GENETIC DIVERGENCE FOR YIELD AND YIELD CONTRIBUTING CHARACTERS IN MUNGBEAN *(Vigna radiata* L.)

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CERTIFICATE

*This is to certify that thesis entitled, "**GENETIC DIVERGENCE FOR YIELD AND YIELD CONTRIBUTING CHARACTERS IN MUNGBEAN (Vigna radiata L.)**" submitted to the faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE IN GENETICS AND PLANT BREEDING**, embodies the result of a piece of bonafide research work carried out by A. H. M. Rakibul Hasan, Registration No.: 08-02699 under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.*

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

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THESIS ABSTRACT

GENETIC DIVERGENCE FOR YIELD AND YIELD CONTRIBUTING CHARACTERS IN MUNGBEAN *(Vigna radiata*L.)

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An experiment was conducted to study on genetic divergence for yield and its contributing characters among 32 genotypes of mungbean. The study was carried out at the experimental field of the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka- 1207 during period of March to July, 2015. The results indicated that the genotypes differed regarding all the characters studied. The phenotypic variance was higher than genotypic variance in all the characters studied. The phenotypic coefficients of variation were also higher than genotypic coefficients of variation in all the characters studied. Moderate to high heritability was observed for all characters. High heritability coupled with high genetic advance in percent mean were observed for peduncles per plant, pods per plant, 100 seed weight and seed yield per plant. The characters peduncle per plant and pods per plant showed highly significant positive correlation with seed yield per plant. Days to 50% flowering, branches per plant, branch length, peduncles per plant, pods per plant, seeds per pod and 100 seed weight showed positive direct effect on yield. All the genotypes were grouped into five clusters having 10, 10, 5, 5 and 2 genotypes, respectively. Cluster I and II comprised the maximum number (10) of genotypes followed by cluster III and IV (5). The cluster V comprised 2 genotypes. The highest inter-cluster distance (42.06) was observed between the clusters III and cluster IV and highest distant genotypes were G11 and G22 followed by G32 and G27. The lowest inter-cluster distance was observed (18.05) between the clusters between clusters I and II, The lowest distance was observed between genotype G8 and G9. Among the characters studied peduncles per plant, pods per plant, 100 seed weight, seed yield per plant were major characters that contributed most towards genetic divergence.

CHAPTER I

INTRODUCTION

Mungbean (*Vigna radiata* L.) is a self-pollinated leguminous pulse crop belongs to the family Leguminoseae sub family papilionaceae, grown principally for its protein rich edible seeds. It is one of the important crops well suited to dry areas, mainly under irrigated conditions. The mungbean is a short day, warm season crop, grown mainly in semi-arid to sub-humid lowland, tropical and sub-tropical region in the world (Poehlman, 1991a).It is cultivated traditionally by small landholders throughout tropical, subtropical and temperate tones of Asia including Bangladesh, Pakistan, India, Sri Lanka, Nepal, Thailand, Burma, Iran, Vietnam, Indonesia, China, Korea and Japan. Since mungbean has a short maturity span (60-75 days) it is grown under various cropping systems, hence contributing to the increase income of the small landholders' as well as to the improvement of the soil conditions (Fernandez and Shanmugasundaram, 1988).In the South Asia, mungbean is used to make curry. Daal is the most common dish which is made from various kinds of split legumes with spices. In the Southeast and East Asian countries, it is used to make various kinds of sweet, bean jam, sweetened bean soup, vermicelli, and bean sprout. In Bangladesh it is grown under a wide range of agro-ecological zones of both rainfed and irrigated nature mainly cultivated in the Barisal and Patuakhali district. During 2011-2012, it was cultivated over an area of 91,000acres with 26 thousand tones production (Statistical Year book of Bangladesh, 2012). The average yield is much low than its potential and the yield obtained in other countries. One of the

reasons of low yield is unavailable of high yielding cultivars with better adaptability.

The major mungbean producing country is India (around 55% of the world hectarage and 45% of the world production) (Singh and Yadav, 1978). Production of mungbean is increasing more rapidly than the production of other pulse species. According to FAO (1999) a minimum intake of pulse by a human should be 80gm per head day by day where as it is only 14.19gm in Bangladesh (BBS, 2007). Mungbean is playing an important role in our nutrition. It is a very economical source of quality plant protein food. Mungbeancontains about 23.86 percent protein, this being about two-third of the protein content of soybean, twice that of wheat and three fold that of rice. It also contains 1.5 % lipids. 62.6% CHO, 436% lysine, 75mg methionine, 55mg cystine. (Poehlman, 1991).It offers potential in solving the malnutrition problems in developing nations. The mungbean has easily digestibility coefficient (79%), Biological value (72%) and Nutritional value (32%).

Mungbean can fix atmospheric nitrogen with association of particular soil bacteria and root nodules which are available for use by the plants. According to Morris, *et al.,* 1986, mungbean can be fixed about 86 kg/ha atmospheric nitrogen.Mungbean plant could be used as good fodder after the pods have been picked. Mungbean may be grown as a green manure crop to be ploughed under or as combined cash and soil improvement crops with the residues incorporated into the soil after pods have been harvested. In Bangladesh, mungbean is one of the major pulse crop ranking 5^{th} in acreage, 6^{th} in production, 3^{th} in protein (%)

content and 1st in respect of price. Mungbean is generally cultivated during early Rabi. But it is also grown in rabi after rice (January to March) in Summer (April to June) and after Jute (September to November) (Islam, 1978). 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. 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. The production is declining due to introduction of high yielding varieties of wheat and winter rice. At the present situation, increasing per unit area is the only way to increase production because it is not possible to afford much land to this crop. The low production syndrome results from several factors; (1) low genetic potential in native varieties; (2) yield fluctuations due to drought and floods; (3) losses from disease and insect pest; and (4) poor cultural practices. The per acre productivity of all pulses including mungbean are growing down steadily in Bangladesh.

Genetic diversity is one of the most important criteria for parent selection. Genetic diversity is a prerequisite for an efficient plant breeding program. The availability of transgressive segregants in any breeding program depends upon the diversity of involving parents. The importance of genetic diversity in the improvement of crop has been stressed in both self and cross-pollinated crops. (Griffin &Lindtorm, 1954; Murty and Anand, 1966; Gaur,*et al.* 1978).The quantification of genetic diversity through biometrical procedure (Anderson,

1957; Rao, 1952) has made it possible to choose genetically diverse parents for a successful hybridization program. Genetic diversity is important to know the source of genes for a particular trait within the available germplasms. (Tomooka, 1991). In order to increase the frequency of desired genotypes in breeding progenies, superior parents with high breeding values are needed.

The supreme parents having desired characters could be identified through divergence analysis. Several statistical methods are known for discriminating divergence viz., Mahalanohis's generalized distance (Mahalanobis, 1936), Fishers discriminant analysis, inspection of biometric data and totals of grouped data and Coopers's statistical classification with quadratic forms. Among them Mahalanobis's D^2-statistics based on multivariate analysis appears to be a good index. This technique has been followed by many researchers on a wide range of crops. Based on the above information, the present experiment was conducted to study the available variation, genetic nature and genetic diversity of 32 mungbean genotypes collected from BARI for more promising and necessary study to develop new varieties of mungbean. An intensive genetic restructuring program is necessary to evolve high yielding varieties of mungbean suitable for Bangladesh agro-climatic condition (Bhadra and Dev, 1985). To achieve this breeding goal an understanding of a genetic architecture of the yield determining characters will be helpful in yield improvement (Bhadra and Ali, 1986). A logical way to start any breeding program is to collect precise information on the nature and degree of genetic divergence that would help the plant breeder in

choosing the right type of parents for purposeful hybridization in heterosis breeding (Patel *et al.*, 1989).

Since mungbean is considerably less improved than its field demand it is necessary to choose genetically diverse parents to achieve heterotic cross for further transgression and to identify direct and indirect associations among yield attributes. To generate information on the degree of genetic diversity and coefficient of direct and indirect association among yield contributing characters this study was undertaken with the following objectives:

to study the genetic variability for different quantitative and qualitative characters.

to determine the nature of relationship between yield and yield contributing characters and relative contribution of each character towards seed yield in mungbean through the correlation co-efficient analysis.

to find out diverse germplasm suitable for the utilization in varietal improvement and future hybridization program.

CHAPTER II

REVIEW OF LITERATURE

Genetic divergence analyses is an initial systematic breeding methods for improvement of crops including mungbean. A few literatures of these works in mungbean are available. The literatures available on genetic analysis is summarized below:

2.1 Origin and Distribution

The mungbean is an annual herbaceous legume belonging to the family papilionaceae, includes the genus *vigna*, and subgenus *ceratotropics* distinguished two species (*Vigna radiata)* the mungbean and (*Vigna mungo)* the blackgram. The genus *Vigna* is pan tropical and now has been broadened to include about 170 species, 120 from Africa, 22 from Indo-Pak sub-continent and Southeast Asia and a few from other parts of the world (Ghafoor, *et al.,* 2001). Only seven species of *Vigna* are cultivated as pulse crops mostly in Asia, Africa and some parts of Latin America (Anishetty and Moss, 1988).

