GENETIC DIVERSITY ANALYSIS AND CHARACTER ASSOCIATION IN YIELD AND YIELD CONTRIBUTING TRAITS OF MUNGBEAN (*Vigna radiata* L.)

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CERTIFICATE

This is to certify that thesis entitled, "GENETIC DIVERSITY ANALYSIS AND CHARACTER ASSOCIATION IN YIELD AND YIELD CONTRIBUTING TRAITS OF MUNGBEAN (Vigna radiata L.)" 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 bona fide research work carried out by Marzana Rahman, Registration No. : 11-04276 under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.*

I further certify that such help or source of information, as has been availed of during the course of this investigation has been duly been acknowledged.

Dated: June, 2017
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Prof. Dr. Md. Sarowar Hossain
(Supervisor)

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SOME COMMONLY USED ABBREVIATION

Full word	Abbreviation
Agroecological zone	AEZ
and others (*at elli*)	*et al.*
Asian Vegetable Research and Development Center	AVRDC
Bangladesh Agricultural Research Institute	BARI
Bangladesh Bureau of Statistics	BBS
Centimeter	cm
Crop Growth Rate	CGR
Degree celsius	^{o}C
Environmental coefficient of variation	ECV
Environmental variance	σ^2e
Genetic advance	GA
Genotypic coefficient of variation	GCV
Genotypic variance	σ^2g
Gram (s)	g
Hectare	ha
Hour	hr
Kilogram	Kg
Leaf Area Index	LAI
Milliequivalents	meq
Millimeter	mm
Metric ton	MT
Mungbean Yellow Mosaic Virus	MYMV
Parts per million	ppm
Percent	%
Phenotypic coefficient of variation	PCV
Phenotypic variance	σ^2p
Random amplified polymorphic DNA	RAPD
Randomized Complete Block Design	RCBD
Regional Agricultural Research Station	RARS
Sher-e-Bangla Agricultural University	SAU
Soil Resources Development Institute	SRDI
Total Dry Matter	TDM

GENETIC DIVERSITY ANALYSIS AND CHARACTER ASSOCIATION IN YIELD AND YIELD CONTRIBUTING TRAITS OF MUNGBEAN (*Vigna radiata* L.)

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ABSTRACT

The present research was undertaken to determine the genetic variability, correlation among different yield contributing characters of mungbean (*Vigna radiata* L.). The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. The research was done based on 33 genotypes collected from Bangladesh Agricultural Research Institute, considering eight quantitative characters during Kharif season from March to June, 2017 in research farm of Sher-e-Bangla Agricultural University. The analysis of variance showed significant variation in all the traits studied. The phenotypic variances were greater than the genotypic variances with little differences in all traits except plant height, number of branches per plant and pods per plant. High heritability coupled with high genetic gain was observed in days to 50% flowering, plant height, pod length, 100 seed weight and seed yield per plant which indicated the effect of additive genes. In the correlation study seed yield per plant had highly significant positive relation with number of pods per plant, number of branches per plant and number of seeds per pod. Pods per plant followed by pod length showed the highest positive direct effect on the seed yield per plant. Selection of these traits might cause the probability of simultaneous improvement of mungbean. The genotypes were grouped into four clusters by diversity (D^2) analysis where cluster I comprised 13 genotypes and cluster III and IV had 6 genotypes in each. The highest inter cluster distance was found between cluster II and cluster IV (10.425) and intra cluster distance in cluster II (2.45). Principal component analysis revealed first two components contributed 68.11% towards genetic diversity in mungbean. Therefore, it might be concluded that considering group distance and other agronomic performance G_1 (BD-6874), G_2 (BD-6875), G_{14} (BD-6904), G_{27} (BD-6929), G_{28} (BD-6932) had potential for improvement for further hybridization in breeding program.

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CHAPTER I
INTRODUCTION

For the majority of the people of Bangladesh pulse crop is important as protein source in their diet. It contains protein about twice as much as cereals. It also contains amino acid lysine, which is generally deficit in food grains (Elias, 1986). It has the ability to fix nitrogen and addition of organic matter to the soil is important factors in maintaining soil fertility (Senanayake *et al*., 1987; Zapata *et al*., 1987). Among several pulses mungbean is more important and valuable crop.

Mungbean (*Vigna radiata* L.) is one of the most important pulse crops belonging to the papilionoid subfamily of the Fabaceae and has a diploid chromosome number of $2n=2x=22$ and widely grown in Bangladesh but production is lower. The mungbean is also known as greengram or mung. The mungbean is mainly cultivated in Pakistan, India, Bangladesh, Nepal, China, Korea, South Asia and Southeast Asia. It is used as an ingredient in both savory and sweet dishes. Mungbean is cultivated mostly in South, East and Southeast Asia by small holder farmers for its edible seeds and sprouts. Mungbean seeds are a good source of dietary protein and contain higher levels of folate and iron than most other legumes (Keatinge *et al*., 2011). Intercropping mungbean in rice–rice and rice–wheat systems increases the yield of the subsequent cereal crop and reduces pest incidence (Yaqub *et al*., 2010). Genetic diversity data and archaeological evidence suggest that mungbean was domesticated in India (Fuller, 2007). India is also the world's largest producer of mungbean, accounting for over 50% of the global annual production (~6 million tons), followed by China and Myanmar (Nair, 2012). Because of short duration mungbean can fit in as a cash crop between major cropping seasons. It is grown three times in a year. About 60-65% of the total mungbean is grown under the boro (winter) rice mungbean-aus (rainfed) rice

cropping system. It is covering 105166 acres with an average yield of 36954 MT (BBS, 2016).

Mungbean grain contains 19.5% to 28.5% protein (AVRDC, 1988). Mungbean also contains 51% carbohydrate, 4% mineral, and 3% vitamins (Afzal *et al.*, 2008). Besides providing protein in the diet, mungbean has the remarkable quality of helping the symbiotic root rhizobia to fix atmospheric nitrogen and hence to enrich soil fertility (Anjum *et al.*, 2006). It supplies a substantial amount of nitrogen to the succeeding non-legume crops (i.e., rice) grown in rotation (Sharma and Prasad, 1999). Major area of mungbean is replaced by cereals (Abedin *et al.*, 1991).

Now a day, it is being cultivated after harvesting of Rabi crops (wheat, mustard, lentil, etc.). Six varieties of mungbean have been developed by Pulses Research Centre, BARI and disseminated with the package of management technologies to the farmers for cultivation. But limited study was done on mungbean and the area covered by this crop is not satisfactory. There are few constraints such as several biotic and abiotic stresses, low yield; rice cultivation all year round mainly on winter (Boro) season which limit pulse cultivation. So it is necessary to improve yield and quality of mungbean. Several activities like building up diverse germplasm, selection and evaluation of genotype from germpasm etc. should be used in improvement program. For a successful breeding program we need better genotypes as parent material. Improved knowledge on genetic diversity and characterization will help to yield and quality improvement. So we need to do more research and study on mungbean to develop high yielding varieties to fulfill our national demand. In Bangladesh several genotypes having diverse characteristics are grown in several parts of the country. Available genotypes in the market do not have uniformity in nomenclature. A better knowledge of genetic resources may help in identifying desirable cultivars for commercial cultivation. So the present research was undertaken with the following objectives:

- To study the genetic diversity among the genotypes of mungbean
- To study the interrelationships of yield contributing characters among themselves and with seed yield; and their direct and indirect effects
- To screen out suitable parental groups with better performances for future breeding program.

CHAPTER II
REVIEW OF LITERATURE

In spite of the best efforts for improving the mungbean varieties, the yield of this crop remains low. Several studies have been made to understand their performances which mainly include the contribution of various yield components towards yield. The yield components depend on some physiological traits. To understand the physiological 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 utilized in crop improvement (Hassan *et al*., 1995 and Hakim *et al*., 2008). Egli and Zhen-wen (1991) suggested that seeds per unit area were related to canopy photosynthesis during flowering and pod set and canopy photosynthesis rate was determined through LAI and CGR. Datta and Mandal (1998) studied that a plant with optimum LAI may produce higher biological yield as well as seed yield. Sarwar *et al*., 2004 and Khan and Khalil, 2010 said that the dry matter accumulation may be the highest if LAI attains its maximum value within the shortest possible time. Mondal *et al*. (2011) revealed that not only TDM production, but also the capacity of efficient partitioning between the vegetative and reproductive parts may produce high economic yield.

Studies on genetic variability with the help of suitable biometrical tools such as coefficient of variability, heritability, genetic advance and genetic diversity become indispensable in breeding programs for tangible results of desired values. To obtain a better insight of ancillary characters under selection, correlation and path coefficient 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. Keeping in view the objectives of the present investigation, the review of literature concerned to the studies on “Genetic diversity analysis and character association in yield and

yield contributing traits of mungbean" was conducted for this thesis outlined under the following major heads.

2.1. GENETIC VARIABILITY, HERITABILITY, GENETIC ADVANCE

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 in their environment and become more resistant to disease, climate change and competition from invading species and so on. Heritability is a statistic used in the fields of breeding and genetics that estimates the degree of variation in a phenotypic trait in a population that is due to genetic variation between individuals in that population (Wray *et al*., 2008). Heritability measures the fraction of phenotype variability that can be attributed to genetic variation. Estimates of heritability use statistical analysis to help 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 is the measure of genetic gain under selection. So it is important to measure these genetic parameters to select more diverse genotype. Several scientists evaluated few experiment on mungbean and their findings are given below-

Pande *et al*. (1975) and Malik *et al*. (1983) revealed that high heritability associated with genetic advance was high for number of pods and plant height show that it was due to additive gene effects and selection may be effective on basis of these characters. Narasimhulu *et al.* (2013) studied the genetic variability and character association in forty mungbean genotypes for different quantitative characters. The highest genotypic and phenotypic variances were observed for number of branches per plant, pods per plant, biological yield and harvest index. So, it is evident that genetic variability is very important for breeding programs. Therefore, present experiment was conducted to assess the

genetic variability for the desirable character in mungbean genotypes. It will help in the selection of promising lines which can be used for further breeding program. Mehetre *et al.* (2000) reported that pods per plant and seed yield per plant had high genotypic and phenotypic coefficient of variation by studying variability for 11 characters with 60 diverse genotypes of soybean. They also reported high heritability associated with high genetic advance as percentage of mean. They studied that plant height and pods per plant had high genotypic and phenotypic coefficient of variation.

Islam *et al.* (1999) studied the genetic variability and correlation between yield and yield components in mung bean and observed the significant differences among the various genotypes and Yimram *et al.* (2009) studied genetic variation in cultivated germplasm of mungbean for breeding for high yielding. He assessed broad sense heritability and estimated genetic advance for selection of major quantitative traits. Again Denton and Nwangburuka (2011) revealed that estimates of genetic parameters provide an indication of the relative importance of the various types of gene effects affecting the total variation of a plant character. Genotypic and phenotypic coefficients of variation and heritability accompanied with genetic advance are very important parameters in improving traits. Jonson *et al.* (1955) reported the immense importance of selecting and evaluating varieties for quantitative and yield ability in any breeding program, before such varieties can be introduced to a given local environment.

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 and correlation studies between yield and yield components in mung bean. 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. However, proper evaluation of the extent of genetic variation available for yield components, their

heritability values and genetic advance could be of great significance for the breeders in order to choose best genotypes for improvement. Gadakh *et al.* (2013) and Byregowada *et al.* (1997) reported that the magnitude of PCV and GCV was the highest for seed yield followed by pods per plant and pods per cluster in greengram.

Siddique and Gupta (1991) reported that genetic coefficient of variation together with heritability estimates would give the best indication of the amount of gain due to selection. Therefore there could be better chance for improvement of the above traits with the relatively highest value of genotypic coefficient of variation. Degefa *et al.* (2014) studied that days to flowering (10%) and seeds per plant (7.22%) were accompanied with the relatively very low PCV and GCV, respectively at Hirna whereas at Rare, days to flowering had the lowest PCV (7.7%) and GCV (7.19), respectively. The same was true for a combined analysis where PCV and GCV values were the lowest (8.7% and 8.3%) for days to flowering, respectively. For all traits the values of phenotypic variance (σ^2p) exceeded that of genotypic variance (σ^2g), though the difference was small. This indicated that environmental variance (σ^2e) had its own contribution on the performance of the traits in addition to genotypic variance.

Alom *et al.* (2014) revealed that including seed yield, all the characters, except seeds per pod exhibited high heritability accompanied by medium to high genetic advance as percent of mean. These characters also showed medium to high GCV and PCV. However seeds per pod showed moderate heritability and genetic advance as present of mean. Similarly Sabu *et al.* (2009) stated that the magnitude of the estimated broad sense heritability in this study ranged from 9.52% for seeds per plant to 98.85% for days to maturity in Hirna while it ranged from 27.84% for number of primary branches to 97.79% for days to maturity at Rare. The existence of relatively high heritability in a given trait indicated the presence of more additive gene effects for possible improvement.

