CORRELATION, CO-EFFICIENT AND GENETIC VARIABILITY ANALYSIS IN MUNGBEAN (*Vigna radiata* L. wilczek)

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CERTIFICATE

*This is to certify that thesis entitled, "**Correlation, Co-efficient and Genetic variability analysis in Mungbean (Vigna radiata 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 in GENETICS AND PLANT BREEDING**, embodies the result of a piece of bonafide research work carried out by **MD. EYAHIA SHEAK** Registration **No.10-04104** under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.*

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

(Prof. Dr. Md. Sarowar Hossain)

Supervisor

Dated: December, 2017
Place: Dhaka, Bangladesh


DEDICATED
TO
MY PARENTS

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SAU, Dhaka

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.*		

CORRELATION, CO-EFFICIENT AND GENETIC VARIABILITY ANALYSIS IN MUNGBEAN (*Vigna radiata* L. wilczek)

BY

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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 2017 to 5 March 2018. 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 plant height, number of pod per plant, thousand seed weight and seed yield indicating that these trait was under additive gene control and selection 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 days to first flowering, seeds per pod 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 Therefore considering group distance and other agronomic performances the inter-genotypic crosses between G7 and G30; G8 and G7; G15 and G30; G15 and G8; G19 and G30, G7 and G29, G9 and G19; G10 and G11; G24 and G30; G24 and G8, might be suggested for future hybridization program.

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CHAPTER I

INTRODUCTION

The mungbean, *Vigna radiata* (L.) Wilczek has been grown in India since ancient times. It is still widely grown in southeast Asia, Africa, South America and Australia. It was apparently grown in the United States as early as 1835 as the Chickasaw pea. It is also referred to as green gram, golden gram and chop soybean. Mungbeans are grown widely for use as a human food (as dry beans or fresh sprouts), but can be used as a green manure crop and as forage for livestock.

Mungbean 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 is an important crop in our country. Bangladesh grows various types of pulse crops. Among them grass pea, lentil, field pea and cowpea are important. Mungbean belongs to the family Leguminoseae, sub family papilionaceae. Mungbean is an annual food legume. Since mungbean has a short maturity span (60-75 days) it is grown under various cropping systems, hence contributing to the increase of the small landholders income as well as to the improvement of the soil conditions (Fernandez and Shanmugasundaram, 1988). In the south Asia mungbean is use to make daal. Daal is the most common dish in the south asia. In Bangladesh it is grown under a wide range of agro-ecological zones of both rainfied and irrigated nature. One of the reasons of low yield is unavailability of high yielding cultivars with better adaptability. Recently Bangladesh achieved self sufficiency in cereal production. Vegetables production trend is also positive for its ready market, high demand and availability of good variety, though fruits production remains static. But the production of grain legumes (pulses) and oilseeds declined sharply, mostly for decreasing of cultivation area. The country has to import more than 50% of its

requirement for pulses, spending hard currency. According to FAO (1999) recommendation a minimum intake of pulse by a human should be 80g/day. Whereas it is 14.19g in Bangladesh (BBS,2007). A lot of research have been done to increase the present yield of grain legumes including mungbean. Research have shown that the ultimate yield components that contribute directly to the grain yield are in order of development , the number of pods , average seed number and average seed size.

Mungbean seeds are sprouted for fresh use or canned for shipment to restaurants. Sprouts are high in protein (21%–28%), calcium, phosphorus and certain vitamins. Because they are easily digested they replace scarce animal protein in human diets in tropical areas of the world. Because of their major use as sprouts, a high quality seed with excellent germination is required. The food industry likes to obtain about 9 or 10 grams of fresh sprouts for each gram of seed. Larger seed with a glassy, green color seems to be preferred.

If the mungbean seed does not meet sprouting standards it can be used as a livestock food with about 1.5 ton of mungbean being equivalent to 1.0 tons of soybean meal for protein content. Feeding trials have been conducted at Oklahoma State University for swine and young calves with good results.

Mungbeans are a warm season crop requiring 90–120 days of frost free conditions from planting to maturity (depends on variety). Adequate rainfall is required from flowering to late pod fill in order to ensure good yield. Late plantings which result in flowering during the high temperature-low moisture period in July and August will reduce yield. High humidity and excess rainfall late in the season can result in disease problems and harvesting losses due to delayed maturity.

Mungbeans (if proper varieties are used) are adapted to the same climatic areas as soybean, drybean and cowpea. Mungbeans are responsive to length of daylight so short days hasten flowering and long days delay it. Varieties differ in their photoperiod response.

Mungbeans do best on fertile sandy, loam soils with good internal drainage. They do poorly on heavy clay soils with poor drainage. Performance is best on soils with a pH between 6.2 and 7.2 and plants can show severe iron chlorosis symptoms and certain

micronutrient deficiencies on more alkaline soils. Mungbean has phosphorus, potassium, calcium, magnesium and sulfur requirements similar to other legumes which must be met by fertilizer additions if the soil is deficient in these elements.

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.

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 30 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.

Lush (1947) defined heritability in broad sense as well as in narrow sense. Broad sense, heritability is the proportion of total genetic variance in the total phenotypic variance, while narrow sense heritability is the ratio of additive genetic variance to the total phenotypic variance. Selection (natural or artificial), provides improved or more fit genotypes only by acting on genetic variance or genetic differences which are inherited to the next generation. Thus heritability estimate which provides the assessment of ratio of transmissible genetic variation to the total variation happens to be the most important basic factor that determines genetic improvements or response to selection. The two other important factors which play crucial role in determining the response to selection are the genetic variability estimate and the intensity of the selection. The estimate of genetic advance as per cent of mean provides more reliable information regarding the effectiveness of selection in improving a trait because its estimate is derived by involving heritability, phenotypic standard deviation and selection intensity. Thus the estimate of heritability and genetic advance are of great significance to plant breeders for developing suitable selection strategy.

Rathnaswamy et al. (1978) observed variability in different characters of 24 early maturity *Vigna radiata* cultivars. The range if variation was 10.15 - 26.05 for pods per plant, 6.21-8.72 cm for pod length, 9.38 -13.45 for seeds per pod 2.95 - 7.4 g for 100-seed weight and 4.28 - 7.25 g for seed yield per plant.

Singh and Malhotra (1976) observed high heritability for seed weight which was also accompanied with high genetic advance indicating that high heritability coupled with

high genetic advance could be due to additive gene action. Genetic advance was also observed to be high for pod number, branch number and seed yield but these traits had also low heritability estimates.

Miah and Bhadra (1989) obtained information on genetic variation and heritability derived from data on yield and yield components in 7 varieties of *Vigna radiata* (greengram). High values for expected genetic advance were found for number of days to flowering, height and number of pods per plant and seeds per pod and it was thought that selection for these traits would be effective.

Ali and Shaikh (1987) grew 30 mungbean genotypes at 2 sites and evaluated them for 10 traits. Significant "genotype x site" interactions were observed in all the character, except days to maturity. Seed yield per plant exhibited the highest genotypic (30.67%) and phenotypic (49.66%) coefficients of variation. Least phenotypic variation was observed for days to maturity and the least genotypic variation for days to maturity and number of seeds per pod.

Khan (1988) observed that the estimates of heritability and expected genetic advance for pods per plant and 100-seed weight were the highest, following gamma irradiation and for plant yield following combined treatment. In general, the values of heritability and genetic advance were low for all the characters.

Gupta et al. (1978) noted that 100-seed weight, plant height and days to maturity in mungbean (*Vigna radiata*) were influenced by additive gene action.

Ahuja (1980) reported that non additive gene effects were important for all the traits, in mungbean, except 100-seed weight and harvest index for which additive gene effects were more important for number of pods per plant, seed yield per plant and number of seeds per pod. Non additive gene action was low for days to first flowering, plant height, number of branches per plant, number of pods per plant and 100-seed weight. They suggested that recurrent selection may be useful for improvement of yield.

Mahendra (1980) reported that additive gene action controlled plant height, pod length, seeds per pod and days to flowering. The branches, number, pod number and seed yield were found controlled by non additive gene action.

Deshmukh and Manjare (1980) reported that additive gene action predominated for height, pods per cluster, clusters per plant and 100-seed weight, while non additive gene effects were more important for days to flowering, days to maturity and pods per plant in mungbean.

Loganathan et al. (2001a) made experiments with 50 genotypes of greengram to estimate genetic variability for 10 quantitative characters during Rabi 1999. High phenotypic coefficient of variability indicated the favorable effects of environment for number of clusters per plant and seed yield per plant. High genotypic coefficient of variability suggested the substantial effects of genotype for number of pods per plant and seed yield per plant. Due to high genetic advance and additive gene action, phenotypic selection were considered effective for number of pods per plant, seed yield per plant and number of seeds per pod. Non additive gene action was low for days to first flowering, plant height, number of branches per plant, number of pods per plant and 100-seed weight. They suggested that recurrent selection may be useful for improvement of yield.

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.

Lavanya et al. (2005) studied variability and genetic parameters in 20 mung bean genotypes. Results revealed significant differences for seven yield and yield attributing traits viz. number of primary branches, pod length, plant height, pods per plant, seeds per pod, 100-seed weight and seed yield per pod. Pods per plant and seed yield per plant exhibited high phenotypic coefficient of variation that indicated the favorable effect of environment on these characters. High genotypic coefficient of variation suggested the presence of substantial amount of genetic variability for 100-

seed weight, seed yield per plant and pod length along with high heritability and high genetic advance as percentage of mean.

Chakraborty and Borah (2001) studied genetic variability, heritability and genetic advance for 5 root characters viz. root length, root nodules plant, number of secondary roots per plant, root dry weight and root/shoot ratio and seed yield. Relatively, large differences between phenotypic and genotypic coefficient of variability were observed for root length, root nodules per plant and root-shoot ratio indicating that the environment greatly influences these characters. Moderately high heritability with high genetic advance for seed yield per plant, nodules per plant and root dry weight suggested the partial additive gene effects in their inheritance. However, low genetic advance for root length, nodules per plant and root shoot-ratio indicated that these traits were predominantly governed by non-additive gene effects .

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 F2 progenies during mean-kharif 1981-82. High variability was found in the F2 for days to maturity,

clusters/plant, harvest index, pod length and 100-seed weight. Clusters/plant and 100-seed weight had high heritability. In parents, high heritability was found for plant height, seed yield/plant and harvest index, and in the F2 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 of mungbean 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 to differ 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 number of pod, 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 mungbean varieties 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 of pods, 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.

In this crop studies on genetic variability and heritability were also made by several workers (Imrie et al. 1985, Holkar and Raut 1993, Singh and Singh 1996, Sarkar et al. 1996, Tiwari et al. 1997, Vikas et al. 1998, Borah Chakraborty 2001, Singh et al. 2001, Khan et al. 2004.

