GENETIC VARIABILITY, CORRELATION AND PATH CO-EFFICIENT ANALYSIS OF YIELD AND YIELD CONTRIBUTING CHARACTERS IN MUNGBEAN (*Vigna radiata* L. Wilczek)

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CERTIFICATE

This is to certify that thesis entitled, "GENETIC VARIABILITY, CORRELATION AND PATH CO-EFFICIENT ANALYSIS OF YIELD AND YIELD CONTRIBUTING CHARACTERS IN MUNGBEAN(Vignaradiata L. wilczek)" 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 inGENETICS AND PLANT BREEDING, embodies the result of a piece of bonafide research work carried out byShakila SultanaRegistration No.09-03559under 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 duly been acknowledged.

(Prof. Dr. Md. SarowarHossain)
Supervisor

Dated: December, 2015
Place: Dhaka, Bangladesh

DEDICATED

TO

MY PARENTS

SOME COMMONLY USED ABBREVIATIONS

Full Word	Abbreviation	Full Word	Abbreviation
Advanced	*Adv.*	Etcetera	etc.
Agricultural	*Agril.*	Genetic Advance	GA
Agriculture	*Agric.*	Genetics	*Genet.*
Agriculturist	*Agricult.*	Genotype	G
Agronomy	*Agron.*	Genotypic coefficient of variation	GCV
Analysis of Variance	ANOVA	Genotypic variance	σ^2g
And others (at elli)	*et al.*	Gram	G
Applied	*Appl.*	Hectare	Ha
As for example	e.g.	Heritability in broad sense	h^2b
Bangladesh	BD	Horticulture	*Hort.*
Bangladesh Agricultural Development Corporation	BADC	Kilogram	Kg
Bangladesh Agricultural Research Institute	BARI	Leaf area index	LAI
Biology	*Biol.*	National	*Natl.*
Biotechnology	*Biotechnol.*	Newsletter	*Newsl.*
Botany	*Bot.*	Opinion	*Opin.*
Brasleira	*Bras.*	Particular pages	Pp.
Breeding	*Breed.*	Percent	%
Bulletin	*Bull.*	Phenotypic variance	σ^2g
Centimeter	Cm	Phenotypic coefficient of variation	PCV
Chronica	*Chron.*	Physiology	*Physiol.*
Company	Co.	Proceeding	*Proc.*
Completely Randomized Design	CRD	Progress	*Progr.*
Current	*Curr.*	Research	*Res.*
Days after sowing	DAS	Science	*Sci.*
Degree Celsius	°C	Technical	*Tech.*
Degrees of freedom	Df	University	*Univ.*
Ecology	*Ecol.*	Veterinary	*Vet.*
Economy	*Econ.*	Weight of hundred seed	WHS
Environment	*Env.*		
Environmental	*Environ.*		

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ABSTRACT

A field experiment was conducted in the experiment field of SAU and Genetics and Plant Breeding laboratory of Sher-e-Bangla Agricultural University, Dhaka, Bangladesh during the period of 6 December 2015 to 5 March 2016. The experiment was conducted in Randomized Complete Block Design (RCBD) with three replications. There were great deal of significant variations for many characters among the genotypes. 30 Mungbean (*Vigna radiata* L. Wilezek) genotypes were tested for genetic variability and correlation co-efficient and path analysis among 11 yield contributing traits i.e., plant height, pods per plant, pod length, seed per pod, primary and secondary branches, thousand seed weight and grain yield etc. Considering genetic parameter high genotypic co-efficient of variation (GCV) was observed for seed primary branches, number of pod per plant, thousand seed weight and seed yield whereas days of first flowering, days of 50% flowering, days to 80% maturity and number of seed per pod showed low GCV. In all cases phenotypic variance was higher than genotypic variances. High heritability with high genetic advance in percent of mean was observed in primary branches, number of pod per plant, thousand seed weight and seed yield indicating that these trait was under additive gene control and seletion for genetic improvement for these trait would be effective. High heritability with low genetic advance with percent of mean was observed for days to first flowering, days to 50% flowering, days to 80% maturity, number of seed per pod, secondary branches and pod length which indicated that non-additive gene effects were involved for the expression of this character and selection of this character might not be rewarding. The result obtained from the study showed that seed yield per plant had highest significant positive correlation with plant height, primary branches, number of pod per plant, pod length and thousand seed weight which indicated that these characters are important and can be used for direct selection for yield. Based on genotypic correlation analysis characters like pods per plant, pod length and on phenotypic basis, grain yield and seed per pod could be the best criteria in any breeding program for increasing yield in mungbean genotypes. Considering group distance and other agronomic performance the inter genotypic crosses between G15 and G27; G15 and G11; G23 and G21; G1 and G15; G4 and G29; G15 and G29; G4 and G16 may be suggested for future hybridization program.

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CHAPTER I
INTRODUCTION

Mungbean is one of the most important food legumes grown worldwide and the most common crops in most tropical and sub-tropical regions (Allahmoradi, 2011). Mugbean is one of the leading pulse crop of Bangladesh. This commonly grown pulse crop belongs to the family Fabaceae. It holds 3rd in protein content and 4th in acreage in production in Bangladesh (Sarkar *et al.*, 1982). The agro ecological condition is favorable for growing this crop. Pulse constitute the main source of protein for the people, particularly the poor sections of Bangladesh.

Mungbean (*Vigna radiata* L. Wilczek), a photo-periodic insensitive crop. It is well-adapted to low water and soil fertility, and has a short growth duration. In addition, it can be used in crop rotation practices (Somta and Srinives, 2007; Lavanya *et al*., 2008). It plays an important role in human feeding of developing country (Majnon Hoseini, 2009). The importance of this legume is related to desirable characteristics such as high protein content, broad adaptation, low need for agricultural inputs and high ability to increase soil fertility (Makeen *et al*. 2007). It is one of the important sources of protein for both man and domestic animals. Generally mungbean seeds contain 22-28% protein, 60-65% carbohydrates, 1-1.5 % fat and 3.5-4.5% fibers. Another important feature of mungbean is its ability to fix atmospheric nitrogen in symbiosis with nodule forming rhizobium bacteria. At AVRDC (The world vegetable centre), Taiwan, where the largest mungbean collection is maintained, the majority of the germplasms were originated from India (2705), Iran (579) and Afghanistan (281) (AVRDC, 2008). Evaluation of germplasm is useful in selection of core collection as well as for breeding programs

However, the present yield is not high enough to meet the demand of consumers and farmers because of its low yield potential, small seed size and

susceptibility to disease (Srivastava and Singh, 2013). Bangladesh is a developinng country. The land of our country is limited. But the population is very high. More food is required for its over growing population. We have to produce more food in decreasing agricultural land. To meet up the increased demand of food farmers are growing more cereal crops. Due to high population pressure, the total cultivable land is decreasing day by day along with the pulse cultivable land. So at present the cultivation of pulse has gone to marginal land because farmers do not want to use their fertile land in pulse cultivation. Pulse cultivation also decreasing due to its low yield and production.

It is grown three times in a year covering 43,680 ha with an average yield of 0.78 ton/ha (BBS, 2010). It is observed that area, production and yield were fluctuating since 1995/96 to 2005/06. Area decreased but yield increased, thereby production remained more or less same with wide fluctuation.

About 3 ton per ha. of seed yield has been reported in a trial in Taiwan (Lawn, 1978). The yield difference indicate wide scope for increasing yield of mungbean. The climatic condition of Bangladesh is favorable for mungbean production almost throughout the year. A lot of research have been carried out to increase the present yield of mungbean. But so far, no breakthrough has occurred in the yield ceiling of mungbean. Research has shown that the ultimate yield components contribute directly to the grain yield are in order to development, the number of pods per plant, average seed number and average seed size (Adams, 1967). Among these yield components the most dominant contributor to grain yield is the number of pods per plant are more precisely pods per unit land area in various legumes (Mackenzie *et al.* 1975) including mungbean (Prasanna and George,1982).

Genetic variability is a prerequisite for a successful breeding program of any crop species and a critical survey of genetic variability is essential before initiating an improvement program aiming to develop high yielding varieties.

The correlation coefficients between yield components usually show a complex chain of interacting relationship. Path coefficient analysis partitions the components of correlation coefficient into direct and indirect effects and visualize the relationship in more meaningful way.

Multivariate statistics help the researcher to summarize data and reduce the number of variables necessary to describe it (Anderson, 1972). The multivariate techniques, such as cluster analysis and principal component analysis may be an efficient tool in the quantitative estimation of genetic variation. To select germplasm in a more systemic and effective way and to develop strategies to incorporate useful diversity in their breeding programs, study of genetic diversity in genetic resources is a critical factor for breeders to better understand the evolutionary and genetic relationships among accessions (Lavanya *et al.*, 2008). Multivariate technique also plays an important role in choice of divergent parents for hybridization to exploit maximum heterosis.

Yield is the complex end product of many factors which jointly or singly influence the seed yield. Mungbean yield is depend on many important characters as well as on the environmental influence. For yield improvement it is essential to have knowledge on genetic variability of a biological population. A survey of genetic variability with the help of suitable parameter such as genotypic coefficient of variation, heritability and genetic advance are absolutely necessary to start a breeding program. Genetic variation of various attributes are useful for effective selection. These yield contributing attributes are correlated with pod yield and also among themselves. Path analysis find out the real contribution of this traits to yield and desired genotypes can be traced through diversity analysis

Keeping this view in mind, for better genotype searching as well as find out a better parent for hybridization, a study was conducted on diverse mungbean genotypes using agro-morphogenic characters and analysis of yield and yield contributing characters was performed with the following objective:

- To assess the variability present in different genotypes of mung bean.
- To evaluate the performance of 40 mungbean genotypes.
- To assess the characters association and contribution of characters for yield and yield contributing characters.
- To screen out the best genotypes for further use in breeding.

CHAPTER II
REVIEW OF LITERATURE

For planning a breeding program, a thorough knowledge about genetic parameter, correlation coefficient, path coefficient, and multivariate analysis of yield contributing characters are important. Information on genetic x environmental interaction helps to assess the suitability of growing the same strain in different locations. The genus *Vigna* is pan tropical and now has been broaden to include about 170 species, 120 from Africa, 22 from Indo-Pak sub-continent and south east asia and a few from other part of the world (Ghafoor *et al*., 2001). Only 7 species of *Vigna* are cultivated as pulse crop mostly in Asia, Africa and some parts of Latin America (Anishetty and Moss, 1988). It is generally considered that 2 of its cultivated species are of African origin (sub genus *Vigna*) and 5 are Asiatic origin (sub genus *Ceratotropis*). The Asiatic group consists, mungbean / greengram (*Vigna radiata* L. Wilczek), blackgram (*Vigna mungo* L. Hepper), mothbean (*Vigna aconitofolia* Jack. Marechal), adzukibean (*Vigna angularis* wild, Ohwi and Ohashi) and ricebean (*Vigna umbellata* Thunb, Ohwi and Ohashi). The sub genus *Ceratotropis* of the genus *Vigna* includes five important Asian pulses;mungbean, blackgram, ricebean, mothbean and adzukibean. Mungbean and blackgram have been the major pulses in Asia since ancient times (Arora and Mauria, 1989). At present mungbean cultivation spreads worldwide because it is digested compared to black gram (Smartt, 1990). The sub genus *Ceratotropis* is considered to have originated in Asia is called Asian *Vigna*. It forms a discrete group of about 17 species largely confined to Asia and the Pacific.

Research done over the several decades on Genetic parameter, correlation coefficient, path coefficient and multivariate analysis in mungbean is insufficient. Literature concerning the genotype x environmental interactions are also very limited. The available important literature and their findings which are related to the present study are presented in the following sections:

2.1. GENETIC PARAMETER

Makeen *et al*. (2007); studied twenty diverse Mungbean genotypes which were evaluated in Uttar Pradesh, India, to estimate the genetic variation, heritability, genetic advance for 10 quantitative characters. The genotypes differed significantly for all characters studied. Maximum heritability values were recorded in seed protein content, plant height and test weight. High heritability coupled with high genetic advance was observed in pods per plant, plant height and test weight, indicating the importance of additive gene effect for the expression of these characters.

Abrahim *et al.*(2007); evaluated genetic variability and heritability analyses for yield and yield components which were conducted for 646 accessions of green gram grown in Coimbatore, Tamil Nadu, India, during the Rabi and kharif of 2002-04. The estimates of phenotypic (PCV) and genetic (GCV) coefficients of variation were higher for single plant yield, number of branches per plant, number of pods per plant, number of clusters per plant, plant height, and length of branch, indicating greater scope of selection for these traits. Dry matter production and number of clusters per branch revealed wide differences between the estimates of PCV and GCV values, indicating the highly significant effect of environmental factors. The number of days to initial flowering, number of days to 50% flowering, number of days to initial maturity, number of days to full maturity, 100-seed weight, seed length, seed breadth, length of pod, and protein content were less affected by environmental factors, as the difference between the estimates of PCV and GCV was low. The estimates of heritability in the core collection indicated that the number of days to full maturity, number of days to initial maturity, number of days to initial flowering, number of days to 50% flowering, seed length, seed breadth, plant height, length of branch, 100-seed weight, and length of pod were highly heritable. High genetic advance as a

percentage of mean was recorded for the number of clusters per branch, length of branch, single plant yield. and number of pods per plant, number of clusters per plant, plant height and number of branches per plant, suggesting the possibility of selection for these traits in the core collection. High genetic advance coupled with high heritability and GCV was observed for length of branch, number of branches per plant, number of clusters per branch, number of clusters per plant, number of pods per plant, single plant yield and plant height indicating the predominance of additive gene action for this traits.

Rao *et al*. (2006); studied sixty genotypes of Mungbean (*Vigna radiata*) which were evaluated during 2000 in Guntur, Andhra Pradesh, India for 13 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 thirty-six genotypes of Mungbean for genetic variability of seed yield and its contributing characters in summer 2000 at Tirupati, Andbra Pradesh, India. High magnitude of variability was observed for pods per plant and grain yield per plant, while moderate variability was recorded for pods per cluster, clusters per plant, plant height and days to 50% flowering suggesting the possibility of their improvement by selection. 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 additivegene action.

Khairnar *et al.* (2003); evaluated twenty-two Mungbean genotypes for genetic variability in the kharif season of 1997, in Rahuri, Maharashtra, India. A wide range of variability was observed for plant height, clusters per plant, pods per plant, grain yield per plant and 100 grain weight. The estimates of genotypic as well phenotypic coefficients of variation were highest for pods

per plant followed by 100-grain weight. High heritability coupled with high genetic advance was observed for clusters per plant, pods per plant, grain yield and 100- grain weight indicating that these characters can be improved by selection.

Bangar *et al.* (2003); revealed that phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV). The GCV and PCV estimates were highest for branch number per plant and plant height among the characters. The GCV and PCV were of 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.

Pandey and Singh (2002), studied the genetic variability performance of green gram cultivars ML 552, PS 16, ML 371, LM 1510, PDM 11, PusaBaishakhi 1, PDM 84-139, PDM 54, ML 374 and ML 574 in rice-wheat cropping system in a field experiment conducted in Mccrut, Uttar Pradesh, India during the kharif season of 1998 and summer of 1999. Significant differences among the genotypes were observed in terms of plant height, number of days to 50% flowering and maturity, number of seeds per pod.