It is generally considered that two of these cultivated species are of African origin (sub genus *vigna*) and five are Asiatic origin (sub genus *Ceratotropis*). The Asiatic group consists, mungbean per 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 (Paroda and Thomas, 1988). At present, mungbean cultivation spreads worldwide because it is easily digested as compared to blackgram (Smartt, 1990).

The subgenus *Ceratotropis* is considered to have originated in Asia and is called Asian *Vigna*. It forms a discrete group of about seventeen species

largelyconfined to Asia and the Pacific.The origin and progenitor of mungbean is *Vigna sublobatus* acoording to Verdcourt (1970).The primary centers of origin of mungbean are the mountainous regions of Southwest-Asia, particularly Indian subcontinent.

2.2 Botany

Mungbean is an annual herbaceous plant. It has a tap root system, stems are slender usually branched, and upright in growth and leaves are pinnately compound with three to several leaflets. There are large stipules clasping the stem. The inflorescence is raceme arising from the axil of a leaf. The lowest node at which flower initiation occurs is quite constant under a given set of conditions and is used in classifying the varieties with respect to flowering and fruiting duration.

2.3 Genetic variability

Makeen *et al.,* (2007) studied twenty diverse mung bean 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.

Rohman *et al.,* (2003) studied on phenotypic and genotypic variance, correlation coefficient of variance, heritability conducted for yield and yield components in 82 genotypes of mungbean. High heritability estimates coupled with high genetic advance were observed for seed yield per plant, 100 grain weight, plant height, seed per pod and days to 50% flowering.

Swamy *et al.,* (2002) studied genetic divergence and stability analyses for 12 quantitative traits (number of days to 50% flowering, number of days to

maturity, plant height, number of branches per plant, number of clusters per plant, number of pods per cluster, pod length, number of seeds per pod, 100-seed weight, seed protein content, harvest index and seed yield per plant) in 50 mungbean genotypes. The genotypes were grouped into nine clusters based on Mahalanohis D^2 statistics. Superior genotypes from clusters I (WGG-37 and TARM-2). II (TAP-7), VII (LGG-441), IX (LGG-452), VIII (PDM-89-221), III (LGG471), IV (LGG-450), V (LGG-421) and VI (LGG427) were selected based on genetic divergence and stability for yield and yield components. These genotypes may be used for the selection of genetically divergent and stable segregants for future breeding programs.

In another report it was mentioned that genetic divergence following multivariate analysis from 34 genotypes of green gram grown in summer and pre-kharif season. Ten morpho-economic characters like days to flowering, number of primary branches, plant height, pod length, locules per pod, seeds per pod, pods per plant, 100 seed weight, yield per plant and seed protein content were taken into account. Thirty-four genotypes of green gram fall under eight clusters and four clusters in summer and pre-kharif season, respectively. Some genotypes were clubbed together under the same cluster irrespective of season indicating narrow genetic diversity among them. The genetic divergence was independent of geographical diversity. Greater magnitude of genetic diversity among the population of 34 genotypes could be recorded in summer than pre-kharif season. The character 100-seed weight had the highest contribution towards total divergence followed by seed protein content and yield per plant in summer season whereas in pre-kharif the greatest divergence was due to the seed protein content followed by 100 seed weight and days to flowering. 100 seed weight, seed protein content, days to flowering, yield per plant and pods per plant having maximum contribution towards genetic divergence should form the basis of selection of parents to obtain combinations having high heterotic effects (Moloy Roy *et al.*,2007).

Abrahim *et al.*, (2006) evaluated genetic variability and heritability analyses for yield and yield components which were conducted for 646 accessions of green gram grown in Coimbatore, Tamil Nadu, India during the rabi and kharif of 2002-04. The estimates of phenotypic (PCV) and genetic (GCV) coefficients of variation were higher for single plant yield, number of branches per plant, number of pods per plant, number of clusters per plant, plant height, and length of branch, indicating greater scope of selection for these traits. Dry matter production and number of clusters per branch revealed wide differences between the estimates of PCV and GCV values, indicating the highly significant effect of environmental factors. The number of days to initial flowering, number of days to 50% flowering, number of days to initial maturity, number of days to full maturity, 100-seed weight, seed length, seed breadth, length of pod and protein content were less affected by environmental factors as the difference between the estimates of PCV and GCV was low. The estimates of heritability in the core collection indicated that the number of days to full maturity, number of days to initial maturity, number of days to initial flowering, number of days to 50% flowering, seed length, seed breadth, plant height, length of branch, 100-seed weight, and length of pod were highly heritable. High genetic advance as a percentage of mean was recorded for the number of clusters per branch, length of branch, single plant yield, number of pods per plant, number of clusters per plant, plant height and number of branches per plant, suggesting the possibility of selection for these traits in the core collection.

Days to flowering, 100 seed weight was found to be maximum contributive towards genetic divergence in mungbean (Ramana and Singh, 1987). Pods per plant, seeds per pod and 100 seed weight contributed towards genetic diversity in mungbean (Malik *et al.*, 1985). Ghaderi *et al.*, (1979) found pods per plant, Seeds per pod and 100 seed weight were contributive to genetic diversity in mungbean. Flowering time, maturity, seed density and 100 seed weight were maximum towards genetic diversity in mungbean (Ramanujam *et al.*, 1974).

Upadhyaya *et al.,* (2002) studied phenotypic diversity for morphological and agronomic characteristics in 1956 accessions of chickpea core collection, comprising desi, Kabuli and intermediate types. The Kabuli and intermediate types were not significantly different for growth habit and seed color, while they differed significantly from desi types for both traits. Principal component analysis showed that days to 50% flowering, flowering duration. Apical secondary branches, tertiary branches, 100-seed weight, seed color and seed testa texture were important traits in explaining multivariate polymorphism.

PCA was used as a means of assessing progress toward achieving multiple breeding target of the mungbean breeding program reported by Asian Vegetables Research and Development Center (AVRDC, 1987). A hypothetical ideal mungbean cultivar was defined with the characteristics of 2.5 t per ha yield potential, synchronous maturity, early flowering at 38 days, seed weight of 60 g per l000 seeds, highly resistant to *cercospora* leaf streaks (CLS) and powdery mildew (PM) as compared with elite lines and check lines.

A field experiment was conducted by Jitender Kumar *et al.,* (2002) to study the response of methods of sowing (normal and paired row) and irrigation (controlled flooding and furrow) and irrigation schedules (one irrigation at 20 days after sowing (DAS), one irrigation at 35 DAS. 2 irrigation, one each at 20 and 35 DAS, and 3irrigations, one each at 20, 35 and 50 DAS) to mungbean cultivar M 11-85-111 grown in sandy loam soil. Among various characters influencing ultimate grain yield, number of branches per plant, number of pods per plant, number of grains per pod. 1000 grain weight and grains per plant, all had positive and significant association with final grain yield. Path analysis revealed that number of branches per plant, number of pods per plant and grain yield per plant was some of the most cordial characters of grain yield of mungbean.

Thirty seven diverse genotypes of blackgram and three of mungbean resembling to blackgram, are studied by Ghafoor *et al.,* (2002) to determine the extent of genetic variation based on morphological characters. High variance was

observed for plant height, days to maturity, branches per plant, pods per plant, pod length, seeds per pod, biological yield per plant, grain yield per plant and harvest index (%). First four components of PCA with eigen value >1 contributed 78.7% and 79. 1% of the total variance amongst 40 genotypes during two consecutive years.

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

In another report it was mentioned that utilized generalized distance and canonical analysis in 8 genotypes of mungbean and their 15 hybrids. The study yielded 5 clusters among the genotypes and hybrids. Harvest index was identified as one of the large source of divergence and clustering patterns were confirmed to a large extent by canonical analysis (Natarajan and Palanisamy, 1990).

Shamsuzzaman and Shaikh (1982a) 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 per plant displayed the highest (91.7) and the lowest (31.2) heritability respectively. Number of mature pods per plant showed the highest values for both genetic advance expressed as percentage of the mean.

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 per ha. (35.5%). A considerable variation was also obtained for number for pods per plant (25.9%) and seed yield per plant (24.6%).

Sandhu (1979) studied variability among 435 strains of mungbean for the characters, days to 50% flowering and maturity, plant height, number of branches, pods per p1ant, seeds per pod, 1000-seed weight and grain yield and sufficient variability for all the characters. The phenotypic correlation coefficient of variation was the highest (50.4 for total number of branches per plant. Grain yield per plant, pods per plant and clusters per plant also showed considerable phenotypjc correlation coefficient of variation 34.4, 32.7 and 30.1 percent, respectively.

Ahmad *et al.,* (1997) observed that cluster analyses on the basis of quantitative characters were phenotypically more distinct and exhibited more breeding value. Though cluster analyses grouped together accessions with greater morphological similarity, the cluster did not necessarily include all the accessions per genotypes from the same or nearby sites. Maqbool *et al.,* (1997) reported phylogenetic relationship of 15 genotypes of the genus *Lens* and seven of their interspecific hybrids were determined by morphological (quantitative and qualitative) characters.

Shanmugam and Rangasamy (1982a) observed significant differences among the types of green gram for all the nine characters indicating the presence of high variability among the forty genotypes clustered in sixteen groups. The grouping did not conform to the geographic origin. One cluster contained all types of the genotypes from the same region showing similar genetic architecture among the types of these clusters.