2.2 Correlation and path coefficient

The seed yield has very complex inheritance because its expression depends upon several other plant characters referred to as yield components. The genetic architecture of seed yield can be better resolved through components rather than yield per se as the yield is the end product of multiplicative interaction between various components (Grafius 1959). Therefore, yield is also designated as 'super character'. Consequently this, motioned Donald (1968) to put forth the concept of plant ideotypes that refers to the ideal plant structure which possesses optimum balance of all the yield components and other important plant characters so that maximum economic yield can manifest under the environment for which it is aimed. Therefore, selection for yield per se will not mater as such unless accompanied by the selection for important characters responsible for conditioning it.

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.

Sawarker (1978) studied correlation in this crop and found that genotypic correlations were higher than corresponding phenotypic and environmental correlations and grain yield had high correlation with number of pods, number of clusters and seeds per pod.

Vikas *et. al* (1999) studied correlation and direct and indirect relationship of yield components with seed yield in mungbean over environments. They found that genotypic correlation were higher than corresponding phenotypic correlation. Seed

yield per plant showed positive association with number of clusters per plant, number of pods per plant, number of seeds per pod, 100-seed weight and harvest index. The path analysis revealed that seed yield per plant was influenced directly by biological yield and harvest index in most of the environments and by plant height, number of clusters per plants and pods per plant and 100-seed weight in few environments. However, yield was indirectly influenced by plant height, number of pods per plant, days to biological yield via harvest index.

Miah *et al.* (1989) reported highly significant GCA and SCA variances for seed yield. Pods per plant, seed weight, pod length and pods per plant were most important yield contributing characters which should be used in selection pogram.

Chaudhury *et al.* (1979) made experiment using 40 cultivars of mungbean crop on 3 dates during each season for 4 years. They observed positive association of seed yield with pods per plant, seeds for pod and plant height but negative correlation of seed yield with days to flowering and days to first mature pods.

Chakraborty et al. (2004) studied susceptibility of 37 mungbean (*Vigna radiata*) genotypes to pulse beetle and the correlation between pest susceptibility and different seed parameters in pre-monsoon (March-May) and monsoon (July-September) seasons. The susceptibility parameters i.e. percentage of affected seeds, number of eggs laid, number adults emerged, and percentage of weight loss, were significantly and positively correlated with seed weight, but were negatively and significantly correlated with seed coat width. The moisture and protein contents of seeds had no effects on the susceptibility of mungbean to pulse beetle. The coefficients of variation for seed weight and seed coat width were less than 20%, thus, both characters may be used as indirect selection criteria for resistance to *Callosobruchus chinesisin* mungbean.

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.

Singh and Singh (1981) reported that seed yield in 6 *Vigna radiata* cultivars in the summer and kharif(Monsoon) seasons was positively influenced, directly and indirectly by NAR, RGR and specific leaf weight, but not by leaf weight ratio and specific leaf area. The association between different physiological characters is discussed.

Rajput et al. (2004) noted that pod number and seed weight of branches were positively correlated with economic yield where pod number and seed weight in the main stem were negatively correlated with economic yield. Economic yield was positively correlated with harvest index and negatively correlated with biological yield. Plant height was positively correlated with number of nodes. Pod number, pod weight, and seed weight in the main stem were positively correlated with each other. Seed weight on the main stem and branches were negatively correlated.

Chaudhary (1985) observed highest positive association of seed yield with number of seeds per pod followed by branches per plant and clusters per plant The low but negative estimates of correlation of seed yield with plant height and 100-seed weight were recorded. Strong positive correlation between clusters per plant and pods per plant and between branches per plant and clusters per plant were also observed. Path analysis identified seeds per pod and clusters per plant as most important yield influencing traits.

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.

Malik *et al.* (1987) reported that yield was positively and significantly correlated with plant height, primary branches per plant, pods per plant, clusters per plant, and biological yield. The path analysis revealed that days to pod initiation, plant height and biological yield had the highest direct positive effect on seed yield, per plant. The direct effect of days to flower, days to maturity, clusters per plant, pod length and seeds per pod on seed yield were high but negative.

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.

Nafade (1988) reported that plant height, number of clusters per plant, number of pods per plant, number of seeds per pod and shelling percentage showed significant and positive correlation with seed yield at genotypic level, whereas path analysis revealed that number of pods per plant, number of seeds per pod, and shelling percentage were the major yield contributing characters.

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.

Patil and Deshmukh (1988) evaluated 89 diverse genotypes of mungbean and found significant positive association of seed yield with 100-seed weight, seeds per pod and pods per plant. Path analysis indicated that days to flowering and 100-seedweightweremostimportant traits as positive direct contributors towards seed yield. Days to maturity and seeds per pod had high order direct effect on seed yield.

Dhuppe *et al.* (2005) reported that 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 and 100- seed weight were correlated with grain yield at phenotypic level. Path analysis revealed that the number of seeds per plant and 100-seed weight were the major yield contributing characters.

Pundir *et al.* (1992) recorded significant and positive correlation of seed yield with number of branches, clusters and pods per plant, pod length, seeds per pod and 100-seed weight, along with negative correlation of seed yield with plant height and fruiting height in an experiment based on evaluation of 351 germplasm collections.

Significant and positive correlation between branches per plant, clusters per plant, and pods per plant and between pods per plant and 100-seed weight were also observed. In path analysis, pods per plant and 100-seed weight emerged as characters making positive direct and indirect effects on seed yield.

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 and plant height.

Sirohi and Kumar (2006), studied path-coefficient analysis for yield and yield components which were conducted for 19 diverse genotypes of mungbean (*Vignaradiata*) 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 mungbean (*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.

Naidu et al. (1994) carried out path coefficient analysis by evaluating 20 genotypes of Mungbean under 6 environments. They found that shoot dry weight, shoot nitrogen and pods per plant exerted high order positive direct effect, while clusters per plant and branches per plant had negative direct effect on seed yield. Number of pods per plant, 100- seed weight and shoot nitrogen showed considerable positive indirect effect on seed yield through shoot dry weight.

Rajan *et al*. (2000); were studied path coefficients in 7 parents and F2 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.

Rajan et al. (2001) observed that seed yield had significant positive genotypic correlation with number of secondary roots at maturity and dry weight of plants at maturity, plant height cluster per plant, pods per plant, seed per pod and 100-grain weight and harvest index. Number of pods per plant and harvest index showed high positive correlation on grain yield and also with each other. Path analysis reviled that pods per plant had the highest positive direct effect, followed by 100- grain weight on grain yield. The study revealed that improvement of grain yield is possible by selecting characters having high positive correlation and positive direct effect.

Sharma and Gupta (1994) carried out correlation and path analysis in mungbean in which seed yield was found to be positively correlated with biological yield per plant, harvest index, clusters per plant, pods per plant, height and 100-seed weight. Path analysis showed that biological yield per plant had the highest positive direct effect on seed yield, followed by harvest index, pods per plant, seed sulphur content, days to maturity, day to flowering, clusters per plant, 100-seed weight and pod length. Considerable negative direct effect on seed yield per plant were exerted by seeds per pod, seed phosphorus content, seed crushing hardness, plant height and protein content in 32 lines of "urd bean x mungbean" crossing.

Singh and Singh (2000) observed maximum positive and significant correlation coefficient (0.79) in non segregating generation between number of pods per plant and seed yield per plant, whereas in segregating (F2) generation, maximum positive and significant correlation (0.874) was found between seed yield and harvest index in the cross Ma-46 x PDM-146. Seed yield per plant had positive and significant correlation with biological yield, number of pods and harvest index of the parents.

Sharma and Talukdar (1996) studied correlation and path analysis for yield components in 34 M7 gernerations of green gram micro mutant lines and their 2 base genotypes. They found that seed yield per plant was positively correlated with plant height, number of primary branches, pods per cluster, days to maturity, seeds per pod and 100-seed weight. Plant height and pods per cluster had maximum direct effect on seed yield per plant.

Kalpande et al. (1997) reported significant positive association of seed yield with primary branches and clusters per plant on the basis of evaluation of 24 mungbean lines for12 yield components in all the three environments viz. Kharif, late Kharif and Rabi. Path analysis reviled that primary branches and secondary branches per plant had direct positive effects on seed yield through days to 50% flowering. Secondary branches per plant clusters per plant, pods per cluster and seeds per pod were important in almost all the three environments.

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.

Yaqqob et ah (1997) conducted correlation and path analysis in 30 genotypes (mutants) of mungbean under rainfeid conditions. Grain yield had positive genotypic association with days to 50% flowering, number of branches, number of pods per plant, number of clusters, 100- seed weight, dry matter yield and harvest index on grain yield. Negative direct effect of plant height, number of pods and cluster on grain yield was observed.

Gill et al. (2000) reported that seed yield per plant had significant positive correlation with pods per plant, seeds per pod and 100-seed weight in all the 3 crosses except in cross II in F5. Seeds per pod had negative association with 100-seed weight in most of the cases. Pods per plant and 100-seed weight were important yield components in all the crosses both U1F5 and F6 germinations. Direct effects of pods per plant accounted for its high genotypic and phenotypic correlation with yield per plant to a great extent, suggesting that direct selection through pod number and seed yield.

Inter character correlation and path analysis in mungbean were studied by some other investigators also (Shamsuzzaman et al. 1983, Reddy et al. 1994, Sharma, 1995, Vikas et al. 1999, Sharma et al. 2004).

2.3 Genetic Divergence

Mishra (1986) reported cluster analysis assigning the varieties to 10 groups. Genetic diversity was not related to geographical diversity. Highly significant differences were observed among 30 Indian varieties for yield and 7 related characters.

Ramana and Singh (1987) reported that 39 *Vigna radiata* genotypes grown in the spring and kharif seasons of 1984 were grouped into 8 clusters following analysis of data on 8 yield related characters by means of Mahalanobis D statistic. A total of 21 genotypes occurred in cluster in the spring and 28 in cluster in the kharif. A considerable number of genotypes were common to cluster I in both seasons. The effect of season on cluster distances and hence cluster and genotype divergence are considered. Days to flowering and 100-seed weight contributed most to genetic divergence in the kharif season and spring, respectively.

Tawar et al. (1988) obtained information on genetic divergence (D) by analysis of data on 9 quantitative traits in 34 (*Vigna radiata*) genotypes grown in 1982. Five clusters, each containing 5-8 genotypes were obtained.

Natarajan and Palanisamy (1990) found agreement for clustering determined by multivariate analysis, identifying petiole, stem and root weight as the main source of divergence. Canonical analysis additionally identified harvest index as a source of divergence. Divergence between parents as measured by generalized distance analysis corresponded well superiority of the F1 over the mid parental values for pod weight and seed yield.

Satyan et al. (1991) obtained information on genetic diversity derived from an analysis of data on 11 yield components in 12 genotypes. The analysis identified a broad group based on seed yield and pod breaking habit.