Similarly, Agarwal *et al.* (2001); studied genetic variability using 196 soybean germplasm. They found that GCV were moderate for days to flower initiation, days to flower termination, whereas low for days to maturity. Heritability and genetic advance as percentage of mean were high for all the plant growth characters (except moderate GAM for days to maturity).

Loganathan *et al*. (2001); studied Genetic variability in green gram (*Vigna radiata* L.). Fifty genotypes of green gram were used to estimate genetic variability for 10 quantitative characters in Tamil Nadu, India, during Rabi 1999. High phenotypic coefficient of variability indicated the favorable effect of environment for number of clusters per plant and seed yield per plant, and

high genotypic coefficient of variability suggested substantial amount of genetic variability for number of pods per plant and seed yield per plant. High genetic advance, additive gene action and phenotypic selection were effective for number of pods per plant, seed yield per plant and number of seeds per pod. Non-additive gene action, low heritability and low genetic advance were noted for days to first flowering, plant height, number of branches per plant, pod length and 100-seed weight.

Venkateswarlu *et al*. (2001); were assessed genotypic coefficients of variations (GCV), heritability and genetic advance in 17 diverse genotypes of green gram, grown during 1998/99 in Palem, Andhra Pradesh, India. Data were recorded for days to 50% flowering, days to maturity, plant height, number of clusters per plant, number of pods per plant, pod length, number of seeds per pod, 100-seed weight and seed yield per plot. Genotypes differed significantly for all the characters studied except 100-seed weight. Most of the characters showed high heritability values. Seed yield expressed high genetic advance coupled with high heritability and GCV, indicating the predominance of additive gene effects for this trait.

Mehetre *et al.* (2000); studied variability for 11 characters with 60 diverse genotypes of soybean. They reported that pods per plant and seed yield per plant had high genotypic and phenotypic coefficient of variation. They also reported that plant height and pods per plant had high genotypic and phenotypic coefficient of variation and high heritability associated with high genetic advance as percentage of mean.

Similarly Bhandarkar (1999), observed high co-efficient of variation and moderate heritability for pods per plant and seed yield per plant in soybean. He also observed high heritability and genetic advance as percent of mean for plant height and days to maturity.

Islam *et al.* (1999); studied on genetic variation, heritability on 9 yield components in 53 genotypes studied in Joydevpur during 1993. High values

for heritability and genetic advance were estimated for plant height, number of pods per plant, seeds per pod, 1000- seed weight and yield per plant.

Sharma (1999), studied on genotypic and phenotypic coefficients of variation, heritability derived from data on 9 yield-related traits in 15 Mungbean crosses and their six parents grown at Raipur during 1995-96. There was a high degree of genetic variability for all the yield-related traits studied. High heritability and high genetic advance were observed for days to flowering, pods/plant, seeds/plant, l000 seed weight and seed yield the predominance of additive gene effects for this trait.

Vikas *et al.* (1998); evaluated eighteen Mungbean parents (15 females and 3 males) and their 45 F_1 progeny for 12 yield-related traits at 4 sites in India (Simbhaoli, 2 sites in Meerut, and New Delhi) during kharif 1993. The genotypes differed significantly for most of the characters in all the environments. Estimates of components of variation showed that the variability of the material was not influenced by environmental differences. High components of genetic variation, heritability and genetic advance were obtained for plant height, number of clusters per plant, days to 50% flowering, number of pods per plant and biological yield. For these characters, additive gene effects were more important than non- additive gene effects, indicating the scope for improvement of these characters through selection.

Das *et al.* (1998); studied some 22 genotypes of green gram for genetic variability of seed yield and its contributing characters at Nagaon. Plant height, branches/plant, pods/plant, pod length and yield/plant recorded high genotypic coefficient of variation suggesting the possibility for improvement by selection breeding. High heritability associated with high genetic advance over mean was observed for plant height, branches/plant, pods/plant and pod length. It indicates that these traits were mostly controlled by additive gene action. Seeds/pod and yield/plant recorded low heritability coupled with low and high genetic advance, respectively.

Reddy *et al.* (1997); evaluated seventy genotypes of green gram from different geographical regions for 10 yield components at Tirupati in 1994. Genotypic and phenotypic variation was highest for branches/plant followed by grain yield/plant and pods/plant. Days to maturity followed by plant height and pod length had the highest heritability and were least influenced by the environment. Clusters/plant, pods/cluster, seeds/pod, 100seed weight and grain yield showed high differences in phenotypic and genotypic variation, indicating that the expression of these traits was influenced by environmental components.

Tiwari *et al.* (1995); evaluated six parents and their 15 F_2 progenies during mean-kharif 1981-82. High variability was found in the F_2 for days to maturity, clusters/plant, harvest index, pod length and 100-seed weight. Clusters/plant and 100-seed weight had highheritability. In parents, high heritability was found for plant height, seed yield/plant and harvest index, and in the F_2 for days to maturity, clusters/plant, pod length and 100-seed weight. High heritability estimates were generally associated with low genetic advance.

Shamsuzzaman and Shaikh (1982), performed an experiment with 169 local and exotic genotypes of Mungbean and found a significant difference among all the characters studied. Number of mature pods showed higher phenotypic and genotypic coefficients of variability. Number of branches and yield/plant displayed the highest (91.7) and the lowest (31.2) heritability, respectively. Number of mature pods/plant showed the highest values for both genetic advances expressed as percentage.

Rahman (1982), conducted a study on 9 varieties of Mungbean and found minimum coefficient of variation for pod length (0.4%) and maximum for yield/ha (35.5%).A considerable variation was also obtained for number for pods/plant (25.9%) and seed yield plant (24.6%).

Sandhu *et al*.(1979); studied variability among 435 strains of Mungbean for the characters, days to flowering and maturity, plant height, number of branches, fruit clusters and pods/plant, pod length, seeds/pod, 100-seeds weight and grain yield and found sufficient variability for all the characters. The phenotypic coefficient of variation was the highest (50.40) for total number of branches/plant. Grain yield/plant, pods/plant, fruit clusters/plant also showed considerable phenotypic coefficient of variation (3404, 32.7 and 30.1 percent respectively).

Nag *et al*. (1977); conducted two trails with 30 cultivars of Mungbean of diverse origin and found significant differences between cultivars in height, days to first ripening of pods, yield and yield components. Considering that large shiny bright-green seeds are preferred, M-374 and M-394 from the Philippines and AVRDC and 3404 from Thailand were the best.

Veeraswamy *et al.* (1973); conducted an experiment in 22 varieties ofmungbean to estimate genetic variability in some quantitative characters and high genetic coefficient of variation for the characters like number of flower clusters, pods and branches and plant height also reported high estimates of heritability and of genetic advance as a percentage of the number of clusters and branches and plant height.

Yohe and Poehlman (1972), studied the genetic variability of 300 strains of mungbean originated from 18 American, Asian, African and Middle Eastern countries and found a wide range of genetic variability for the characters like days to first ripening of pods, plant height, pods per plant, seed numbers per pod and 1000 seed weight. They also reported that moderately large size and as long as it was associated with flowering appeared to be desirable for high yield.

Chowdhury *et al.* (1971); studied genetic variability in 21 varieties of mungbean and found significant differences in the range of variability for all the ten characters studied but number of days to flowering, plant height and

pod length and 100 seed weight gave higher estimates heritability associated with higher genetic gain.

Singh and Malhotra (1970); estimated the genetic and environmental variability in 75 indigenous and exotic strains of mungbean that appear todiffer in high quantitative characters contributing yield and found wide genotypic and phenotypic for all the characters. They also concluded that selection based on100 seed weight, which had the highest genetic variability and very high genetic advance, would be the most effective. Genetic advance was also observed to be high for numberofpod, branches and seed yield per plant but these characters had low heritability estimates.

Gupta and Singh (1969), estimated variability, heritability and genetic advance in 10 quantitative characters of 36 mungbeanvarieties and reported that 87% of variation in yield accounted for the number of pods, pod length and weight.

Chowdhury *et al*. (1968); performed an experiment on 16 Indian and 5 Japanese varieties of mungbean and found a great variation in different varieties for the characters like plant height, number of branches, number ofpods, number of seeds/pod, 1000 seed weight ad yield. Desirable characters such as high yield of grain, earliness and grain quality in terms of size was found in different varieties. They also suggested that these desirable characters from different varieties should be combined into one variety by hybridization.

2.2 Correlation coefficient

Makeen *et al.* (2007); studied twenty diverse mungbean genotypes which were evaluated in Uttar Pradesh, India to estimate correlation coefficient for 10 quantitative characters. Higher genotypic and phenotypic coefficients of variation were observed for seed yield and number of pods per plant. Character association indicated that pods per plant and plant height had significant positive correlation with seed yield.

Sirohi and Kumar (2006), studied correlation analysis for yield and yield components which were conducted for 19 diverse genotypes of mungbean (*Vigna radiata*) grown in Berthin, Himachal Pradesh, India, during the spring of 1999. The genotypic correlation was dominant to the phenotypic correlation. The number of clusters per plant and number of productive pods per plant exhibited significant and positive correlation with seed yield per plant.

Rao *et al.* (2006); studied sixty genotypes of mungbean (*Vigna radiata*) which were evaluated during 2000 in Guntur, Andhra Pradesh, India. Correlation studies indicated that the total dry matter, number of pods per plant, number of clusters per plant, number of branches per plant and days to 50% flowering were positive and significantly associated with seed yield.

Dhuppe *et al.* (2005); studies on correlation which were carried out in 35 genotypes (11 parental lines and 24 hybrids) of mung bean, grown in Parbhani, Maharashtra, India, in 1998. Data were recorded for days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per plant, 100-seed weight and yield per plant. Grain yield per plant showed positive and significant correlation with days to maturity, number of secondary branches per plant, number of pods per plant and 100-seed weight at genotypic level, whereas secondary branches per plant and100-seed weight were correlated with grain yield at phenotypic level. 1-781 K-H x AKM-9242 were found.

Pandey *et al*. (2002); studied yield correlations and performance of green gram cultivars MT 552 PS 16, ML 371, LM 1510, PDM 11, PusaBaishakhi 1. PDM 84- 139, PDM 54, ML 374 and ML 574 in rice-wheat cropping system in a field experiment conducted in Meerut, Uttar Pradesh, India during the kharif season of 1998 and summer of 1999. Grain yield had significant positive association with number of seeds per pod and test weight. A 300%

cropping intensity can be achieved using the compatible cultivars of rice (Pant Dhan 12 or 10), wheat (UP 233 8/PBW 343) and green gram (PS 16).

Rajan *et al*. (2000); were studied the correlation in 7 parents and F2 population of their 21 crosses in green gram for 13 characters. Seed yield had significant positivegenotypic correlation with number of secondary roots at maturity, dry weight ofplants at maturity, plant height, pods per plant, seeds per pod and thousand grain weight and harvest index. Number of pods, pod per plant and harvest mdcx showed high positive correlation on grain yield and also with each other.

Rajanna *et al.* (2000); estimated significant and positive correlation of number pods per plant, number of clusters per plant and 100-seed weight with seed yield in soybean. Days to maturity, plant height and number of branches per plant exhibited significant and positive correlation with number of clusters per plant and number of pods per plant. Path analysis indicated effect on seed yield per plant.

Islam *et al*. (1999); studied on genetic correlation on 9 yield components in 53 genotypes studied in Joydebpur during 1993.Yield per plant was significantly and positively, correlated with plant height, number of primary branches per plant, number of pods per plant, pod length, number of seeds per pod and 1000-seed weight.

Sharma *et al*. (1999); studied on correlation coefficients is derived from data on 9 yield-related traits in 15 mung bean crosses and their six parents grown at Raipurduring 1995-96. Seed yield was significantly correlated with branches/plant, seeds/plant, pods/plant, pod clusters/plant, seeds/plant and 1000 seed weight

Niazi *et al*. (1999); evaluated genotypic correlation and path-coefficient analysis for 8 agronomic characters affecting seed yield which was accomplished in 15 elite genotypes of mungbean. All the correlation coefficients were significant, whilst number of filled pods per plant, plant

height, number of columns and seed per pod and number of clusters per plant revealed a strong positive association with seed yield per plant. Pods per plant emerged as a reliable component that can serve as a selection criterion in breeding high yielding cultivars of mungbean.

Yaqoob *et al*. (1997); studied ten important agronomic characters for estimation of co-efficient of correlation in 30 genotypes/mutants of Mungbean grown under rain fed conditions at Dera Ismail Khan in 1991. The results showed that grain yield had a positive genotypic relationship with days to 50% flowering, number of branches, number of pods, 1000-seed weight, dry matter yield and harvest index.

Sharma (1995), observed highly significant and positive correlations for number of seeds/plant and 100-seed weight with seed yield in 6 mung bean (*Vigna radiata*) genotypes and then 6 F_1 and 6 F_2 hybrids grown at Jabalpur, Madhya Pradesh in1985.

Kumar *et al*. (1995); studied on yield correlations is derived from data on 6 yield components in 16 genotypes grown during kharif 1989. Pods/plant and 100-seed weight were significantly and positively correlated with seed yield.

Singh and Pathok (1993), recorded on 11 quantitative traits in 20 *Vigna radiata* parents, 90 F_1s and 90 F_2s. Seed yield was positively correlated with plant height, clusters/plant, number of pods/cluster, number of pods/plant, pod length, seeds/pod and 100-seed weight.

Shamsuzzaman and Shaikh (1982), studied the characters association of 169 local and exotic genotypes of Mungbean and observed significant positive correlation of yield/plant with number of primary branches, mature pods/plant and seeds/plant while maturity period, plant height and 1000-seed weight exhibited negative correlated with seed yield. They also reported the height and 1000-seed weight exhibited negative correlated with seed yield. They also reported the highest association of yield/plant with number of mature pod/plant.

Rahman (1982), performed an experiment with 9 varieties/lines of Mungbean study to the correlation and coefficients in some agronomic characters and obtained positive correlation of days to 50% flowering with days to maturity and plant height of days to maturity with plant height, pod length, 1000-seed weight and seed yield/plant of plant height with pod length and seed yield/plant, of number of pods/plant with seed yield/plant, of pod length with 1000-seed weight and seed yield, number of seeds/pod with yield/ha and of 1000-seed weight with seed yield/plant.

Bhaumik and Jha (1980), estimated the biometrical relationships in 2 cultivar of Mungbean and found positive correlation of seed Yield/plant with 1000-seed weight seed/pod and pods/plant. They also reported negative correlation between seed and plant height.

2.3 Path coefficient:

Makeen *et al*. (2007); evaluated twenty diverse Mungbean genotypes and found maximum direct effect on seed yield was observed in pods per plant, test weight andplant height.

Sirohi and Kumar (2006), studied path-coefficient analysis for yield and yield components which were conducted for 19 diverse genotypes of mung bean (*Vigna radiata*) grown in Berthin, Himachal Pradesh, India, during the spring of 1999. All the traits except plant height and number of productive branches per plant had higher magnitude of indirect effects than the direct effects on seed yield per plant. The number of productive branches per plant had a direct significant contribution to seed yield per plant.