Dabholkar (1992) suggested that heritability estimates are classified as low (5-10%), medium (11-30%), high (31-70%) and the highest for the value greater than this. An estimate of heritability is essential for applying optimum breeding strategy. Ilhamuddin *et al.* (1989) and Degefa *et al.* (2014) reported that traits like numbers of primary branches, seeds per plant, numbers of secondary branches, pods per plant, seeds per pod, harvesting index, days to flowering, days to maturity, hundred seed weight, pod length and seed yield in kg/ha, hundred seed weight, days to maturity and days to flowering had very high heritability on mungbean. Sarwar (2004) carried out a study on mungbean and found that heritability estimates were high for pods per plant, hundred seed weight and seed yield per plant.

Johnson and Frey (1967) and Adhikari and Pandey (1982) studied that the characters which exhibited high heritability suggests that the selection will be more effective whereas the characters showing low heritability indicated that the selection will be effected by the environmental factors. Generally, for traits having highest phenotypic heritability value which was close to 1 show a good index of genotypic merit, so genetic gain can be made easily through selection. Therefore heritability determines the effectiveness of selection, though the effectiveness of selection for a given trait depending on relative importance of both genetic and environmental factors in the expression of phenotypic differences among genotypes in a population. Malik *et al*. (1983) also reported high heritability coupled with high genetic advance for seed per plant and number of pods in mung bean indicating that these traits were controlled by additive genes and can easily be transferred to succeeding generations. But, relatively low genetic advance was observed for number of primary branches (1.75), number of secondary branches (2.28), 100 seed weight (2.28), and pod length (2.93). This low estimate of genetic advance arises from low estimate of phenotypic variance or it was observed as a result of non-additive gene action which may be epistatic and/or dominance effects.

Rao *et al*. (2006) researched on 60 genotypes of mungbean (*Vigna radiata*) which were evaluated during 2000 in Guntur, Andhra Pradesh, India for thirteen characters to assess genetic variability, heritability and genetic advance. Total dry matter, plant height, number of pods per plant and yield per plant exhibited high variability and heritability coupled with genetic advance, indicating the influence of additive gene action.

Reddy *et al.* (2003) studied 36 genotypes of mungbean (*Vigna radiate*) for genetic variability of seed yield and its contributing characters in summer 2000 at Tirupati, Andbra Pradesh, India. For pods per plant and grain yield per plant high magnitude of variability was observed, while moderate variability was recorded for pods per cluster, clusters per plant, possibility of their improvement by selection was suggested by plant height and days to 50% flowering. High heritability coupled with high genetic advance was observed for pods per plant, grain yield per plant, pods per cluster, clusters per plant, plant height and days to 50% flowering, while high heritability and moderate genetic advance was recorded for seeds per pod, 100 seed weight and days to maturity suggesting that these traits were controlled by additive gene action.

Bangar *et al.* (2003) reported that phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV). The GCV and PCV estimates were the highest for branch number per plant and plant height among the characters and moderate magnitude for the pod number per plant 100-seed weight (g) and seed yield per plant (g). Days to 50% flowering and days to maturity had very low GCV and PCV estimates. The differences between GCV and PCV magnitudes were very high for 1000-seed weight and number of pods per plant.

2.2. CORRELATION COEFFICIENT

Correlation coefficient 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 coefficient 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. Kritika and Yadav (2017) evaluated evenly mungbean (F_6 generation) and seed yield was found to have positive significant correlation with plant height, number of branches per plant, number of pods per plant, number of seeds per pod, 100-seed weight, biological yield and harvest index and negatively with days to flowering, days to maturity and reaction to MYMV. Zinc content exhibited significant positive correlation with iron content, however, no association of the micronutrients was observed with seed yield.

Kritika and Yadav (2017) studied that the direct effect of biological yield per plot was positive and its association with seed yield per plot was positively significant due to high positive indirect effects via number of branches per plant, number of pods per plant and number of seeds per pod in both the environments. Similarly, harvest index exerted positive indirect effects via number pods per plant and number of seeds per pod and resulted in significant positive association with seed yield. Number of seeds per pod exerted the highest negative indirect effect on seed yield per plot. Plant height and number of branches per plant recorded high positive indirect effect on seed yield via number of pods per plants.

According to Reddy *et al.* (2011) days to flowering, days to maturity, number of pods per plant, shoot dry matter per plant and 100-seed weight had positive

direct effects on seed yield whereas, Srivastava and Singh (2012) indicated that number of pods per plant, number of seeds per pod, number of clusters per plant had maximum direct contribution on seed yield. Garje *et al.* (2014) reported that number of pod per plant had the maximum direct effect on seed yield followed by number of cluster per plant and number of secondary branches per plant.

Makeen *et al.* (2007) evaluated an experiment in Uttar Pradesh, India on twenty diverse mungbean genotypes to estimate correlation coefficient for 10 quantitative characters. They observed higher genotypic and phenotypic coefficients of variation for seed yield and number of pods per plant. They also showed that pods per plant and plant height had significant positive correlation with seed yield. Sirohi and Kumar (2006) performed an experiment in Berthin, Himachal Pradesh, India, during the spring of 1999 on 19 diverse genotypes of mungbean (*Vigna radiata*) and studied 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 per plant and number of productive pods per plant with seed yield per plant.

Khorgade *et al.* (1990) evaluated 30 genotypes of mungbean to determine genotypic and phenotypic correlation coefficients. The grain yield was significantly and positively associated with number of pods per plant, number of cluster per plant and plant height at both genotypic and phenotypic levels. Naidu *et al*. (1991) found that number of pods per plant, seeds per pod and 100-seed weight were positively and significantly associated with seed yield in mungbean. They found higher values of genotypic correlation than their corresponding phenotypic correlation. Seed yield per plant showed positive association with number of cluster per plant, number of pods per plant, number of seeds per pod and 100-seed weight.

Naik *et al.* (2000) studied correlation coefficients in 37 local land races of mungbean and revealed significant association of protein content with early flowering, pod length, pod number, seed number and yield per plant. Manivannan (2002) studied correlation between yield and yield components in eight F_3 populations of mungbean. The study revealed that clusters per plant, pods per cluster and pods per plant had positive correlation with yield.

Kumar *et al.* (2005) revealed that the maximum positive and significant phenotypic correlation coefficient (0.825) was between the number of pods per plant and seed yield per plant, followed by seed yield per plant with harvest index (0.822), days to 50% flowering and plant height (0.752), number of pods per plant and harvest index (0.670), days to 50% flowering and biological yield (0.663), plant height and biological yield (0.599). Alom *et al.* (2014) studied on the variability, heritability, genetic advance and interrelationship via correlation coefficient and path coefficient analysis among the important eight characters in relation to seed yield. They studied that significant genotypic correlation coefficient were found to be higher than their corresponding phenotypic ones. The character 100 seed weight showed significant positive relationship with seed yield. Rajanna *et al.* (2000); estimated that number pods per plant, number of clusters per plant and 100-seed weight had significant and positive correlation with seed yield in soybean. They also reported significant and positive correlation of days to maturity, plant height and number of branches per plant with number of clusters per plant and number of pods per plant.

Prakash *et al.* (2007) showed that seed yield had significant positive correlation with pods per cluster and pod length whereas, characters like days to 50% flowering and days to maturity revealed significant negative correlation with grain yield, indicating that yield increase can be obtained in short duration genotypes. Verma and Garg (2007) found that genotypic correlation were higher than their phenotypic correlation. Seed yield per plant showed positive

association with biological yield and harvest index while it was negatively associated with days to 50% flowering.

Arshad *et al.* (2009) found that amongst the character studied plant height was positive and significant association with yield per plant at both genotypic and phenotypic levels. In addition, positive and significant correlation of plant height with days to flowering and secondary branches per plant was also observed. Primary branches per plant and days of flowering also revealed significant and positive association. Only negative and significant association was noted between secondary branches and pod length. Association among other traits was either positive or negative but non-significant.

Tejbir *et al*. (2009) evaluated 40 genotypes of mungbean under four diverse environments to study the correlations (genotypic and phenotypic) on the basis of twelve morpho-physiological characters. The seed yield showed positive and significant association with number of pods per cluster, number of pods per plant, number of seeds per pod, 100-seed weight, biological yield and harvest index.

2.3. PATH CO-EFFICIENT

Path coefficient analysis permits the separation of direct and indirect effect through the other related characters by partioning the correlation coefficients. The review of the work done utilizing path coefficient analysis in mung bean is presented below. The method of path coefficient 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.

Kritika and Yadav (2017) revealed that path coefficient analysis indicated that number of pods per plant, number of seeds per pod, biological yield per plot and harvest index had the maximum direct contribution on seed yield hence these characters should be given due importance while formulating selection criteria for seed yield.

Degefa *et al.* (2014) studied 30 genotypes of mungbean for path analysis and revealed that at genotypic level, maximum positive direct effect was exerted on seed yield per plot by number of primary branches, plant height and pods per plant. This indicated that the high yielding mungbean could be obtained by selecting pods per 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 per plot. So, direct and indirect selection through these characters should be effective. Alom *et al.* (2014) revealed that path co efficient analysis suggested that pods per plant contributed the maximum direct effects having positive on seed yield. Plant height, pod length and 100 seed weight had also positive direct effect on seed yield. Thus selection based on pods per plant, days to first flowering, plant height and 100 seed weight might be effective for improving seed yield in mungbean.

Sandhu *et al.* (1980) performed path coefficient analysis in mungbean using 86 varieties. They found that number of pods per plant, days to maturity and 100-seed weight had high positive direct effects on grain per plant. Naidu *et al.* (1991) assessed path analysis in 49 genotypes of mungbean and reported that number of pods per plant had the maximum positive direct effect on seed yield. Mishra and Yadav (1992) carried out path analysis of yield components in 15 varieties and noticed that harvest index, plant height and number of branches had direct positive influence on seed yield.

Pathak and Patel (1993) determined path coefficients in 44 diverse genotypes and found that clusters per plant followed by pod length, pods per cluster and days to flowering had the highest positive direct effects while days to maturity, plant height, branches per plant, pods per plant and seeds per pod showed negative direct effects on grain yield per plant. Veerbadhiran and Jehangir (1995) carried out a study to estimate path coefficients using 27 genotypes of mungbean. The study revealed that number of pods had the highest positive direct effect on seed yield followed by number of clusters per plant.

Sbaghpour *et al.* (1998) evaluated 49 varieties of mungbean and revealed that seeds per plant and 100-seed weight had the largest positive direct effects on mungbean yield. Joseph and Santhosh (1999) analyzed path coefficients in five hybrids of mungbean and found that number of pods per plant had high positive direct effect on seed yield. Seeds per pod and test weight had low direct and indirect effects on yield, respectively.

Venkateswarlu (2001) screened thirteen genotypes of mungbean for path coefficients analysis and found that pods per plant and seeds per pod had maximum positive direct effect on seed yield. Days to maturity, clusters per plant, plant height, number of seeds per pod, 100-seed weight exhibited high indirect effects on seed yield via pods per plant.

Haritha and Reddy (2002) examined 50 genotypes of mungbean for path coefficients analysis and revealed that clusters per plant exhibited maximum direct effect followed by pods per cluster on grain yield. Asifa *et al.* (2005) observed that plant height (0.12), clusters per plant (0.47), pods per plant (0.64), pod length (0.33) and harvest index (0.52) had positive direct effects on seed yield. Bais *et al.* (2007) showed that pods per plant, 100-seed weight and nodule dry weight had significant direct positive effect on grain yield. Pods per cluster had indirect positive effect via pods per plant on grain yield. Pods per plant, 100-seed weight and nodule dry weight are the important components of

grain yield in summer mungbean which may be exploited for the improvement of grain yield.

Pundri *et al.* (1992) suggested that pods per plant should be given priority in selecting for high yielding varieties in mungbean as it had positive direct and indirect effects on seed yield. In addition, seeds per plant, harvest index and biomass affected seed yield positively and directly as well as indirectly via all characters except via 100 seed weight which showed a negative effect indicating that part of variability observed in seed yield could be explained by those traits. Haritha and Sekhar (2002) and Hassan *et al*. (2003) showed that seed yield can be directly and positively influenced by biomass yield in mungbean. Days to flowering and 100 seed weight had negative direct effect on seed yield. The residual (0.0015) indicated that characters which included in genotypic path analysis explained (99.8%) of the total variation in seed yield.

Kumar *et al.* (2005) revealed that number of pods per plant (0.561), harvest index (0.425), 1000 seed weight (0.261), had positive effect towards seed yield, whereas at phenotypic level biological yield (0.195), number of seeds per pod (0.087), days to 50% flowering (0.011) had relatively low direct effect, therefore, these characters may be selected directly to improve seed yield.

Saxena *et al.* (2007) reported that days to maturity, biological yield per plant, harvest index and plant height had high direct effect, so emphasis should give to an early maturing dwarf plant with high biological yield and harvest index for higher seed yield in mungbean. Sirohi *et al.* (2007) studied that at phenotypic level harvest index showed the maximum (0.456) direct and positive contribution towards seed yield followed by biological yield. Harvest index and biological yield are two main characters which are contributing directive towards seed yield. Hence, selection based on these characters would bring an improvement in mungbean. Ved prakash *et al.* (2007) showed that a

great contribution through high direct effect of pods per cluster, pod length and seeds per pod toward grain yield.