Naidu and Satyanarayana (1991) recorded data for 13 yield related and agronomic characters. D2 analysis grouped the genotypes into 14,11 and 8 clusters for the 3 respective environments, which showed the influence of environments on clustering pattern and also indicated the importance of studying materials in more than one

environment. No relationship between geographic diversity and genetic diversity was observed.

Holkar and Yadava (1995) used D analysis and grouped 36 genotypes into 9 and 10 clusters for the S1 and S2 seasons, respectively. The characters biological yield, harvest index and number of pods per plant made greater contribution to genetic divergence and were suggested for use as to selection criteria for improvement of seed yield in this crop .

Mishra et ah (1995) reported significant differences occurred among genotypes which were grouped into 6 clusters. VG 135, ML 125, PDM-14 and TT-2E were the most diverse genotypes.

Reddy (1997) grouped genotypes into 8 clusters. The pattern of distribution of genotypes from different geographical regions into various clusters was random demonstrating that geographical isolation may not be the only factor for genetic diversity. Days to maturity, pod length, grain yield, plant height, branches per plant and pods per cluster contributed 85% of total divergence.

Lai et al. (1998) studied D analysis of 84 genotypes of different geographical regions and grouped them into 17 clusters. Pods per plant contributed most to cluster differentiation. Genetic diversity was independent of geographic origin and parentage. Glutamate oxaloacetate transaminase activity was high in high yielding clusters. They suggested the importance of biochemical divergence in relation to morphological divergence.

Miranda et al. (1999) and Satyan et al. (1999) studied genetic divergence in this crop and grouped the genotypes into clusters.

Loganathan et al. (2001) studied multivariate analysis of 10 quantitative traits. The grouping of material into 7 clusters indicated the presence of wide range of genetic diversity among the genotypes.

Sandhu et al. (1979) observed the existence of a substantial amount of diversity in the mutant isolated from the gama-ray induced population of 3 mungbean cultivars (Ml-131, ML-267 and ML- 337). The mutants were grouped into 8 clusters. Clusters I to

VIII were the largest with 8 mutants in each and cluster VII was the smallest with two mutants only. Except for cluster III mutants, all other mutants were derived from2 or 3 cultivars. All the 3 mutants grouped in cluster III were isolated from one cultivar (ML-337). Plant height, pods per plant, seeds per pod, biological yield per plant, grain yield per plant and harvest index accounted for 99.92% of the total divergence.

Reddy et al. (2003) studied genetic divergence analysis for 12 quantitative traits viz. days to 50% flowering, days to maturity, plant height, branches per plant, clusters per plant, pods per cluster, pod length, seeds per pod, 100-seed weight, seed protein content, harvest index and seed yield per plant. The 50 mungbean genotypes were grouped into 9 clusters based on Mahalanobis-D statistic. Superior genotypes from different groups i.e. I (WGG-37 and Tarm- 2), II (TPA-7), VII (LGG-441), IX (LGG-452), VIII (PDM-89-221), III (LGG-471), IV (LGG-450), V (LGG421) and VI (LGG-427) were selected based on genetic divergence for yield and yield components.

Patil et al. (1991) recorded data for plant height, branches per plant, clusters per plant, pods per plant, seeds per pod, 100-seed weight, biological yield, harvest index, days to first flowering, days to 50% flowering, days to initiation of pod maturity, days to 75% maturity, powdery mildew at 45 and 60 days and mungbean yellow mosaic virus. The simultaneous test of significance for pooled effect of all the characters in all the test environments showed significant differences among the genotypes, indicating the presence of considerable genetic variability for different characters. The genotypes fall into 5 clusters in environments (E 3), 10 clusters in E 2 and 9 clusters inE1. The maximum number of genotypes (30) were included in cluster I under E 3. In contrast the number of clusters containing single genotypes were highest in E 2, followed by E 1 and E 3. Under E 3, only 5 clusters were obtained. The factors responsible for differentiation of intra and inter-cluster levels were different in different environments as indicated by the clusters means of various characters. In all the 3 environments, the pathological characters contributed the maximum. Among the genotypes K-851, LM-608 and LM -512 were the most genetically diverse in all the 3 environments.

CHAPTER III

MATERIALS AND METHODS

This chapter shows information concerning methodology that was used in execution of the experiment. It comprises a brief description of experimental site location, planting materials, climate and soil, seed bed preparation, experimental layout and design, 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, Sher-e-Bangla Nagar, Dhaka-1207. Bangladesh during the period from December 2017 to March 2018. The experimental site location 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 field was situated in the subtropical zone. The soil of the experimental site belongs to Agro ecological region of —Madhupur Tract (AEZ- 28). The soil of the experimental field 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 temperature, humidity, air 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 2017 (Table 1).

3.4 Design and Layout of the Experiment

The experiment was laid out and evaluated during Rabi season 2017-2018 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 field 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 2017.

3.6 Manure and Fertilizer Application

Mungbean requires less nitrogen application because mungbean is able to fix nitrogen from atmosphere. 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 well decomposed cowdung 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	2.11	48
TSP	3.62	92
MP	1.55	38
Cow dung	Applied earlier	2 ton

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

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

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.

7 Sowing of Seed and Intercultural Operation

The seed of thirty mungbean genotypes were sown in the experimental field on 6 December 2017. 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.

3.8 Crop Harvesting

After maturity stage harvesting of mungbean pods was done. Different genotypes matured at different times. Mature pods were harvested when fruits turned to brown in color and the pods per plant were allowed to ripe and then seeds were collected. Harvesting was completed on 5 March 2018.

3.9 Data Collection

Based on different agro-morphogenic traits data were recorded from each plot. 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. When first flower of a plot were at the opened flowered then days to first flowering was recorded

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.

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. multivariate 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).

Plate 2: A pictorial view showing intercultural operation

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

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^2_g= Genotypic standard deviation

δ^2_p= Phenotypic standard deviation

–

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 by Allard (1960).

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

Where, GA = Genetic advance

δ^2_g= Genotypic variance

δ^2_p= Genotypic 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).

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

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).

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

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):

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

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.

R_{iy} = 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^2 statistic is more reliable as requisite knowledge of parents in respect of a mass of characteristics is available prior to crossing. Rao (1952) suggested that the quantification of genetic diversity through biometrical procedures had made it possible to choose genetically diverse parents for a hybridization program. Multivariate analysis viz. Principal Component analysis, 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:

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

Where,

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

x = Number of characters.

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

3.10.9.5 Computation of average intra-cluster distances

Average intra-cluster distances were calculated by the following formula as suggested by Singh and Chowdhury (1985).

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

Where ,

$\sum D_i^2$ = 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).

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.

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

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 (D2) express the maximum divergence among the genotypes included into these different clusters. Varieties or lines 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

RESULT AND DISCUSSION

The present study was carried out with a view to determine the variability, character association and genetic diversity among 30 genotypes of mungbeans 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 nonexistence of variation among the genotypes for this trait. The maximum days to first flowering was found as 41 and the minimum was recorded as 44 with mean value of 42.58 (Table 2). The genotypic variance (0.27) and phenotypic variance (1.05) , genotypic coefficient of variation (1.21) and phenotypic coefficient of variation (2.41) were close to each other indicating less environmental influence in case of first flowering (Table 2). Heritability for this trait was low (25.42) and genetic advance (0.54) and genetic advance in percent of mean (1.26) was found low, indicated that selection for this character would not 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 47.67 days to 50.33 days after sowing with mean value 49.16 days (Table 2). The Genotypic, phenotypic and environmental variances observed were 0.39, 1.42 and 1.02, 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 a little difference between the genotypic co-efficient

of variation (1.27) and phenotypic coefficient Variation (2.42) (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 (27.75%) estimates for this trait was low, genetic advance (0.68) was at low and genetic advance over percentage of mean (1.38) were found low (Table 2), selection of this character would be effective. Genetic advances in percent of mean were low with the findings of Nehru *et al.* (1999).

4.2.3 Days to 80% maturity

The variance due to days to 80% maturity showed that the genotypes differed significantly and ranged from 83.00 days to 87.00 days after sowing with mean value of 85.28 days (Table 2). The Genotypic, phenotypic and environmental variances observed were 0.54, 2.20 and 1.66, 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 a little difference between the genotypic co-efficient of variation (0.86) and phenotypic coefficient of variation (1.74) (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 (24.59%) estimates for this trait was low, genetic advance (0.75) was low and genetic advance over percentage of mean (0.88) were found low (Table 2and Figure 2), indicated that 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 (74.00 cm) and the lowest plant height (56.00 cm) were recorded (Table 2). The genotypic and phenotypic variance was observed as 11.29 and 18.68, respectively for plant height with low environmental influence. The phenotypic co-efficient of variation (6.78) was higher than the genotypic co- efficient of variation (5.27), which indicated presence of considerable variability among the genotypes for this trait. The heritability (60.45%) estimates for this trait was high, genetic advance (5.38) was low and genetic advance in per cent of mean (8.44) was found low, 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 was recorded as 3.00 and the minimum number of primary branches 1.33 (Appendix IV). The phenotypic variance (0.46) appeared to be higher than the genotypic variance (0.09) 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 12.78 and 29.06, respectively which indicated presence of considerable variability among the genotypes. The heritability (19.34%) estimates for this trait was low, genetic advance (0.27) was low and genetic advance in per cent of mean (11.58) were found very high, revealed that this trait was governed by additive gene. Selection for this trait would be effective.

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

Traits	Range		Mean	MSS	CV (%)	$\pm^2$g	$\pm^2$e	$\pm^2$p	GCV	ECV	PCV	h^2_b	GA (5%)	GA (% mean)
	Min.	Max.												
DFF	41.00	44.00	42.58	1.58**	2.08	0.27	0.78	1.05	1.21	2.08	2.41	25.42	0.54	1.26
D50%F	47.67	50.33	49.16	2.20**	2.06	0.39	1.02	1.42	1.27	2.06	2.42	27.75	0.68	1.38
DM	83.00	87.00	85.28	3.29**	1.51	0.54	1.66	2.20	0.86	1.51	1.74	24.59	0.75	0.88
PH	56.00	74.00	63.77	41.27**	4.26	11.29	7.39	18.68	5.27	4.26	6.78	60.45	5.38	8.44
PBP	1.33	3.00	2.32	0.63*	26.10	0.09	0.37	0.46	12.78	26.10	29.06	19.34	0.27	11.58
SBP	5.67	8.00	6.54	1.11	13.58	0.11	0.79	0.90	5.02	13.58	14.48	12.03	0.23	3.59
PPP	14.67	31.67	23.93	54.47**	9.88	16.29	5.59	21.88	16.87	9.88	19.55	74.46	7.17	29.98
SPP	10.33	12.00	11.16	0.57	5.42	0.07	0.37	0.43	2.33	5.42	5.90	15.66	0.21	1.90
PL	5.33	7.67	6.82	1.19*	12.25	0.16	0.70	0.86	5.93	12.25	13.61	18.98	0.36	5.32
TSW	24.33	39.67	29.92	66.45**	8.61	19.94	6.63	26.57	14.92	8.61	17.23	75.04	7.97	26.63
YPP	4.00	9.67	7.04	5.40**	13.40	1.50	0.89	2.39	17.40	13.40	21.96	62.78	2.00	28.40