Loganathan *et al.,* (2001a) studied the Genetic diversity using multivariate analysis of 10 quantitative characters (days to first flowering, plant height, number of branches per plant. number of clusters per plant, number of pods per cluster, number of seeds per pod, pod length, 100- seed weight and seed yield per plant) among 42 F3 and eight varietal genotypes of (*Vigna radiata* L). The grouping of material into seven clusters indicated the presence of wide range of genetic diversity among the genotypes. The study indicated no definite relationship between geographic and genetic diversity and geographic diversity

cannot be used as an index of genetic diversity. In general, genetic diversity among the parents was reflected in their progenies. Seed yield per plant contributed maximum, accounting for 41.4% of total divergence. The diverse clusters derived could be used in hybridization program to generate wide range of transgressive segregants in population to develop high yielding green gram varieties with superior yield component traits.

Ghafoor *et al.,* (2000) conducted cluster analysis in mungbean for nine quantitative traits. They observed significant negative correlation of days to maturity with all the characters except branches per plant and suggested that short to medium maturity mungbean cultivars were to be selected for high yield. They identified 44 pure lines on the basis of important agronomic traits that were recommended for testing under wide range of agro-ecological condition in pursuit of best mungbean cultivars.

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

Reddy (1997) evaluated seventy genotypes of greengram from different geographical regions for 10 yield components at Tirupati in 1994. Genotypic and phenotypic variations were highest for branches per plant followed by grain yield per plant and pods per plant. Days to maturity followed by plant height and pod length had the highest heritability and were least influenced by the environment. Clusters per plant, pods per cluster, seeds per pod, 100-seed weight

and grain yield showed high differences in phenotypic and genotypic variation, indicating that the expression of these traits was influenced by environmental components.

Twenty two blackgram genotypes representing a broad based germplasm were analyzed by Ghafoor *et al.,* (2003) using multivariate analyses for two consecutive years. High genetic variance was observed for plant height, maturity, pods, seed weight, biomass, grain yield and harvest index. First four PCs contributed 80.0% of the variation during 1998 and 80.9% during 1999. Five yield contributing traits, i.e. branches, pods, pod length, biomass and grain yield were observed important for first component during both the years. PC2 was more related to maturity rather than reproductive traits. First two PCs which exhibited about 60% of the variance were plotted to observe the relationship between the cultivars. Five genotypes were separated from others during both the years.

Tiwari *et al.,* (1995) evaluated six parents and their 15 F2 progenies during kharif 1981-82. High variability was found in the F2 for days to maturity, clusters per plant, harvest index, pod length and 100-seed weight. Clusters per plant and 100-seed weight had high heritability. In parents, high heritability was found for plant height, seed yield per plant and harvest index and in the F2 for days to maturity, clusters per plant, pod length and 100-seed weight. High heritability estimates were generally associated with low genetic advance.

Reddy *et al.,* (2003) studied thirty-six genotypes of mungbean for genetic variability of seed yield and its contributing characters in summer 2000 at Tirupati, Andhra Pradesh, India. High magnitude of variability was observed for pods per plant and grain yield per plant, while moderate variability was recorded for pods per cluster, clusters per plant, plant height and days to 50% flowering suggesting the possibility of their improvement by selection. High heritability coupled with high genetic advance was observed for pods per plant, grain yield per plant, pods per cluster, clusters per plant, plant height and days to 50% flowering, while high heritability and moderate genetic advance was recorded

for seeds per pod, 100-seed weight and days to maturity suggesting that these traits were controlled by additive gene action.

Loganathan *et al.,* (2001b) studied on Genetic variability in greengram (*Vigna radiata* L.). Fifty genotypes of green gram were used to estimate genetic variability for 10 quantitative characters in Tamil Nadu, India, during rabi 1999. High phenotypic coefficient of variability indicated the favorable effect of environment for number of clusters per plant and seed yield per plant and high genotypic coefficient of variability suggested substantial amount of genetic variability for number of pods per plant and seed yield per plant, high genetic advance, additive gene action and phenotypic selection were effective for number of pods per plant, seed yield per plant and number of seeds per pod. Non-additive gene action, low heritability and low genetic advance were noted for days to first flowering, plant height, number of branches per plant, pod length and 100-seed weight.

Islam *et al*., (1999) studied on genetic variation, heritability on 9 yield components in 53 genotypes studied in Joydebpur 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.

Malhotra and Singh (1971) while working on genetic divergence in blackgram reported narrow range of variability for l00-seed weight and pod length whereas, Shanmugam and Rangaswamy (1982) while analyzing45 genotypes of blackgram reported that yield per plant contributed most to the genetic diversity.

Malik *et al.,* (1985) studied genetic divergence in 12 indigenous varieties of mungbean for six quantitative characters. The study indicated the presence of ample genetic variation among the cultivars irrespective of their origin. They suggested that plant height, days to flowering and grain yield should be considered for selecting genetically divergent lines in mungbean.

Khaimar *et al*., (2003) evaluated twenty-two mung bean genotypes for genetic variability in the kharif season of 1997, in Rahuri, Maharashtra, India. A wide

range of variability was observed for plant height, clusters per plant, pods per plant, grain yield per plant and 100 grain weight. The estimates of genotypic as well phenotypic coefficients of variation were highest for pods per plant followed by 100-grain weight. High heritability coupled with high genetic advance was observed for clusters per plant, pods per plant, grain yield and 100-grain weight indicating that these characters can be improved by selection.

Das and Chakraborty (1998) studied some 22 genotypes of greengram for genetic variability of seed yield and its contributing characters at Nagaon. Plant height, branches per plant, pods per plant, pod length and yield per plant recorded high genotypic coefficients 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 per plant, pods per plant and pod length. It indicates that these traits were mostly controlled by additive gene action. Seeds per pod and yield per plant recorded low heritability coupled with low and high genetic advance, respectively.

Kumar *et al*., (2003b) studied a total of 40 green gram cultivars during the 1998 wet season to determine genetic variability analysis. Data were recorded for days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, pod length, number of seeds per pod, 100-seed weight and grain yield per plant.

Pandey and Singh (2002) studied the genetic variability performance of green gram cultivars ML 552, PS 16, ML 371, LM 1510, PDM 11, Pusa Baishakhi 1, PDM 84-139, PDM 54, ML 374 and ML 574 in rice-wheat cropping system in a field experiment conducted in Meerut, Uttar Pradesh, India during the kharif season of 1998 and summer of 1999. Significant differences among the genotypes were observed in terms of plant height, number of days to 50% flowering and maturity, number of seeds per pod, 100-seed weight, yield and infection by yellow mosaic virus.

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

2.4 Correlation coefficients

Investigation on yield contributing characters with 169 local and exotic mungbean genotypes revealed that mature pods per plant, primary branches per plant and seeds per pod showed significantly positive correlation with yield per plant while maturity, plant height and 100 seed weight were negatively correlated with seed yield (Shamsuzzaman *et al.,* 1983).

Shamsuzzaman and Shaikh (1982a) studied the characters association of 169 local and exotic genotypes of mungbean and observed significant positive correlation of yield per plant with number of primary branches, mature pods per plant and seeds per plant while maturity period, plant height and 1000- seed weight exhibited negatively 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 per plant with number of mature pods per plant.

Correlation studies in agronomic characters of 70 mungbean strains showed that number of pods per plant had strongest association with seed yield. There were negative associations of seed size, plant height and days from sowing, on first flowering and to maturity with seed yield (Ahmed *et al.,* 1981).

Sandhu *et al.,* (1979) studied correlation ship among yield attributes in mungbean and found negative correlation of yield with days to flowering, positive correlation with plant height and branches per plant, highly positive significant correlation with clusters per plants pod length, positive correlation with days to maturity, high positive significant correlation with seed weight,

seeds per pod. The correlation study concluded that pods per plant, cluster per plant, seeds per pod, pod length and 100 seed weight were important attributes of grain yield.

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

Dhuppe *et al*., (2005) studies on correlation which were carried out in 35 genotypes (11 parental lines and 24 hybrids) of mungbean grown in Parbhanj, Maharashtra, India, in 1998. Data were recorded for days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per plant, l00-seed weight and yield per plant. Grain yield per plant showed positive and significant correlation with days to maturity, number of secondary branches per plant, number of pods per plant and 100- seed weight at genotypic level, whereas secondary branches per plant and 100-seed weight were correlated with grain yield at phenotypic level.

In a study of 20 diversed mungbean genotypes, seed yield per plant showed positive correlation with pod and seed yield per plant, seeds per pod and branch number, plant height and seed numbers per pod. Pod length had the greatest positive direct effect on yield as revealed by path coefficient analysis followed by number branches per plant number per plant and plant height (Khan, 1988).

Sirohi and Kumar (2006) studied correlation analysis for yield and yield components which were conducted for 19 diverse genotypes of mungbean (*V. 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.

Kumar *et al.,* (2003) studied on correlation for yield and yield components of pea. The number of days to flowering showed a positive association with number of days to maturity and number of seeds per pod.

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

Yadav (2000) found positive correlation between seed yield and seeds per pod in black gram. Chakraborty and Haque (2000) got the same type of result in lentil. Tiwari *et al.,* (2001) found a significant and positive correlation between seed yield per plant and number of seeds per pod in pea.