Arshad *et al.* (2009) observed that the maximum direct positive effect for plant height (1.114) and days to flowering 90.424) on yield per plant. Among the characters having high positive indirect effect, pod length showed the higher value (1.161) with yield per plant through secondary branches per plant. The results suggest that selection for genotypes having high yield potential may based on days to flowering and plant height. Peerajade *et al.* (2009) observed that in kharif number of pods per plant, pod length and number of pods per cluster contributing the maximum positive and direct effect on yield, while in summer same trend but in addition to plant height on yield indicating these characters should be given emphasis for selecting high yielding greengram cultivars for rainfed condition. Tejbir *et al.* (2009) identified biological yield and harvest index as important parameters as these showed the maximum and positive direct effect on yield and also all other characters contributed indirectly towards seed yield, via these characters.

2.4. GENETIC DIVERSITY

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 D^2 form of a generalized distance, which considers the variation produced by any characterstatistic to measure the distance between two populations. Mahalanobis technique is in th and their conjoint effect that it bears on other character. Mahalanobis also pointed out that D^2 would be remaining constant when samples were drawn from two different populations irrespective of the size of the representative sample. This indicates that D^2 provided a measure of actual magnitude of divergence between two individuals under comparison.

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 OPF 1), 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.

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 per plant and number of pod clusters per plant. Low variability was found for number of fruiting branches per plant, pod length, and number of seeds per pod.

Venkatakrishna *et al.* (2000) estimated genetic divergence among 40 genotypes of greengram and grouped then into 15 clusters. No relationship between geographic and genetic divergence was observed. They revealed that number of pods per plant, days to maturity, days to flowering and plant height are the main characters contributed the maximum towards divergence. Backiyarani *et al.* (2000) employed Mahalanobis's D^2 statistics conducted experiment in a set of 32 genotypes of cowpea and reported that no parallelism was observed

between geographic origin and genetic diversity. Single plant yield, harvest index and earliness in flowering contributed 80% towards total divergence.

Raje and Rao (2001) conducted experiment in a set of 200 germplasm lines along with six commercial varieties of mungbean in four different environments. They indicated that no linear relationship was observed between geographic and genetic diversity. Manivannan (2002) reported that multivariate analysis of divergence in greengram for 10 quantitative characters, led to grouping of 33 genotypes into seven clusters, 100-seed weight contributed the maximum towards total divergence followed by powdery mildew reaction.

Vendakumari and Rajendraprasad (2003) studied genetic divergence in 24 landraces of grass pea and were grouped into five clusters. Inter cluster distance was the maximum between cluster VI and VII which serve as potential parents for hybridization. Haritha and Reddy (2003) evaluated 50 genotypes of mungbean for 13 traits through D^2 and metroglyph methods and grouped them into 10 and eight clusters and reported that the characters viz. 100-seed weight and seed yield contributed more towards the total divergence and indicated that D2 analysis was more potent compared to metroglyph analysis. Reddy *et al.* (2004) conducted experiments with 69 genotypes of mungbean were grouped into 11 clusters and the maximum inter clustered distance was observed between cluster II and X which serve as potential parents for hybridization. Dasgupta *et al.* (2005) studied genetic divergence in 50 horde gram accessions using Mahalanobis's D^2 technique and canonical analysis. They observed no significant relationship between geographic origin and genetic diversity.

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

characters viz. days to maturity, 100-seed weight, number of pods per plant and dry matter contributed through 80% of total divergence. 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.

Konda *et al.* (2007) conducted experiment with 40 genotypes of blackgram were grouped into seven clusters and noticed that their inter cluster distance was the maximum between cluster II and cluster IV serve as potential parents for hybridization. Genotypes in cluster IV showed the highest mean value for seed per pod, 100 seed weight, grain yield per plant and potential content. Indradeo (2007) evaluated 44 genotypes of cowpea through Mahalanobi's D^2 statistics and grouped them into 13 clusters and reported the maximum genetic diversity by number of pods per plant, number of grain per pod, pod length, 100-grain weight and seed yield per plant.

Roy *et al.* (2007) conducted a genetic divergence study in 34 genotypes of greengram grown in summer and kharif seasons and were grouped into eight clusters and four clusters, respectively. They revealed that the genetic diversity was independent of geographical diversity. The character 100-seed weight had the highest contribution towards total divergence followed by seed protein content and yield per plant in summer season and the characters seed protein content followed by 100-seed weight contributed the maximum to the divergence. Sankaran (2008) evaluated a study by using Mahalanobi's D^2 statistics for evaluating 31 land races of lablab bean. They reported that the Inter cluster distance were the maximum between cluster VI and cluster V which serve as potential parents for hybridization. Elangaimannan *et al.* (2008) studied genetic divergence in 34 genotypes of blackgram, grouped them into

seven clusters by using Mahalanobi's D^2 statistics. Inter Cluster distance was the maximum between cluster II and cluster IV which 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. 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.

CHAPTER III
MATERIALS AND METHODS

This chapter explains information concerning methodology that was used in execution of the experiment. It contains a brief description of experimental site location, experimental materials, climate and soil, seed bed preparation, layout and design of the experiment, land preparation, fertilization, , intercultural operations, harvesting, data recording procedure, statistical analysis etc., which are presented as follows:

3.1. Experimental site and geographical location

The experiment was carried out at the agronomic field of Sher-e-Bangla Agricultural University, Dhaka-1207, Bangladesh during the period from March to June 2017. The research site was found at an altitude of 8.6m from the sea level with latitude of 23°74' N and longitude of 90°35' E in Agro-ecological zone of Madhupur Tract (AEZ-28) (Anonymous, 1988).The experimental site is shown in the map of AEZ of Bangladesh in (Appendix I).

3.2. Soil and climate

The experimental site was situated in the subtropical zone. The soil was clay loam in texture with pH ranges from 6.00 to 6.63. The soil was olive gray in color with common fine to medium distinct dark yellowish brown mottles. The organic carbon content is 0.84% (Appendix II). The records of temperature of air, humidity and rainfall during the period of experiment were presented from the Bangladesh Meteorological Department, Agargaon, Dhaka (Appendix III).

3.3. Experimental materials

For this study thirty three genotypes of mungbean (*Vigna radiata.*L) were used. Purity and germination percentage were leveled as around 100 and 80, respectively. These genotypes were collected from Plant Genetic Resources

Centre (PGRC) of Bangladesh Agricultural Research Institute (BARI), Gazipur on December 2017 (Table 1).

3.4. Design and layout of the experiment

The experiment was laid out and evaluated during kharif season 2017 in Randomized Complete Block Design (RCBD). The experiment was conducted in three replications. Plant to plant distance was 15 cm and line to line distance was 30 cm. The total land size was 120.75 m^2 and the plot to plot distance was 2.5m. The genotype was randomly distributed to each line.

3.5. Land preparation

The experiment plot was prepared by several and cross ploughing followed by laddering and harrowing with tractor and power tiller which brought good tilth in the first week of March, 2017. Weeds and other stables were removed carefully and leveled properly. Manures and fertilizers were applied as per the recommended dose before the final land preparation. The final land preparation was done on 15 March, December 2017.

3.6. Manure and fertilizer application

Mungbean has the ability of nitrogen fixation from atmosphere so it requires less nitrogen application. But for initial establishment of plant up to the stage of nodule formation 20-40-20 NPK, respectively was applied as a starter dose. Well decomposed cow dung was mixed with the soil according to the recommendation guide BARI, 2006 and pulverized well and dried in the sun. TSP, MP and Gypsum were applied at the time of final land preparation and cow dung was applied two weeks before seed sowing during the land preparation. The recommended doses of manure and fertilizers were given in (Table: 2)-

Table 1. Sources of 33 genotypes of Mungbean

SL.NO.	DESIGNATION	SOURCES
1	G_1	BD-6874
2	G_2	BD-6875
3	G_3	BD-6876
4	G_4	BD-6878
5	G_5	BD-6879
6	G_6	BD-6896
7	G_7	BD-6898
8	G_8	BD-9835
9	G_9	BD-9837
10	G_{10}	BD-6900
11	G_{11}	BD-6901
12	G_{12}	BD-6902
13	G_{13}	BD-6903
14	G_{14}	BD-6904
15	G_{15}	BD-6906
16	G_{16}	BD-6907
17	G_{17}	BD-6909
18	G_{18}	BD-6917
19	G_{19}	BD-6918
20	G_{20}	BD-6920
21	G_{21}	BD-6923
22	G_{22}	BD-6924
23	G_{23}	BD-6925
24	G_{24}	BD-6926
25	G_{25}	BD-6927
26	G_{26}	BD-6928
27	G_{27}	BD-6929
28	G_{28}	BD-6932
29	G_{29}	BD- 6933
30	G_{30}	BD-6934
31	G_{31}	BD-6935
32	G_{32}	BD-6936
33	G_{33}	BD-6937

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

Fertilizers/ Manures	Doses (kg)	
	Applied in the plot	**Quantity /ha**
Urea	2.27	53
TSP	4.00	99
MP	1.70	41
Cow dung	Applied earlier	2.5 ton

3.7. Sowing of seed and intercultural operation

The seed of 33 genotypes of mungbean were sown in the field on 17 March, 2017. Weeding was done properly and timely. Intercultural operations were done uniformly for all the genotypes. Thinning was done 25 days after sowing. Weeding was done twice. The first weeding was done during thinning and the second one after about two months of sowing. Recommended insecticide and fungicide were applied when needed. Some pictorial views (A, B, C, D) of different stages plants of experiment in the field are showing in Plate 1(a) and plate 1(b).

3.8. Crop 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 per plant were allowed to ripe and then seeds were collected and different genotypes with different replications were collected separately. Harvesting was completed on 26 June 2017. A view of field during maturity and harvesting stage is given in Plate 2.

3.9. Data collection

Data were recorded from each plot based on different agro-morphogenic traits throughout the life cycle of the plant. With the guidance of supervisor data were recorded in respect of the following parameters.

(A)

(B)

Plate 1(a). Different stages of mungbean. (A). Germination of seedling, (B). Growing stage

(C)

(D)

Plate 1(b). Different stages of mungbean. (C). Flowering stage, (D). Fruiting stage

Plate 2. Pictorial views showing field view at maturity and harvesting stage

3.9.1. Days to 50% flowering

Days to 50% flowering were recorded from the sowing date to the date of 50% flowering of every entry.

3.9.2. Plant height (cm)

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

3.9.3. Number of branches per plant

The total number of branches arisen from the main stem of a plant was counted as the number of branches per plant.

3.9.4. Pod per plant

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

3.9.5. Pod length (cm)

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

3.9.6. Seed per pod

Well filled seeds were counted from each pod of a plant and it was considered as the number of seeds per pod.

3.9.7. 100 seed weight (g)

Weight in grams of randomly counted hundred seeds of each entry was recorded

3.9.8. Yield per plant (g)

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

3.10.1. Statistical analysis

The mean values of five randomly selected plants used for recording observations were computed for each of nine 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 MSTAT-C 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 MSTAT-C. 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), Cluster Analysis (CA) and Canonical Vector Analysis (CVA).

3.10.1.1. Analysis of variance

The analysis of variance for different characters was carried out using mean data in order to assess the genetic variability among genotypes 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 in Table 3.

Table 3. Analysis of variance (ANOVA)

Sources of variation	Degrees of freedom (df)	Mean sum of squares (MSS)	Expected MSS
Replication	(r-1)	Mr	g$б_r^2$+ $б_e^2$
Genotypes	(g-1)	Mg	r $б_g^2$+ $б_e^2$
Error	(g-1) (r-1)	Me	$б_e^2$
Total	(rg-1)		

Where, r = number of replications

g = number of treatments (genotypes)

$б\,^2_r$ = variance due to replications.

$б^2_g$ = variance due to treatments (genotypes)

$б^2_e$ = 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

$$S.E = \sqrt{\frac{2\,Ee}{r}}\ (1+\frac{rqu}{q+1})$$

Where, S. E = standard error of mean

Ee = mean sum of squares for error (Intra block)

r = number of replications

q = number of genotypes in each sub-block

u = weightage factor computed

3.10.1.2. Genotypic variance and phenotypic variance

Phenotypic and genotypic components of variance were estimated by using the formula given by Cochran and Cox (1957).

$$\text{Genotypic variance } (\sigma^2 g) = \frac{\text{MSS due to genotypes} - \text{MSS due to error}}{R}$$

Where, R= number of replication

Phenotypic variance ($\sigma^2 p$) = Genotypic variance (σ^2g) + Error variance (σ^2e)

3.10.1.3. Estimation of genotypic and phenotypic co-efficient of variation

Genotypic and phenotypic co-efficient of variation were calculated by the formula suggested by Burton (1952)

$$\text{Phenotypic Co efficient of Variability (PCV \%)} = \frac{\sqrt{\text{Phenotypic variance}}}{\text{Grand mean}} \times 100$$

$$= \sqrt{\frac{\sigma_p^2}{\bar{x}}} \times 100$$

Genotypic Co efficient of Variability (GCV %) = $\frac{\sqrt{\text{Genotypic variance}}}{\text{Grand mean}} \times 100$

$$= \sqrt{\frac{\sigma_g^2}{\bar{x}}} \times 100$$

PCV and GCV were classified into three following categories as suggested by Sivasubramanian and Menon (1973).