DFF = days to 1st flowering, D50%F = days to 50% flowering, DM = days to 80% flowering, PH = plant height (cm), PBP = primary branches per plant, SBP = secondary branches per plant, PPP = pods per plant, SPP = seeds per pod, PL = pod length (cm), TSW = thousand seed weight (g) and YPP = yield per plant (gm). MS = mean sum of square, δ^2 p = Phenotypic variance, δ^2g = Genotypic variance, δ^2e = Environmental variance, PCV = Phenotypic Coefficient of Variation, GCV= Genotypic Coefficient of Variation and ECV= Environmental Coefficient of Variation, h^2 = Heritability in broad sense, GA= Genetic advance

4.2.6 Number of secondary branches per plant

Number of secondary branches per plant was ranged from 5.67 to 8.00 with mean value of 6.54 (Appendix IV). The genotypic variance and phenotypic variance for this trait were 0.11 and 0.90, 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 (5.02) was close to phenotypic co-efficient of variation (14.48) which was desirable for the improvement of this crop. The heritability estimates for this trait was (12.03%) with low genetic advance (0.23) and high genetic advance in percent of mean (3.59) 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 (31.67) and the minimum was recorded (14.67) with mean value (23.93) (Table 2). The genotypic variance (16.29) and phenotypic variance (21.88), genotypic coefficient of variation (16.87) and phenotypic coefficient of variation (19.55) were close to each other indicating less environmental influence in case of number of pod per plant (Table 2). Heritability for this trait was high (74.46%) but genetic advance (7.17) and genetic advance in percent of mean (29.98) 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 (7.67) and the minimum was recorded (5.33) with mean value (6.82) (Table 2). The genotypic variance (0.16) and phenotypic variance (0.86), genotypic coefficient of variation (5.93) and phenotypic coefficient of variation (13.61) were not close to each other indicating environmental influence in case of pod length (Table 2).

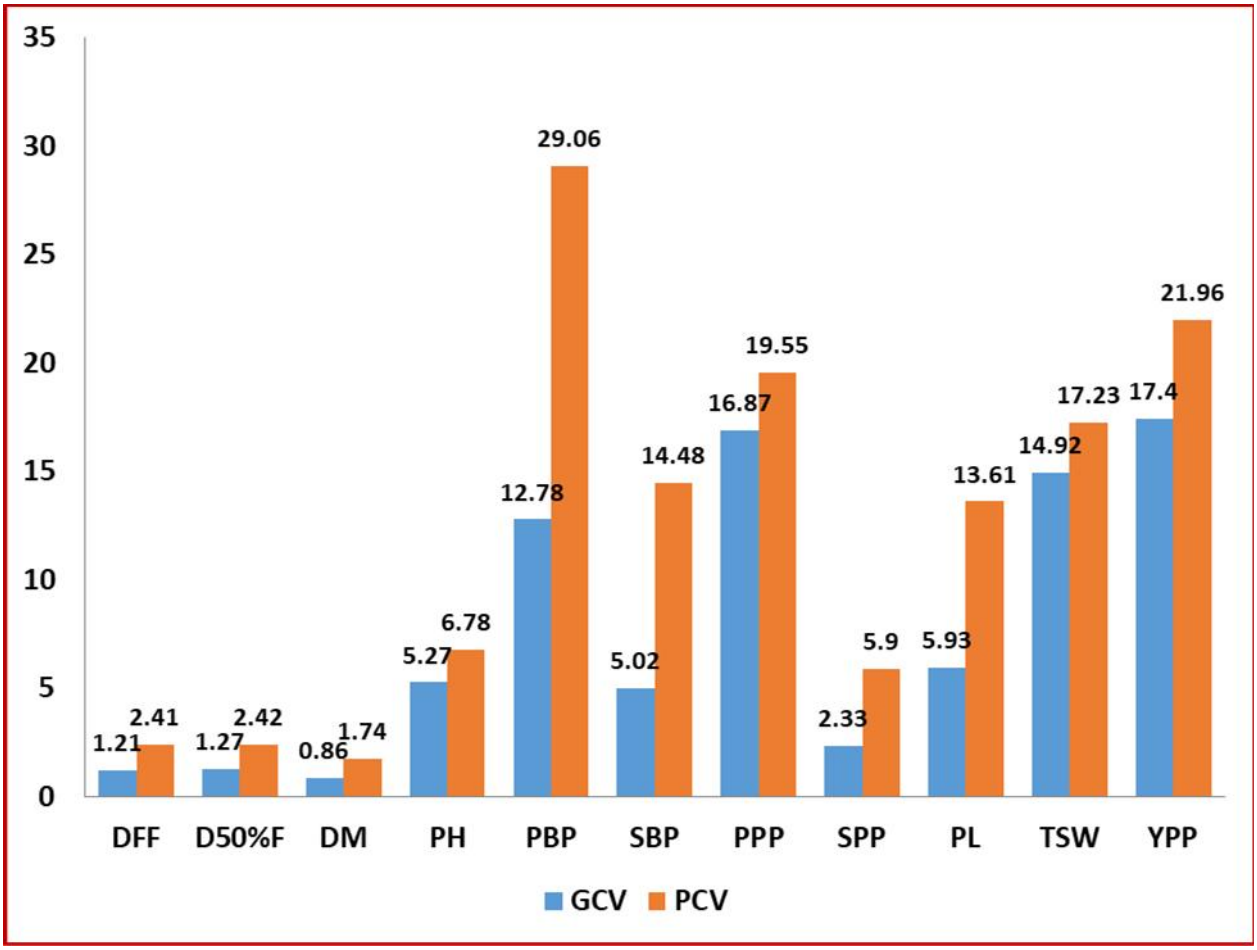

Figure 1. Genotypic and phenotypic variability in Mungbean

(DFF = days to 1st flowering, D50%F = days to 50% flowering, DM = days to 80% flowering, PH = plant height (cm), PBP = primary branches per plant, SBP = secondary branches per plant, PPP = pods per plant, SPP = seeds per pod, PL = pod length (cm), TSW = thousand seed weight (g) and YPP = yield per plant (g)).

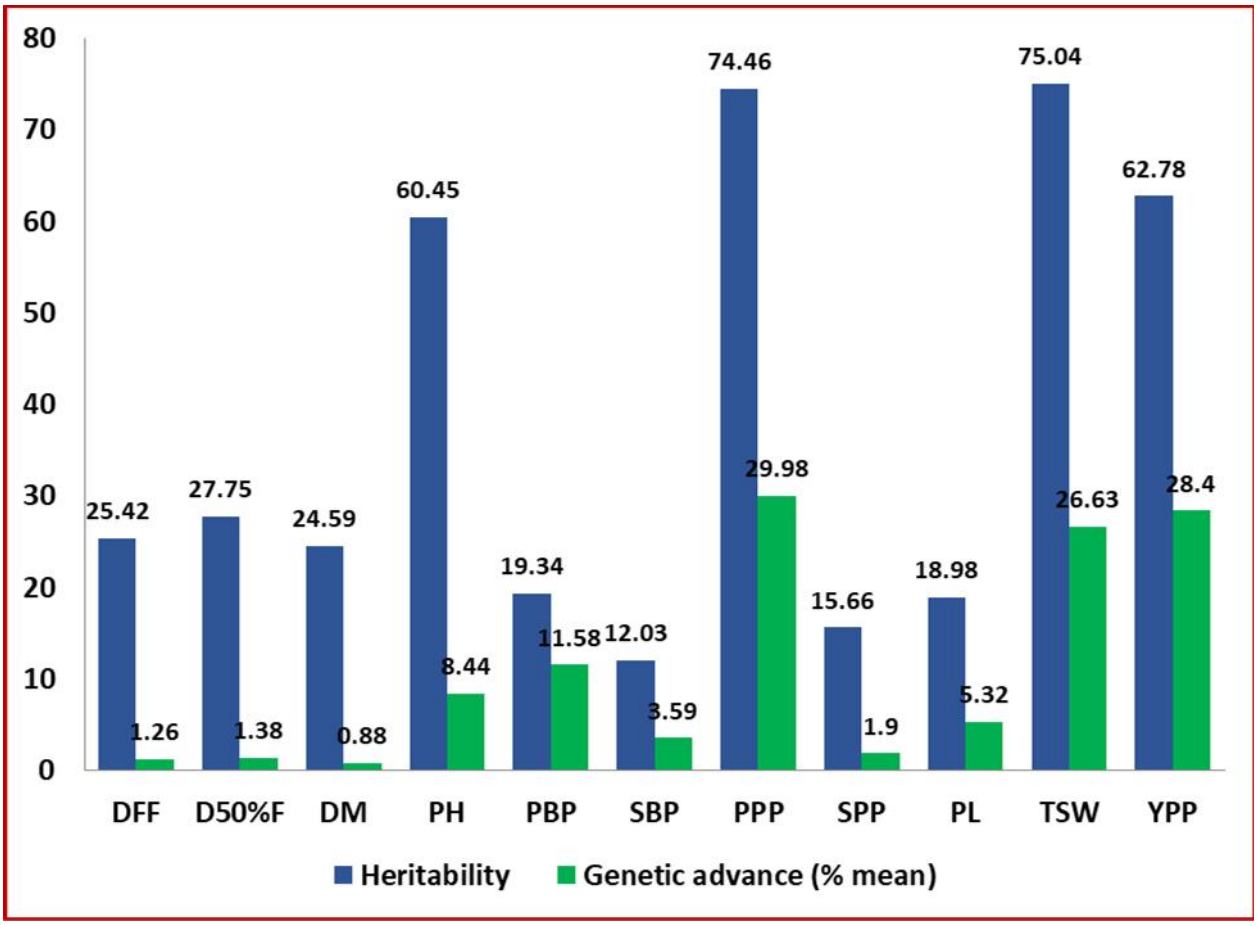

Figure 2. Heritability and genetic advance (% mean) of Mungbean

(DFF = days to 1st flowering, D50%F = days to 50% flowering, DM = days to 80% flowering, PH = plant height (cm), PBP = primary branches per plant, SBP = secondary branches per plant, PPP = pods per plant, SPP = seeds per pod, PL = pod length (cm), TSW = thousand seed weight (g) and YPP = yield per plant (g)).

trait was low (18.98%) and genetic advance (0.36) and genetic advance in percent of mean (5.32) was found low, indicated that selection for this character would be less 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 seeds per pod was found (12.00) and the minimum was recorded (10.33) with mean value (11.16) (Table 2). The genotypic variance (0.07) and phenotypic variance (0.43), genotypic coefficient of variation (2.33) and phenotypic coefficient of variation (5.90) were close to each other indicating less environmental influence in case of number of pod per plant (Table 2). Heritability for this trait was low (15.66%) and genetic advance (0.21) and genetic advance in percent of mean (1.90) was found low, indicated that selection for this character would be less effective.