In another report it was mentioned that positive significant correlation of yield with branches per plant, positive correlation with plant height, highly negative correlation with days to flowering, highly positive correlation with clusters per plant, pods per plant, pod length and days to maturity, positive correlation with seeds per pod. They suggested that seed weight should be highest priority in selecting genotypes in mungbean (Ali and Shaikh, 1987).

Rohman *et al.,* (2003) studied on correlation coefficient analysis which was conducted for yield and yield components in 82 genotypes of mungbean. Yield was positive and significantly correlated with pod per plant, seed per pod and 100 grain weight, pod per plant, seed per pod and 100 grain weight contributed maximum positive and direct effect on yield indicating these two traits should be given emphasis while selecting high yielding mungbean cultivar for rainfed conditions.

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

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

Bhaumik and Jha (1980) estimated the biometrical relationship in 2 cultivar of mungbean and found positive correlation of seed yield per plant with 1000 seed weight, seed per pod and pods per plant. They also reported negative correlation between seed and plant height.

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

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

Digby *et al.,* (1989) reported that coordinates obtained from PCA is used as input of PCO analysis in calculation of distances among the points. Thus PCA is

used for graphical representation of the points while PCO to calculate the minimum distance in a straight line between each pair of points.

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

Wani *et al.*, (2007) determined the genetic variability among 20 genotypes of green gram (*Vigna radiata*) for quantitative characters and protein content. High heritability, coupled with high genetic advance, was observed for number of pods per plant, number of pods per cluster, plant height and seed yield, suggesting the importance of additive genetic control in the inheritance of these characters. Seed yield exhibited a positive and significant correlation with number of pods per plant followed by number of pods per cluster and pod length. These characters were the major yield-contributing characters. Therefore, the seed yield of green gram may be improved through the direct selection of these characters.

Siddique *et al.*, (2006) determined the genetic divergence and trait association in mungbean genotypes (01CMG511, 01CMG512, 01CMG513, 01CM6514. 01CMCI516. 01CMG517 and 01CMG5518). Analysis of variance indicated highly significant differences for all the traits except grains per pod, which showed non-significant results. Genotype 01CMG515 recorded the lowest number of days to maturity (66), whereas 01CMG518 showed the highest number of days to maturity (76). The highest grain yield (859.26 kg per ha) was recorded for NM-98. Genotypic variance was highest for grain yield followed by 1000-grain weight. The highest value of heritability was recorded for grain yield (99.81%) followed by 1000-grain weight (92.18%), number of days to flowering

(19.06%) and number of days to maturity (88.50%). Grain yield (11765.58) and 1000-grain weight (1568.54) showed the highest genetic advance followed by number of days to flowering (1162.29) and to maturity (655.03). Positive and significant correlation was exhibited by most of the traits.

Yaqoob *et al.,* (1997) studied ten important agronomic characters for estimation of co-efficient of correlation in 30 genotypes per mutants of mungbean grown under rainfed 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.

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

Nazir *et al.,* (2005) determined the direct and indirect effects of different genetic parameters in different mungbean lines per cultivars. Twenty mungbean lines per cultivars were evaluated to exploit yield components to the maximum extent and formulate selection criteria in mungbean. According to the results, high heritability coupled with moderate to high genetic advance was observed for plant height (97.00 and 23.40), seed yield (86.00 and 32.41), harvest index (86.00 and 36.78) and 100-seed weight (74.00 and 17.01). It indicated that additive genes mainly control such characters. Clusters per plant (0.47), pods per plant (0.57), pod length (0.30) and 100-seed weight (0.38) showed positive and significant genotypic correlation with seed yield. Clusters per plant (0.71), pods per plant (0.69), pod length (0.45), 100-seed weight (0.41) and seeds per pod (0.77) also had significant phenotypic correlation with seed yield. Plant height (0.12), clusters per plant (0.47), pods per plant (0.64), pod length (0.33) and harvest index (0.52) showed positive direct effects on seed yield.

In another report it was mentioned that sixty genotypes of mungbean (*Vigna radiata*) for 13 characters to assess genetic variability, heritability, correlation,

genetic advance and genetic diversity. Total dry matter, plant height, number of pods per plant and yield per plant exhibited high variability and heritability coupled with genetic advance, indicating the influence of additive gene action. Correlation studies indicated that the total dry matter, number of pods per plant, number of clusters per plant, number of branches per plant and days to 50% flowering were positive and significantly associated with seed yield, total dry matter and number of pods per plant had direct positive effect on seed yield while plant height had negative effect. The results of multivariate analysis indicated the presence of considerable genetic divergence among the genotypes. The genotypes were grouped into eight clusters. Days to maturity, 100-seed weight, number of pods per plant and total dry matter contributed maximum towards diversity. Crosses can be effective between the genotypes of cluster V and VII followed by cluster I and VII where the maximum inter-cluster distance was exhibited for getting desirable segregants (Rao *et al.*, 2006).

Singh and Pathok (1993) recorded on 11 quantitative traits in 20 (*Vigna radiata)* parents, 90 F1s and 90 F2s. Seed yield was positively correlated with plant height, clusters per plant, number of pods per cluster, number of pods per plant, pod length, seeds per pod and 100-seed weight.

Niazi *et al.,* (1999) evaluated genotypic correlation and path-coefficient analysis for 8 agronomic characters affecting seed yield which was accomplished in 15 elite genotypes of mungbean. All the correlation coefficients were significant, whilst number of tilled pods per plant, plant height, number of columns and seed per pod, and number of clusters per plant revealed a strong positive association with seed yield per plant. Pods per plant emerged as a reliable component that can serve as a selection criterion in breeding high yielding cultivars of mungbean.

Sharma (1995) observed highly significant and positive correlations for number of seeds per plant and 100-seed weight with seed yield in 6 mungbean (*Vigna radiata*) genotypes and their GF1 and GF2 hybrids grown at Jabalpur, Madhya Pradesh in 1985.

In another report it was mentioned that twenty-five diverse genotypes of mungbean to study the variability and character association of eight quantitative characters. The estimates of high heritability with high genetic advance observed for the characters biological yield, days to 50% flowering, number of pods per plant, plant height indicated the presence of additive gene action for these characters. The phenotypic and genotypic coefficients of variation were high for biological yield, number of pods per plant, harvest index, seed yield per plant. The maximum positive and significant phenotypic correlation coefficient (0.825) was observed between the number of pods per plant and seed yield per plant, followed by seed yield per plant with harvest index (0.822), days to 50% flowering and plant height (0,752), number of pods per plant and harvest index (0.670), days to 50% flowering and biological yield (0.663), plant height and biological yield (0.599). Path coefficient analysis showed that number of pods per plant (0.561), harvest index (0.425), 1000 seed weight (0.216), had positive and direct effect towards seed yield, whereas at phenotypic level biological yield (0.195) number of seeds per pod (0.087), days to 50% flowering (0.011) had relatively low direct effect. Therefore, these characters may be selected directly to improve seed yield (Kumar *et al.,* 2005).

A study was conducted by Reddy *et al.,* (2005) to derive information on genotypic and phenotypic correlations, direct and indirect effects of various traits (days to 50% flowering. days to maturity, plant height. branches per plant, pod length. pods per plant. seeds per pod, nodules per plant, clusters per plant, protein content, harvest index, test weight and seed yield per plant) in greengram. The number of seeds per plant was significantly and positively correlated with plant height and number of clusters per plant at both genotypic and phenotypic levels, and significantly and positively associated with the number of seeds per pod, test weight, days to maturity and days to 50% flowering at the genotypic level and with number of pods per plant at the phenotypic level. Path analysis indicated that plant height, days to 50% flowering and test weight recorded the highest direct effect in the desirable direction. Their association with seed yield was significant and positive,

indicating that there exists a true and perfect association between these characters and suggesting that direct selection for these characters will help in isolating early and high yielding genotypes.

Thirteen genotypes of green gram were studied for seven characters by Venkateswarlu (2001a) for association analysis and revealed that pods per plant, days to maturity, plant height, 100-seed weight, seeds per pod and pod length showed significant and positive association with seed yield. Pods per plant and seeds per pod had maximum positive direct effect on seed yield. Days to maturity, clusters per plant, plant height, 100-seed weight and seeds per pod exhibited high indirect effect on seed yield via pods per plant.

In another report it was mentioned that the genetic variation, heritability and characters association 9 yield components in 53 genotypes of mungbean. 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. Yield per plant was significantly and positively correlated with plant height, number of primary branches per plant, number of pods per plant, pod length, number of seeds per pod and 1000-seed weight. Pod length exerted the highest positive direct effect on yield. (Islam*et al.,* 1999).

Manivannan *et al.,* (1998) evaluated thirty green gram (*Vigna radiata*) genotypes for 8 yield components. Genotypes were grouped into 8 clusters based on their genetic diversity. Highest inter-cluster values were observed between clusters VI and VIII, VII and VIII and IV and VII. Plant height contributed most towards divergence followed by length, pods, seeds per pod and clusters. Genotypes KMGI, MGG319, WGG47 and PLM292 were recommended for breeding purposes.