Rao *et al.* (2006); studied sixty genotypes of mung bean (*Vigna radiata*) which were evaluated during 2000 in Guntur, Andhra Pradesh, India.Total dry matter and number of pods per plant had direct positive effect on seed yield while plant height had negative effect.

Dhuppe *et al*. (2005); studies on correlation and path analysis which were carried outin 35 genotypes (1 parental lines and 24 hybrids) of mungbean,

grown in Parbhani. Maharashtra, India, in 1998. Data were recorded for days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per plant, 100-seed weight and yield per plant. Path analysis revealed that the number of seeds per plant and 100-seed weight were the major yield contributing characters. The performance of Jal-781 x AKM-9504 and Jal-781 K-H x AKM-9242 were found.

Rajan *et al*. (2000); were studied path coefficients in 7 parents and F_2 population of their 21 crosses in green gram for 13 characters. Path analysis revealed that pods per plant had the highest positive direct effect on grain yield, followed by hundred grain weight on grain yield. The study revealed that genetic improvement of grain yield is possible by selecting characters having high positive correlation and positive direct effect.

Sharma *et al*. (1999); studied on correlation coefficients is derived from data on 9 yield-related traits in 15 mung bean crosses and their six parents grown at Raipur during 1995-96.Phenotypic and genotypic path analysis revealed that seeds/plant had the highest positive direct effect on grain yield followed by 1000 seed weight, plant height and pods/plant..

Sabaghpour *et al*. (1998); evaluated path analysis of yield components in Mungbean varieties. Some 49 varieties of mung bean (*Vigna radiata*) at Gorgan in 1993.Seed yield/plant had highly significant and positive correlation with seeds/plant and pods/plant. Path coefficient analysis revealed that seeds/plant and 100-seed weight had the largest positive direct effect on mung bean yield.

Yaqoob *et al*. (1997); studied ten important agronomic characters for estimation of co-efficient of correlation in 30 genotypes/mutants of mung bean grown under rain fed conditions at Dera Ismail Khan in 1991. Path co-efficient analysis revealed positive direct effects of days to 50% flowering, days to maturity, number of branches, 1000-seed weight, dry matter yield and

harvest index on grain yield. A negative direct effect of plant height, number of pods and number of clusters on grain yield was observed in this study.

Rahman (1982), studied the path-coefficient analysis in some quantitative characters of 9 Mungbean varieties and showed that pod length, 1000 seed weight, days to 50% flowering, plant height and number of pods/plant had direct contribution to yield to the extent of 0.560 to 1.470, while days to maturity (-2.039) and number of seeds/pod (-0.800) had negative direct contribution to yield.

Bhaumik and Jha (1980), conducted path coefficient analysis in 20 Mungbean cultivars and found indirect effect of number of nodes on the main stem and number of primary branches on the yield through the number of pods/plant and that of pod length was through number of seeds/pod and 1000-seed weight. They also reported negative correlation of yield with plant height both directly and indirectly.

Singh and Malhotra (1976), performed an experiment with 75 strains of Munbean to estimate path coefficient and observed that seed yield was influenced by pods/plant, seed/pod and 1000-seedweight if other yield components were kept constant. However, 1000-seedweight had a negative indirect effect on yield by affecting the number of seeds/pod and pod per plant.

2.4 Multivariate analysis

Twenty eight crosses resulting from 8 x 8 diallel excluding reciprocal were studied by Srivastava and Singh (2013) to know the magnitude of heterosis over better parent and standard variety for yield and its components in mungbean. The highest heterosis to the extent of 80.76% over standard variety and 72.39% over better parent for seed yield per plant was observed in the cross Narendra Mung-1 x PS-16 which exhibited high heterosis percentage for yield and yield components. The promising hybrids viz. Pusa Baisakhi x Pusa bold (vishal), Pusa Baisakhi x Pant M-3, Narendra Mung-1 x

PS-16, Pusa Baisakhi x Pusa-105, Pusa Baisakhi x ML-613 were identified which have increased potential to exploit the hybrid vigor or to isolate the desirable segregants.

Allahmoradi *et al*. (2011); conducted field experiment to investigate the resistance of mung bean and its physiological responses to drought stress. Results showed that there was no significant difference in yield and yield components between control and drought stress during reproductive growth stage, whereas drought stress during vegetative growth stage significantly decreased yield and yield components. Relative water content of leaves appeared to be the most limiting factor responsible for the differences in yield between treatments.

Yimram *et al.*(2009); cultivated 340 mungbean accessions to study the extent and pattern of their diversity with respect to the traits measured. They also estimated broad-sense heritability (H) and expected genetic advance (GA) from selection of major quantitative traits. The germplasm displayed a wide range of diversity for most of the traits evaluated. High genetic variability, moderate to high H and GA were found in yield components, i.e. 100-seed weight, seed weight per plant, and number of pods per plant. Principal component analysis revealed that the first three PCs explained 74.9% of the total variation. The variance explained by PC1 was due to the variation in almost all traits. PC2 originated principally from number of pods per plant, number of branches per plant, pod width and seed length.

Lavanya *et al*. conducted an experiment in 2008. They used RAPD profiles which were used to identify the extent of diversity among 54 accessions of mung bean that included both improved and local land races. Out of the 40 primers screened, seven primers generated 174 amplification products with an average of 24.85 bands per primer. The RAPD profiles were analysed for Jaccard's similarity coefficients that was found to be in the range from 0 to 0.48, indicating the presence of wide range of genetic diversity at molecular level. This study indicated that the RAPD profiles provide an easy and simple

technique for preliminary genetic diversity assessment of mung bean accessions that may reflect morphological trait differences among them.

Somta and Srinives (2007), conducted an experiment on Genome research of mungbean and black gram. They improved genetic transformation protocols for the crops have been developed recently. High-throughput markers such as SSRs and SNPs has been developed for closely related legumes with mungbean and black gram will be helpful to accelerate genome research and molecular breeding in these crops.

Makeen *et al.* (2007); conducted an experiment to study genetic variability, heritability and genetic advance to utilize mungbean gene pool effectively under rain-fed conditions during kharif. The number of pods per plant and seed yield were recorded with significantly higher heritability (>60%), corresponding PCV (>25%) and GCV (>20%) coupled with more than 30% genetic advance. The correlation studies exhibited highly significant and positive association of all the quantitative characters with seed yield except with that of days to 50% flowering. The number of pods per plant had the maximum direct effect followed by plant height and 1000-seed weight indicating their direct contribution towards seed yield.

Zubair *et al.* (2007); conducted an experiment with forty diverse Mungbean (*Vigna radiata* L. *Wilczck*) genotypes were evaluated for 14 quantitative traits at National Agricultural Research Centre, Islamabad, Pakistan during 1999-2000 under rain fed conditions. All the traits were analyzed using multivariate analysis technique (cluster and principal component analyses). The first four PCs with eigenvalues >1 contributed 85.49% of the variability amongst genotypes. Populations with high PC1 values were high yielding and early in maturity. The populations with high PC2 were late in flowering and maturity, and contributed more towards vegetative growth rather than reproductive. The genotypes were categorized iti four clusters based on average linkage. Clusters I, II and IV were more clearly separated from

cluster III. Cluster analysis revealed that genotypes under investigation displayed a wide range of variation for most of the traits that could be exploited in breeding program to enrich the Mungbean genetic treasure.

Raje and Rao (2000), conducted an experiment with two hundred germplasm lines along with 6 commercial mung bean cultivars were evaluated in Jabalpur. Madhya Pradesh, India over 4 environments (2 sowing dates during summer, and 2 sowing dates during kharif). Multivariate linear regression analysis was conducted on various characteristics contributing to seed yield Days to maturity, plant height, clusters per plant, pods per cluster, pods per plant, pod length, seeds per pod, seeds per plant and hundred seed weight contributed mainly to seed yield, while days to 50% flowering, days from flowering to maturity, plant height, primary branches per plant, pod length, seeds per pod and hundred seed weight contributed mainly to biological yield and harvest index.

Ghavami and Rezai (2000), performed to investigate the genetic and geographic diversity of 193 *Vigna radiata* accessions from the Iran Mungbean Collection, from the view point of phenology and some morphological characters, and to study the relation between various characters by multivariate analysis, a field experiment was conducted in Isfahan, Iran [date not given]. Results indicated the presence of high variability for yield and other yield components, but low variation for phenological traits. Cluster analysis grouped the genotypes into 6 clusters. Genotypes in groups 5 and 6, because of having short growth duration and high seed yield, were distinguished as being very suitable. Grouping of countries and cities indicated that the pattern of genetic diversity followed the geographic diversity for countries, but this relation was not detected for the cities. Factor analysis revealed 2 factors, the first one with a major impact on lateness, reduction of 1000-seed weight and seed yield, and the second one with effects on number of pods per plant and seed yield. Canonical correlation analysis for phenological and morphological traits led to

introduction of 2 pairs of variables: ‘lateness’ and ‘seed and pod smallness’, and ‘vegetative growth rate’ and ‘yield specific’.

Jain and Ramgiry (2000), showed significant variation for yield per plant. High heritability values accompanied by genetic advance as a percentage of mean were noticed for seed yield, plant height and pods per plant.

Nehru *et al.* (1999); estimated genetic advance and heritability for 16 yield and quality components in 49 genotypes of soybean. They found days to maturity and 100 seed weight had high heritability but low genetic advance.

CHAPTER III
MATERIALS AND METHODS

This chapter illustrates information concerning methodology that was used in execution of the experiment. It comprises a brief description of locations of experimental site, planting materials, climate and soil, seed bed preparation, layout and design of the experiment, pot preparation, fertilization, transplanting of seedlings, intercultural operations, harvesting, data recording procedure, statistical and nutritional analysis etc., which are presented as follows:

3.1 Experimental site

The experiment was accomplished at the agronomic field of Sher-e-Bangla Agricultural University, Dhaka-1207, Bangladesh during the period from December 2015 to March 2016. Location of the site is 23°74' N latitude and 90°35' E longitude with an elevation of 8 meter from sea level (Anonymous, 2014) 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 of the experimental site belongs to Agro ecological region of "Madhupur Tract" (AEZ No. 28). The soil was clay loam in texture and olive gray with common fine to medium distinct dark yellowish brown mottles. The pH was 6.00 to 6.63 and organic carbon content is 0.84% (Appendix II). The records of air temperature, humidity and rainfall during the period of experiment were noted from the Bangladesh Meteorological Department, Agargaon, Dhaka (Appendix III).

3.3 Experimental materials

Thirty genotypes of mungbean were collected from Plant Genetic Resources Centre (PGRC), Bangladesh Agricultural Research Institute (BARI), Gazipur

and from Bangladesh Agricultural Development Corporation (BADC) on December 2015 (Table 1).

3.4 Design and layout of the experiment

The experiment was laid out and evaluated during Rabi season 2015-16 in Randomized Complete Block Design (RCBD). The experiment was conducted in 3 replications and plant to plant distance was 15 cm and line to line distance was 30 cm. The total land size was 126.75 m^2. The plot to plot distance was 2.5m. The genotype was randomly distributed to each line.

3.5 Land preparation

The experimental plot was prepared by ploughing with tractor followed by harrowing and laddering by cows. Weeds and stables were removed. Manures and fertilizers were applied as per the recommended dose before the final land preparation. The final land preparation was done on 4 December 2015.A pictorial view showing, A. design and layout.B. sowing of seed in Plate 1.

3.6 Manure and fertilizer application

Due to ability of nitrogen fixation from atmosphere mungbean requires less nitrogen application. But for initial establishment of plant up to the stage of nodule formation a starter dose of 20-40-20 NPK, respectively was applied. Soil was well pulverized and dried in the sun and only well decomposed cow dung was mixed with the soil according to the recommendation guide BARI, 2006.The doses of manure and fertilizers were given below-

Fertilizers/ Manures	**Dose (kg)**	
	Applied in the plot	**Quantity /ha**
Urea	2.01	47
TSP	3.56	88
MP	1.51	36
Cow dung	Applied earlier	2 ton

Table no. 1. List of mungbean genotypes with their Accession No.

Serial No.	Genotype No.	Name/Acc No.(BD)
1	G1	BD-6875
2	G2	BD-6876
3	G3	BD-6878
4	G4	BD-6881
5	G5	BD-6882
6	G6	BD-6884
7	G7	BD-6885
8	G8	BD-6886
9	G9	BD-6887
10	G10	BD-6888
11	G11	BD-6890
12	G12	BD-6891
13	G13	BD-6892
14	G14	BD-6893
15	G15	BD-6895
16	G16	BD-6897
17	G17	BD-6899
18	G18	BD-6902
19	G19	BD-6906
20	G20	BD-6908
21	G21	BD-6909
22	G22	BD-10022
23	G23	BD-10023
24	G24	BD-10024
25	G25	BD-10026
26	G26	BD-10027
27	G27	BD-10028
28	G28	BD-10029
29	G29	BD-10030
30	G30	BD-10032

A

B

Plate 1: A pictorial view showing. A. design and layout. B. sowing of seed

TSP, MP and Gypsum were applied at the time of final land preparation. Cow dung was applied two weeks before seed sowing during the land preparation.

3.7 Sowing of seed and intercultural operation

The seed of 30 mungbean genotypes were sown in the field on 6 December 2016. Intercultural practices were done uniformly for all the genotypes. Thinning was done 25 days after sowing and weeding was done twice-the first during thinning and the second after about two months of sowing.A pictorial view showing intercultural operation is presented in Plate 2.

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. Harvesting was completed on 5 March 2016.A pictorial view showing the mungbean field at maturity stage in Plate 3.

3.9 Data collection

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

3.9.1 Days to first flowering

Difference between the dates of sowing to the date of a plot was counted as days to first flowering. Days to first flowering was recorded when first flower of a plot were at the opened flowered.

3.9.2 Days to 50% flowering

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

Plate 2: A pictorial view showing intercultural operation

Plate 3: A pictorial view showing the mungbean field at maturity stage

3.9.3 Days to 80% maturity

Difference between the dates of sowing to the date of maturity of a plot was counted as days to maturity. Days to maturity was recorded when 80% pod of a plot were matured.

3.9.4 Plant height (cm)

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

3.9.5 Number of main branches per plant

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

3.9.6 Days Number of secondary branches per plant

The total number of branches arisen from the primary branch of a plant was counted as the number of secondary branches per plant.

3.9.7 Number of pod per plant

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

3.9.8 Pod length (cm)

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

3.9.9 Number of seeds per plant

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

3.9.10 1000 seed weight (g)

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

3.9.11 Yield/plant

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 Statistical analysis

Mean data of the characters were subjected to multivariate 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 2000 software through four techniques viz., Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CA) and Canonical Vector Analysis (CVA).

3.10.1 Estimation of genotypic and phenotypic variances

Genotypic and phenotypic variances were estimated according to the formula of Johnson *et al.* (1955).