4.2.10 Thousand 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 (39.67) and the minimum was recorded (24.33) with mean value (29.92) (Table 2). The genotypic variance (19.94) and phenotypic variance (26.57), genotypic coefficient of variation (14.92) and phenotypic coefficient of variation (17.23) were close to each other indicating less environmental influence in case of thousand seed weight (Table 2). Heritability for this trait was high (75.04%) and genetic advance (7.97) and genetic advance in percent of mean (26.63) 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

seed yield per plant was found (9.67) and the minimum was recorded (4.00) with mean value (7.04) (Table 2). The genotypic variance (1.50) and phenotypic variance (2.39)was found, genotypic coefficient of variation (17.40) and phenotypic coefficient of variation (21.96) were close to each other indicating less environmental influence in case of seed yield per plant (Table 2). Heritability for this trait was high (62.78%) but genetic advance (2.00) and genetic advance in percent of mean (28.40) 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 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, a highly significant positive correlation was observed in days to 50% flowering (G=0.549), secondary branches per plant (G=0.595), yield per plant (G=0.568) and seeds per pod (G=0.759). This character also showed non-significant positive correlation with thousand seed weight at both levels. It has showed a highly significant negative correlation with pods per plant (G=-0.467). It also showed insignificant negative correlation with days to 80% maturity, plant height, and pod length both at genotypic and phenotypic levels.

4.3.2 Days to 50% flowering

The correlation of days to 50% flowering was highly significant negative correlation in primary branches per plant (G=-0.568), and secondary branches per plant (G=-0.506). It also showed insignificant negative correlation with pod per plant. This character also showed non-significant positive correlation with plant height, seeds per pod, thousand seed weight and yield per plant. 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.

4.3.3 Days to 80% maturity

Highly significant and positive correlation was observed in case of pod length (G=0.547).a significant and positive correlation was found in thousand seed weight (G=0.375). The correlation with plant height (G=-0.517,P=-0.187), number of primary branches per plant (G=-0.684), secondary branches per plant (G=-0.956), seeds per pod (G=-0.990) was negative and highly significant. This character also showed non-significant negative correlation with 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=0.429, P=0.231), and number of secondary branches per plant (G=0.736, P=0.168) at both the genotypic and phenotypic levels was observed.it has also showed highly significant and negative correlation with thousand seed weight (G=-0.318, P=-0.246) and yield per plant (G=-0.257). This character also showed insignificant negative

correlation with number of primary branches per plant, seeds per pod and pod length 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 highly significant and positive association of number of primary branches with number of secondary branches (G=0.840, P=0.96).A non-significant positive correlation was found in number of seeds per pod (G=0.113, P=0.116), and thousand seed weight (G=0.164, P=0.020) 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 highly significant and negative association of number of secondary branches with number of seeds per pod (G=-0.508), thousand seed weight (G=-0.458) and pod length (G=-0.468) (Table 3) at the genotypic and levels were observed. Non-significant positive correlation was found with yield per plant and number of pods per plant at both levels

4.3.7 Number of pod per plant

Significant and positive correlation was observed with pod length and yield per plant. Pods per plant showed significant negative correlation with thousand seed weight (G=-0.268). Pods per plant showed insignificant negative correlation with seed per pod (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 yield per plant (G=0.461) (Table 3).

Plate 4: Seeds of different mungbean genotypes

Plate 5: Mungbean plants with mature pods

Table 3: Genotypic and phenotypic correlation co-efficient among different pairs of yield and yield contributing characters for different genotypes of mungbean

Traits		D50%F	DM	PH	PBP	SBP	PPP	SPP	PL	TSW	YPP
DFF	G	0.549**	-0.081	-0.242	-0.015	0.595**	-0.467**	0.759**	-0.199	0.186	0.568**
	P	0.187	-0.076	-0.087	0.002	-0.006	-0.130	0.068	-0.037	0.123	0.148
D50%F	G		0.170	0.058	-0.538**	-0.506**	-0.228	0.212	0.090	0.015	0.269
	P		-0.009	0.068	-0.202	-0.069	-0.153	0.080	-0.026	0.007	0.169
DM	G			-0.517**	-0.684**	-0.956**	-0.148	-0.990**	0.547**	0.375*	0.089
	P			-0.087	-0.059	-0.026	-0.130	-0.016	0.233*	0.156	0.118
PH	G				-0.296	0.736**	0.429**	-0.225	-0.120	-0.318*	-0.257*
	P				-0.108	0.168	0.231	-0.133	-0.066	-0.246*	-0.112
PBP	G					0.840**	-0.047	0.113	-0.030	0.164	-0.264
	P					0.096	-0.034	0.116	0.020	0.020	-0.023
SBP	G						0.145	-0.508**	-0.468**	-0.458**	0.036
	P						0.058	0.031	0.104	-0.130	0.007
PPP	G							-0.238	0.198	-0.268*	-0.001
	P							-0.092	0.128	-0.206	-0.043
SPP	G								0.267	0.438**	0.316*
	P								-0.027	0.290*	0.052
PL	G									0.175	-0.877**
	P									0.010	-0.977**
TSW	G										0.461**
	P										0.286

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

DFF = days to 1st flowering, D50%F = days to 50% flowering, D80F = days to 80% flowering, PH = plant height (cm), PBP = primary branches per plant, SBP = secondary branches per plant, PPP = pods per plant, SPP = seeds per pod, PL = pod length (cm), TSW = thousand seed weight (g) and YPP = yield per plant (gm).

4.4 Path coefficient analysis

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 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 first flowering

Path analysis revealed that days to first flowering had positive direct effect (0.2340) on yield. Days to first flowering showed negative indirect effect with pod length (-0.0028) and pod per plant (-0.1948). Days to first flowering has indirect positive effect with number of seeds per pod (0.0005), plant height (0.0369), days to 50% maturity, primary branches per plant, secondary branches per plant, and days to 80% maturity (Table 4).

4.4.2 Days to 50% flowering

Path analysis revealed that days to 50% flowering had positive direct effect (0.2180) on yield. Days to 50% flowering showed negative indirect effect with days to 80% flowering (-0.005), plant height (-0.0151) number of secondary branches per plant (-0.0406) and pod per plant (-0.0428). Days to 50% flowering has indirect positive effect with primary branches per plant, number of seeds per pod (0.0002) and pod length (0.0004) (Table 4).

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

	DFF	D50%F	DM	PH	PBP	SBP	PPP	SPP	PL	TSW	Correlation with yield
DFF	**0.2340**	0.0294	0.0007	0.0369	0.0009	0.0330	-0.0649	0.0005	-0.0028	0.0599	0.327
D50%F	0.0316	**0.2180**	-0.0005	-0.0151	0.0548	-0.0406	-0.0428	0.0002	0.0004	0.0048	0.21
D80%F	-0.0180	0.0116	**-0.0090**	0.0651	0.0448	-0.0696	-0.0313	-0.0006	0.0108	0.0997	0.104
PH	-0.0356	0.0135	0.0024	**-0.2430**	0.0317	0.0763	0.0808	-0.0003	-0.0027	-0.1154	-0.192
PBP	-0.0012	-0.0667	0.0023	0.0430	**-0.1790**	0.0600	-0.0092	0.0008	0.0002	0.0314	-0.119
SBP	0.0346	-0.0397	0.0028	-0.0831	-0.0482	**0.2230**	0.0193	-0.0002	-0.0009	-0.0929	0.015
PPP	-0.0646	-0.0397	0.0012	-0.0836	0.0070	0.0183	**0.2350**	-0.0003	0.0050	-0.0977	-0.019
SPP	0.0620	0.0259	0.0026	0.0389	-0.0671	-0.0192	-0.0329	**0.0020**	0.0016	0.1302	0.144
PL	-0.0201	0.0024	-0.0029	0.0199	-0.0009	-0.0062	0.0355	0.0001	**0.0330**	0.0302	0.091
TSW	0.0349	0.0026	-0.0022	0.0697	-0.0140	-0.0515	-0.0571	0.0006	0.0025	**0.4020**	0.387*

DFF = days to 1st flowering, D50%F = days to 50% flowering, D80F = days to 80% flowering, PH = plant height (cm), PBP = primary branches per plant, SBP = secondary branches per plant, PPP = pods per plant, SPP = seeds per pod, PL = pod length (cm), TSW = thousand seed weight (g) and YPP = yield per plant (gm).

4.4.3 Days to 80% maturity

Days to 80% maturity had negative direct effect (-0.0090) on yield per plant. Days to 80% maturity had indirect positive effect on number of primary branches per plant (0.0448), plant height (0.0651), pod length (0.0108) and weight of 1000 seed (0.0997). It had a negative indirect effect on secondary branches per plant (-0.0696), pod per plant (-0.0313) and seeds per pod (-0.0006) (Table 4).

4.4.4 Plant height (cm)

Plant height had negative direct effect (-0.2430) on yield (Table 4). It had a negative indirect effect through thousand seed weight (- 0.1154). Number of seeds per pod (-0.0003), and pod length (-0.0027). Number of pods per plant (0.0808), days to 50% flowering (0.0135), primary branches per plant (0.0317) and secondary branches per plant (0.0763), 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.

4.4.5 Number of primary branches per plant

Number of primary branches per plant had negative direct effect (-0.1790) on yield per plant (Table 4). Number of primary branches per plant had indirect positive effect on days to 80% flowering (0.0023), plant height (0.0430), number of secondary branches per plant (0.0600), number of seed per pods (0.0008), pod length (0.0002) and weight of 1000 seed (0.0314). It had a negative indirect effect on days to 50% flowering (-0.0667) and number of pods per plant (-0.0092).

4.4.6 Number of secondary branches per plant

Number of secondary branches per plant had positive direct effect (0.2230) on yield per plant (Table 4). Number of secondary branches per plant had indirect positive effect on yield via days to 80% maturity (0.0028), and number of pods per plant (0.0193). It had a negative indirect effect on days to 50% flowering (-0.0397), primary branches per plant (-0.0482), plant height (-0.0831) and thousand seed weight (-0.0977).

Plate 6: Pods of different mungbean genotypes

4.4.7 Number of pod per plant

Number of pod per plant had the direct positive effect on yield (0.2350) whereas it had positive indirect effect through days to 80% flowering (0.0012), pod length (0.0050), number of primary branches (0.0070), and number of secondary branches per plant (0.0183). and number of seeds per plant (0.1695) (Table 4). However, it had indirect negative effects through days to 50% flowering (- 0.0397), plant height (-0.0836), number of seeds per pod (-0.0003) and thousand seed weight (-0.0977).