2.5 D^2- Statistic

Nath *et al.,* (2005) estimated the genetic divergence among 19 genotypes of *Vigna* comprising wild and cultivated species following Mahalanohis' D^2 technique and canonical analysis. The genotypes formed three different clusters.

Close correspondence in cluster composition was found between D^2 analysis and canonical analysis. Genotypes belonging to *Vigna radiata*, *V. mungo*. *V. aconitifolia, V. irilobata* and *V. sinensis* [*V. unguiculata*] formed a single cluster. Genotypes of *V. umbellate*, *V. hiniana* [*V. hainiana*] and *V. trichuriensis* formed another cluster. Genotype of *V. minima* formed a third cluster. Wide variability among the germplasms was found. Parental selection in hybridization programs to increase variability in black gram and mungbean is suggested.

Genetic diversity in 39 mutants of mungbean was assessed by Sandhu and Brar *et al.,* (2002) using Mahalanobis' D^2- statistics. The results revealed the existence of a substantial amount of diversity in the mutants isolated from the gamma ray-induced populations of three mungbean cultivars (ML 131, ML 267 and ML 337). The mutants were grouped into eight clusters. Cluster I and VIII were the largest with eight mutants each and cluster VII was the smallest with two mutants. Except for cluster III mutants, all other mutants were derived from two or three cultivars. All the three mutants grouped in cluster III were isolated from a single 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.

Sinha *et al.,* (1999) estimated the genetic divergence using Mahalanobis's D^2 statistic. Altogether 8 clusters were formed. Cluster I alone accommodated 30 genotypes. Inter-cluster distance was maximum (471.66) between cluster VII and VIII followed by clusters IV and VIII. There was no strict relationship between geographical distribution and genetic divergence. However, there was a tendency to be grouped in a cluster for cultivars belonging to a zone. Intra-cluster D^2 value was maximum in cluster III, which has 3 cultivars. The trait seed weight (100-seed weight) had the highest contribution to genetic divergence.

In another report it was mentioned that 40 genotypes of greengram through D^2 analysis and revealed a wide genetic variability among the genotypes. There was no relationship between geographic and genetic diversity as genotypes chosen

from same eco-geographical region were found in different clusters as well as in the same clusters. The maximum inter-cluster distance was observed between clusters I and XIV and as followed by clusters VIII and IX, clusters III and IX and clusters I and IX indicating wide divergence among these clusters. The variance of cluster means revealed that number of pods per plant, days to maturity, days to flowering and plant height were the main characters contributing 10 the genetic divergence in the present material (Kishore *et al.,* 2000).

Some 84 genotypes of mungbean from different geographical regions were grouped into 17 clusters using D^2 analysis. Pods per plant contributed most to cluster differentiation. Genetic diversity was independent of geographic origin and parentage. Glutamate oxaloacetate transaminase (aspartate aminotransferase) activity was high in high-yielding clusters. The present study suggests the importance of biochemical divergence in relation to morphological divergence (Lal *et al.,* 1998).

Miranda *et al.,* (1999) studied thirty mungbean lines using canonical variate and cluster analysis for yield components. D^2- statistics of Mahalanobis' generalized distance identified 9 heterotic groups. The genotypes Ouro Verde and KY-8 were the most similar, while KY1945 and V3726 were the most dissimilar: KY 1945 was recommended for crossing with V3726; breeding efforts should be based on crosses between heterotic groups as determined by cluster analysis, graphics analysis of canonical varieties was in agreement with cluster analysis.

A study on genetic divergence was carried out by Singh and Pathak (1987) using Mahalanohis' D^2- statistics in 20 genotypes of mungbean of diverse origin with 112 quantitative traits including yield per plant. The genotypes were grouped into six clusters; the members of all clusters were geographically unrelated. Cluster 2 with eight genotypes had the maximum values for pods per plant and seed yield per plant. These eight genotypes with four others were recommended for hybridization.

Manivannan (2002) analyzed 33 mungbean genotypes derived from ten crosses to determine genetic diversity using multivariate analysis. The genotypes were grouped into seven clusters. Among the characters studied, 100-seed weight and powdery mildew reaction contributed them towards the total divergence. Based on the performance they suggested seven genotypes to be included in the hybridization program.

Ramanujam *et al.,* (1974) explained that in mungbean flowering time, maturity, seed density and 100 seed weight contributed maximum toward genetic diversity from a study of D^2 analysis. They suggested that in general there was fair agreement between the extent of heterosis and genetic divergence between the parents. Seed density, maturity time, seed size and flowering lime recorded maximum and yield components as pods per plant and seeds per pod had limited influence in genetic divergence was found by Shanmugam and Rangasamy, (1982a) in forty genotypes in greengram clustered in 16 groups. Yield per plant followed by clusters per plant and pods per cluster contributed maximum towards genetic divergence. Natarajan *et al.,* (1988) studied 45 greengram genotypes which was clustered into 4 groups and suggested that seed weight followed by days to flowering contributed maximum towards genetic diversity. Seed size and pod length contributed maximum towards genetic divergence in mungbean reported by Gupta and Singh. (1970). Thulasidass. (1984) classified 30 mungbean genotypes into 7 clusters and reported that 100 seed weight, pods per plant, plant height, and pod length had maximum contribution. Days to flowering, seed size and primary branches per plant was main components to genetic diversity in mungbean (Malhotra *et al.,* 1974).

In a field experiment conducted by Saxena *et al.,* (2002) 59 cultivars of greengram were grouped into sixteen clusters utilizing data on a set of twelve characters related to yield and its contributing characters (days to maturity, plant height. number of primary branches per plant, height of first fruiting internode, cluster per plant, number of pods per plant, number of pods per cluster, 100-seed weight, biological yield per plant, seed yield per plant and harvest index). Major

clusters in divergence analysis contained cultivars of heterogeneous origin, indicating no parallelism between genetic and geographic diversity. The cluster pairs exhibiting very high inter cluster distances were cluster IX and XIV, cluster IX and XII, cluster VII and X. cluster V and XII, and cluster V and XIV. Days to maturity, followed by plant height, seed yield, height of first fruiting internode, biological yield and number of clusters per plant showed high percent contribution towards genetic divergence. Therefore, crosses between members of clusters having high cluster means for important characters coupled with high inter cluster distances between them are likely to be more rewarding.

Mishra and Rao (1990) reported thirteen clusters in a comparative study of D^2 and meteroglyph analyses of 117 chickpea genotypes. Cluster I had the maximum number of genotypes. Meteroglyph analysis did not show similar type of clustering as observed in D^2 analysis, but canonical analysis showed similar type of clustering.

Tawar *et al.,* (1988) conducted genetic divergence using D^2 analyses in 34 genotypes of mungbean and these were grouped in five clusters. Variability observed in the parents was related to genetic diversity of the parents selected under study. First canonical root contributed 88% of the total variation. Inclusion of such genotype from distinct clusters and their implication in mungbean breeding program as suggested by Singh *et al.,* (1991) examined the organization of diversity for morphological and agronomic characters in 306 landraces of cultivated common bean (*Phaseolus vulgaris* L.) by analyzing data for multivariate statistical analyses and observed genetic variance within and between groups. Kumar and Arora (1992) presented observation of 40 genotypes of chickpea collected from various geographical regions for 18 character s including seed yield, Multivariate analyses revealed 10 clusters. No definite relationship was established between genetic diversity and geographical distribution. Maximum hybrid vigor was observed among most diverse genotypes.

CHAPTER III

MATERIALS AND METHODS

A field experiment was conducted at the experimental field of Genetics and Plant Breeding department of Sher-e Bangla Agricultural University, Dhaka Bangladesh during March 2015 to July 2015 to study on the inter genotypic variability, genetic divergence and path coefficient in Mungbean (*Vigna radiata* L.).The materials and methods of this experiment are presented in this chapter under these following headings:

3.1 Site of experiment:

The research work was conducted at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka- 1207. The experimental site was at $90^0 22'$ E longitude and $23^0 41'$ N latitude at an altitude of 8.6 meters above the sea level.

3.2 Soil and Climate of the experimental Site

The experimental area was under the sub-tropical monsoon climate zone, which is characterized by heavy rainfall, high humidity, high temperature and relatively long day during the *Kharif* season while hardly rainfall, low humidity, low temperature and short day during the Rabi season. Rabi season is favorable for mungbean cultivation but it also be cultivated as summer crops in kharif-1 season. The land belongs to agro-ecological region of 'Madhupur Tract' (AEZ 28) of Nodda soil series. The soil was sandy loam in texture having pH 5.47-5.63. The mean temperature of the growing period was 26.43°C with average maximum and minimum being 36°C and 20.54°C respectively. Details of the meteorological data in respect of temperature, rainfall, relative humidity, total sunshine and soil temperature during the period of experiment were collected from the weather station, Dhaka, Bangladesh.