Categories: Low: Less than 10% Moderate: 10-20% High: More than 20%

3.10.1.4. Estimation of heritability

The broad sense heritability (h^2_{bs}) was estimated for all characters as the ratio of genotypic variance to the total of phenotypic variance as suggested by Lush (1949) and Hanson *et al*. (1956).

$$h^2_{bs} = \frac{\text{Genotypic variance}}{\text{Phenotypic variance}} \times 100$$

$$= \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Heritability estimates in cultivated plants could be placed in the following categories as suggested by Robinson *et al*. (1966).

Categories: Low: 0-30%; Moderate: 30-60%; High: >60%

3.10.1.5. Genetic advance (GA):

The expected genetic gain or advance for each character was estimated by using the following method suggested by Johnson *et al*. (1955).

$$GA = h^2_{bs} \times \sigma_p \times K$$

Where,

h^2_{bs} = Heritability estimate in broad sense

σ_p = Phenotypic standard deviation of the trait

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

Categories: High (>20%) Moderate (10-20%) Low (<10%)

Further the Genetic advance as per cent of mean was computed by using the following formula

GA (% of mean) = $\frac{\text{GA}}{\text{Grand mean}} \times 100$

Genetic advance as per cent mean was categorized into following groups as suggested by Johnson *et al.* (1955).

Categories: High (>20%) Moderate (10-20%) Low (<10%)

3.10.1.6. Correlation coefficient analysis

To determine the degree of association of characters with yield and also among the yield components, the correlation coefficients were calculated. The genotypic co-variance component between two traits and have the phenotypic covariance component were derived in the same way as for the corresponding variance components. The co-variance components were used to compute genotypic and phenotypic correlation between the pairs of characters. Both genotypic and phenotypic coefficients of correlation between two characters were determined by using the variance and covariance components as suggested by Al-Jibouri *et al*. (1958).

Genotypic correlation coefficients, $r_g(xy) = \frac{Cov_g\ xy}{\sqrt{\sigma_x^2}.\sqrt{\sigma_y^2}}$

Phenotypic correlation coefficients, $r_p(xy) = \frac{Cov_p\ xy}{\sqrt{\sigma_x^2}.\sqrt{\sigma_y^2}}$

Where,

Cov_g, Cov_p are the genotypic and phenotypic covariance of xy, respectively.

σ_g^2 and σ_p^2 are the genotypic and phenotypic variance of x and y, respectively.

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.

3.10.1.7. Path co-efficient analysis

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

$$r_{yx_1} = P_{yx_1} + P_{yx_2} r_{x_1x_2} + P_{yx_3} r_{x_1x_3}$$
$$r_{yx_2} = P_{yx_2} + P_{yx_1} r_{x_1x_2} + P_{yx_3} r_{x_2x_3}$$
$$r_{yx_3} = P_{yx_3} + P_{yx_1} r_{x_1x_3} + P_{yx_2} r_{x_2x_3}$$

Where, r's denotes simple correlation co-efficient and P's denote path co-efficient (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_{yx_1} = the direct effect of x1 on y.

$P_{yx_2} r_{x_1x_2}$ = the indirect effect of x1 via x2 on y.

$P_{yx_3} r_{x_1x_3}$= 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,

$P_{RY}^2 = (R^2)$; and hence residual effect, $R = \sqrt{P_{RY}^2}$

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

r_{iy}=Correlation of the character with yield

3.10.2. Multivariate analysis

The genetic diversity among the genotypes was assessed by Mahalanobis's (1936) general distance (D^2) statistic and its auxiliary analyses. The parents selection in hybridization programme 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), Cluster Analysis (CA) and Canonical Vector Analysis (CVA), which quantify the differences among several quantitative traits, are efficient method of evaluating genetic diversity. These are as follows:

3.10.2.1. 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.

3.10.2.2. 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.

3.10.2.3. Canonical Vector Analysis (CVA)

Canonical Vector Analysis (CVA) finds linear combination of original variability that maximize the ratio of between group to within group variation, thereby giving functions of the original variables that can be used to discriminate between the groups. Thus, in this analysis a series of orthogonal transformations sequentially maximizing of the ratio of among groups to the within group variations. The canonical vector is based upon the roots and vectors of WB, where W is the pooled within groups covariance matrix and B is the among groups covariance matrix.

3.10.2.4. 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 Caudhury (1977). The D^2 values were estimated for all possible combinations between genotypes. In simpler form D^2 statistic is defined by the formula

$$D^2 = \sum_{i}^{x} d_i^2 = \sum_{i}^{x} (Y_i^j - Y_j^k) \quad (j \neq k)$$

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.

3.10.2.5. Computation of average intra-cluster distances

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

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

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.

3.10.2.6. Computation of average inter-cluster distances

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

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

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.

3.10.2.7. 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.

3.10.2.8. 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:

i. Choice of cluster from which genotypes are selected for use as parent(s)
ii. Selection of particular genotype(s) from the selected cluster(s)
iii. Relative contribution of the characters to the total divergence
iv. Other important characters of the genotypes performance

CHAPTER IV
RESULTS AND DISCUSSION

The present experiment was conducted to study the genetic variability, character association and genetic diversity among 33 genotypes of mungbean as well as to study the correlation and path co-efficient for seed yield and different yield contributing characters. The data were recorded on different parameters such as days to 50% flowering, plant height (cm)**,** number of branches per plant, pods per plant, pod length (cm), seeds per pod, 100 seed weight (g), yield per plant (g). Data on different yield and yield contributing characters of mungbeans were computed and statistically analyzed and the obtained results of the present study have been presented and discussed in this chapter as follows-

4.1. Genetic Variability

The analysis of variance indicated significantly higher amount of variability present among the genotypes for all the characters studied viz., days to 50% flowering, plant height (cm)**,** number of branches per plant, pod per plant, pod length (cm), seed per pod, 100 seed weight (g), yield per plant (g) (Appendix V). The results clearly indicated that there existed high variability for yield and yield components among the genotypes studied. Therefore there was a lot of scope for selection for majority of the traits in the genotypes. The ANOVA of all the eight characters is presented in Appendix V. The mean, range, mean sum of square, variance components, genotypic and phenotypic co-efficient of variance, heritability, genetic advance, and genetic advance in percentage of mean are presented in Table 4.

4.1.1. Days to 50% flowering

The variance due to days to 50% flowering showed that the genotypes differed significantly (Appendix V) and it ranged from 7.67 days to 19.33 days after

Table 4. Estimation of genetic parameters in eight characters of 33 mungbean genotypes

Parameters	Range	Mean	Mean sum of square(MS)	σ^2p	σ^2g	σ^2 e	PCV (%)	GCV (%)	ECV (%)	Heritability (%)	Genetic advance (5%)	Genetic advance (% mean)
Days to 50% flowering	7.67-19.33	14.99	33.61**	11.52	11.05	0.47	22.64	22.18	4.56	95.95	6.71	44.75
Plant height (cm)	33.20-72.87	49.32	253.09**	99.93	76.58	23.35	20.27	17.74	9.80	76.63	15.78	31.99
No. of branches per plant	1.74-3.61	2.41	0.83**	0.46	0.19	0.27	28.14	17.90	21.72	40.43	0.57	23.44
Pods per plant	6.00-22.40	11.15	49.11**	20.71	14.20	6.51	40.80	33.78	22.88	68.56	6.43	57.62
Pod length (cm)	5.42-8.98	6.43	2.24**	0.85	0.69	0.16	14.35	12.95	6.19	81.42	1.55	24.07
Seeds per pod	8.11-12.80	10.14	0.78**	1.48	0.70	0.78	11.99	8.22	8.73	47.01	1.18	11.61
100 seed weight (g)	2.01-7.30	3.11	3.18**	1.16	1.01	0.16	34.64	32.23	12.68	86.59	1.92	61.78
Seed yield per plant (g)	1.52-4.34	2.70	1.49**	0.66	0.42	0.25	30.20	23.89	18.46	62.61	1.05	38.94

σ^2p = Phenotypic variance, σ^2g = Genotypic variance and σ^2 e = Environmental variance, PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, ECV = Environmental coefficient of variation.

sowing with mean value 14.99 days (Table 4). The Genotypic, phenotypic and environmental variances observed were 11.05, 11.52 and 0.47, respectively. The phenotypic variance appeared to be closed to the genotypic variance suggested least influence of environment in expression of the genes controlling this trait. It was observed that there was little difference between the genotypic co-efficient of variation (22.18) and phenotypic coefficient of variation (22.64) (Figure 1) indicating minor environmental influence on this character. Therefore, selection based upon phenotypic expression of this character would be effective for the improvement of this crop. Bangar *et al.* (2003) reported that phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) which agrees with the result of this experiment. The heritability (95.95%) estimates for this trait was very high, genetic advance (6.71) was at lower level and genetic advance over percentage of mean (44.75) were found high (Table 4 and Figure 2) indicated that this trait was controlled by additive genes and selection of this character would be effective. Reddy *et al.* (2003) reported high heritability coupled with high genetic advance for days to 50% flowering, which also agreed with the result of this experiment.

4.1.2. Plant height (cm)

The mean for plant height was recorded and it ranged from 33.20 cm to 72.87 cm (Table 4). The analysis of variance revealed highly significant differences among the genotypes with respect to plant height (Appendix V). The genotypic and phenotypic variance was observed as 76.58 and 99.93, respectively for plant height with low (23.35) environmental influence. The phenotypic co-efficient of variation (20.27) was higher than the genotypic co-efficient of variation (17.74), which indicated presence of considerable variability among the genotypes for this trait. The heritability (76.63%) estimates for this trait was high, genetic advance (15.78) was moderate and genetic advance in per cent of mean (31.99) was found high, revealed that this trait was governed by additive