4.4.8 Pod length

Pod length had the direct positive effect on yield (0.0330). whereas it had positive indirect effect through number of pods per plant (0.0355),plant height (0.0199) and number of seeds per plant (0.0001), days to 50% flowering (0.0024) and thousand seed weight (0.0302) (Table 4). However, it had indirect negative effects through days to 80% flowering (-0.0029), number of secondary branches (-0.0062), number of primary branches (-0.0009). Bhaumik and Jha (1980) found similar result.

4.4.9 Number of seed per pod

Number of seeds per pod had the direct positive effect on yield (0.0020) whereas it had negative indirect effect through number of primary branches per plant (-0.0671), number of secondary branches per plant (-0.0192) and pods per plant (-0.0329). However, it had indirect positive effects through days to 50% flowering (0.0259), pod length (0.0016), plant height (0.0389) and days to 80% flowering (0.0026). (Table 4).

4.4.10 Thousand seed weight (g)

Thousand seed weight had positive direct effect (0.4020) on yield per plant. Thousand seed weight had indirect positive effect through days to 50% flowering (0.0026), plant height (0.00697), number of seeds per pod (0.0006) and pod length (0.0025) (Table 4). It had a negative indirect effect on number of pods per plant (-0.0571) number of primary branches (-0.0140) and number of secondary branches per plant (-0.0515). 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 79.43% 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 five apparent clusters. The genotypes were distantly located from each other, which indicated that considerable diversity existed among the genotypes.

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 (D2) 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 II (13.446), followed by between clusters II and IV (11.781), V and III (10.375). In contrast, the lowest inter-cluster distance was observed between cluster I and V (3.919).

However, the maximum inter-cluster distance was observed between the clusters III and II (13.446) indicating genotypes from these two clusters if involved in hybridization may produce a wide spectrum of segregating population. On the other hand, the maximum intra-cluster distance was found in cluster II (2.76), which contained only 7 genotype, while the minimum distance was found in cluster I (0.45) that comprises 6 genotype. Inter and intra cluster distances are show in Table 6. Cluster I consists of nearest cluster with D2 values cluster V (3.919) and farthest

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

Principle component axes	Eigen values	Percent variation	Cumulative % of percent variation
I	2.330	21.18	21.18
II	1.868	16.98	38.16
III	1.440	13.09	51.25
IV	1.211	11.00	62.25
V	1.031	9.37	71.62
VI	0.859	7.81	79.43
VII	0.686	6.24	85.67
VIII	0.585	5.32	90.99
IX	0.422	3.83	94.82
X	0.297	2.70	97.52
XI	0.272	2.48	100.00

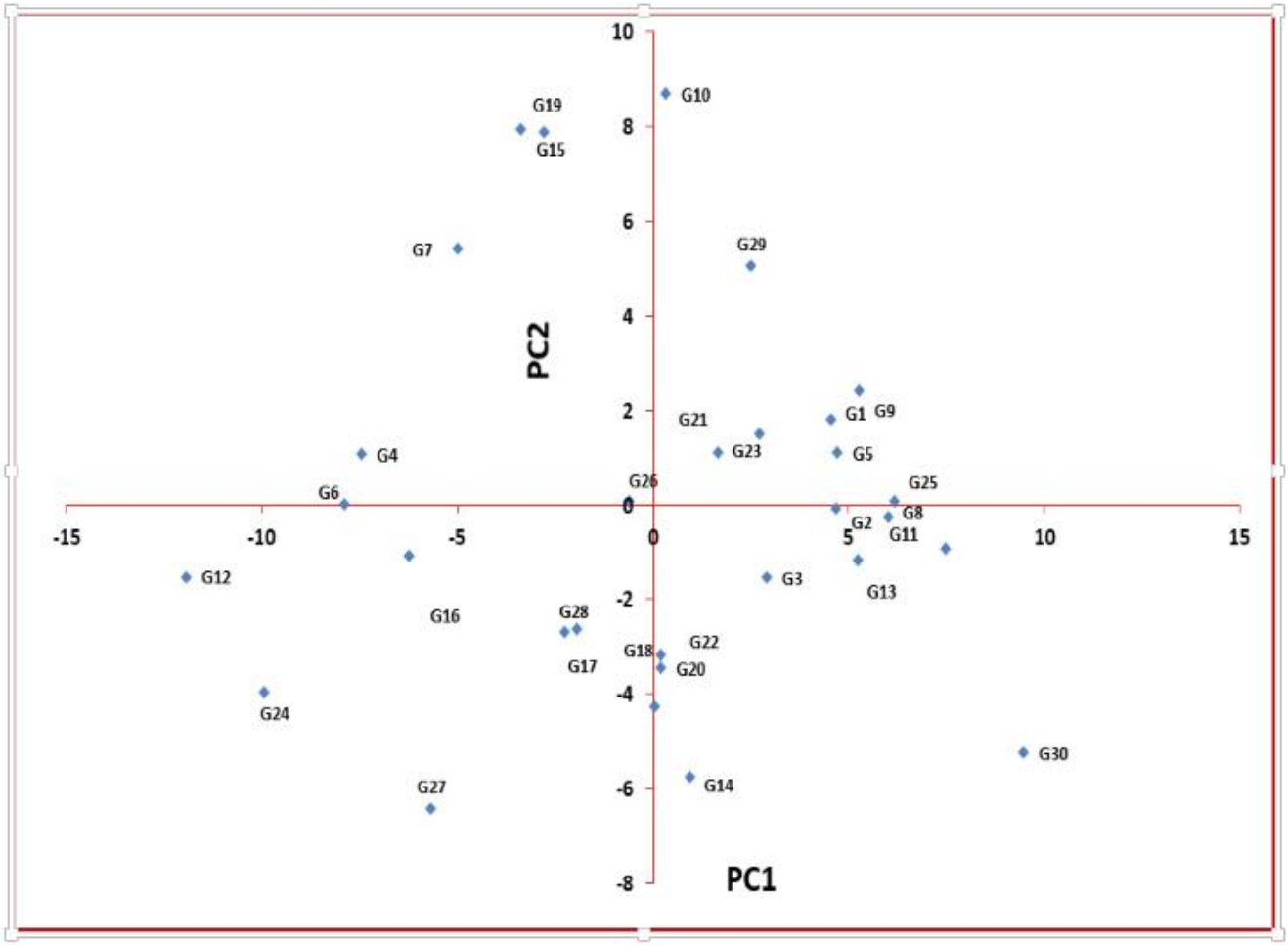

Figure 3. Scatter diagram of 30 genotypes of mungbean based on their principal component scores.

cluster with D2 values III (9.015) (Table 7). Cluster II consists of nearest cluster with D2 values cluster I (5.104) and farthest cluster with D2 values III (13.446). Cluster III consists of nearest cluster with D2 values cluster IV (6.709) and farthest cluster with D2 values II (13.446). Cluster IV consists of nearest cluster with D2 values cluster V (6.528) and farthest cluster with D2 values II (11.781). Cluster V consists of nearest cluster with D2 values cluster I (3.919) and farthest cluster with D2 values III (10.375). 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 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 II (13.446). So the crosses between the genotypes belonging cluster III and II might produce high heterosis. Also the crosses between genotypes from cluster III and II might produce high level of segregating population. So the genotypes belonging to cluster III and cluster II might be selected for future hybridization program .

4.5.3 Principal coordinate analysis (PCO)

Inter genotypic distances (D2) 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 G5 and G24 (Table 8). The lowest distance was observed between the G9 and G25. The difference between the highest and the lowest inter genotypic distance indicated the prevalence of variability among the 30 genotypes of Mungbean studied.

Table 6. Intra (Bold) and inter cluster distances (D^2) for 30 genotypes

Cluster	I	II	III	IV	V
I	**0.45**	5.104	9.015	7.986	3.919
II		**2.76**	13.446	11.781	6.284
III			**1.02**	6.709	10.375
IV				**1.54**	6.528
V					**1.74**

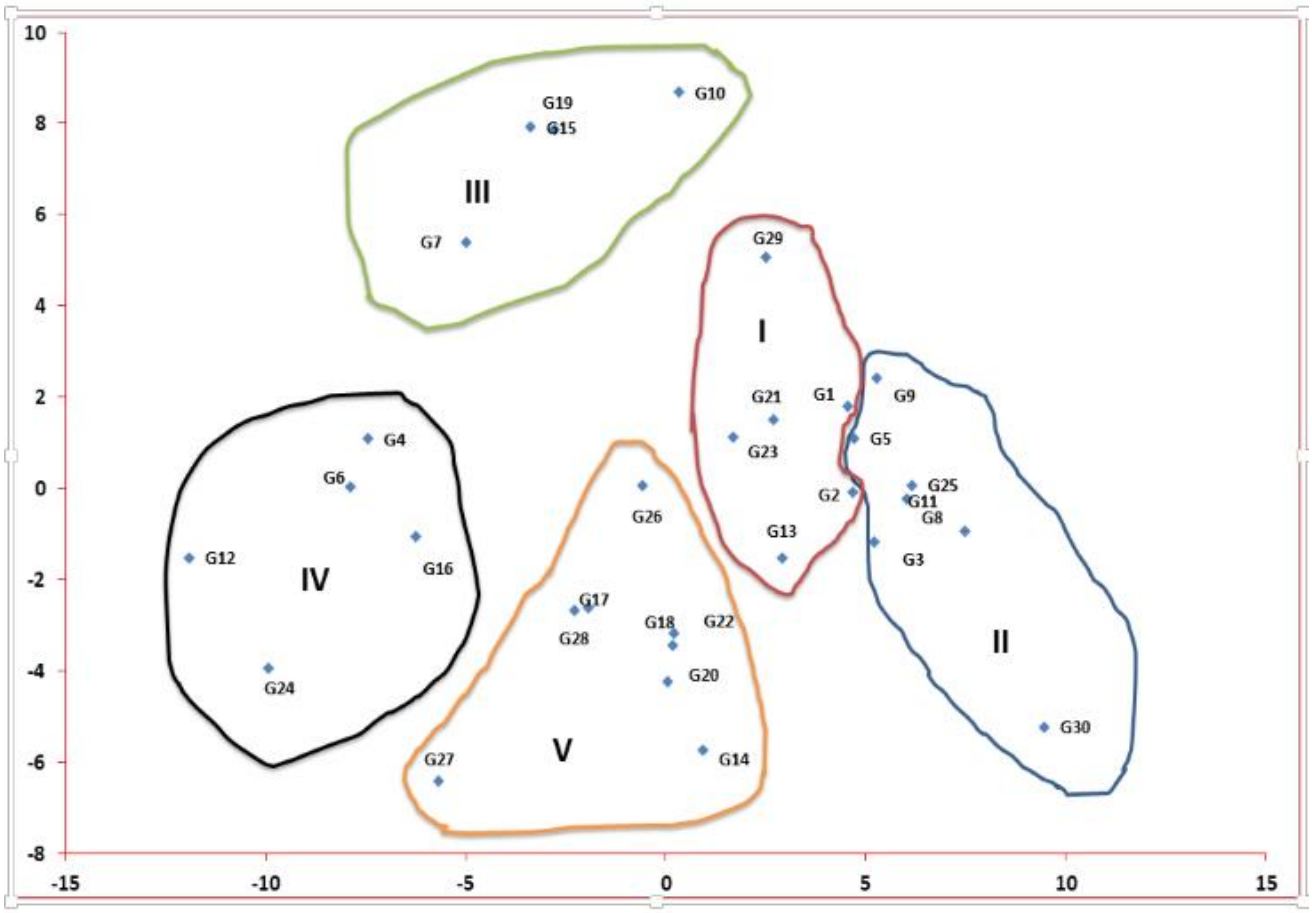

Figure 4. Scatter distribution of 30 genotypes of Mungbean based on their principal component scores super imposed with clustering.