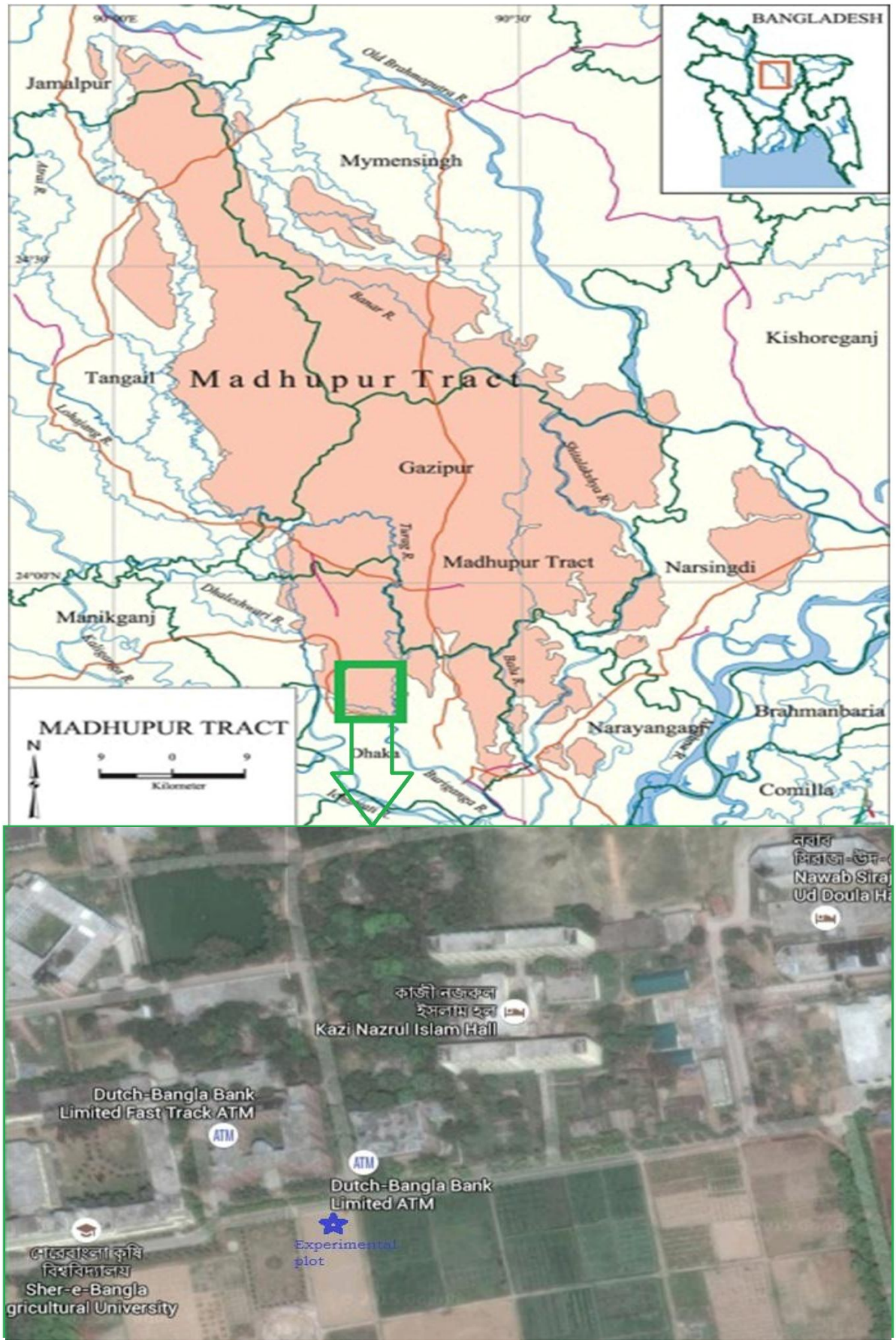

Figure 1. Location of the experimental site

3.3Genetic materials used for the experiment

Thirty two (32) genotypes were used in the study. The seeds of 32 accession lines were collected from Plant Genetic Resources Center (PGRC) of Bangladesh Agricultural Research Institute (BARI). Descriptions of the genotypes are given in (Table 1).

Table 1. The code, accession name and source of collection of the 32 genotypes of mungbean used in the experiment

Sl No.	Code	Accession number	Source of Collection
1	G1	BD-6875	BARI
2	G2	BD-6876	BARI
3	G3	BD-6878	BARI
4	G4	BD-6881	BARI
5	G5	BD-6882	BARI
6	G6	BD-6884	BARI
7	G7	BD-6885	BARI
8	G8	BD-6886	BARI
9	G9	BD-6887	BARI
10	G10	BD-6888	BARI
11	G11	BD-6890	BARI
12	G12	BD-6891	BARI
13	G13	BD-6892	BARI
14	G14	BD-6893	BARI
15	G15	BD-6894	BARI

Table 1. Continued

Sl No.	Code	Accession number	Source of Collection
16	G16	BD-6895	BARI
17	G17	BD-6897	BARI
18	G18	BD-6902	BARI
19	G19	BD-6905	BARI
20	G20	BD-6906	BARI
21	G21	BD-6908	BARI
22	G22	BD-6909	BARI
23	G23	BD-10022	BARI
24	G24	BD-10023	BARI
25	G25	BD-10024	BARI
26	G26	BD-10026	BARI
27	G27	BD-10027	BARI
28	G28	BD-10028	BARI
29	G29	BD-10029	BARI
30	G30	BD-10030	BARI
31	G31	BD-10031	BARI
32	G32	BD-10032	BARI

3.4 Design and layout of the experiment

The experiment was laid out in Randomized Complete Block Design (RCBD) with 3 replications. The field was divided into 3 blocks then the blocks were further sub-divided into 4 plots each of which was (2 m × 3 m) where genotypes were randomly assigned. Total land size was 120 m^2. The individual block size was 2m ×12m. Block to Block distance was 70 cm, plant to plant distance was 20 cm and row to row distance was 40 cm. The genotypes were distributed to each row with each block randomly.

3.5 Preparation of the experimental field

The selected field for growing mungbean was first opened with power tiller and was exposed to the sun for a week. Then the land was prepared to obtain good tilth by several ploughing, cross ploughing and laddering. Subsequent operations were done with harrow, spade and hammer. Weeds and stubbles were removed, larger clods were broken into small particles and finally attained into a desirable tilth to ensure proper growing conditions. The plot was partitioned into the unit plots according to the experimental design as mentioned earlier. Recommended doses of well decomposed cowdung, manure and chemical fertilizers were applied and mixed well with the soil each plot. Proper irrigation and drainage channels were also prepared around the plots. Each unit plot was prepared keeping 5 cm height from the drains. The bed soil was made friable and the surface of the bed was leveled.

3.6 Manure and fertilizer application:

Due to its ability of nitrogen fixation from the atmosphere mungbean requires less nitrogen than other pulse crops. But for initial establishment of plant up to the stage of nodule formation a starter dose of 20-40-20 NPK respectively was applied. The unit plots were fertilized with cow dung, urea, TSP and MP @ 10 ton, 50 kg, 85 kg, 35 kg per ha respectively. The entire cow dung, TSP, MP and half of the urea was applied at the time of final land preparation. The remaining

half of urea was applied as top dressing in two installments. First top dressing was done at 20 days after and second at 35 days after sowing.

In this study fertilizer was applied as per the recommendation of Bangladesh Agricultural Research Institute (BARI). The following doses of fertilizers and manures were applied to the plot for mungbean cultivation.

Table 2. Doses of different fertilizers used in the experimental field

Fertilizers/ manures	Doses (kg)	
	Applied in the plot	Quantity/ ha
Urea	2.01	47
TSP	3.50	88
MP	1.50	36
Cow dung	20	2.00 ton

3.7 Seed sowing

Seeds of 32 accession were sown on 23 March, 2015. The seedlings were emerged 4-5 days after seed sowing.

3. 8 Intercu1tural operations

The growing seedlings were always kept under care observation. After sowing the seeds, the following intercu1tural operations were accomplished for their better growth and development

3.8.1 Irrigation

A shallow irrigation was applied in the experimental field just after sowing the seeds. Here after the crop was irrigated when needed depending on the moisture status of the soil and requirement of plants.

3.8.2 Weeding and mulching

Weeding and mulching were necessary to keep the plots free from weeds, easy aeration and for conserving soil moisture. When the plants were well established, the soil around the base of plants was pulverized.

3.8.3 Top dressing

The remaining doses of Urea were applied as top dressing in two equal installments. First top dressing was done at 20 DAS and second at 35 DAS.

3.8.4 Plant protection measures

The established plants were affected by aphids. Diazinon 60EC (l5cc per 10 liter) was applied against aphids and other insects. Few plants found to be infected by yellow mosaic were uprooted and destroyed.

3.9 Harvesting

Different genotypes matured at different times. The harvesting was completed by 30 May 2015. Ten plants from each plot were randomly selected to collect data and these were harvested by uprooting. Border plants were discarded to avoid border effect.

3.10 Data collection

In order to study the genetic divergence among the genotypes, the data were collected in respects of 13 parameters. Data on germination, flowering and maturity was recorded on whole plant basis. The other following parameters were noted on individual plant basis from five randomly selected competitive plants.

3.10.1 Days to first flowering (DF): Determined as the days from sowing to first begun to flower of the plant.

3.10.2 Days to 50% flowering (D50F): Determined as the days from sowing to 50% of plants had begun to flower.

3.10.3 Days to first mature pod (DM): Determined as the days from sowing to first mature pod when the pod color change from green to black.