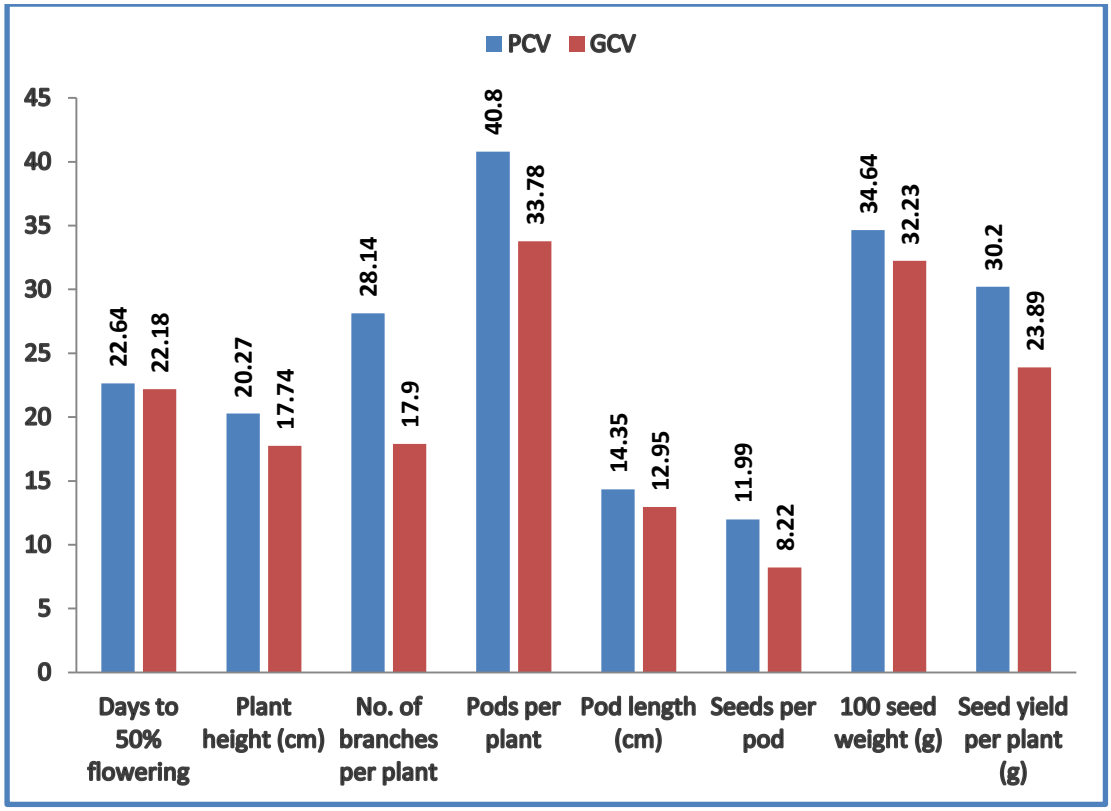

Figure 1. Genotypic and phenotypic coefficient of variation in mungbean

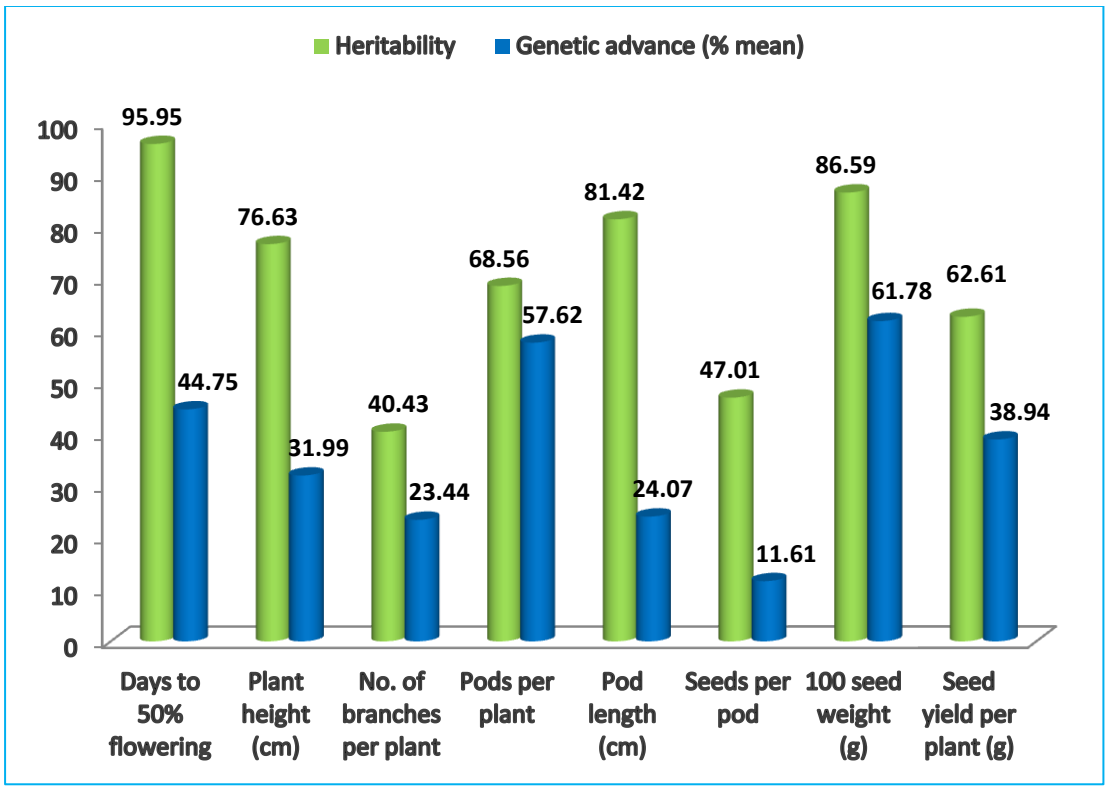

Figure 2. Heritability and genetic advance over mean in mungbean

gene. Therefore, selection for this trait will be effective. Rao *et al*. (2006) reported that plant height exhibited high variability and heritability coupled with genetic advance which was similar to this experiment.

4.1.3. Number of branches per plant

Considerable differences among the genotypes studied in case of number of branches per plant are observed and the range was recorded from 1.74 to 3.61(Table 4). The phenotypic variance (0.46) appeared to be higher than the genotypic variance (0.19) suggested considerable influence of environment on the expression of the genes controlling this trait. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 17.90 and 28.14, respectively which indicated presence of considerable variability among the genotypes. The heritability (40.43%) estimates for this trait was moderate, genetic advance (0.57) was low and genetic advance in per cent of mean (23.44) were found high, revealed that this trait was governed by additive gene. Selection for this trait may be effective.

4.1.4. Number of pods per plant

Mean sum of square for number of pods per plant was highly significant in mungbean, indicating the existence of considerable difference among the genotypes for this trait (Appendix V). The range of number of pods per plant was recorded from 6.00 to 22.40 with mean value 11.15 (Table 4). The genotypic variance (14.20) was lower than the phenotypic variance (20.71). Phenotypic coefficient of variation (40.80) was higher than the genotypic coefficient of variation (33.78) indicating considerable environmental influence in case of number of pod per plant. Heritability for this trait was high (68.56) but genetic advance (6.43) was low and genetic advance in percent of mean (57.62) was found high, indicated that selection for this character would be effective. Malik *et al.* (1983) also reported high heritability coupled with high genetic advance for number of pods in mungbean indicating that these traits

were controlled by additive genes and can easily be transferred to succeeding generations and it agreed with the findings of this experiment.

4.1.5. Pod length (cm)

Mean sum of square for pod length was highly significant in mungbean, indicating existence of considerable difference for this trait (Appendix V). The maximum pod length was found (8.98) and the minimum was recorded (5.42) with mean value (6.43) (Table 4). The genotypic variance (0.69) and phenotypic variance (0.85), genotypic coefficient of variation (12.95) and phenotypic coefficient of variation (14.35) were close to each other indicating less environmental influence in case of pod length. Heritability for this trait was very high (81.42) but genetic advance (1.55) was low and genetic advance in percent of mean (24.07) was found high, indicated that selection for this character would be effective. Degefa *et al.* (2014) reported that traits like pod length had very high heritability on mungbean. A pictorial view is showing morphological variation of seeds and mature pods of 33 genotypes of mungbean in Plate 3.

4.1.6. Number of seeds per pod

Mean sum of square for number of seeds per pod was highly significant in mungbean, indicating existence of considerable difference for this trait (Appendix V). The maximum number of pod per plant was found (12.80) and the minimum was recorded (8.11) with mean value (10.14) (Table 4). The genotypic variance (0.70) and phenotypic variance (1.48), genotypic co-efficient of variation (8.22), and phenotypic coefficient of variation (11.99) difference indicating considerable environmental influence in case of number of pod per plant (Table 4). Heritability for this trait was moderate (47.01) but genetic advance (1.18) and genetic advance in percent of mean (11.61) was found moderately high, indicated that this character was governed by additive gene effect, where low heritability was being exhibited due to high environmental effects and selection for this character may be effective in such

Plate 3. Pictures showing morphological variation of pod and seed of 33 genotypes of mungbean

cases. Malik *et al.* (1983) reported high heritability coupled with high genetic advance for seeds per plant in mungbean.

4.1.7. 100 seed weight (g)

Mean sum of square for hundred seed weight is highly significant in mungbean, indicating existence of considerable difference for this trait (Appendix V). The maximum hundred seed weight was found (7.30) and the minimum was recorded (2.01) with mean value (3.11) (Table 4). The genotypic variance (1.01) and phenotypic variance (1.16), genotypic coefficient of variation (32.23) and phenotypic coefficient of variation (34.64) were close to each other indicating less environmental influence in case of hundred seed weight. Heritability for this trait was very high (86.59) but genetic advance (1.92) and genetic advance in percentage of mean (61.78) was found high, indicated that selection for this character would be effective and Sarwar *et al.* (2004) reported high heritability for hundred seed weight in mungbean.

4.1.8. Seed yield per plant (g)

Mean sum of square for seed yield per plant (g) was highly significant in mungbean, indicating existence of considerable difference for this trait (Appendix V). The range of seed yield per plant was recorded from 1.52 to 4.34 with mean value (2.70) (Table 4). The genotypic variance (0.42) and phenotypic variance (0.66), genotypic coefficient of variation (23.89) was lower than phenotypic coefficient of variation (30.20) indicating that the apparent variation was not only due to genotypes but also due to the influence of environment. Heritability for this trait was high (62.61) but genetic advance (1.05) and genetic advance in percent of mean (38.94) was found high, indicated that selection for this character would be effective. Reddy *et al.* (2003) reported that high heritability coupled with high genetic advance was observed for seed yield per plant.

4.2. Correlation coefficient analysis

As yield is the resultant of combined effect of several component characters and environment, understanding the interaction of characters among themselves and with environment has been of great use in the plant breeding. Correlation studies along with path analysis provide a better understanding of the association of different characters with fruit yield. So selection may not be effective unless the other contributing components influence the yield directly or indirectly. When selection pressure is applied for improvement of any character highly associated with yield, it simultaneously affects a number of other correlated characters. Hence knowledge regarding association of character with yield and among themselves provides guideline to the plant breeders for making improvement through selection with a clear understanding about the contribution in respect of establishing the association by genetic and non-genetic factors (Dewey and Lu, 1959). Genotypic and phenotypic correlation coefficient between yield and yield contributing traits of mungbean are shown in Table 5.

4.2.1. Days to 50% flowering

The correlation of days to 50% flowering was highly negatively significant in case of seeds per pod at genotypic level (G= -0.610) and negatively significant at phenotypic level (P= -0.391). This character was also negatively significant in case of pods per plant at genotypic level (P= -0.373). Non-significant positive correlation was observed in pod length (G=0.303, P=0.281) and hundred seed weight (G=0.269, P= 0.255) at both the genotypic and phenotypic levels (Table 5). This character also showed non-significant negative correlation with plant height, number of branches per pod and seed yield at both levels. Prakash *et al.* (2007) showed that character like days to 50% flowering revealed significant negative correlation with grain yield, indicating that yield increase can be obtained in short duration genotypes. Verma and Garg (2007) found that seed yield per plant showed negative association with days to 50% flowering which agreed with the result of this experiment.

Table 5. Genotypic (G) and phenotypic (P) correlation coefficient between yield and yield contributing traits of mungbean

	Attribute	Days to 50% flowering	Plant height (cm)	No. of branches per plant	Pods per plant	Pod length (cm)	Seeds per pod	100 seed weight (g)	Seed yield per plant (g)
Days to 50% flowering	G	1	-0.174	-0.250	-0.373*	0.303	-0.610**	0.269	-0.173
	P	1	-0.126	-0.149	-0.293	0.281	-0.391*	0.255	-0.111
Plant height (cm)	G		1	0.641**	0.431*	-0.213	0.600**	-0.323	0.312
	P		1	0.329	0.409*	-0.166	0.431*	-0.234	0.323
No. of branches per plant	G			1	0.437*	-0.402*	0.507**	-0.369*	0.494**
	P			1	0.274	-0.279	0.203	-0.266	0.249
Pods per plant	G				1	-0.378*	0.823**	-0.523**	0.550**
	P				1	-0.272	0.580**	-0.418*	0.563**
Pod length (cm)	G					1	-0.471*	0.770**	0.104
	P					1	-0.220	0.702**	0.160
Seeds per pod	G						1	-0.591**	0.358*
	P						1	-0.366*	0.323
100 seed weight (g)	G							1	-0.094
	P							1	-0.001
Seed yield per plant (g)	G								1
	P								1

** = Significant at 1%. * = Significant at 5%.

4.2.2. Plant height (cm)

A highly significant and positive association of plant height with number of branches per plant (G=0.641) and number of seeds per pod (G=0.600) at genotypic level (Table 5). This character was also showed positive significant correlation with number of seeds per pod (P=0.431) at phenotypic level. Plant height had positive significant correlation with pods per plant at both level (G=0.431, P=0.409). This character also had non-significant positive correlation with seed yield at both level and non-significant negative correlation with pod length and 100 seed weight at both the genotypic and phenotypic levels. Arshad *et al.* (2009) found that amongst the character studied plant height was positive and significant association with yield per plant at both genotypic and phenotypic levels. They also showed that positive and significant correlation of plant height with branches per plant was also observed.

4.2.3. Number of branches per plant

A highly significant and positive association of number of branches with number of seeds per pod (G=0.507) and seed yield (G=0.494) and significant positive correlation with pods per plant (G=0.437) at genotypic level (Table 5). This character had negative significant correlation with hundred seed weight (G= -0.402)) and pod length (G= -0.369) at genotypic level was observed. Insignificant negative correlation was found with pod length (P= -0.279) and 100 seed weight (P= -0.266) and insignificant positive correlation with pod per plant, seeds per plant and seed yield at phenotypic levels. Rajanna *et al.* (2000) estimated significant and positive correlation of number of branches per plant with number of pods per plant that support the findings of this experiment and it indicating that increasing number of branches results increasing number of pods per plant which as well as increases yield.

4.2.4. Number of pods per plant

Highly significant positive correlation was observed with seeds per pod (G=0.823, P=0.580) and seed yield per plant (G=0.550, P=0.563) at both levels (Table 5). Pods per plant showed highly significant negative correlation with hundred seed weight (G= -0.523) at genotypic level. Pods per plant showed significant negative correlation with pod length (G= -0.378) at genotypic level and 100 seed weight (P= -0.418) at phenotypic level. Kumar *et al.* (2005) revealed that the maximum positive and significant phenotypic correlation coefficient (0.825) was between the number of pods per plant and seed yield per plant which was similar to this experiment.

4.2.5. Pod length (cm)

Pod length showed highly significant positive correlation with the 100 seed weight (G=0.770, P=0.702) at both genotypic and phenotypic level (Table 5) indicating with the increasing of pod length increasing hundred seed weight as well as yield. This character was also showed significant negative correlation with seeds per pod (G= -0.471) at genotypic level. Positive non-significant correlation of pod length with seed yield was observed at both levels.

4.2.6. Seeds per pod

Seeds per pod had highly significant negative correlation with 100 seed weight (G= -0.591) at genotypic level and negative significant correlation at phenotypic level (P= -0.366) (Table 5). This character had significant positive correlation with seed yield (G=0.358) at genotypic level and non-significant positive correlation at phenotypic level. Vikas *et al.* (1999) estimated that seed yield per plant showed positive association with number of seeds per pod.

4.2.7. 100 seed weight (g)

This character showed non-significant negative correlation with seed yield at both genotypic and phenotypic level. In this experiment, though 100 seed weight was low but due to higher number of seeds per pod yield was high.