Table 7. The nearest and farthest clusters from each cluster between D2 values in mungbean

Cluster	Nearest Cluster with D^2 values	Farthest Cluster with D^2 values
I	V (3.919)	III (9.015)
II	I (5.104)	III (13.446)
III	IV (6.709)	II (13.446)
IV	V (6.528)	II (11.781)
V	I (3.919)	III (10.375)

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 V had highest number of eight genotypes followed by cluster II and cluster I and IV constituted by seven, six and also five genotypes, respectively. On the other hand, cluster III constituted by only four genotype. Cluster V had maximum eight genotypes namely G14, G17, G18, G20, G22, G26, G27, G28. Cluster II represents 7 genotypes namely G3, G5, G8, G9, G11, G25, G30. and Last of all cluster III had minimum genotype and it was G7, G10, G15, G19. 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 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 III (43.00), whereas minimum days to first flowering in cluster II (42.05). Maximum days to 50% flowering were observed in cluster I (49.55).

Whereas minimum days to 50% flowering in cluster II (48.71). Maximum days to 80% flowering were observed in cluster IV (85.80), whereas minimum days to 80% flowering in cluster I (85.06). Then maximum plant heights were observed in I (66.11) whereas minimum plant height were observed in cluster IV (59.73). Maximum number of primary branches was observed in cluster IV (2.47) and minimum (2.22) in cluster I. Number of secondary branches per plant was observed

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

Lowest distance			Highest distance		
Genotypes		**Distance**	**Genotypes**		**Distance**
G9	G25	0.142	G5	G24	0.864
G12	G16	0.202	G5	G27	0.852
G17	G22	0.202	G10	G27	0.839
G21	G23	0.212	G15	G30	0.825
G21	G26	0.213	G5	G15	0.813
G20	G22	0.216	G5	G21	0.802
G23	G29	0.217	G5	G18	0.792
G17	G20	0.217	G4	G5	0.787
G2	G3	0.223	G5	G12	0.779
G23	G26	0.223	G11	G24	0.775

Table 9. Distribution of genotypes in different clusters

Cluster	No. of genotypes	Genotypes
I	6	G1, G2, G13, G21, G23, G29
II	7	G3, G5, G8, G9, G11, G25, G30
III	4	G7, G10, G15, G19
IV	5	G4, G6, G12, G16, G24
V	8	G14, G17, G18, G20, G22, G26, G27, G28
Total	30	

maximum in cluster I (6.83) and minimum to cluster V (6.37). Maximum (28.57) and minimum (16.50) number of pods per plant were observed in cluster II and III, respectively. The maximum pod length (7.00) was observed in the cluster II, whereas minimum pod length (6.58) was observed in cluster III. Number of seeds per pod was maximum in cluster V (11.37) and minimum number in cluster II (10.81). Weight of 1000 seed was highest in cluster IV with a mean value of (36.80) and it was least in genotypes belongs to the cluster II (25.86). 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 II was far diverse from the genotypes of the cluster III and where the genotypes belonging to I and IV were the least diverse. Genotypes of cluster I-IV and III-IV were moderately diverse from each other. The similar diverse genotypes were included between the cluster I-III and I-II.

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 (Z1 and Z2) obtained from principal component analysis (PCA). The important characters responsible for genetic divergence in the axis of differentiation in vector I (Z1) were days to first flowering (0.6008), days to 80% flowering (0.5493), number of primary branches per plant (0.3280), number of seeds per pod (1.8681), thousand seed weight (0.0936) and yield per plant (0.3363).

Table 10. Cluster mean for ten yield and yield related characters in 30 mungbean genotypes

Characters	I	II	III	IV	V
Days to 1st flowering	42.67	42.05*	43.00**	42.73	42.67
Days to 50% flowering	49.55**	48.71*	48.92	48.93	49.50
Days to 80% flowering	85.06*	85.14	85.33	85.80**	85.21
Plant height (cm)	66.11**	64.62	62.17	59.73*	64.58
Primary branches per plant	2.22*	2.28	2.42	2.47**	2.29
Secondary branches per plant	6.83**	6.62	6.50	6.40	6.37*
Pods per plant	24.28	28.57**	16.50*	20.33	25.58
Seeds per pod	11.11	10.81*	11.17	11.33	11.37**
Pod length (cm)	6.78	7.00**	6.58*	6.80	6.83
Thousand seed weight (g)	26.44	25.86*	27.25	36.80**	33.13
Yield per plant (g)					

* Lower value

** Higher value

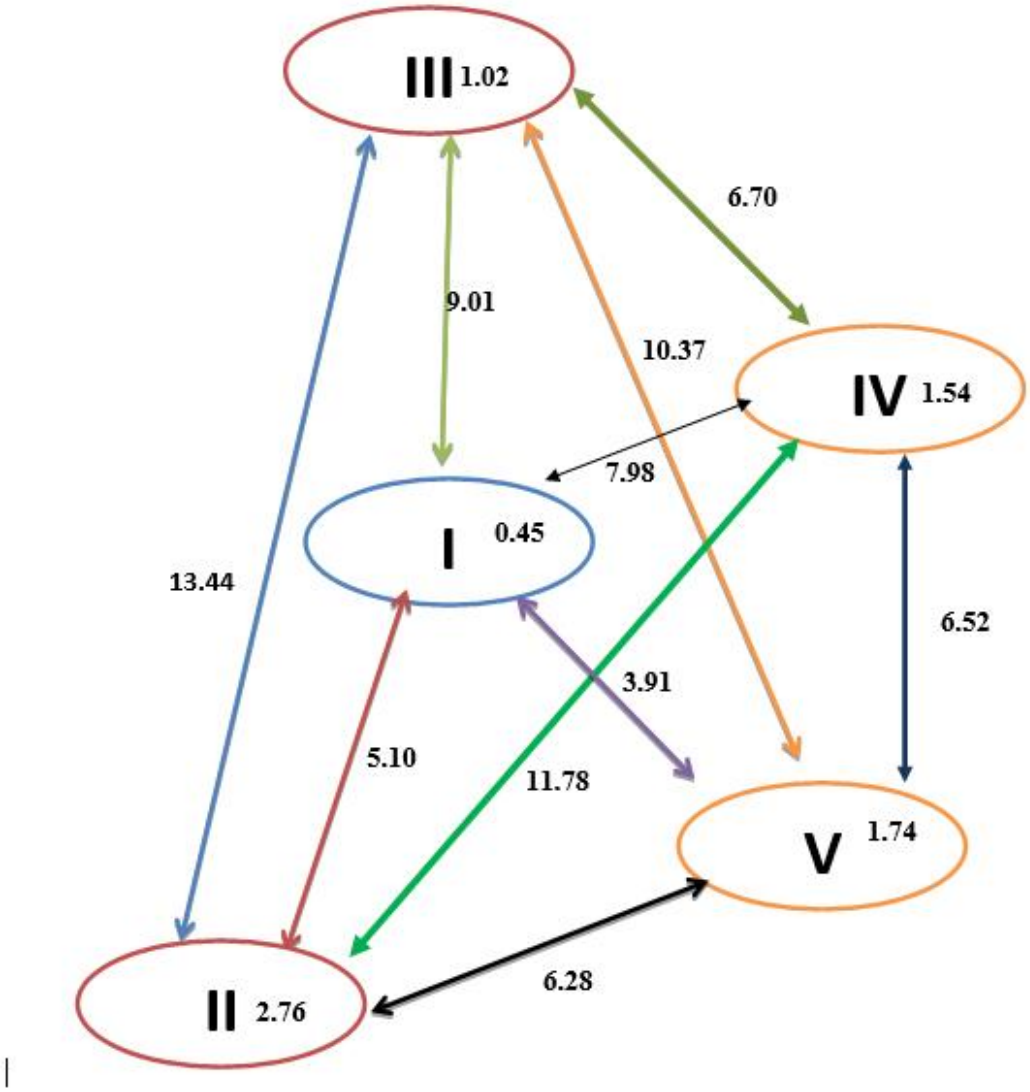

Figure 5. Intra and inter cluster distances (D2) of Mungbean genotypes

These characters were important because all these characters had positive signs in first axis. Days to 80% flowering (0.0569), days to first flowering (0.3236), plant height (0.0811), primary branches per plant (0.1449) and pod length (0.4352) had positive sign in vector II (Z2), second axis of differentiation. On the other hand, days to 50% maturity, plant height, number of secondary branches per plant, number of pods per plant, pod length possessed the negative sign in the first axis of differentiation and days to 50% flowering, number of secondary branches per plant, number of pod per plant, seeds per pod, yield per plant 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 80% flowering, primary branches per plant and days to first flowering had positive sign in both the axis, which indicated that they were the important component 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 G7, G11, G30 for minimum days to 50% flowering from cluster II (G7) and III (G11, G30), for maximum plant height and pod per plant G30 from cluster II; G24 for maximum weight of 1000 seed from cluster IV, G7 and G8 for maximum days to 80% flowering from cluster III and II. G30 for 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 G7 and G30; G8 and G7; G15 and G30; G15 and G8; G19 and G30, G7 and G29, G9 and G19; G10 and G11; G24 and G30; G24 and G8, might be suggested for future hybridization program.

Table 11 Relative contributions of the ten characters of 30 varieties to the total divergence

Characters	Principal Component	
	Vector-1	Vector-2
Days to 1st flowering	0.6008	0.3236
Days to 50% flowering	-1.2006	-0.6634
Days to 80% flowering	0.5493	0.0569
Plant height (cm)	-0.0013	0.0811
Primary branches per plant	0.3280	0.1449
Secondary branches per plant	-0.2612	-0.3146
Pods per plant	-0.9473	-0.2991
Seeds per pod	1.8681	-0.6008
Pod length (cm)	-0.7779	0.4352
Thousand seed weight (g)	0.0936	-0.4970
Yield per plant (g)	0.3363	-0.1384

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 2017 to 5 March 2018. 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 genotypic coefficient of variation ranged from 0.86% (days to 80% flowering) to 17.40% (yield per plant) and phenotypic coefficient of variation ranged from 1.74% (days to 80% flowering) to 29.06% (primary branches per plant).It has been also observed that difference between GCV and PCV for primary branches per plant (12.78% and 29.06%), secondary branches per plant (5.02% and 14.48%) and pod length (5.93% and 13.61%) suggested a highly significant influence of environment on the expression of the traits. The heights estimated heritability among eleven yield contributing characters 75.04%, 74.46%, 62.78%, 60.45% was in 1000 seed weight, number of pod per plant, yield per plant and plant height. The lowest heritability was 12.03 in number of secondary branches per plant.