3.10.4 Days to 50% mature pod (D50M): Determined as the days from sowing to 50% mature pod when the pod color change green to black

3.10.5 Branches per plant (BP): Count only pod-bearing branches whose origin was in the leaf axils on the main stem.

3.10.6 Branch length (BL): length (in cm) of longest branch from main stem to the branch top.

3.10.7 Plant height (PH): The length of the main stem from the ground level to the tip, what was measured in centimeter (cm).

3.10.8 Peduncles per plant (PeP): Number of peduncles having at least one fully grown pod at first harvest including both main stem and branches.

3.10.9 Pods per plant (PP): The pods per plant was calculated from the five randomly selected plants.

3.10.10 Pod length (PL): Mean length (in cm) of pods from ten randomly selected mature pods.

3.10.11 Seeds per pod (SP): It was the mean number of seeds from ten randomly selected pods.

3.10.12 100 seed weight (SW): One hundred seed weight (g) was taken randomly from the bulk sample of each genotype and adjusted to the 12% moisture content and measured the weight by an electrical balance.

3.10.13 Yield per plant (YP): Total weight of seeds per plant (at mature stage) after pod shelling was measured in gram.

3.11Data analysis

3.11.1 Univariate analysis

The collected data were statistically analyzed. The mean, maximum, minimum and standard deviation for each character have been calculated and analysis of variance for each of the character was performed. The mean square (MS) at error and phenotypic variances were estimated as per Johnson, *et al.* (1995).

$$\sigma^2_g = \frac{GMS - EMS}{r}$$

Where,

GMS and EMS are the genotypic and error mean square and r is the number of replication.

The phenotypic variances (σ^2_p), were derived by adding genotypic variances with the error variances (σ^2_e), as given by the following formula,$\sigma^2_p = \sigma^2_g + \sigma^2_e$

3.11.2 Estimation of genotypic and phenotypic co-efficient of variation

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

Genotypic co-efficient of variation (GCV) = $\frac{\sigma_g \times 100}{\bar{X}}$

Where,

σ_g= Genotypic standard deviation

$\bar{X}$ = Population mean

Similarly,

The phenotypic co-efficient of variation was calculated from the formula:

Phenotypic co-efficient variation (PCV) = $\frac{\sigma_p \times 100}{\bar{X}}$

Where,

σ_p=Phenotypic standard deviation

$\bar{X}$= Population mean

3.11.3 Estimation of genetic advance

The expected genetic advance for different characters under selection was estimated using the formula suggested by Lush (1949) and Johnson, *et al.*, (1955).

Genetic advance (GA) = K. $h^2.\sigma_p$

Where,

K = Selection differential, the value of which is 2.06 at 5% selection,

σ_p= Phenotypic standard deviation estimating from Genetic advance in percentage of mean

3.11.4 Estimation of heritability

Broad sense heritability was estimated (defined by Lush. 1949) by the following formula suggested by Hanson, *et al.*, (1956) and Johnson, *et al,* (1955).

$$h^2_b\% = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where,

h^2_b= Heritability in broad sense, σ^2_g= Genotypic variance, σ^2_p= Phenotypic variance.

3.11.5 Genetic advance in percent mean

Genetic advance as percentage of mean was calculated from the following formula:

$$\text{Genetic advance (\% of mean)} = \frac{\text{Genetic advance}}{\text{Population mean}} \times 100$$

3.11.6 Estimation of genotypic and phenotypic Correlation co-efficient

For calculating the genotypic and phenotypic correlation coefficient for all possible combination the formula suggested by Johnson, *et al.,* (1955) and Hanson, *et al.*, (1956) were adopted.

The genotypic covariance components between two traits and of the phenotypic covariance component were derived in the same way as for the corresponding variance components. The covariance components are used to compute genotypic and phenotypie correlation between the pairs of the characters as follows:

Genotypic correlation = $\frac{\sigma^2_{gxy}}{\sqrt{\sigma^2_{gx}+\sigma^2_{gy}}}$

Where,

σ^2_{gxy}= Genotypic covariance between the traits x and y.

σ^2_{gx}= Genotypic variance of the trait x

σ^2_{gy}= Genotypic variance of the trait y thus,

Phenotypic correlation (rph_{xy}) = $\frac{\sigma^2_{phxy}}{\sqrt{\sigma^2_{phx}+\sigma^2_{phy}}}$

Where,

σ^2_{phxy}= Phenotypic covariance between the traits x and y.

σ^2_{phx}= Phenotypic variance of the trait x

σ^2_{phy}= Phenotypic variance of the trait y thus,

3.11.7 Multivanate analysis (D^2 Statistics)

Mean data for each character was subjected to multivariate analysis methods viz, principal component analysis (PCA), principal coordinate analysis (PCO), canonical variate analysis (CVA) and cluster analysis (CLSA) using GENSTAT 4.2 program.

3.11.8 Principal component analysis (PCA)

Principal component analysis is one of the multivariate techniques to know the interrelationships among several characters and can be done from the sum of squares and product matrix for the characters. Principal components were computed from the correlation matrix and genotypic scores obtained for the first

component and succeeding components with latent roots greater than unity (Jager, *et al.,* 1983).

3.11.9 Principal coordinate analysis (PCO)

Principal coordinate analysis is equivalent to PCA but it is used to calculate inter-unit distances. Through the use of all dimensions of p it gives the minimum distances between each pair of n points using similarity matrix (Digby *et al.,* 1989). Inter-distances between genotypes were studied by PCO.

3.11.10 Canonical variate analysis (CVA)

The canonical variate analysis is based upon the roots and vectors of W-IB, where W is the pooled within groups covariance matrix and B is the among groups covariance matrix. It provides two-dimensional plots that helped in separating different populations involved.

3.11.11 Cluster analysis (CLSA)

Genotypes were divided into groups on the basis of a data set into some number of mutually exclusive groups. The clustering was done using non-hierarchical classification. In GENSTAT, the algorithm is used to search for optical values of the chosen criterion. The optimal values of the criteria followed by some initial classification of the genotypes into required number of groups, the algorithm repeatedly transfers genotypes from one group to another so long as such transfer improved the value of the criterion. When no further transfer can be found to improve the criterion, the algorithm switches to second stage that examine the effect of two genotypes of different classes and so on.

3.11.12 Computation of average intra-cluster distance

Computation of average Intra-cluster distance for each cluster was calculated by taking possible D^2 values within the members of a cluster obtained from the PCO after the clusters are formed. The formula utilized was $\sum D^2/n$, where $\sum D^2$ is the sum of distances between all possible combinations (n) of the genotypes

included in a cluster. The square root of the average D^2 values represents the distance (D) within cluster.

3.11.13 Cluster diagram

It was drawn using the values between and within clusters distances, which presents a momentary idea of the pattern of diversity among the genotypes included in a cluster.

3.11.14 Computation of average inter-cluster distances

The procedures of calculating inter-cluster distance between cluster II and I and between cluster Ill and I and between I and IV, between II and IV and so on. The clusters were taken one by one and their distances from other clusters were calculated.

CHAPTER IV

RESULTS AND DISCUSSION

In the present investigation 32 genotypes of mungbean were studied. The results presented here provide some information on genetic variability, correlation and D^2- statistic. Mean values for different characters, mean squares from analysis of variance, genotypic and phenotypic co-efficient of variation, heritability; genetic advance and partitioning of genotypic correlation into direct and indirect effect and multivariate analysis are presented in Table 3 to 11. The results obtained from this study are presented and discussed under the following headings:

4.1 Univariate analysis

4.1.1 Analysis of variance and genetic parameters

The analysis of variance (Table 3) indicated the existence of significant variability for all the characters studied. The mean, range, genotypic, phenotypic and environmental variance, genotypic, phenotypic and environmental coefficients of variation, heritability estimates, genetic advance and genetic advance in percent mean are presented in (Table 4). The results are discussed character wise as follows:

4.1.2 Days to 50% flowering

The analysis of variance showed that the genotypes varied significantly for 50 % flowering. The minimum and maximum duration for 50% flowering was observed in the genotypes G14, G23, G30, G32 (35 days) and G29 (41 days), respectively (Appendix III). The estimates of GCV (3.29) and PCV (4.51) were moderate with very little difference, heritability (53.15) of this trait was moderate and GA% was low (4.94) but genetic advance (1.81) was also low (Table 4). It reveals non-additive gene action and high heritability was exhibited due to influence of favorable environment rather than genotypes, so selection may not be rewarded. But Mohar *et al.,* (1999) reported that days to 50% flowering showed higher estimates of heritability along with genetic advance.

4.1.3 Days to 50% maturity

The mean square due to genotypes differed significantly for days to maturity. The mean for this character was 60.44, which ranged from 50 - 67. The minimum days required for 50% maturity was in G32 (50 days) and maximum days were for G12 (67 days) (Appendix III). The phenotypic variance (18.64) was a little higher than genotypic variance (15.25). The genotypic (6.46) and phenotypic (7.14) coefficient of variation were moderate with a little difference indicates that environment have a little effect on the expression of this character. High heritability (81.82) was obtained due to this low environmental influence but genetic advance in percent of mean was medium (12.04) (Table 4). Such results indicated that selection based on this trait might be effective. Chakraborty and Haque (2000) found high heritability and low genetic advance in lentil for this trait.