Genotypic variance, $\delta^2 g = \frac{MSG - MSE}{r}$

Where, MSG = Mean sum of square for genotypes

MSE = Mean sum of square for error, and

r = Number of replication

Phenotypic variance, $\delta^2 p = \delta^2 g + \delta^2 e$

Where, $\delta^2 g$ = Genotypic variance,

$\delta^2 g$ = Environmental variance = Mean square of error

3.10.2 Estimation of genotypic and phenotypic co-efficient of variation

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

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

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

Where, GCV = Genotypic co-efficient of variation

PCV = Phenotypic co-efficient of variation

δ_g = Genotypic standard deviation

δ_p = Phenotypic standard deviation

$\bar{x}$ = Population mean

3.10.3 Estimation of heritability

Broad sense heritability was estimated by the formula suggested by Singh and Chaudhary (1985).

$$h^2_b(\%) = \frac{\delta^2_g}{\delta^2_p} \times 100$$

Where, h^2_b = Heritability in broad sense

δ^2_g = Genotypic variance

δ^2_p = Genotypic variance

3.10.4 Estimation of genetic advance

The following formula was used to estimate the expected genetic advance for different characters under selection as suggested byAllard (1960).

$$GA = \frac{\delta^2_g}{\delta^2_p} . K . \delta_p$$

Where, GA = Genetic advance

δ^2_g = Genotypic variance

δ^2_p = Phenotypic variance

δ_p = Phenotypic standard deviation

K = Selection differential which is equal to 2.06 at 5% selection intensity.

3.10.5 Estimation of genetic advance in percentage of mean

Genetic advance in percentage of mean was calculated by the following formula given by Comstock and Robinson (1952).

$$\text{Genetic Advance in percentage of mean} = \frac{\text{Genetic advance}}{\bar{x}} \times 100$$

3.10.6 Estimation of simple correlation co-efficient

Simple correlation co-efficient (r) was estimated with the following formula (Singh and Chaudhary, 1985; Clarke, 1973).

$$r = \frac{\sum xy - \frac{\sum x \cdot \sum y}{N}}{\sqrt{[\{\sum x^2 - \frac{(\sum x)^2}{N}\}\{\sum y^2 - \frac{(\sum y)^2}{N}\}]}}$$

Where, $\sum$ = Summation

x and y are the two variables correlated

N = Number of observation

3.10.7 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:

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

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

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

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_{yx1} = The direct effect of x1 on y.

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

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

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

$$P^2_{RY} = 1 - \sum P_{iy} \cdot riy$$

Where, P^2_{RY} = (R^2); and hence residual effect, $R = (P^2_{RY})^{1/2}$

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

Riy = Correlation of the character with yield.

3.10.8 Multivariate analysis

The genetic diversity among the genotypes was assessed by Mahalanobis (1936) with general distance (D^2) statistic and its auxiliary analyses. The parent's selection in hybridization program based on Mahalanobis's D^2statistic 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, Principal Coordinate analysis, Cluster analysis and Canonical Vector analysis (CVA),

which quantify the differences among several quantitative traits, are efficient method of evaluating genetic diversity. These are as follows:

3.10.9 Estimation of genetic diversity

3.10.9.1 Principal Component Analysis (PCA)

Principal component analysis, one of the multivariate techniques, is used to examine the interrelationship among several characters and can be done from the sum of squares and product matrix for the characters. Therefore, principal component were computed from the correlation matrix and genotype scores obtained from the first components (which has the property of accounting for maximum variance) and succeeding components with latent roots greater than the unity (Jager *et al.* 1983). Contribution of the different morphological characters towards divergence is discussed from the latent vectors of the first two principal components.

3.10.9.2 Principal Coordinate Analysis (PCO)

Principal coordinate analysis is equivalent to principal component analysis but it is used to calculate inter-unit distances. Through the use of all dimensions of P it gives the maximum distances between each pair of the n point using similarity matrix (Digby *et al.*, 1989).

3.10.9.3 Canonical Vector Analysis (CVA)

The canonical vector analysis compute a linear combination of original variabilities that maximize the ratio in between group to within group variation to be finding out and thereby giving functions of the original variabilities that can be used to discriminate between groups. Finally, a series of orthogonal transformations sequentially maximizing the ratio of the among groups to the within group variations.

3.10.9.4 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 Chaudhury (1985). The D^2 values were estimated for all possible

combinations between genotypes. In simpler form D^2 statistic is defined by the formula

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

Where,

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

x = Number of characters.

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

3.10.9.5 Computation of average intra-cluster distances

Average intra-cluster distances were calculated by the following formula as suggested by Singh and Chowdhury (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.

3.10.9.6 Computation of average inter-cluster distances

Average inter-cluster distances were calculated by the following formula as suggested by Singh and Chowdhury (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. and n_j= Number of populations in cluster j.

3.10.9.7 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 Chowdhury (1985). It gives a brief idea of the pattern of diversity among the genotypes included in a cluster.

3.10.9.8 Clustering

To divide the genotypes of the study into some number of mutually exclusive groups clustering were done using non-hierarchical classification. Starting from some initial classification of the genotypes into required groups, the algorithm repeatedly transfers genotypes from one group to another so long as such transfers improve the criterion, the algorithm switches to a second stage which examine the effect of swapping two genotypes of different classes and so on.

3.11 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 Chowdhury (1985). According to them the following points should be considered while selecting genotypes for hybridization program:- Choice of cluster from which genotypes are selected for use as parent (s)- Selection of particular genotype(s) from the selected cluster(s)- Relative contribution of the characters to the total divergence- Other important characters of the genotypes performance.

CHAPTER IV
RESULTS AND DISCUSSION

The present study was carried out with a view to determine the variability, character association and genetic diversity among 30 genotypes of mungbeanas 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 plant height, days to first flowering, days to 50% flowering, days to 80% flowering, number of pod per plant, days to maturity, number of primary branches per plant, number of pod per plant, number of seeds per pod, pod length, seed yield per plant and thousand seed weight. The data were statistically analyzed and results obtained from statistical analysis are described below under the following sections.

4.1 Genetic parameters

The analysis of variance indicated significantly higher amount of variability present among the genotypes for all the characters studied viz., days to first flowering, days to 50% flowering, plant height (cm), main branches per plant, number of flowers per plant, number of pods per plant, seeds per plant, pod length, hundred seed weight, number of seed per plant, yield per hectare (Appendix V). The results clearly indicated that there exists high variability for yield and yield components among the genotypes studied. Therefore there is a lot of scope for selection for majority of the traits in the genotypes. The ANOVA of all the 11 characters is presented in Appendix V.

4.2 Genetic variability, heritability and genetic advance

Heritability estimates help in determining the relative amount of heritable portion of variation. Presence of narrow gap between PCV and GCV for all the characters under these study, suggested that these traits studied has low environmental influence. The estimates of heritability alone fail to indicate the response to selection (Johnson *et al*. 1955). Therefore, the heritability estimates

appears to be more meaningful when accompanied by estimates of genetic advance. The genetic advance as percent of mean (GAM) was also estimated. The extent of variation among the genotypes in respect of thirteen characters was studied and estimates of mean, range, genotypic and phenotypic coefficients of variation, heritability, genetic advance and genetic advance as percent mean for all the characters were studied and the results are shown in Table 2 and illustrated in Figure 1 and 2. The mean performance of mungbean genotypes for various yield components is presented in Appendix IV.

4.2.1 Days to first flowering

Mean sum of square for days to flowering was non-significant (Table 2) indicating non existence of variation among the genotypes for this trait. The maximum days to first flowering was found as 42.33 and the minimum was recorded as 45.33 with mean value of 44.03 (Table 2). The genotypic variance (0.95) and phenotypic variance (0.95) , genotypic coefficient of variation (2.21) and phenotypic coefficient of variation (2.21) were close to each other indicating less environmental influence in case of first flowering (Table 2). Heritability for this trait was very high (99.99) but genetic advance (2.00) and genetic advance in percent of mean (4.55) was found low, indicated that selection for this character would be effective.

4.2.2 Days to 50% flowering

The variance due to days to 50% flowering showed that the genotypes differed non-significantly and ranged from 48.33 days to 52.33 days after sowing with mean value 50.67 days (Table 2). The Genotypic, phenotypic and environmental variances observed were 2.10, 2.10 and 0.0001, respectively (Table 2). 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 no difference between the genotypic co-efficient of variation (2.86) and phenotypic coefficient of

Table 2. Estimation of genetic parameters in eleven characters of thirty genotypes in mungbean

Traits	Range	Mean	MSS	CV (%)	σ^2_g	σ^2_e	σ^2_P	GCV	ECV	PCV	h^2_b	GA (5%)	GA(% mean)
DFF	42.33-45.33	44.03	1.89	0.023	0.95	0.0001	0.95	2.21	0.02	2.21	99.99	2.00	4.55
D50F	48.33-52.33	50.67	4.21	0.020	2.10	0.0001	2.10	2.86	0.02	2.86	100.00	2.99	5.90
D80F	83.33-88.33	86	5.24	0.012	2.62	0.0001	2.62	1.88	0.01	1.88	100.00	3.33	3.88
PH	46.73-74.676	60.703	16.35**	5.937	6.99	2.3660	9.36	10.20	5.94	11.81	74.71	4.71	18.17
PB	1.00-3.17	2.33	0.69**	9.862	0.32	0.0528	0.37	24.25	9.86	26.18	85.81	1.08	46.27
SB	5.50-7.73	6.78	0.90**	5.443	0.38	0.1362	0.52	9.13	5.44	10.63	73.79	1.10	16.16
NP/P	13.18-34.45	20.82	149.52**	4.088	74.40	0.7243	75.12	41.43	4.09	41.63	99.04	17.68	84.93
NS/P	10.12-12.33	11.12	1.20**	4.860	0.45	0.2921	0.75	6.06	4.86	7.77	60.82	1.08	9.73
PL	5.93-7.90	6.82	0.92**	5.574	0.39	0.1445	0.53	9.16	5.57	10.72	72.97	1.10	16.12
TSW	21.02-45.98	26.73	75.45**	3.941	37.17	1.1095	38.28	22.81	3.94	23.15	97.10	12.38	46.30
YIELD	3.49-11.61	6.29	19.67**	9.009	9.68	0.3211	10.00	49.45	9.01	50.27	96.79	6.30	100.23

DFF= Days to first flowering, D50F= Days to 50% flowering, D80F= Days to 80% maturity, PH= Plant height, PB= Primary branches, SB= Secondary branch, NP/P= No. of pod /plant, NS/P= No. of seed/pod, PL= Pod length, TSW= 1000 seed weight and YIELD= Yield/plant, MS = mean sum of square, σ^2 p = Phenotypic variance, σ^2g = Genotypic variance, σ^2e = Environmental variance, PCV = Phenotypic Coefficient of Variation, GCV= Genotypic Coefficient of Variation and ECV= Environmental Coefficient of Variation, h^2_b = Heritability in broad sense, GA= Genetic advance

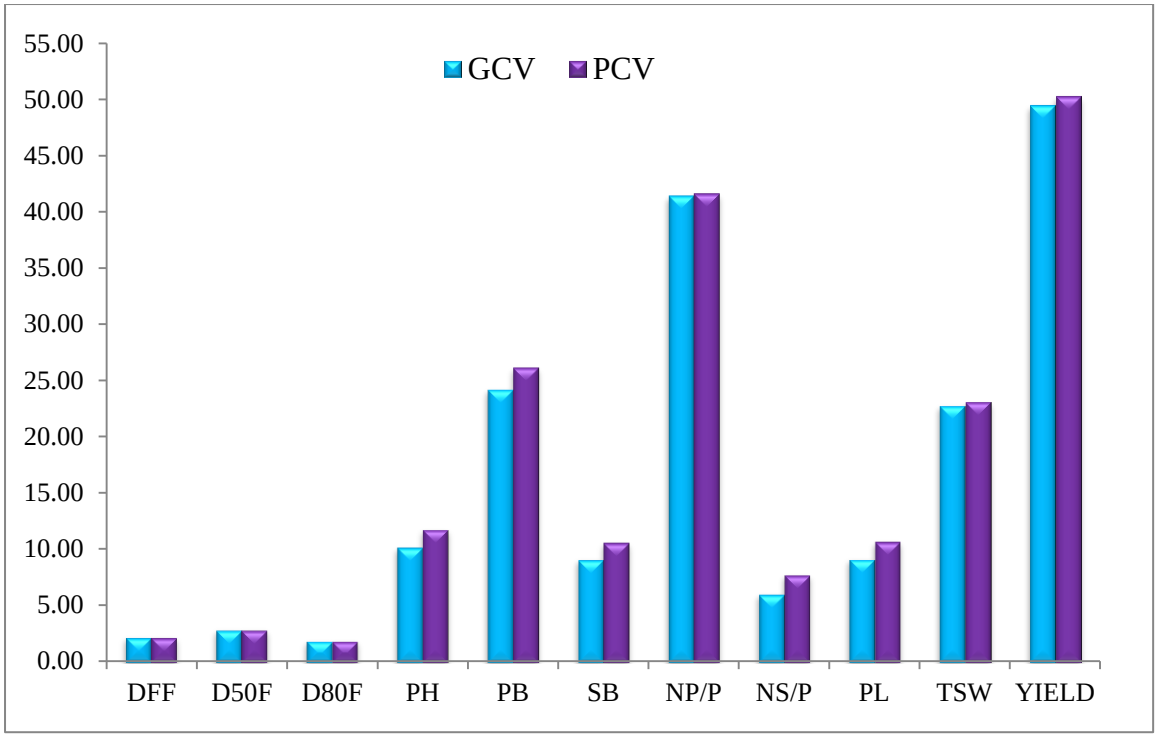

Figure 1.Genotypic and phenotypic variability in Mungbean.