The genetic advance (GA 5%) ranged from 0.21 (seeds per pod) to 7.97

thousand seed weight. The maximum genetic advance (GA 5%) was observed in respect of thousand in seed weight (7.97%) in eleven characters of Mungbean genotypes. The maximum genetic advance in percent of mean (GAMP) was obtained in pod per plant (29.98%) and the lowest was for 80% maturity (0.88%).

The significant positive correlation at the 5% level was observed for days to 80% maturity with pod length, days to 80% maturity and thousand seed weight at genotypic and phenotypic level. The significant positive correlation at the 1% level days to 50% flowering, yield per plant and weight of thousand seed 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, 4, 5 and 8 genotypes respectively.

The maximum cluster distance was observed between cluster III and II (13.446) followed by the distance between cluster II and IV (11.781). The lowest inter– cluster distance was observed between cluster I and V (3.919) followed by cluster I and II (5.104).

The highest intra cluster distance was identified in cluster II (2.76) and the lowest intra cluster distance was observed in cluster I (0.45). 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.

Therefore considering group distance and other agronomic performances the inter-genotypic crosses between G7 and G30; G8 and G7; G15 and G30; G15 and G8; G19 and G30, G7 and G29, G9 and G19; G10 and G11; G24 and G30; G24 and G8, might 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. 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 mungbean germplasms 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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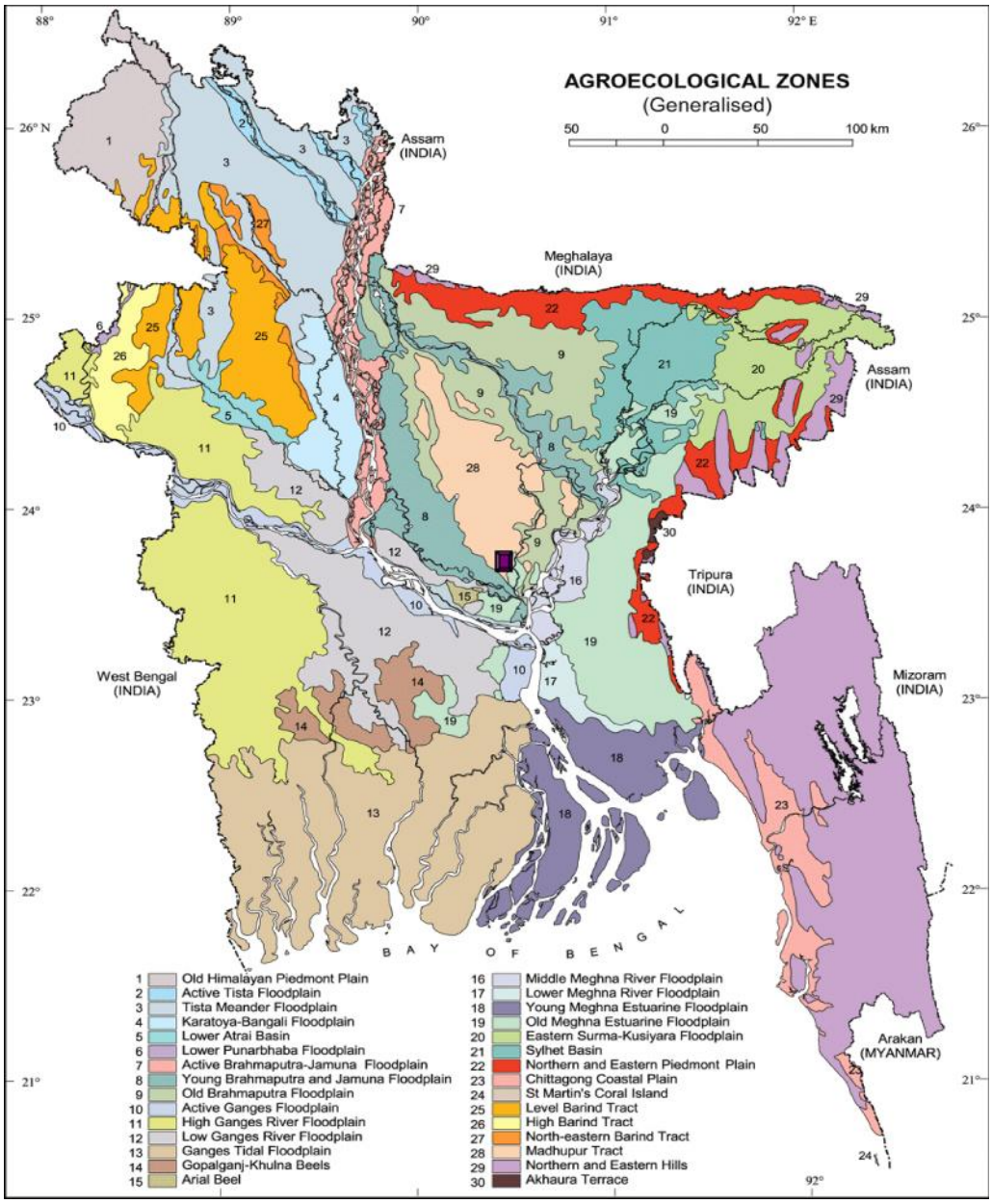
APPENDICES

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
PH	6.00 – 6.63
Organic matter	0.84
Total N (%)	0.46
Available phosphorous	21 ppm
Exchangeable K	0.41 meq / 100 g soil

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

Appendix III. Monthly average temperature, relative humidity and total rainfall and sunshine of the experimental site during the period from November, 2017 to May, 2018.

Month	Air temperature (°C)		Relative humidity (%)	Rainfall (mm) (total)	Sunshine (h)
	Maximum	Minimum			
November, 2017	34.8	18.0	77	227	5.8
December, 2017	32.3	16.3	69	0	7.9
January, 2018	29.0	13.0	79	0	3.9
February, 2018	28.1	11.1	72	1	5.7
March, 2018	33.9	12.2	55	1	8.7
April, 2018	34.6	16.5	67	45	7.3
May, 2018	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

Gen	DFF	D50F	DM	PH	PBP	SBP	PPP	SPP	PL	TSW	YPP
1	42.00	49.33	85.00	68.00	1.67	7.00	23.67	11.33	7.00	25.00	7.00
2	42.00	49.00	86.00	68.67	2.67	7.00	25.00	11.00	6.67	27.33	5.33
3	41.00	50.00	85.00	63.33	2.67	6.00	27.67	11.67	7.33	28.67	5.00
4	42.00	50.33	86.67	62.00	1.33	6.00	18.33	10.33	5.33	35.00	7.00
5	42.00	48.33	84.00	63.00	2.33	5.67	27.00	10.67	6.67	25.67	4.00
6	43.00	49.00	84.67	56.00	2.67	6.00	22.00	12.00	6.33	34.67	8.00
7	42.33	47.67	87.00	58.67	2.67	6.33	18.33	11.00	7.00	29.67	5.67
8	43.00	49.00	87.00	60.33	2.33	6.00	30.67	10.67	7.00	24.33	7.00
9	42.00	50.00	85.33	61.67	2.00	7.33	27.00	10.67	7.67	24.67	7.00
10	43.33	48.33	83.33	63.00	2.67	7.00	17.33	11.67	5.33	24.33	6.00
11	41.67	47.67	84.67	67.00	2.00	6.00	28.67	10.67	6.67	25.33	5.00
12	43.67	48.67	85.67	57.67	3.00	6.67	19.33	11.33	7.33	39.33	7.33
13	42.33	49.33	85.67	68.67	2.00	6.00	26.33	11.33	7.33	27.33	7.00
14	42.67	50.00	84.00	74.00	2.67	7.00	24.00	11.33	6.67	35.00	6.33
15	43.00	50.33	86.00	64.00	2.00	5.67	14.67	10.67	7.00	27.67	7.67
16	43.00	48.67	86.00	62.00	2.67	7.00	21.00	11.67	7.67	35.33	6.67

Continued Appendix IV

Gen	DFF	D50F	DM	PH	PBP	SBP	PPP	SPP	PL	TSW	YPP
17	42.00	49.00	86.00	63.33	2.67	7.00	24.67	11.00	6.00	33.33	7.33
18	42.00	48.33	84.67	62.67	2.33	6.00	28.00	11.33	6.67	32.00	9.67
19	43.33	49.33	85.00	63.00	2.33	7.00	15.67	11.33	7.00	27.33	5.67
20	43.00	49.00	83.67	62.33	2.67	7.00	27.67	11.33	7.33	31.67	7.33
21	44.00	50.00	84.67	64.33	2.00	7.00	24.00	11.00	7.00	27.67	9.67
22	42.67	50.00	85.33	64.00	3.00	6.00	26.67	11.67	6.33	31.67	7.67
23	43.33	49.33	86.00	64.00	2.33	7.00	24.67	10.67	6.67	26.67	8.00
24	42.00	48.00	86.00	61.00	2.67	6.33	21.00	11.33	7.33	39.67	9.00
25	41.33	48.33	86.00	66.00	2.33	7.33	27.33	10.33	7.67	25.33	6.67
26	42.67	50.00	86.00	63.33	2.33	6.33	23.67	11.67	7.67	30.00	8.67
27	42.67	49.33	85.67	63.67	1.33	6.00	25.00	11.00	7.00	38.33	8.67
28	43.67	50.33	86.33	63.33	1.33	5.67	25.00	11.67	7.00	33.00	6.67
29	42.33	50.33	83.00	63.00	2.67	7.00	22.00	11.33	6.00	24.67	7.33
30	43.33	47.67	84.00	71.00	2.33	8.00	31.67	11.00	6.00	27.00	7.00

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	PCA 1	PCA 2
G1	5.270	2.407
G2	4.680	-0.074
G3	2.904	-1.543
G4	-7.458	1.076
G5	4.699	1.101
G6	-7.886	0.022
G7	-4.985	5.406
G8	6.016	-0.243
G9	4.554	1.807
G10	0.330	8.677
G11	7.473	-0.938
G12	-11.927	-1.525
G13	5.224	-1.179
G14	0.935	-5.746
G15	-3.376	7.923
G16	-6.234	-1.073
G17	-2.265	-2.685
G18	0.042	-4.248
G19	-2.783	7.867
G20	0.190	-3.454
G21	1.675	1.114
G22	0.208	-3.169
G23	2.705	1.506
G24	-9.938	-3.945
G25	6.161	0.070
G26	-0.595	0.071
G27	-5.667	-6.430
G28	-1.941	-2.615
G29	2.516	5.054
G30	9.476	-5.232

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