4.3. Path coefficient analysis

Though correlation analysis indicates the association pattern of components traits with yield, they simply represent the overall influence of a particular trait on yield rather than providing cause and effect relationship. In order to find out a clear picture of the inter relationship between yield per plant and other yield attributes, direct and indirect effects were worked out using path coefficient analysis technique developed by Wright (1921) and demonstrated by Deway and Lu (1959) at phenotypic level which also measured the relative importance of each component. Such information would be of great value in enabling the breeder to specifically identify the important component traits of yield and utilize the genetic stock for improvement in a planned way and here In path coefficient analysis, the direct effect of a trait on yield of plant and its indirect effect through other characters were computed and the results are presented in Table 6.

4.3.1. Days to 50% flowering

Path analysis revealed that days to 50% flowering had negative direct effect (-0.0400) on yield (Table 6). Days to 50% flowering showed negative indirect effect with plant height (-0.0044), number of branches per plant (-0.0600), pods per plant (-0.2158) and 100 seed weight (-0.0003). This character also had indirect positive effect with number of seeds per pod (0.0467) and plant length (0.1254) which was contributed to result non-significant negative genotypic correlation with yield per plant (-0.148). On the other hand Kumar *et al*. (2005) revealed that days to 50% flowering (0.011) had relatively low positive direct effects on yield which disagreed with the findings of this experiment.

4.3.2. Plant height (cm)

Plant height showed positively direct effect (0.0280) on yield (Table 6). This character showed highest positive indirect effect through pods per plant (0.2663) followed by number of branches per plant (0.1458), days to 50% flowering (0.0062), 100 seed weight (0.0003). The character also produced

Table 6. Partitioning of pearson correlations into direct (bold) and indirect effects by path analysis

	Days to 50% flowering	Plant height (cm)	No. of branches per plant	Pods per plant	Pod length (cm)	Seeds per pod	100 seed weight (g)	Pearson correlation with yield
Days to 50% flowering	**-0.0400**	-0.0044	-0.0600	-0.2158	0.1254	0.0467	-0.0003	-0.148
Plant height (cm)	0.0062	**0.0280**	0.1458	0.2663	-0.0825	-0.0477	0.0003	0.316
No. of branches per plant	0.0080	0.0136	**0.3000**	0.2227	-0.1437	-0.0316	0.0003	0.370*
Pods per plant	0.0137	0.0118	0.1059	**0.6310**	-0.1424	-0.0650	0.0005	0.556**
Pod length (cm)	-0.0118	-0.0054	-0.1014	-0.2114	**0.4250**	0.0327	-0.0007	0.127
Seeds per pod	0.0203	0.0145	0.1029	0.4455	-0.1509	**-0.0920**	0.0005	0.340
100 seed weight (g)	-0.0106	-0.0081	-0.0942	-0.3035	0.3162	0.0448	**-0.0010**	-0.057

Residual effect: 0.381 ** = Significant at 1%. * = Significant at 5%.

negative indirect effect on yield via pod length (-0.0825) and seeds per pod (-0.0477) which were contributed to result non-significant positive genotypic correlation with yield per plant (0.316). Degefa *et al*. (2014) revealed that at genotypic level, the maximum positive direct effect was exerted on seed yield per plot by plant height and it was similar to this experiment and it indicated that the high yielding mungbean could be obtained by selecting plant height.

4.3.3. Number of branches per plant

Number of branches per plant showed positively direct effect (0.3000) on yield (Table 6). This character showed highest positive indirect effect through number of pods per plant (0.2227) followed by plant height (0.0136), days to 50% flowering (0.0080) and 100 seed weight (0.0003). The character also produced negative indirect effect on yield via pod length (-0.1437) and seeds per pod (-0.0316) which were contributed to result significant positive genotypic correlation with yield per plant (0.370). Mishra and Yadav (1992) noticed that number of branches had direct positive influence on seed yield.

4.3.4. Number of pods per plant

Number of pods per plant showed positively direct effect (0.6310) on yield (Table 6). This character showed the highest positive indirect effect through number of branches per plant (0.1059) followed by days to 50% flowering (0.0137), plant height (0.0118) and 100 seed weight (0.0005). The character also produced negative indirect effect on yield via pod length (-0.1424) and seeds per pod (-0.0650) which were contributed to result highly significant positive genotypic correlation with yield per plant (0.556). Pundri *et al.* (1992) suggested that pods per plant should be given priority in selecting for high yielding varieties in mungbean as it had positive direct and indirect effects on seed yield which supported this experiment.

4.3.5. Pod length (cm)

Pod length showed positively direct effect (0.4250) on yield and positive indirect effect through seeds per pod (0.0327) (Table 6). The character also produced negative indirect effect on yield via 100 seed weight (-0.0007) followed by plant height (-0.0054), days to 50% flowering (-0.0118), number of branches per plant (-0.1014) and pods per plant (-0.2114) which were contributed to result non-significant positive genotypic correlation with yield per plant (0.127). Asifa *et al.* (2005) observed that pod length (0.33) had positive direct effects on seed yield as this experiment.

4.3.6. Number of seeds per pod

Number of seeds per pod showed negatively direct effect (-0.0920) on yield and negative indirect effect through pod length (-0.1509) (Table 6). The character also produced positive indirect effect on yield via pods per plant (0.4455) followed by number of branches per plant (0.1029), days to 50% flowering (0.0203), plant height (0.0145) and 100 seed weight (0.0005) which were contributed to result non-significant positive genotypic correlation with yield per plant (0.340). Pathak and Patel (1993) determined that seeds per pod showed negative direct effects on grain yield per plant which agreed with the result of this experiment.

4.3.7. 100 seed weight (g)

100 seed weight showed negatively direct effect (-0.0010) on yield (Table 6).This character also showed positive indirect effect through pod length (0.3162) and seeds per pod (0.0448). The character also produced negative indirect effect on yield via plant height (-0.0081) followed by days to 50% flowering (-0.0106), number of branches per plant (-0.0942) and pods per plant (-0.3035) which were contributed to result non-significant negative genotypic correlation with yield per plant (-0.057). Haritha *et al.* (2002) and Hassan *et al.* (2003) showed that 100 seed weight had negative direct effect on seed yield which similar to this experiment.

4.4. Genetic Diversity

4.4.1 Principal component analysis (PCA)

Principal component analysis was carried out with 33 genotypes of mungbean. The computed Eigen values for the 8 variables subjected to principal component analysis together with the corresponding proportion and cumulative explained variance are given in Table 7. First two Eigen values for four principal coordination axes of genotypes accounted for 68.11% variation showed in Table 7. Based on principal component scores I and II obtained from the Principal component analysis (Appendix VI), a two-dimensional scatter diagram (Z_1-Z_2) using component score I as X axis and component score II as Y axis was Constructed, which has been presented in Figure 3. The scatter diagram revealed that there were four apparent clusters. The genotypes were distantly located from each other, which indicated that considerable diversity existed among the genotypes. The first principal component accounted for 47.42 % of the total variation while principal components two and three accounted for 20.69 % and 11.63 %, respectively (Table 7).

4.4.2. Non-Hierarchical Clustering

Thirty three mungbean genotypes were grouped into four different clusters nonhierarchical clustering (Table 8). These results confirmed the clustering pattern of the genotypes obtained through principal component analysis. In this study cluster I had the highest number of genotypes and it was thirteen, cluster II constitute eight genotypes. Cluster III and cluster IV had six genotypes (Table 8). Cluster I had G_3 (BD 6876), G_5 (BD 6879), G_7 (BD 6898), G_{10} (BD 6900), G_{15} (BD 6906), G_{19} (BD 6918), G_{20} (BD 6920), G_{21} (BD 6923), G_{23} (BD 6925), G_{27} (BD 6929), G_{29} (BD 6933), G_{31} (BD 6935) and G_{33} (BD 6937). Cluster II consisted G_1 (BD 6874), G_2 (BD 6875), G_9 (BD 9837), G_{12} (BD 6902), G_{13} (BD 6903), G_{14} (BD 6904), G_{16} (BD 6907), and G_{17} (BD 6909). Cluster III consisted G_4 (BD 6878), G_6 (BD 6896), G_{11} (BD 6901), G_{18} (BD 6917), G_{26} (BD 6928) and G_{32} (BD 6936). Cluster IV consisted G_8 (BD 9835),

Table 7. Eigen values and yield percent contribution of eight characters of 33 genotypes

Principal component axes	Eigen values	Percent variation	Cumulative % of Percent variation
I	3.320	47.42	47.42
II	1.449	20.69	68.11
III	0.814	11.63	79.74
IV	0.632	9.03	88.77
V	0.352	5.00	93.78
VI	0.234	3.35	97.14
VII	0.200	2.80	99.94
VIII	0.156	0.06	100.00

Z_1-Z_2 Graph

Figure 3. Scatter diagram of mungbean genotypes of based on their principal component scores

Table 8. Distribution of 33 genotypes in different clusters

Cluster no.	Genotypes	No. of populations
I	3, 5, 7, 10, 15, 19, 20, 21, 23, 27, 29, 31, 33	13
II	1, 2, 9, 12, 13, 14, 16, 17	8
III	4, 6, 11, 18, 26, 32	6
IV	8, 22, 24, 25, 28, 30	6
	Total	33

G_{22} (BD 6924) G_{24} (BD 6926), G_{25} (BD 6927), G_{28} (BD 6932) and G_{30} (BD 6934). Among the eight characters cluster II earned the highest cluster mean value for plant height (63.09), number of branches per plant (2.80) and seeds per pod (11.01) (Table 9). The genotypes included in cluster III were the highest mean value for days to 50% flowering (16.11), pods per plant (13.66) and seed yield per plant (3.18). Cluster IV produced the maximum cluster mean for pod length (6.90) and 100 seed weight (3.81) (Table 9). Konda *et al.* (2007) conducted experiment with 40 genotypes of blackgram were grouped into seven clusters and noticed that their inter cluster distance was the maximum between cluster II and cluster IV serve as potential parents for hybridization. Genotypes in cluster IV showed the highest mean value for seed per pod, 100 seed weight, grain yield per plant and potential content.

4.4.3. Canonical variate analysis (CVA)

Canonical Variate Analysis (CVA) was done to compute the inter-cluster distances. The intra and inter-cluster distance (D^2) values are shown in Table 10. In this experiment, the inter-cluster distances were higher than the intra-cluster distances thus indicating broader genetic diversity among the genotypes of different groups. The highest inter-cluster distance was observed between clusters II and IV (10.425), followed by between clusters I and II (7.450), and III and IV (5.892). In contrast, the lowest inter-cluster distance was observed between cluster I and III (3.199). However, the maximum inter-cluster distance was observed between the clusters II and IV (10.425) indicating genotypes from these two clusters if involved in hybridization may produce a wide spectrum of segregating population. On the other hand, the maximum intra-cluster distance was found in cluster II (2.45) which contained only 8 genotypes while the minimum distance was found in cluster IV (1.73) that comprises 6 genotypes. Inter and intra cluster distances are show in Table 10. Cluster I consists of nearest cluster with D^2 values cluster III (3.199) and farthest cluster with D^2 values II (7.450) (Table 11). Cluster II consists of the nearest cluster with D^2 values of cluster III (5.110) and farthest cluster with D^2

Table 9. Cluster mean for eight yield and yield related characters in 33 mungbean genotypes

Characters	I	II	III	IV
Days to 50% flowering	15.77	13.13	16.11	14.67
Plant height (cm)	45.11	63.09	51.07	38.35
No. of branches per plant	2.47	2.80	2.27	1.91
Pods per plant	10.38	13.42	13.66	7.30
Pod length (cm)	6.40	6.36	6.14	6.90
Seeds per pod	9.79	11.01	10.31	9.58
100 seed weight (g)	3.18	2.80	2.69	3.81
Seed yield per plant (g)	2.48	2.97	3.18	2.33

Table 10. Intra (Bold) and inter cluster distances (D^2) for 33 genotypes

Cluster	I	II	III	IV
I	**2.21**	7.450	3.199	3.261
II		**2.45**	5.110	10.425
III			**1.87**	5.892
IV				**1.73**

Table 11. The nearest and the farthest clusters from each cluster between D^2 values in mungbean

Sl No.	Cluster	Nearest Cluster with D^2 values	Farthest Cluster with D^2 values
1	I	III (3.199)	II (7.450)
2	II	III (5.110)	IV (10.425)
3	III	I (3.199)	IV (5.892)
4	IV	I (3.261)	II (10.425)

values of IV (10.425). Cluster III consists of the nearest cluster with D^2 values cluster I (3.199) and farthest cluster with D^2 values IV (5.892). Cluster IV consists of nearest cluster with D^2 values cluster I (3.261) and farthest cluster with D^2 values II (10.425). A two-dimensional scatter diagram was constructed using component I as X-axis and component II as Y-axis, showing in the relative position. According to scatter diagram all the genotypes were apparently distributed into five clusters (Figure 4). It is assumed that the maximum amount of heterosis will be manifested in cross combination involving the genotypes belonging to the most divergent clusters and furthermore, for a practical plant breeder, the objective is to achieve high level production in addition to high heterosis. In the present study, the maximum distance existed between cluster II and IV, so the crosses between the genotypes belonging cluster II with cluster IV might produced high heterosis and also the crosses between genotypes from cluster II with IV might produced high level of segregating population. So the genotypes belonging to cluster II and cluster IV might be selected for future hybridization program.