(DFF= Days to first flowering, D50F= Days to 50% flowering, D80F= Days to 80% maturity, PH= Plant height, PB= Primary branches, SB= Secondary branch, NP/P= No. of pod /plant, NS/P= No. of seed/pod, PL= Pod length, TSW= 1000 seed eight and YIELD= Yield/plant, MS = mean sum of square, σ^2 p = Phenotypic variance, σ^2g = Genotypic variance, σ^2e = Environmental variance, PCV = Phenotypic Coefficient of Variation, GCV= Genotypic Coefficient of Variation and ECV= Environmental Coefficient of Variation, h^2_b = Heritability in broad sense, GA= Genetic advance)

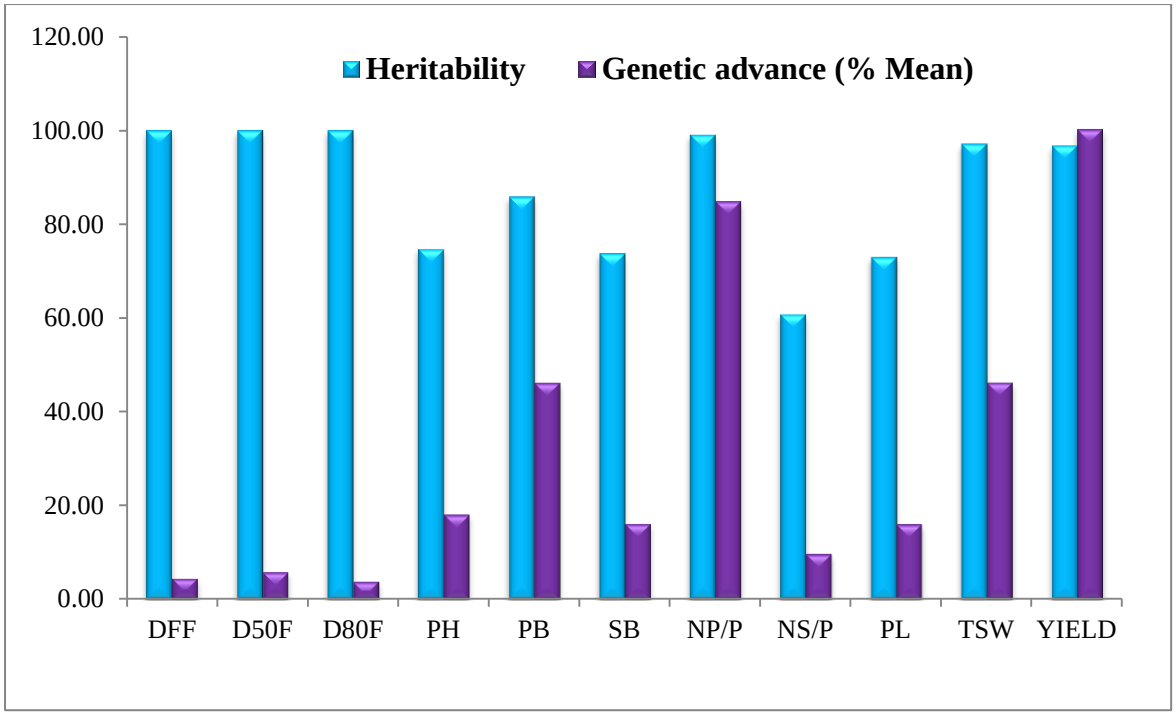

Figure 2. Heritability and genetic advance over mean in mungbean

(DFF= Days to first flowering, D50F= Days to 50% flowering, D80F= Days to 80% maturity, PH= Plant height, PB= Primary branches, SB= Secondary branch, NP/P= No. of pod /plant, NS/P= No. of seed/pod, PL= Pod length, TSW= 1000 seed weight and YIELD= Yield/plant, MS = mean sum of square, σ^2 p = Phenotypic variance, σ^2g = Genotypic variance, σ^2e = Environmental variance, PCV = Phenotypic Coefficient of Variation, GCV= Genotypic Coefficient of Variation and ECV= Environmental Coefficient of Variation, h^2_b = Heritability in broad sense, GA= Genetic advance)

Variation (2.86) (Table 2 and 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 disagrees with the result of this experiment. The heritability (100%) estimates for this trait was very high, genetic advance (2.99) was at moderate level and genetic advance over percentage of mean (5.90) were found high (Table 2), indicated that this trait was controlled by additive genes and selection of this character would be effective. Genetic advances in percent of mean were low with the findings of Nehru *et al.* (1999). On the other hand high heritability with high genetic advance in percent of mean was observed by Agarwal *et al.* (2001), Jain and Ramgiry (2000) and Mehetre *et al.* (2000).

4.2.3 Days to 80% maturity

The variance due to days to 80% maturity showed that the genotypes differed significantly and ranged from 83.33 days to 88.33 days after sowing with mean value of 86.00 days (Table 2). The Genotypic, phenotypic and environmental variances observed were 2.62, 2.62 and 0.0001, respectively (Table 2). 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 no difference between the genotypic co-efficient of variation (1.88) and phenotypic coefficient of variation (1.88) (Table 2 and 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 disagrees with the result of this experiment. The heritability (100%) estimates for this trait was very high, genetic advance (2.99) was at moderate level and genetic advance over percentage of mean (5.90) were found high (Table 2and Figure 2), indicated

that this trait was controlled by additive genes and selection of this character would be effective. Genetic advances in percent of mean were low with the findings of Nehru *et al.* (1999). On the other hand high heritability with high genetic advance in percent of mean was observed by Agarwal *et al*. (2001), Jain and Ramgiry (2000) and Mehetre *et al*. (2000).

4.2.4 Plant height (cm)

The mean for plant height was recorded. It ranged from 46.736 cm to 74.676 cm (Table 2). The analysis of variance revealed highly significant differences among the genotypes with respect to plant height (Appendix V). The maximum plant height (74.676 cm) and the lowest plant height (46.23 cm) were recorded (Table 2). The genotypic and phenotypic variance was observed as 6.99 and 9.36, respectively for plant height with low environmental influence. The phenotypic co-efficient of variation (11.81) was higher than the genotypic co-efficient of variation (9.36), which indicated presence of considerable variability among the genotypes for this trait. The heritability (74.71%) estimates for this trait was high, genetic advance (4.71) was low and genetic advance in per cent of mean (18.17) was found high, revealed that this trait was governed by additive gene. Therefore, selection for this trait will be effective.

4.2.5 Number of primary branches per plant

Considerable differences among the genotypes studied in case of number of primary branches per plant (Table 2). Maximum number of primary branches wasa recorded as 3.17 and the minimum number of primary branches 1.00 (Appendix IV). The phenotypic variance (0.37) appeared to be higher than the genotypic variance (0.32) suggested considerable influence of environment on the expression of the genes controlling this trait (Table 2). The genotypic co-efficient of variation and phenotypic co-efficient of variation were 24.25 and 26.18, respectively which indicated presence of considerable variability among the genotypes. The heritability (85.81%) estimates for this trait was high, genetic advance (1.08) was low and genetic advance in per cent of mean

(46.27) were found very high, revealed that this trait was governed by additive gene. Selection for this trait would be effective.

4.2.6 Number of secondary branches per plant

Number of secondary branches per plant was ranged from 5.50 to 7.73 with mean value of 6.78 (Appendix IV). The genotypic variance and phenotypic variance for this trait were 0.38 and 0.52, respectively (Table 2). The phenotypic variance appeared higher than the genotypic variance which suggested influence of environment on the expression of the genes controlling this character. The genotypic co-efficient of variation (9.13) was close to phenotypic co-efficient of variation (10.63) which was desirable for the improvement of this crop. The heritability estimates for this trait was (73.79) with low genetic advance (1.10) and high genetic advance in percent of mean (16.16) indicated that this trait was controlled by additive gene and selection for this character would be effective.

4.2.7 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 maximum number of pod per plant was found (34.45) and the minimum was recorded (13.18) with mean value (20.82) (Table 2). The genotypic variance (74.40) and phenotypic variance (75.12), genotypic coefficient of variation (41.43) and phenotypic coefficient of variation (41.63) were close to each other indicating less environmental influence in case of number of pod per plant (Table 2). Heritability for this trait was very high (99.04) but genetic advance (17.68) and genetic advance in percent of mean (84.93) was found high, indicated that selection for this character would be effective.

4.2.8 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 (7.73) and the minimum was recorded (5.93) with mean value (6.82) (Table 2). The genotypic variance (0.39) and phenotypic variance (0.53), genotypic coefficient of variation (9.16) and phenotypic coefficient of variation (10.72) were close to each other indicating less environmental influence in case of pod length (Table 2). Heritability for this trait was very moderately high (72.97) but genetic advance (1.10) and genetic advance in percent of mean (16.12) was found moderately high, indicated that selection for this character would be effective. Roy *et al.* (1993) found similar results in mungbean.

4.2.9 Number of seeds per pod

Mean sum of square for number of seeds per pod was not highly significant in mungbean, indicating non-existence of considerable difference for this trait (Appendix V). The maximum number of pod per plant was found (12.33) and the minimum was recorded (10.12) with mean value (11.12) (Table 2). The genotypic variance (0.45) and phenotypic variance (0.75), genotypic coefficient of variation (6.06) and phenotypic coefficient of variation (7.77) were close to each other indicating less environmental influence in case of number of pod per plant (Table 2). Heritability for this trait was moderately high (60.82) but genetic advance (1.08) and genetic advance in percent of mean (9.73) was found moderately high, indicated that selection for this character would be less effective.

4.2.10Thousand seed weight (g)

Mean sum of square for thousand seed weight is highly significant in mungbean, indicating existence of considerable difference for this trait (Appendix V). The maximum thousand seed weight was found (45.98) and the minimum was recorded (21.02) with mean value (26.73) (Table 2). The genotypic variance (37.17) and phenotypic variance (38.28), genotypic coefficient of variation (22.81) and phenotypic coefficient of variation (23.15) were close to each other indicating less environmental influence in case of thousand seed weight (Table 2). Heritability for this trait was very high (97.10)

but genetic advance (12.38) and genetic advance in percent of mean (46.30) was found high, indicated that selection for this character would be more effective. A pictorial view of seeds of different genotypes is presented in Plate 4.

4.2.11 Seed yield per plant (g)

Mean sum of square for seed yield per plant (gm) was highly significant in mungbean, indicating existence of considerable difference for this trait (Appendix V). The maximum thousand seed weight was found (11.61) and the minimum was recorded (3.49) with mean value (6.29) (Table 2). The genotypic variance (9.68) and phenotypic variance (10.00), genotypic coefficient of variation (49.45) and phenotypic coefficient of variation (50.27) were close to each other indicating less environmental influence in case of thousand seed weight (Table 2). Heritability for this trait was very high (96.79) but genetic advance (6.30) and genetic advance in percent of mean (100.00) was found very high, indicated that selection for this character would be more effective. The very high heritability with moderate genetic advance provided opportunity for selecting high valued genotypes for breeding program.A pictorial view of seeds of different genotypes of mungbean with mature pods is presented in Plate 5.

4.3 Correlation co-efficient

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

Plate 4: Seeds of different mungbean genotypes

Plate 5: Mungbean plants with mature pods

about the contribution in respect of establishing the association by genetic and non-genetic factors (Dewey and Lu, 1959). Pearson correlation analysis among yield and its contributing characters are shown in Table 3. The genotypic correlation coefficients in most cases were higher than their phenotypic correlation coefficients indicating the genetic reason of association. While phenotypic correlation coefficient were higher than genotypic correlation coefficient indicating suppressing effect of the environment which modified the expression of the characters at phenotypic levels. The depicted genotypic and phenotypic correlation coefficient among yield and yield contributing characters of mungbean are shown in Table 3.

4.3.1 Days to first flowering

In case of days to first flowering, highly significant positive relationship was observed in days to 50% flowering (G=0.910) and days to 80% maturity (G=0.75). But non-significant positive correlation was observed in number of primary branches, number of secondary branches, and number of pods per plant at both genotypic and phenotypic levels (Table 3). The character reflected highly significant relationships with days to 50% flowering, days to 80% maturity at genotypic and phenotypic levels and highly significant positive association with days to 50% flowering at genotypic and phenotypic levels. It appeared from the results that increasing days to first flowering caused the plant to produce lesser height and pod length. This character also showed insignificant negative correlation with plant height, pod length and number of seeds per pod at both levels. It also showed insignificant positive correlation with the number of primary branches per plant, the number of pods per plant, pod length and yield both at genotypic and phenotypic levels.

4.3.2 Days to 50% flowering

The correlation of days to 50% flowering was highly positive significant in case of 80% maturity (G=0.876, P=0.867). But non-significant positive correlation was observed in plant height (G=0.113,P=0.103), number of pods per plant (G=0.171, P=0.166), thousand seed weight (G=0.141, P=0.166) and

Table 3. Genotypic and phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of mungbean

		DFF	D50F	D80F	PH	PB	SB	NP/P	NS/P	PL	TSW
	G	0.910**									
D50F	P	0.806**									
	G	0.75**	0.876**								
D80F	P	0.722**	0.867**								
	G	-0.091	0.113	0.163							
PH	P	-0.087	0.103	0.149							
	G	0.192	0.192	0.225	0.032						
PB	P	0.187	0.184	0.205	0.023						
	G	0.135	-0.152	0.056	-0.095	0.25					
SB	P	0.103	-0.122	0.046	-0.083	0.15					
	G	0.223	0.171	0.034	0.477**	-0.032	-0.064				
NP/P	P	0.203	0.166	0.026	0.467**	-0.023	-0.044				
	G	-0.066	-0.153	-0.042	0.388*	0.075	0.132				
NS/P	P	-0.056	-0.148	-0.033	0.377*	0.059	0.101	0.219			
	G	-0.106	-0.242	-0.213	0.197	-0.382	0.088	0.123	0.541**		
PL	P	-0.095	-0.229	-0.199	0.185	-0.365*	0.071	0.113	0.508**		
	G	0.042	0.141	0.243	0.394*	0.321	0.212	-0.024	0.498**	0.087	
TSW	P	0.035	0.132	0.230	0.381*	0.309	0.195	-0.016	0.482**	0.075	
	G	0.171	0.197	0.145	0.601**	0.135	0.069	0.834**	0.575**	0.212	0.541**
YIELD	P	0.161	0.184	0.135	0.581**	0.123	0.057	0.817**	0.559**	0.197	0.531**

DFF= Days to first flowering, D50F= Days to 50% flowering, D80%= Days to 80% maturity,PH= Plant Height (cm), PB= Number of Primary branches/plant, SB= Number of secondary branch/plant, , NP/P= Number of pod/plant, PL= Pod length (cm), NS/P= Number of seed/plant.TSW = Weight of 1000 seed (g), YIELD= Yield (gm/plant), G=Genotypic correlation and P=Phenotypic correlation

** Significant at 1% level of probability, * Significant at 5% level of probability,.

seed yield (G=0.197, P=0.184) at both the genotypic and phenotypic levels (Table 3). This character also showed insignificant negative correlation with number of seeds per pod and pod length at both levels. Rao*et al*. (2006), Yaqoob*et al*. (1997) reported that days to 50% flowering were positively and significantly associated with seed yield. Rahman (1982) obtained positive correlation of days to 50% flowering with days to maturity.

4.3.3Days to 80% maturity

Highly significant and positive correlation was observed in case of days to first flowering and days to 50% flowering. The correlation of days to 80% maturity with plant height (G=0.163,P=0.149), number of pods per plant (G=0.034, P=0.026), thousand seed weight (G=0.243, P=0.230) and seed yield (G=0.145, P=0.135) was positive and significant at both the genotypic and phenotypic levels (Table 3). This character also showed non-significant negative correlation with number of seed per pod and pod length at both levels.

4.3.4 Plant height

A highly significant and positive association of plant height with number of pods per plant (G=0.477, P=0.467), number of seeds per pod (G=0.388, P=0.377), thousand seed weight (G=0.394, P=0.381) and seed yield (G=0.601, P=0.581) (Table 3) at both the genotypic and phenotypic levels was observed. This character also showed insignificant negative correlation with number of secondary branches at both levels. Makeen *et al*. (2007), Islam (1999) and Niazi *et al*. (1999) indicated that plant height was significantly and positively correlated with yield.

4.3.5 Number of primary branches per plant

A non-significant and positive association of number of primary branches with number of secondary branches (G=0.25, P=0.15), number of seeds per pod (G=0.075, P=0.059), thousand seed weight (G=0.321, P=0.309) and seed yield (G=0.135, P=0.123) at both the genotypic and phenotypic levels was observed. Insignificant negative correlation was found with pod length and number of pods per plant at both level. Islam *et al.* (1999) studied yield per plant was significantly

and positively correlated with number of primary branches per plant.

