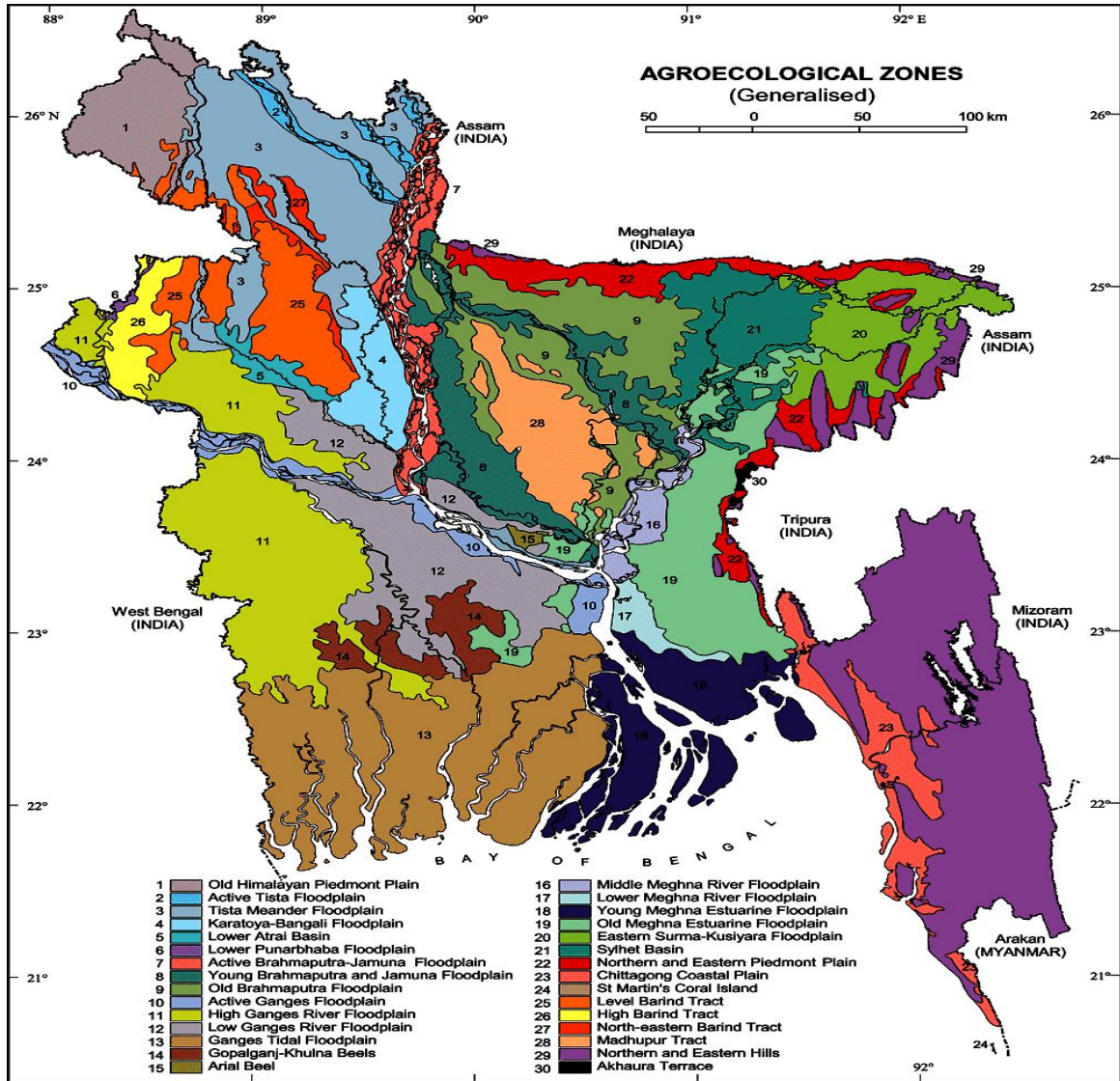
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APPENDICES

Appendix I:

Map showing the experimental site under the study

Legend showing the research site

Appendix II:

Physical and chemical characteristics of initial soil depth of the experimental site

A. Physical composition of the soil:

Soil separates	Percentage (%)	Methods
Sand	36.90	Hydrometer method (Day, 1915)
Silt	26.40	Do
Clay	36.66	Do
Textural class	Clay loam	Do

B. Chemical composition of the soil:

Serial Number	Soil characteristics	Analytical data	Methods
1	Organic carbon (%)	0.82	Walkley and Black, 1947
2	Total N (kg/ha)	1790.00	Bremner and Mulvaney, 1965
3	Total P (ppm)	840.00	Olsen and Sommers, 1982
4	Total S (ppm)	225.00	Bardserial numberey and Lanester, 1965
5	Available P (kg/ha)	69.00	Olsen and Dean, 1965
6	Available N (kg/ha)	54.00	Bremner, 1965
7	Available S (ppm)	16.00	Hunter, 1984
8	Exchangeable K (kg/ha)	89.50	Pratt, 1965
9	CEC	11.23	Chapman, 1965
10	pH(1:2.5 soil to water)	5.55	Jackson, 1958

Appendix III:

Monthly average temperature, average relative humidity and total rainfall and total sunshine of the experimental site during the period from November, 2018 to February, 2019.

Month	Air temperature (°C)		Relative humidity (%)	Total rainfall (mm)	Sunshine (hr)
	Minimum	Maximum			
November, 2018	18	31	63	12.6	5.8
December, 2018	16	28	61	1.9	7.9
January, 2019	13.0	27	57	3.5	3.9
February, 2019	18	28	58	12.3	5.7