4.4.4. Cluster mean analysis

The cluster means of eight different characters (Table 9) were compared and indicated considerable differences between clusters for all the characters studied. The maximum days to 50% flowering were observed in cluster III (16.11) and minimum in cluster II (13.13). The maximum plant height was observed in II (63.09) whereas the minimum in cluster IV (38.35). The maximum (2.80) and the minimum (1.91) number of branches per plant was observed in cluster II and IV, respectively. The maximum (13.66) and the minimum (7.30) number of pods per plant were observed in cluster III and IV, respectively. The maximum pod length (6.90) was observed in the cluster IV, whereas the minimum pod length (6.14) was observed in cluster III. Number of seeds per pod was the maximum in cluster II (11.01) and the minimum number in cluster IV (9.58). Weight of 100 seed was the highest in cluster IV with mean value 3.81 and the lowest in genotypes belong to the cluster III (2.69).

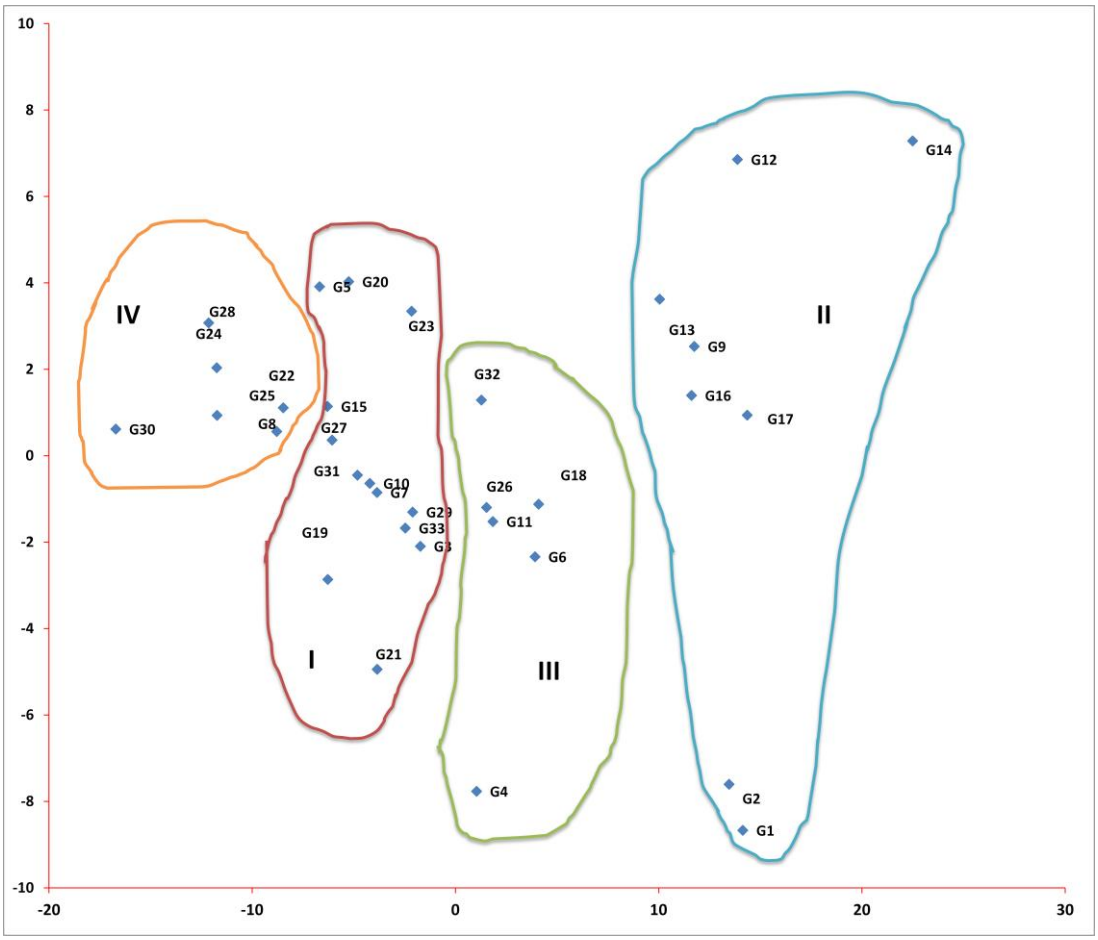

Figure 4. Cluster diagram showing average intra and inter cluster distances of 33 genotypes of mungbean

Seed yield per plant was the maximum in cluster III (3.18) and the minimum in cluster IV (2.33). So to develop high yielding varieties these groups can be used in hybridization program.

4.4.5. Cluster diagram

With the help of D^2 values within and between clusters, an arbitrary cluster diagram (Figure 5) was constructed, which exhibited the relationship between different genotypes. However, the diagram was not following exact scale, it was apparent from the Figure 5 that the genotypes included in the cluster II was far diversed from the genotypes of the cluster IV and where the genotypes belonging to I and III were the least diversed. Genotypes of cluster I-III and III-IV were moderately diverse from each other. The similar diverse genotypes were included between the cluster I-III and I-IV.

4.4.6 Contribution of characters towards divergence of the genotypes

Contribution of characters towards the divergence obtained from canonical variate analysis is presented in Table 11. In this method vectors was calculated to represent the varieties in the graphical form (Rao, 1952). This was helpful in cluster analysis as it facilitated the study of group constellation and also serves as a pictorial representation of the configuration of various groups. The latent vectors (Z_1 and Z_2) obtained from principal component analysis (PCA). The important characters responsible for genetic divergence in the axis of differentiation in vector I (Z_1) (Table 12) were days to 50% flowering (0.3426), number of branches per plant (0.1007), plant height (0.3877), pods per plant (0.1420) and pod length (0.4361) because all of these characters had positive signs in the first axis. Days to 50% flowering (0.0356), plant height (0.0148), number of branches per plant (2.0940), pod length (0.8728), seeds per pod (0.4476) and 100 seed weight (0.0929) had positive sign in vector II (Z_2), the second axis of differentiation.

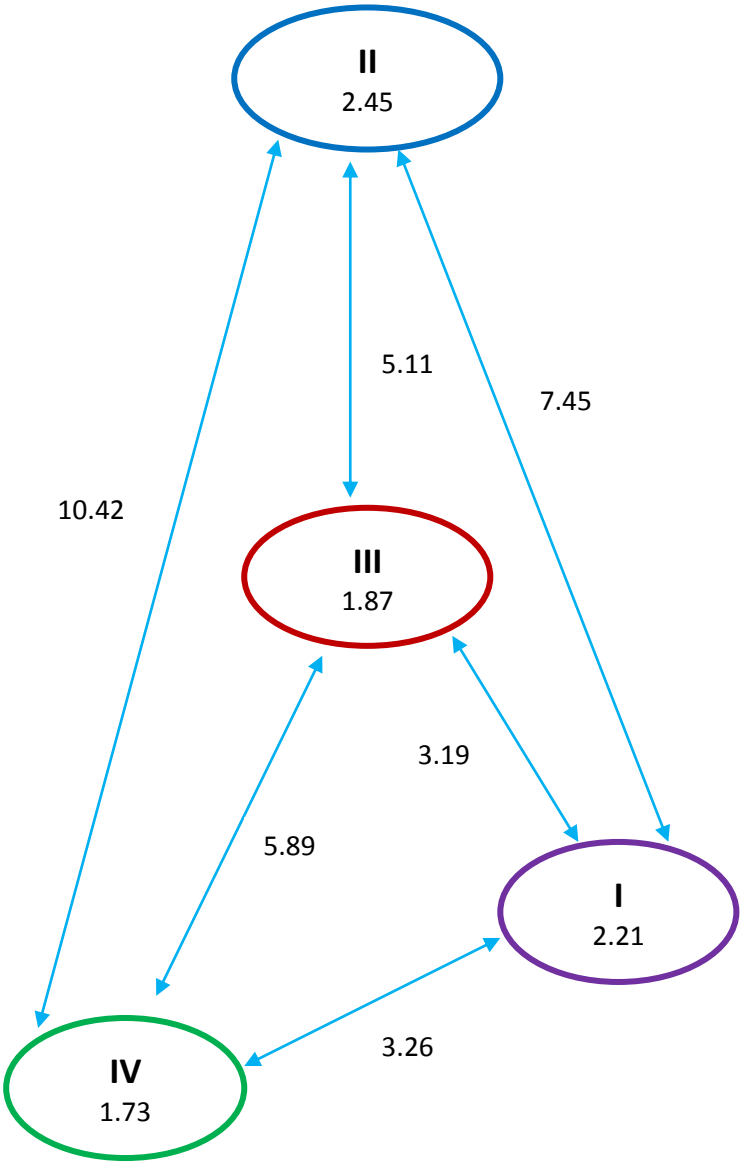

Figure 5. Intra and inter cluster distances of 33 genotypes in mungbean

Table 12. Relative contributions of the eight characters of 33 varieties to the total divergence

Principal component axes	Principal Component	
	Vector-1	Vector-2
Days to 50% flowering	0.3426	0.0356
Plant height (cm)	0.3877	0.0148
No. of branches per plant	0.1007	2.0940
Pods per plant	0.1420	-0.0428
Pod length (cm)	0.4361	0.8728
Seeds per pod	-0.0156	0.4476
100 seed weight (g)	-0.1844	0.0929
Seed yield per plant (g)	-0.1133	-1.5368

On the other hand, seeds per pod, 100 seed weight and seed yield per plant possessed the negative sign in the first axis of differentiation and pods per plant and seed yield per plant possessed negative signs in the second axis of differentiation, which meant these had minor role in the genetic divergence. The role of days to 50% flowering, plant height (cm), number of branches per plant and pod length (cm), in both the vectors was important components for genetic divergence in these materials.

4.4.7. Selection of genotypes as parent for hybridization program

Selection of genetically diversed parents is a most important step for hybridization program, so, in the present study genotypes were to be selected on the basis of specific objectives. From the crosses between genetically distance parents a high heterosis could be produced. Considering the magnitude of cluster mean and agronomic performance the genotype G_2 (BD-6875) for the minimum days to 50% flowering from cluster II; for the maximum number of pods per plants, seeds per pod G_1 (BD-6874) from cluster II; G_{28} (BD-6932) and G_{27} (BD-6929) for the maximum weight of 100 seed and pod length from cluster IV, G_{14} (BD-6904) for the maximum plant height were found promising. Therefore considering group distance and other agronomic performances G_1, G_2, G_{14}, G_{27}, G_{28} genotypes might be suggested as parents for future hybridization program.

CHAPTER V
SUMMARY AND CONCLUSION

Mungbean (*Vigna radiata* L.) provides grain for human consumption and as well as the plant fixes nitrogen to the soil. It supplies a substantial amount of nitrogen to the succeeding non-legume crops (i.e., rice) grown in rotation. Six varieties of mung bean have been developed by Pulses Research Centre, BARI and eight from BINA and disseminated with the package of management technologies to the farmers for cultivation. But limited study was done on mung bean and the area covered by this crop is not satisfactory. So for making more improvement further research was done. The research work was done in the experiment field and laboratory of Genetics and Plant Breeding department of Sher-e-Bangla Agricultural University, Dhaka, Bangladesh during the period from March to June 2017. The experiment was conducted in Randomized Complete Block Design (RCBD) with three replications of 33 genotypes of mungbean collected from BARI. Data on days to 50% flowering, plant height (cm), number of branches per plant, no. of pod/plant, no. of seeds/pod, pod length (cm), 100 seed weight (g), seed yield/plant (g) were recorded. There were great deals of significant variation for all the characters among the genotypes.

The genetic variability is the raw material of cereal breeding on which selection acts to evolve superior genotypes and the wide genetic variability that exists in the available genotypes provides huge scope for further improvement. Yield being a complex quantitative character, direct selection for yield may not result in successful improvement. Therefore, it is necessary to partition the observed variability into heritable and non-heritable components by calculating genetic parameters such as genotypic and phenotypic coefficient of variation, heritability and genetic gain.

The study revealed wide range of variability for most of the characters studied. On the basis of mean performance, genotypes G_2 (7.67) followed by G_8 (8.00), genotype G_1 (9.33) and genotype G_9 (9.33) took the minimum days to 50% flowering. Genotype G_{15} showed the maximum days to 50% flowering (19.33) whereas the yield (2.26) was comparatively lower than other. The highest plant was observed in genotype G_{14} (72.87cm). Genotype G_1 followed by G_2 was recorded to showed the maximum number of pod per plant (22.40, 21.33) and seeds per pod (12.80, 12.27). Genotype G_{28} followed by G_{27} showed the maximum pod length (8.98, 8.48) and 100 seed weight (7.30, 5.71). Seed yield per plant was the maximum in genotype G_1 (4.34 gm). So, these genotypes could be used for future breeding program.

The high magnitude of phenotypic and genotypic coefficient of variation (PCV and GCV) was observed for the characters e.g. days to 50% flowering (22.64, 22.18), plant height (20.27, 17.74), pod length (14.35, 12.95), and 100 seed weight (34.64, 32.23). Except number of pod per plant (40.80, 33.78), and seed yield per plant (30.20, 23.89). The differences between PCV and GCV for the characters were narrow indicating lesser influence of environment on these characters and could be improved by following phenotypic selection.