4.3.6 Number of secondary branches per plant

A non-significant and positive association of number of secondary branches with number of seeds per pod (G=0.132, P=0.101), thousand seed weight (G=0.212, P=0.195) and seed yield (G=0.069, P=0.057)(Table 3)at both the genotypic and phenotypic levels were observed. Insignificant negative correlation was found with pods length and number of pods per plant at both levels.

4.3.7 Number of pod per plant

Highly significant positive correlation was observed with plant height and yield per plant at both levels. Pods per plant showed insignificant negative correlation with thousand seed weight (G=-0.24, P=-0.016), primary branches per plant and secondary branches per plant at both the genotypic and phenotypic levels. Pods per plant showed significant positive correlation with seed yield (G=0.834, P=0.817) (Table 3) at both the genotypic and phenotypic levels which was reported by Makeen et al. (2007), Siroh and Kumar (2006), Rao *et al*. (2006), Rajan *et al*. (2000) and Islam *et al*. (1999). A pictorial view of pods of different mungbean genotypes is presented in Plate 6.

4.3.8 Weight of 1000 seed (g)

A highly significant positive association of weight of 1000 seed at both the genotypic and phenotypic levels was observed with number of seeds per plant and yield (0.541 and 0.531) (Table 3).

4.4 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. The path coefficient analysis technique was developed by Wright (1921) and demonstrated by Deway and Lu (1959) facilitates the portioning of correlation coefficients into direct and indirect contribution of various characters on yield. It is standardized partial regression coefficient analysis. As such, it measures the direct influence of one variable upon

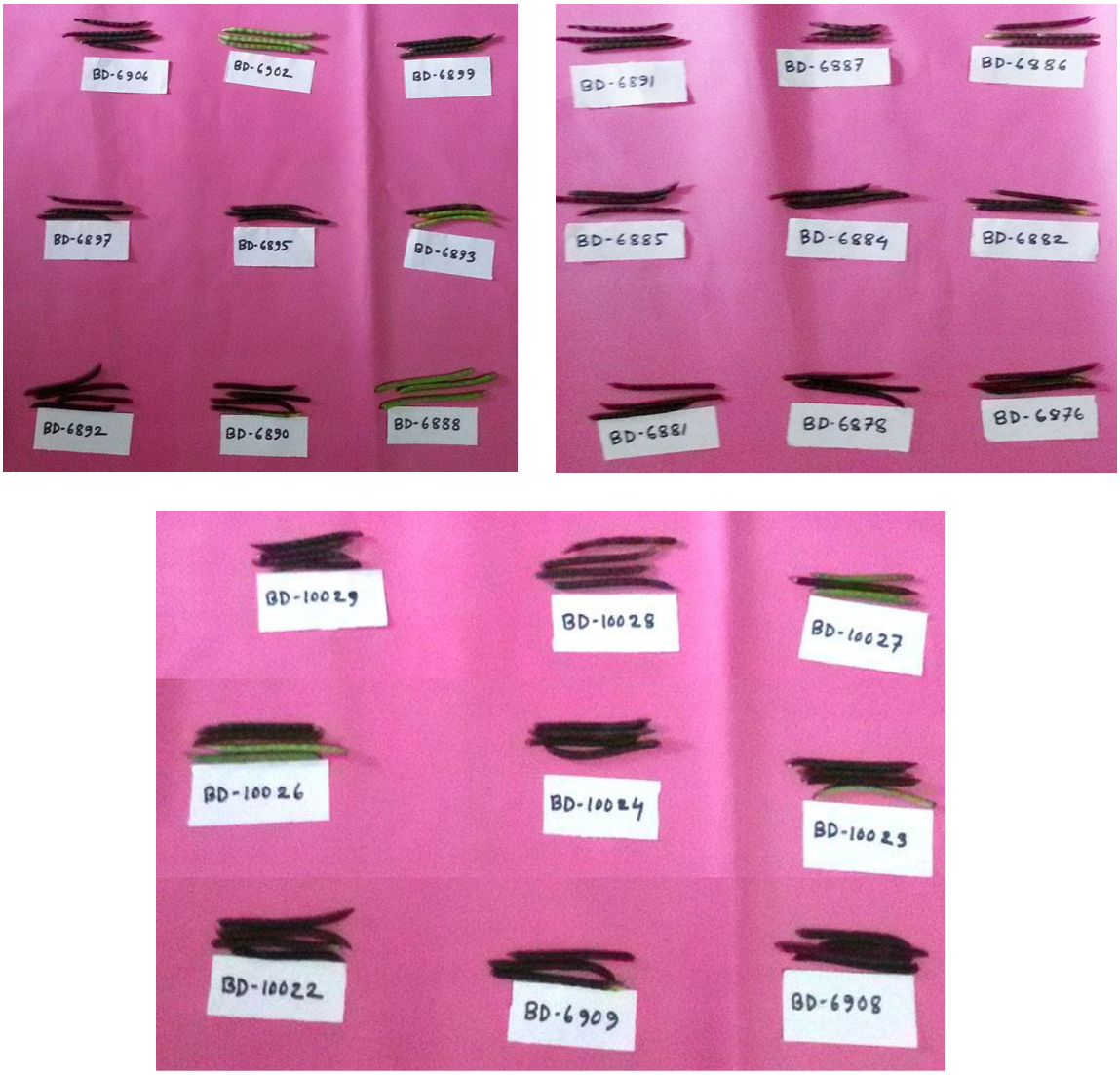

Plate 6: Pods of different mungbean genotypes

other. 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.

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 4.

4.4.1 Days to 50% flowering

Path analysis revealed that days to 50% flowering had negative direct effect (-0.1026) on yield. Days to 50% flowering showed negative indirect effect with days to 80% flowering (-0.0902), plant height (-0.0112) and number of primary branches per plant (-0.1948). Days to 50% flowering has indirect positive effect with number of seeds per pod (0.1538) and plant length (0.2461) (Table 4).

4.4.2 Days to 80% maturity

Days to 80% maturity had positive direct effect (0.1771) on yield per plant. Days to 80% maturity had indirect positive effect on days to 50% flowering (0.1559), number of secondary branches per plant (0.0106), plant height (0.0283), number of pods per plant (0.0531) and weight of 1000 seed (0.4251). It had a negative indirect effect on number of seeds per pod (-0.0709) and pod length (-0.3719) (Table 4).

4.4.3 Plant height (cm)

Plant height had positive direct effect (0.1950) on yield (Table 4). It had a negative indirect effect through number of secondary branches per plant (-0.1755). Number of seeds per pod (0.7606), pod length (0.384), number of pods per plant (0.9361), days to 50% flowering (0.0215) and weight of 1000 seed (0.7684) had indirect positive effect. Maximum direct effect on seed yield was observed in plant height reported by Makeen *et al.* (2007), Sirohi *et al.* (2006) and Sharma *et al.* (1999) found negative direct effect on seed yield which did not support my result.

Table 4. Path coefficient analysis showing direct and indirect effects of different characters on yield of mungbean

Characters	Direct effect	Indirect effect									Genotypic correlation with Yield
		D50F	D80F	PH	PB	SB	NP/P	NS/P	PL	TSW	
D50F	- **0.1026**	-	-0.0902	-0.0112	-0.1948	0.1538	-0.1743	0.1538	0.2461	-0.1436	**0.197**
D80F	**0.1771**	0.1559	-	0.0283	0.3897	0.0106	0.0531	-0.0709	-0.3719	0.4251	**0.145**
PH	**0.1950**	0.0215	0.0312	-	0.5850	-0.1755	0.9361	0.7606	0.3842	0.7684	**0.601**
PB	**0.1873**	0.0356	0.0412	0.0056	-	0.0468	-0.0056	0.1498	-0.7117	0.5993	**0.135**
SB	**0.0441**	-0.0066	0.0026	-0.0039	0.1103	-	-0.0026	0.0574	0.0397	0.0926	**0.069**
NP/P	**0.7371**	0.1253	0.0221	0.3538	-0.0221	-0.4422	-	0.1695	0.8845	-0.1474	**0.834**
NS/P	**0.0007**	-0.0001	-0.0001	0.0003	0.0001	0.0001	0.0002	-	0.0004	0.3660	**0.575**
PL	**0.1625**	-0.0389	-0.0341	0.0320	-0.6174	0.1462	0.1950	0.8773	-	0.1413	**0.212**
TSW	**0.0004**	0.0001	0.0001	0.0002	0.0001	0.0001	-0.0001	0.2119	0.0001	-	**0.541**

Residual value: 0.45. D50F= Days to 50% flowering. D80F=Days to 80% flowering, PH= Plant Height (cm), PB= Number of primary branch/plant, NP/P= Number of pod/plant, PL= Pod length (cm), SB= Number of secondary branch per plant, NS/P= Number of seed/plant, TSW= Thousand seed weight (g).

4.4.4 Number of primary branches per plant

Number of primary branches per plant had positive direct effect (0.1873) on yield per plant (Table 4). Number of primary branches per plant had indirect positive effect via days to 50% flowering (0.0356), days to 80% flowering (0.0412), plant height (0.0056), number of secondary branches per plant (0.00468), number of seed per pods (0.1498) and weight of 1000 seed (0.5993). It had a negative indirect effect on number of pods per plant (-0.0056) and pod length (-0.7117).

4.4.5 Number of secondary branches per plant

Number of secondary branches per plant had positive direct effect (0.0441) on yield per plant (Table 4). Number of secondary branches per plant had indirect positive effect on yield via number of primary branches (0.1103), number of secondary branches per plant (0.00468), number of seeds per pod (0.0574) and weight of 1000 seed (0.0926). It had a negative indirect effect on days to 50% flowering (0.0066), number of pods per plant (-0.0026), plant height (-0.0039).

4.4.6 Number of pod per plant

Number of pod per plant had the direct positive effect on yield (0.7371) whereas it had positive indirect effect through days to 50% flowering (0.1253), pod length (0.8845), plant height (0.3538) and number of seeds per plant (0.1695) (Table 4). However, it had indirect negative effects through number of primary branches (-0.0221), number of secondary branches per plant (-0.4422) and thousand seed weight (-0.1474).

4.4.7 Pod length

Pod length had the direct positive effect on yield (0.1625) whereas it had positive indirect effect through number of pods per plant (0.1950),plant height (0.0320) and number of seeds per plant (0.1695) number of secondary branches per plant (0.1462) and thousand seed weight (0.1413) (Table 4). However, it had indirect negative effects through days to 50% flowering (-0.0389), pod length (0.8845), number of primary branches (-0.6174). Bhaumik and Jha (1980) found similar result.

4.4.8 Number of seed per pod

Number of seeds per pod had the direct positive effect on yield (0.0007) whereas it had positive indirect effect through number of primary branches per plant (0.0001), number of secondary branches per plant (0.0001) and thousand seed weight (0.3660), pod length (0.0003), plant height (0.0003) and number of pods per plant (0.0002) (Table 4). However, it had indirect negative effects through days to 50% flowering (-0.0001).

4.4.9 Thousand seed weight (g)

Thousand seed weight had positive direct effect (0.0004) on yield per plant. Thousand seed weight had indirect positive effect through days to 50% flowering (0.0001), number of primary branches (0.0001), number of secondary branches per plant (0.0001), plant height (0.0002), number of seeds per pod (0.2119) and pod length (0.0001) (Table 4). It had a negative indirect effect on number of pods per plant (-0.0001). Singh and Malhotra (1976) observed 1000 seed weight had a negative indirect effect on yield.

4.5 Multivariate analysis

4.5.1 Principal component analysis (PCA)

Principal component analysis was carried out with thirty genotypes of mungbean which gives Eigen values of principal component axes of coordination of genotypes with the first axes totally accounted for the variation among the genotypes. First six Eigen values for six principal coordination axes of genotypes accounted for 90.95% variation showed in Table 5. Based on principal component scores I and II obtained from the Principal component analysis (Appendix VI), a two-dimensional scatter diagram (Z1-Z2) 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.

Table 5. Eigen values and yield percent contribution of 11 characters of 30 genotypes of mungbean

Principal component axes	Eigen values	Percent variation	Cumulative % of Percent variation
I	3.141	28.56	28.56
II	2.659	24.17	52.73
III	1.453	13.21	65.94
IV	1.168	10.62	76.56
V	0.948	8.62	85.18
VI	0.635	5.77	90.95
VII	0.452	4.11	95.06
VIII	0.301	2.74	97.80
IX	0.159	1.45	99.25
X	0.077	0.69	99.94
XI	0.007	0.06	100.00

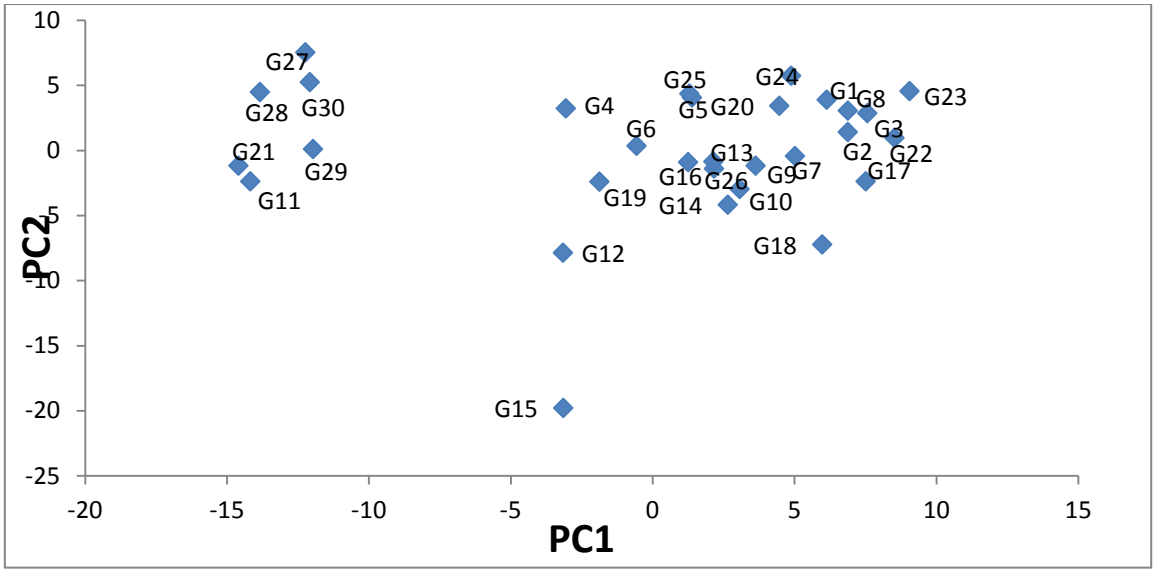

Figure 3. Scatter diagram of 30 genotypes of mungbean based on their principal component scores.

4.5.2 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 6. 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 III and V (12.57), followed by between clusters II and V (11.578), I and III (10.547). In contrast, the lowest inter-cluster distance was observed between cluster II and IV (3.919).

However, the maximum inter-cluster distance was observed between the clusters III and V (12.57) 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 I (1.116), which contained only 6 genotype, while the minimum distance was found in cluster III (0.0) that comprises 1 genotype. Inter and intra cluster distances are show in Table 6. Cluster I consists of nearest cluster with D^2 values cluster II (3.973) and farthest cluster with D^2 values III (10.547) (Table 7). Cluster II consists of nearest cluster with D^2 values cluster I (3.973) and farthest cluster with D^2 values V (11.578). Cluster III consists of nearest cluster with D^2 values cluster IV (6.466) and farthest cluster with D^2 values V (12.527). Cluster IV consists of nearest cluster with D^2 values cluster III (6.466) and farthest cluster with D^2 values V (9.466). Cluster V consists of nearest cluster with D^2 values cluster I (7.863) and farthest cluster with D^2 values III (12.527). 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 maximum amount of heterosis will be manifested in cross combination involving the genotypes belonging to the

Table 6. Intra (Bold) and inter cluster distances (D^2) for 14 genotypes of mungbean

	I	II	III	IV	V
I	**1.116**				
II	3.973	**0.989**			
III	10.547	9.93	**0.0**		
IV	4.282	3.919	6.466	**0.888**	
V	7.863	11.578	12.527	9.466	**0.444**

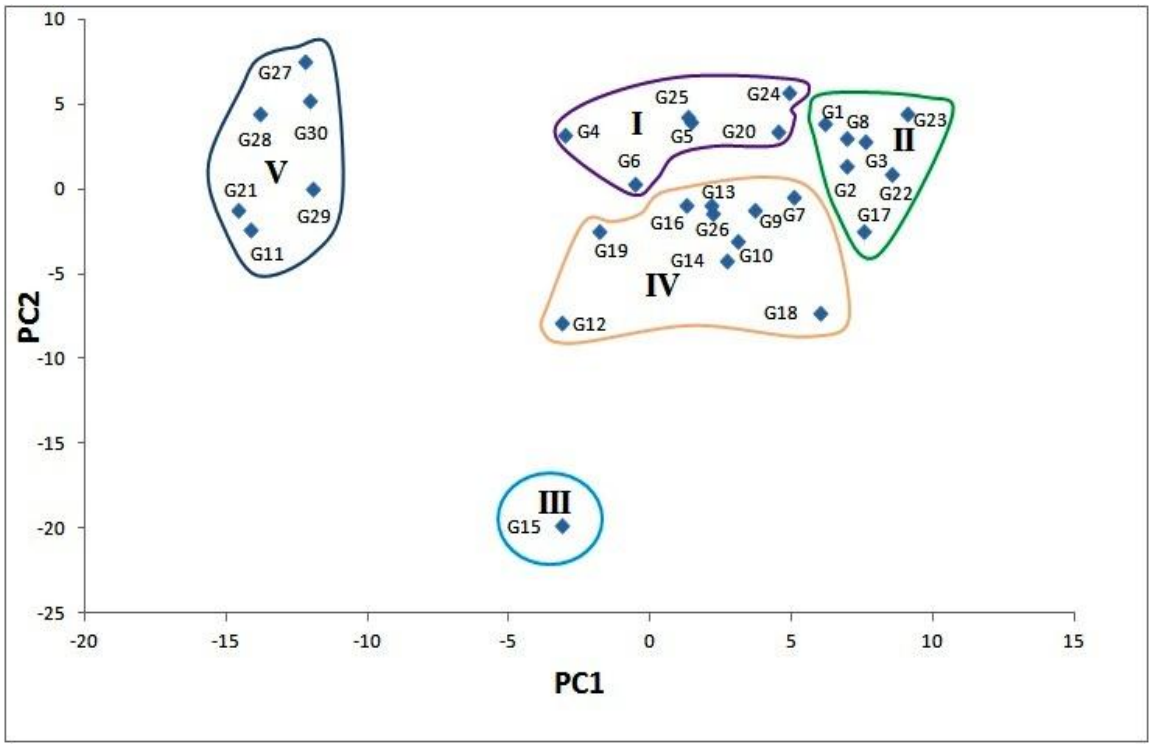

Figure 4. Scatter distribution of 30 genotypes of Mungbean based on their principal component scores super imposed with clustering.

Table 7. The nearest and 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	II (3.973)	III (10.547)
2	II	I (3.973)	V (11.578)
3	III	IV (6.466)	V (12.527)
4	IV	III (6.466)	V (9.466)
5	V	I (7.863)	III (12.527)

most divergent clusters. 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 III and V. So the crosses between the genotypes belonging cluster III with cluster V might produce high heterosis. Also the crosses between genotypes from cluster III with V might produce high level of segregating population. So the genotypes belonging to cluster III and cluster V might be selected for future hybridization program.

4.5.3 Principal coordinate analysis (PCO)

Inter genotypic distances (D^2) as obtained by principal coordinate analysis (PCO) for all possible combinations between the pairs of genotypes. Inter genotypic distances, as obtained from principal coordinate analysis showed that the highest distance was observed between the G23 and G21 (Table 8). The lowest distance was observed between the G26 and G14. The difference between the highest and the lowest inter genotypic distance indicated the prevalence of variability among the 30 genotypes of Mungbean studied.

4.5.4 Nonhierarchical clustering

Thirty mungbean genotypes were grouped into five different clusters through non-hierarchical clustering (Table 9). These results confirmed the clustering pattern of the genotypes obtained through principal component analysis. Cluster IV had highest number of ten genotypes followed by cluster II and cluster I and V constituted by seven, six and also six genotypes, respectively. On the other hand, cluster III constituted by only a genotype. Cluster IV had maximum ten genotypes namely BD-6885, BD-6887, BD-6888, BD-6891,BD-6892, BD-6893, BD-6897, BD-6902, BD-6906 and BD-10027. Cluster II represents 7 genotypes namely BD-6875, BD-6876, BD-6878, BD-6886, BD-6899, BD-10022, BD-10023 and Last of all cluster III had minimum genotype and it was BD-6895. The results confirmed the clustering pattern of the genotypes according to the principal component analysis. The clustering pattern obtained coincided with the apparent grouping patterns performed by PCA. For that reason it can be said that the results

Table 8. Ten highest and ten lowest inter genotypic distance among 30 genotypes of mungbean

Sl.	Genotype combination		Distance
10 highest inter genotypic distances			
1	G23	G21	1.4255
2	G22	G21	1.4069
3	G23	G11	1.3838
4	G21	G3	1.3611
5	G23	G15	1.3565
6	G29	G23	1.3372
7	G21	G8	1.3317
8	G22	G11	1.3196
9	G29	G22	1.3171
10	G21	G2	1.3033
10 lowest inter genotypic distances			
1	G26	G14	0.1347
2	G26	G10	0.1391
3	G22	G8	0.1528
4	G14	G10	0.1557
5	G30	G28	0.1624
6	G16	G6	0.1757
7	G29	G21	0.1821
8	G3	G1	0.1928
9	G8	G3	0.1969
10	G22	G3	0.2015

Table 9. Distribution of genotypes in different clusters

Cluster	Number of genotype	Genotype Number	Genotypes
I	6	G4, G5, G6, G20, G24 and G25	BD-6881, BD-6882, BD-6884, BD-6908, BD-10024 and BD-10026
II	7	G1, G2, G3, G8, G17, G22 and G23	BD-6875, BD-6876, BD-6878, BD-6886, BD-6899, BD-10022 and BD-10023
III	1	G15	BD-6895
IV	10	G7, G9, G10, G12, G13, G14, G16, G18, G19 and G26	BD-6885, BD-6887, BD-6888, BD-6891, BD-6892, BD-6893, BD-6897, BD-6902, BD-6906 and BD-10027
V	6	G11, G21, G27, G28, G29 and G30	BD-6890, BD-6909, BD-10028, BD-10029, BD-10030 and BD-10032

obtained through PCA were established by nonhierarchical clustering (Figure 3 and 4).

4.5.5 Cluster mean analysis

The cluster means of 11 different characters (Table 10) were compared and indicated considerable differences between clusters for all the characters studied. Maximum days to first flowering were observed in cluster V (44.50), whereas minimum days to first flowering in cluster I (43.50). Maximum days to 50% flowering were observed in cluster III (51.33).

Whereas minimum days to 50% flowering in cluster I (49.83). Maximum days to 80% flowering were observed in cluster III (87.33), whereas minimum days to 80% flowering in cluster I(84.66). Then maximum plant heights were observed in III (70.78) whereas minimum plant height were observed in cluster II (60.68). Maximum number of main branches was observed in cluster IV (2.60) and minimum (1.98) in cluster I. Number of secondary branches per plant was observed maximum in cluster III (7.28) and minimum to cluster II (6.60). Maximum (33.54) and minimum (14.19) number of pods per plant were observed in cluster V and II, respectively. The maximum pod length (6.95) was observed in the cluster I, whereas minimum pod length (6.51) was observed in cluster II. Number of seeds per plant was maximum in cluster III (12.14) and minimum number in cluster II (10.69). Weight of 1000 seed was highest in cluster III with a mean value of (45.98) and it was least in genotypes belongs to the cluster I (23.46). To develop high yielding varieties these groups can be used in hybridization program.

4.5.6 Cluster diagram

With the help of D^2 values within and between clusters, an arbitrary cluster diagram (Figure 5) was constructed, which showed 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 V was far diverse from the genotypes of the cluster III and where the genotypes belonging to II and IV were the least diverse. Genotypes of cluster I-IV and

Table 10. Cluster mean values of 11 different characters of 30 genotypes of mungbean

Traits	I	II	III	IV	V
Days to first flowering	43.50	44.19	44.33	43.93	44.50
Days to 50% flowering	49.83	51.04	51.33	50.53	51.16
Days to 80% maturity	84.66	86.62	87.33	86.03	86.33
Plant height	63.14	60.68	70.78	68.04	69.85
Primary branches/plant	1.98	2.21	2.52	2.60	2.32
Secondary branch/plant	6.72	6.60	7.28	6.93	6.70
No. of pods /plant	20.20	14.19	20.50	18.25	33.54
No. of seeds/pod	10.75	10.69	12.14	11.44	11.28
Pod length	6.95	6.51	6.63	6.93	6.91
1000 seed weight	23.46	24.22	45.98	29.21	25.60
Yield/plant	5.17	3.68	11.48	6.19	9.77

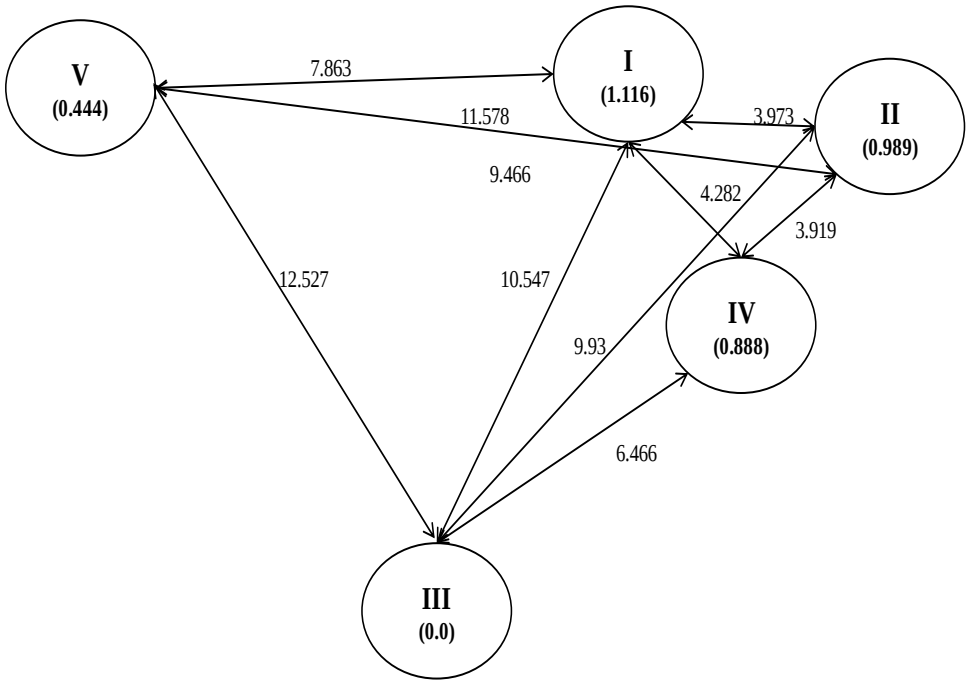

Figure 5. Intra and inter cluster distances (D^2) of Mungbean genotypes

III-IV were moderately diverse from each other. The similar diverse genotypes were included between the cluster I-III and II-III.

4.5.7 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 is 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) were days to 50% flowering (0.8891), number of secondary branches per plant (0.3254), number of seeds per pod (0.8858), thousand seed weight (0.0165) and yield (0.038). These characters were important because all these characters had positive signs in first axis. Days to 50% flowering (0.079), pod length (0.6144) and yield (1.7441) had positive sign in vector II (Z2), second axis of differentiation.

On the other hand, days to first flowering, days to 80% maturity, number of primary branches per plant, number of pods per plant, pod length possessed the negative sign in the first axis of differentiation and days to first flowering, days to 80% maturity, number of secondary branches per plant, number of flower per plant, plant height and weight of 1000 seed possessed negative signs in the second axis of differentiation that means these had minor role in the genetic divergence. Days to 50% flowering and yield had positive sign in both the axis, which indicated that they were the important component

Table 11. Relative contributions of the 11 characters of 30 genotypes of Mungbean to the total divergence

Traits	**Vector-1**	**Vector-2**
Days to first flowering	-0.6637	-0.0598
Days to 50% flowering	0.8891	0.079
Days to 80% maturity	-0.2757	-0.2256
Plant height	0.0329	-0.0736
Primary branches/plant	-0.422	-0.455
Secondary branch/plant	0.3254	-0.3798
No. of pods /plant	-0.6181	-0.5073
No. of seeds/pod	0.8858	-2.4018
Pod length	-0.9028	0.6144
1000 seed weight	0.0165	-0.7313
Yield/plant	0.038	1.7441

characters having higher contribution to genetic divergence among the genotypes studied.

4.5.8 Selection of genotypes as parent for hybridization program

Selection of genetically diverse parents is an urgent 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 G4 (BD-6881) for minimum days to 50% flowering from cluster I; for maximum plant height, pod length and yield G29 (BD-10030) from cluster V; G15 (BD-6895) for maximum weight of 1000 seed from cluster III, G16 for maximum days to 50% flowering, maximum number of secondary branches and maximum weight of 1000 seed from cluster IV were found promising. Therefore considering group distance and other agronomic performances the inter-genotypic crosses between G15 and G27; G15 and G11; G15 and G21; G15 and G28; G15 and G30, G15 and G29, G4 and G29; G1 and G15; G4 and G16; G23 and G21, G15and G16, G4 and G23, G29 and G4 might be suggested for future hybridization program.

CHAPTER V

SUMMARY AND CONCLUSION

The research work was done in the experiment field and laboratory Genetics and Plant Breeding department of Sher-e-Bangla Agricultural University, Dhaka, Bangladesh during the period of 6 December 2015 to 5 March 2016. The seeds were sown by three replications and the experiment was conducted in Randomized Complete Block Design (RCBD). Data on days to first flowering, days to 50% flowering, days to 80% maturity, Plant height (cm), primary branches per plant , secondary branches per plant, No. of pod /plant, No. of seeds/pod, Pod length (cm) 1000 seed weight (g), Yield/plant (g) were recorded. There were great deals of significant variation for all the characters among the genotypes.