The highest estimated heritability among eight yield contributing characters 95.95%, 86.59%, 81.42%, 76.63%, 68.56% and 62.61% was in 50% flowering, 100 seed weight, pod length, plant height, number of pod per plant and seed yield, respectively. The lowest heritability was 40.43% and 47.01% in number of seed per pod and number of branches per plant.

The maximum genetic advance (GA 5%) was observed in plant height (15.78) among eleven characters of mungbean genotypes. The maximum genetic advance in percent of mean (GAMP) was obtained for 100 seed weight (61.78%) and the lowest was for number of seeds per pod (11.61%).

The significant positive correlation at the 5% level was observed for seed yield per plant with number of seed per pod at genotypic level and for plant height with pods per plant at both level and seeds per pod at genotypic level. The significant positive correlation at the 1% level was observed for pods per plant with seeds per pod and seed yield at both genotypic and phenotypic level. Path co-efficient analysis for seed yield revealed that seed yield per plant exerted the highest direct effect on pods per plant (0.631), followed by number of seeds per pods (0.425).

Genetic diversity was assessed by using Mahalanobis D^2 statistic. Grouping the genotypes into clusters using Tocher's method resulted in the formation of four clusters, of which cluster I was the biggest with thirteen genotypes followed by cluster II with eight genotypes. Cluster III and IV had six genotypes.

The maximum inter cluster distance was observed between cluster II and IV (10.425) followed by the distance between cluster I and II (7.450). The lowest inter cluster distance was observed between cluster I and III (3.199) followed by cluster I and IV (3.261). The highest intra cluster distance was identified in cluster II (2.45) and the lowest intra cluster distance was observed in cluster IV (1.73). The highest intra cluster distance between these genotypes indicated to obtain wide spectrum of segregating population if parents chosen from these distant cluster would be rewarding and can be used in hybridization program.

Incase of relative contribution of characters to total divergence days to 50% flowering (0.342, 0.035), plant height (0.387, 0.014), no. of branches per plant (0.100, 2.09) and pod length (0.436, 0.872) showed positive result (in both vector-I and vector-II). Selection of these characters will be effective because of their high relative contribution to total divergence.

Considering group distance and other agronomic performance G_1, G_2, G_{14}, G_{27}, G_{28} showed considerable genetic diversity. So among them crosses between these genotypes would be produced new recombinants with desired traits.

The results of the present study revealed that a wide variability exists among the collected mungbean genotypes and there was also genotypic variability of different yield contributing characters with yield of mungbean. Furthermore, there was also positive association of yield contributing characters with yield of mungbean. So, from the findings of the present study the following conclusions could be drawn:

- High heritability coupled with high genetic advance in percent of mean was observed in days to 50% flowering, pods per plant, pod length, number of pod per plant and 100 seed weight and seed yield. Hence, yield improvement in mungbean would be achieved through selection of these characters.

- Wide range of genetic diversity existed among the mungbean genotypes. The variability could be used for future breeding program of mungbean in Bangladesh.

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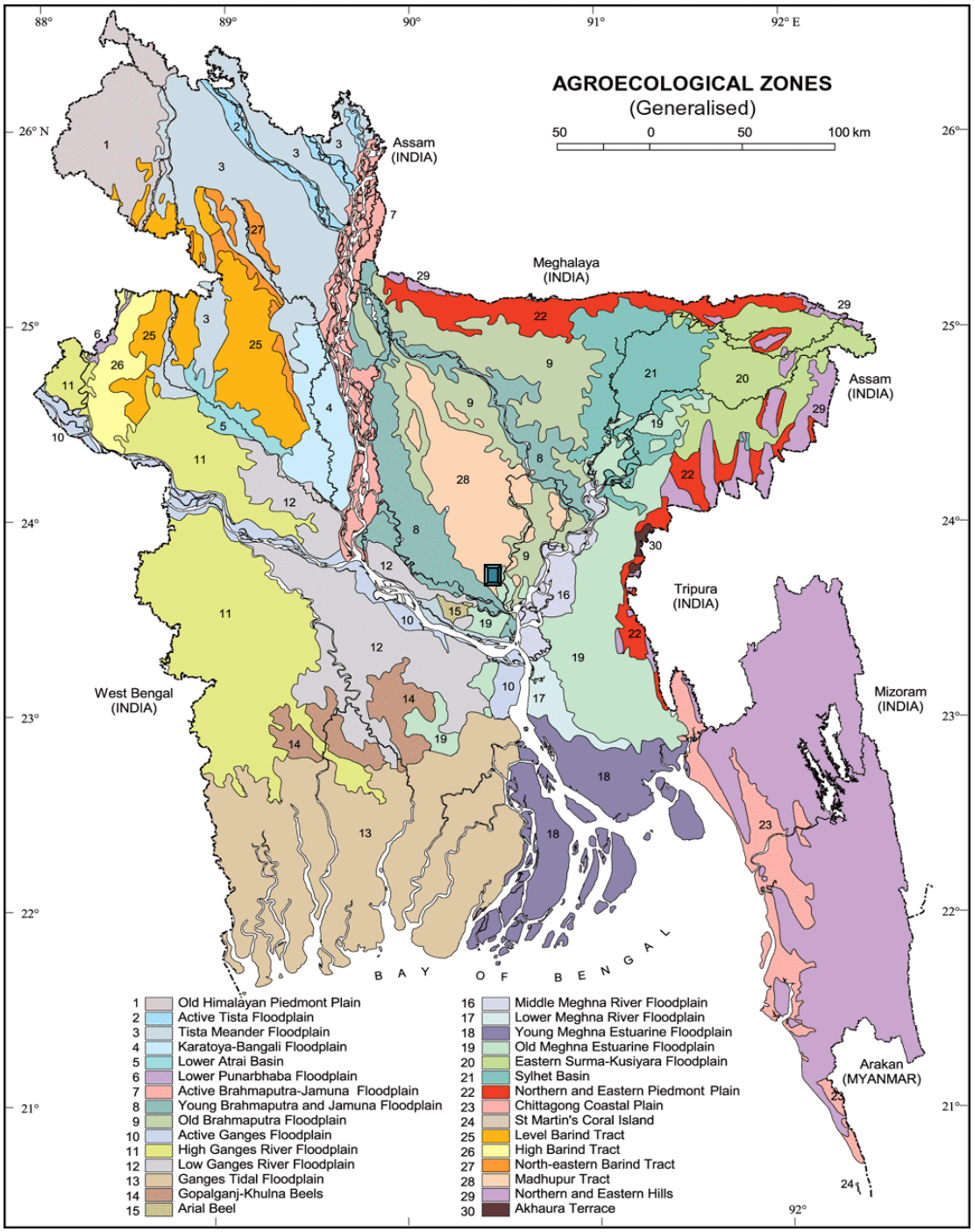
APPENDICES

Appendix I. Map showing the experimental site under the study



The experimental site under study

Appendix II. Monthly average Temperature, Relative Humidity, Total Rainfall and Sunshine of the experimental site from the period of March, 2017 to June, 2017

Month	Air temperature (°C)		Relative humidity (%)	Rainfall (mm)	Sunshine (hr)
	Maximum	Minimum			
March, 2017	32.5	20.4	62	65.8	7.2
April, 2017	33.7	23.6	71	156.3	6.0
May, 2017	32.9	24.5	76	339.4	5.1
June, 2017	32.1	26.1	82	340.4	3.7

Source: Bangladesh Meteorological Department (Climate & Weather Division), Agargaon, Dhaka - 1212

Appendix III. Physical characteristics and chemical composition of soil of the experimental site (0-15 cm depth)

Soil characteristics	Analytical results
Agroecological Zone	AEZ-28: Madhupur Tract
PH	6.00 – 6.63
Organic matter	0.84
Total N (%)	0.46
Available phosphorous	21 ppm
Exchangeable K	0.41 meq / 100 g soil

Source: Soil Resource and Development Institute (SRDI), Dhaka

Appendix IV. Mean performance of different characters of 33 mungbean genotypes

Genotypes	Days to 50% flowering	Plant height (cm)	Branches per plant	Pods per plant	Pod length (cm)	Seeds per pod	100 seed weight (g)	Seed yield per plant (g)
G-1	9.33	61.07	3.61	22.40	5.60	12.80	2.44	4.34
G-2	7.67	60.67	3.27	21.33	6.13	12.27	2.01	3.47
G-3	12.00	47.13	2.88	12.58	5.64	11.16	2.50	2.30
G-4	12.33	48.57	2.38	18.78	5.79	11.02	2.01	3.36
G-5	14.67	43.72	2.27	6.07	6.89	9.00	3.85	1.68
G-6	17.67	52.63	2.23	14.33	5.55	9.60	2.64	3.13
G-7	11.33	45.33	2.37	10.93	6.35	11.47	3.63	3.01
G-8	8.00	41.32	1.84	8.13	6.28	9.93	3.02	2.21
G-9	9.33	61.33	2.07	11.20	6.44	11.07	2.50	2.46
G-10	12.00	45.11	1.74	11.00	5.42	9.44	3.49	1.56
G-11	16.33	50.75	2.42	12.83	5.60	10.75	2.43	3.16
G-12	18.00	64.40	2.70	7.73	6.71	9.73	3.40	2.04
G-13	10.33	59.91	2.63	9.82	6.24	10.62	3.08	2.41
G-14	16.67	72.87	2.92	9.15	6.65	10.47	3.83	3.16
G-15	19.33	43.45	1.98	8.63	6.17	10.07	3.52	2.26
G-16	16.67	60.93	2.62	12.27	6.43	11.00	2.57	2.83
G-17	17.00	63.53	2.60	13.50	6.69	10.13	2.59	3.05
G-18	15.33	53.07	2.03	13.20	6.05	10.13	3.04	2.76
G-19	16.00	42.58	2.48	12.67	6.10	9.28	2.78	3.84
G-20	13.33	45.11	3.47	6.00	8.48	8.11	2.65	1.89
G-21	17.33	44.47	2.10	15.07	5.98	9.75	2.39	3.37
G-22	16.33	40.87	1.78	8.47	5.92	10.40	2.50	1.93
G-23	17.67	47.93	3.17	7.20	5.59	10.48	2.40	1.52
G-24	13.67	38.33	2.10	6.44	6.05	9.67	2.99	2.30
G-25	17.00	38.11	2.03	7.56	6.04	9.62	3.03	2.28
G-26	17.33	50.53	2.22	12.53	7.43	10.70	2.73	4.08
G-27	16.67	43.53	2.19	9.87	6.05	9.42	5.71	3.55
G-28	18.67	38.27	1.87	6.20	8.98	8.42	7.30	2.78
G-29	18.33	47.00	1.77	12.08	8.02	10.02	2.73	2.54
G-30	14.33	33.20	1.83	7.00	8.12	9.42	4.01	2.47
G-31	18.67	44.54	2.24	10.58	6.42	9.53	2.74	2.06
G-32	17.67	50.87	2.36	10.27	6.39	9.67	3.30	2.58
G-33	17.67	46.53	3.50	12.27	6.12	9.60	2.99	2.60
Mean	**15**	**49.32**	**2.41**	**11.15**	**6.43**	**10.14**	**3.11**	**2.70**
Minimum	**7.67**	**33.20**	**1.74**	**6.00**	**5.42**	**8.11**	**2.01**	**1.52**
Maximum	**19.33**	**72.87**	**3.61**	**22.40**	**8.98**	**12.80**	**7.30**	**4.34**

Appendix V. Analysis of variance for different characters in 33 mungbean genotypes

Characters	Mean sum of square		
	Replication (r-1) = 2	**Genotype (g-1) = 32**	**Error (r-1)(g-1) = 64**
Days to 50% flowering	0.74	33.61**	0.47
Plant height (cm)	140.48	253.09**	23.35
No. of branches per plant	0.27	0.83**	0.27
Pods per plant	4.96	49.11**	6.51
Pod length (cm)	0.55	2.24**	0.16
Seeds per pod	2.87	0.78**	2.87
100 seed weight (g)	0.38	3.18**	0.16
Seed yield per plant (g)	0.04	1.49**	0.25

** Denote Significant at 1% level of probability

Appendix: VI. Principal component score I and II

Genotypes	PCA 1	PCA 2
G-1	14.138	-8.668
G-2	13.458	-7.603
G-3	-1.724	-2.094
G-4	1.039	-7.768
G-5	-6.686	3.913
G-6	3.914	-2.339
G-7	-3.864	-0.850
G-8	-8.475	1.109
G-9	11.752	2.529
G-10	-4.216	-0.640
G-11	1.841	-1.523
G-12	13.877	6.855
G-13	10.043	3.624
G-14	22.490	7.285
G-15	-6.297	1.142
G-16	11.613	1.396
G-17	14.356	0.939
G-18	4.089	-1.122
G-19	-6.283	-2.863
G-20	-5.250	4.027
G-21	-3.853	-4.942
G-22	-8.795	0.560
G-23	-2.158	3.343
G-24	-11.750	2.038
G-25	-11.728	0.935
G-26	1.530	-1.195
G-27	-6.075	0.364
G-28	-12.143	3.073
G-29	-2.108	-1.304
G-30	-16.716	0.616
G-31	-4.822	-0.450
G-32	1.275	1.287
G-33	-2.469	-1.673