The phenotypic variance was higher than the corresponding genotype variance in all the characters, indicating greater influence of environment on the expression of these characters. The maximum difference between phenotypic and genotypic coefficient of variation were 80%and 50% respectively which indicated that the plant height mostly depended on environment effect. The height estimated heritability among eleven yield contributing characters 100%, 99.99%, 99.04%, 97.10%,96.79% was in 50% flowering and 80% maturity , days to first flowering, number of pod per plant and 1000 seed weight per plant. The lowest heritability was 60.72 in number of seed per pod.

The maximum genetic advance (GA 5%) was observed in respect of thousand in seed weight (12.38) eleven characters of Mungbean genotypes. The maximum genetic advance in percent of mean (GAMP) was obtained for seed yield (100.23%) and the lowest was for 80% maturity (3.88%).

The significant positive correlation at the 5% level was observed for seed yield per plant with number of pod per plant, number of seed per pod and

thousand seed weight at genotypic and phenotypic level. The significant positive correlation at the 1% level days to 50% flowering, days to 80% maturity and seed yield at both genotypic and phenotypic level.

Multivariate analysis was carried out through principal component analysis (PCA) principal coordinate analysis (PCO),cluster analysis, and canonical vector analysis (CVA) using genstat 5.13 software programmed as per as PCA, $D^2$and cluster analysis using the genotypes were grouped into five different clusters. Cluster I, II, III,IV and V comprised 6, 7, 1, 10 and 6 genotypes respectively.

The maximum cluster distance was observed between cluster III and V (12.527) followed by the distance between cluster II and V (11.578). The lowest inter– cluster distance was observed between cluster II and IV (3.919) followed by cluster I and II (3.973).

The highest intra cluster distance was identified in cluster I (1.116) and the lowest intra cluster distance was observed in cluster III (0.0). The highest intra cluster distance between these genotypes indicate to obtain wide spectrum of segregating population if parents chosen from these distant cluster will be rewarding and can be used in hybridization program.

Considering group distance and other agronomic performance the inter genotypic crosses between G15 and G27; G15 and G11; G15 and G21; G15 and G28; G15 and G30, G15 and G29 may be suggested for future hybridization program.

The result of the present study revealed that a wide variability exists among the collected Mungbean genotypes. In addition, there was also genotypic variability of different yield contributing characters with yield of Mungbean.

The result of the present study revealed that a wide variability exists among the collected Mungbean genotypes. Furthermore, there were also positive associatin yield contributing characters with yield of Mungbean 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 primary branches, number of pod per plant and 1000 seed weight and seed yield. Hence, yield improvement in mungbean would be achieved through selection of these characters.

- ❖ Further collection of mungbeangermplasms would be continued for getting more variability and desired traits inMungbean.

- ❖ 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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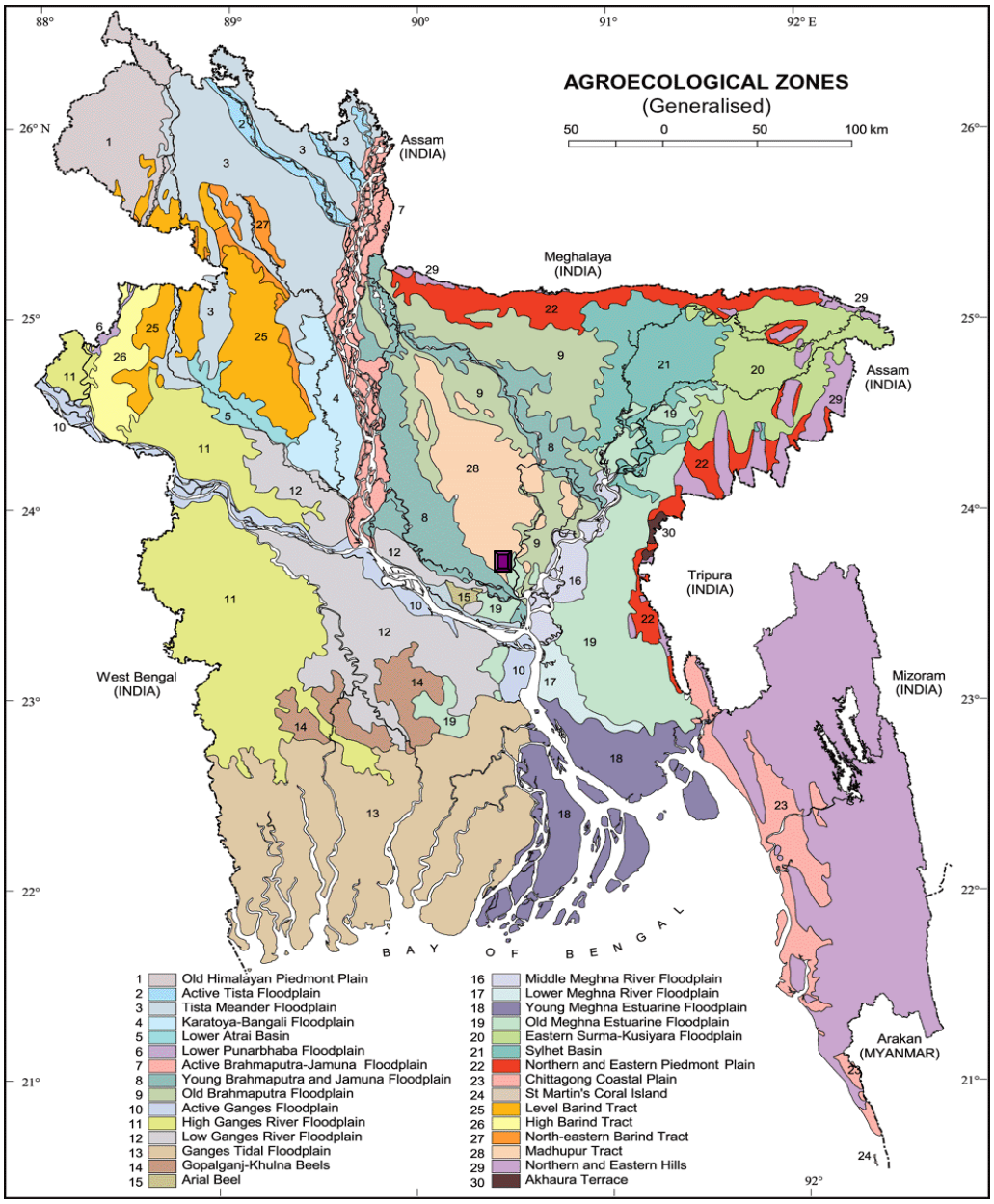
APPENDICES

Appendix I. Map showing the experimental site under the study



The experimental site under study

Appendix II: Morphological, physical and chemical characteristics of initial soil (0-15 cm depth) of the experimental site

Soil characteristics	Analytical results
Agro ecological Zone	Madhupur Tract
P^H	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 III. Monthly average temperature, relative humidity and total rainfall and sunshine of the experimental site during the period from November, 2015 to May, 2016

Month	Air temperature (°C)		Relative humidity (%)	Rainfall (mm) (total)	Sunshine (h)
	Maximum	Minimum			
November, 2015	34.8	18.0	77	227	5.8
December, 2015	32.3	16.3	69	0	7.9
January, 2016	29.0	13.0	79	0	3.9
February, 2016	28.1	11.1	72	1	5.7
March, 2016	33.9	12.2	55	1	8.7
April, 2016	34.6	16.5	67	45	7.3
May, 2016	32.8	23.6	68	245	5.4

Source: Bangladesh Meteorological Department (Climate and Weather Division), Agargoan, Dhaka – 1207.http://bmd.gov.bd/?/home/

Appendix IV. Mean performance of various growth parameter and yield components

Sl.	Genotype	DFF	D50F	D80F	PH	PB	SB	NP/P	NS/P	PL	TSW	YIELD
G1	BD-6875	44.33	51.33	87.33	63.42	1.89	7.50	15.57	10.83	6.40	22.25	3.79
G2	BD-6876	44.33	52.33	87.33	63.16	2.44	5.67	14.58	10.23	6.57	24.75	3.72
G3	BD-6878	44.33	52.33	87.33	66.55	2.11	6.48	14.57	10.42	6.00	22.81	3.49
G4	BD-6881	42.33	49.33	83.33	72.97	1.33	6.46	24.00	10.67	6.87	23.75	6.13
G5	BD-6882	43.33	50.33	85.33	64.18	2.00	5.50	20.23	10.72	6.23	22.84	5.00
G6	BD-6884	44.33	50.33	85.33	62.30	2.11	6.97	21.67	10.84	7.27	26.82	6.33
G7	BD-6885	43.33	49.33	85.33	69.34	1.00	6.82	15.75	11.46	7.80	26.42	4.79
G8	BD-6886	43.33	49.33	85.33	60.70	2.44	6.90	14.25	11.01	6.63	23.48	3.71
G9	BD-6887	44.33	50.33	86.33	64.33	3.17	7.63	17.42	10.12	6.47	27.75	4.92
G10	BD-6888	44.33	51.33	87.33	71.37	2.72	7.30	17.08	11.64	7.27	28.75	5.75
G11	BD-6890	44.33	52.33	88.33	74.67	2.56	6.63	33.67	10.40	6.20	29.99	10.49
G12	BD-6891	43.33	50.33	85.33	65.02	2.67	7.63	22.57	11.72	6.73	34.73	9.51
G13	BD-6892	45.33	52.33	86.33	63.83	3.08	6.48	18.75	10.81	5.93	27.48	5.62
G14	BD-6893	44.33	51.33	86.33	71.45	3.08	6.55	17.32	11.64	6.90	30.08	6.09

Continued Appendix IV

Sl.	Genotype	DFF	D50F	D80F	PH	PB	SB	NP/P	NS/P	PL	TSW	YIELD
G15	BD-6895	44.33	51.33	87.33	70.78	2.52	7.28	20.50	12.14	6.63	45.98	11.48
G16	BD-6897	44.33	52.33	88.33	63.16	2.50	6.85	19.55	11.44	7.03	27.42	6.17
G17	BD-6899	45.33	52.33	88.33	64.01	2.06	6.50	13.42	10.42	7.00	28.35	3.99
G17	BD-6899	45.33	52.33	88.33	64.01	2.06	6.50	13.42	10.42	7.00	28.35	3.99
G18	BD-6902	43.33	49.33	84.33	65.86	2.42	7.07	14.22	11.31	7.00	33.48	5.40
G19	BD-6906	43.33	49.33	85.33	74.24	2.49	6.32	21.67	12.25	6.83	28.59	7.62
G20	BD-6908	42.33	48.33	83.33	64.08	2.13	6.87	17.22	10.75	7.90	23.24	4.33
G21	BD-6909	44.33	51.33	85.33	69.77	2.25	5.83	34.20	11.67	7.60	29.07	11.61
G22	BD-10022	43.33	49.33	85.33	60.19	2.36	6.73	13.18	10.67	5.93	25.37	3.54
G23	BD-10023	44.33	50.33	85.33	46.73	2.18	6.45	13.73	11.28	7.07	22.54	3.52
G24	BD-10024	43.33	49.33	84.33	54.53	2.72	7.33	17.67	10.42	5.97	21.52	4.00
G25	BD-10026	45.33	51.33	86.33	60.78	1.58	7.19	20.42	11.11	7.43	22.60	5.21
G26	BD-10027	43.33	49.33	85.33	71.80	2.90	6.64	18.15	12.03	7.30	27.38	5.99
G27	BD-10028	44.33	50.33	85.33	66.87	2.33	6.42	33.98	10.44	6.13	21.02	7.43
G28	BD-10029	44.33	51.33	86.33	71.12	2.35	6.87	34.45	11.64	7.27	23.42	9.46

Continued Appendix IV

Sl.	Genotype	DFF	D50F	D80F	PH	PB	SB	NP/P	NS/P	PL	TSW	YIELD
G29	BD-10030	44.33	50.33	86.33	69.42	2.08	6.70	31.75	12.33	7.23	27.30	11.06
G30	BD-10032	45.33	51.33	86.33	67.31	2.33	7.73	33.17	11.19	7.00	22.82	8.57
	Mean	44.03	52.33	85.99	65.80	2.33	6.78	20.82	11.12	6.82	26.73	6.29
	Min.	42.33	48.33	83.33	46.73	1	5.5	13.18	10.12	5.93	21.02	3.49
	Max.	45.33	52.33	88.33	74.67	3.17	7.73	34.45	12.33	7.9	45.98	11.61

DFF= Days to first flowering, D50F= Days to 50% flowering, D80F= Days to 80% maturity, PH= Plant height, PB= Primary branches per plant, SB= Secondary branch per plant, NP/P= No. of pod /plant, NS/P= No. of seed/pod, PL= Pod length, TSW= 1000 seed weight and YIELD= Yield/plant

Appendix V. Analysis of variance of 11 yield and yield contributing characters of mungbean

Source	Df	Mean sum of square										
		DFF	**D50F**	**D80F**	**PH**	**PB**	**SB**	**NP/P**	**NS/P**	**PL**	**TSW**	**YIELD**
Genotype	29	1.89	4.21	5.24	16.35**	0.69**	0.90**	149.52**	1.20**	0.92**	75.45**	19.67**
Replication	2	10.00	10.00	10.00	1.27	0.03	0.33	0.45	0.33	0.47*	4.42*	0.02
Error	58	0.0001	0.0001	0.0001	2.3660	0.0528	0.1362	0.7243	0.2921	0.1445	1.1095	0.3211

**** Correlation is significant at the 0.01 level** *** Correlation is significant at the 0.05 level**

DFF= Days to first flowering, D50F= Days to 50% flowering, D80F= Days to 80% maturity, PH= Plant height, PB= Primary branches per plant, SB= Secondary branch per plant, NP/P= No. of pod /plant, NS/P= No. of seed/pod, PL= Pod length, TSW= 1000 seed weight and YIELD= Yield/plant

Appendix VI. Z1-Z2 score of 30 genotypes of mungbean

Genotype	PC1	PC2
G1	6.137	3.883
G2	6.887	1.406
G3	6.892	3.052
G4	-3.052	3.216
G5	1.397	4.051
G6	-0.561	0.349
G7	5.022	-0.432
G8	7.574	2.844
G9	3.641	-1.176
G10	3.073	-2.967
G11	-14.165	-2.378
G12	-3.146	-7.861
G13	2.149	-0.866
G14	2.653	-4.185
G15	-3.141	-19.783
G16	1.258	-0.897
G17	7.516	-2.387
G18	5.979	-7.234
G19	-1.867	-2.399
G20	4.474	3.42
G21	-14.583	-1.183
G22	8.529	0.97
G23	9.062	4.54
G24	4.89	5.72
G25	1.302	4.341
G26	2.169	-1.397
G27	-12.228	7.524
G28	-13.829	4.472
G29	-11.963	0.106
G30	-12.069	5.25