4.1.4 Plant height

The average height of plant was 69.63 cm. The genotype G3 had the shortest (52.60) and genotype G11 produced the tallest (96.13) plant. (Appendix III). Phenotypic variance (80.00) was considerably higher than the genotypic variance (75.36). The phenotypic coefficient of variation (12.85) and genotypic coefficient of variation (12.47) were close to each other indicating negligible influence of environment on this trait. A high heritability (94.19) along with moderate genetic advance (17.36) and genetic advance in percent of mean (24.93) indicated that selection for this trait would be rewarding (Table 4). High heritability and low genetic advance in percent of mean for plant height was also found by Chaudhary and Sharma (2003), Ramesh *et al.*, (2002), Sureja and Sharma (2000), Tyag *et al.*, 2000).

Table 3. Analysis of variance for different morphological plant characters of 32 mungbean genotypes

Sources of variation	d.f	Mean sum squares					
		DF	D50F	DM	D50M	PH	BP
Replication	2	29.656	23.156	17.281**	4.906	9.834	1.531
Genotypes	31	6.408**	5.658**	41.371**	49.149**	230.72**	1.149
Error	62	2.237	1.285	6.701	3.390	4.646	0.370

** indicates significant at 0.01 probability level.

Table 3. Continued

Sources of variation	d.f	Mean sum squares						
		BL	PP	PL	SP	PeP	SW	YP
Replication	2	17.086**	0.500	0.793	10.53	3.406**	0.020	0.948
Genotypes	31	180.595**	1033.50**	1.312	4.424	130.207**	3.631**	158.53**
Error	62	12.900	7.210	0.052	0.725	3.116	0.020	0.475

** indicates significant at 0.01 probability level.

DF = Days to first flowering, D50F = Days to 50% flowering, DM = Days to first mature pod, D50M = Days to 50% mature pod, PH = Plant height, BP = Branches per plant, BL = Branch length, PP= Pods per plant, PL = Pod length, SP = Seeds per pod, PeP = Peduncles per plant, SW=100 seed weight, YP= Yield per plant

Table 4. Genetic component of variation for yield and yield contributing characters in mungbean

SL. No.	Characters	Minimum	Maximum	Mean	Phenotypic variance (δ^2p)	Genotypic variance (δ^2g)	PCV (%)	GCV (%)	Heritability (%)	GA	GA (%)
1	DF	30.00	37.00	33.84	3.63	1.39	5.63	3.48	38.33	1.50	4.44
2	D50F	35.00	41.00	36.72	2.74	1.46	4.51	3.29	53.15	1.81	4.94
3	DM	42.00	55.00	50.88	18.26	11.56	8.40	6.68	63.30	5.57	10.95
4	D50M	50.00	67.00	60.44	18.64	15.25	7.14	6.46	81.82	7.28	12.04
5	PH	52.60	96.13	69.63	80.00	75.36	12.85	12.47	94.19	17.36	24.93
6	BP	3.00	5.00	4.06	0.63	0.26	19.54	12.55	41.24	0.67	16.60
7	BL	36.23	76.87	52.30	68.80	55.90	15.86	14.30	81.25	13.88	26.54
8	PP	34.00	97.00	58.63	349.31	342.10	31.88	31.55	97.94	37.71	64.31
9	PL	5.03	8.10	6.87	0.47	0.42	10.00	9.43	88.98	1.26	18.33
10	SP	9.00	14.00	12.59	1.96	1.23	11.11	8.82	62.97	1.82	14.42
11	PeP	14.00	41.00	21.78	45.48	42.36	30.96	29.88	93.15	12.94	59.41
12	SW	1.20	5.00	2.26	1.22	1.20	48.95	48.55	98.37	2.24	99.18
13	YP	10.67	37.33	20.55	53.16	52.68	35.48	35.32	99.11	14.89	72.44

DF= Days to first flowering, D50F= Days to 50% flowering, DM= Days to first mature pod, D50M= Days to 50% mature pod, PH= Plant height, BP= Branches per plant, BL= Branch length, PP= Pods per plant, PL= Pod length, SP= Seeds per pod, PeP= Peduncles per plant, SW=100 seed weight, YP= Yield per plant,PCV= Phenotypic coefficient of variations, GCV= Genotypic coefficient of variations, GA= Genetic advance, GA (%)= Genetic advance in percent mean

4.1.5 Branches per plant

The maximum branches per plant were found (5) in the genotypes G1, G4, G5, G9, G10, G12 and G13 and minimum branches per plant were found (3) in the genotype G15, G16, G22, G24, G25 (Appendix III). The phenotypic variance (0.63) was slightly higher than genotypic variance (0.26) and the PCV (19.54) was also a little greater than GCV (12.55) indicating the role of environment on the expression of this trait which was low other than high heritability (41.24) of the trait. The genetic advance was also low (0.67) with moderate genetic advance in percent of mean (16.60) for this trait (Table 4).

4.1.6 Branch length

Based on the branch length there was significant variations among the genotypes. Branch length ranged from 36.23 cm to 76.87 cm which was observed in G23 and G11, respectively. Average value for branch length was 52.30 cm. (Appendix III). Phenotypic variance (68.80) was higher than the genotypic variance (55.90). The Phenotypic and genotypic coefficient of variations were 15.86 and 14.30, respectively, which differed each other indicating favorable influence of environment on this trait. Heritability of this trait was high (81.25) but genetic advance was low (13.88) along with moderate genetic advance as a percentage of mean (26.54) (Table 4). The high heritability was exhibited due to influence of favorable environment that means selection may not be effective. Ramesh *et al.*, (2002) found moderate to high heritability coupled with high genetic advance as a percentage of mean for branch length in cowpea.

4.1.7 Peduncles per plant

Significant differences among the genotypes were observed due to pod bearing peduncles per plant. The highest number of pod bearing peduncles per plant was 41.00, produced by the G11 and the lowest number of pod bearing peduncles per plant was 14.00, produced by G16, G29 and G30 and mean of this character was 21.78 (Appendix III). The phenotypic variance (45.48) was

slightly higher than genotypic variance (42.36). Moderate genotypic coefficient of variation (29.88) and phenotypic coefficient of variation (30.96) were found for this trait with a non-significant difference which indicated that there were little environmental effect on the expression of character. The heritability was very higher (93.15) together with high genetic advance (12.94) and genetic advance in percent of mean (59.41) indicating the selection for this character would be effective (Table 4). Devendra *et al.*, (1998) in pea, Arora and Jeena (1999) in chickpea. Yadav and Dahiya (2000) in blackgram found high heritability for this character and it indicates pod bearing peduncles per plant was an important character for selection with restriction and improvement of seed yield.

4.1.8 Pods per plant

The highest and the lowest number of pods per plant were produced by the G12 (97.00) and G18 (34.00) respectively and mean of this character was 58.63 (Appendix III). The phenotypic and genotypic variance was high and the difference between the phenotypic variance (349.31) and the genotypic variance (342.10) was not significant. Moderate genotypic coefficient of variation (31.55) and phenotypic coefficient of variation (31.88) were found for this trait with a non-significant difference which indicated that there was little environmental effect on the expression of the character. This character showed high heritability (97.94) along with high genetic advance (37.71) and high genetic advance in percent of mean (64.31) might indicate that the heritability was due to additive gene effect and phenotypic selection might be effective (Table 4).

4.1.9 Seeds per pod

The variation among the genotypes for seeds per pod was not significant. The mean of all the genotypes for this character was 12.59, which ranged from 9 to 14. The lowest number of seeds per pod was found (9) in G22 and the highest was found (14) in G1, G3, G4, G5, G6, G7, G9, G10, G21 and G28 (Appendix III). The genotypic variance (1.23) and phenotypic variance (1.96) were low for

this trait. The estimates of genotypic coefficient of variation (8.82) and phenotypic coefficient of variation (11.11) were moderate with little difference. Therefore, it can be concluded that there was an environmental influence for expression of this character. Moderate heritability (62.97) and low genetic advance (1.82) and genetic advance in percent of mean (14.42) were also observed for the trait concerned (Table 4).

4.1.10 100- seed weight

Significant differences among the genotypes were observed due to 100 seed weight. Maximum number of 100 seed weight was found in G11 (5.80) and minimum in G31 (1.20) with a mean value of 2.26 (Appendix III). Little influence of environment upon this trait was reported due to difference between the estimation of GCV (48.55) and PCV (48.95). High heritability (98.37) and high genetic advance in percent of mean (99.18) was found for this trait (Table 4). Thus suggesting phenotypic selection for 100 seed weight would be rewarding. Gupta *et al.,* (1998) in pea and Vivek *et al.,* (1999) observed high heritability coupled with genetic advance as a percentage of mean was for 100-seed weight in chickpea.

4.1.11 Yield per plant

The genotypes varied significantly for seed yield per plant. The highest seed yield per plant was observed in the genotype G11 (37.33). The lowest seed yield per plant was observed in the genotype G22 (10.67) (Appendix III). The phenotypic variance (53.16) differed slightly from genotypic variance (52.68) for this trait. Moderate genotypic (35.32) and phenotypic (35.48) coefficient of variation and high heritability (99.11) along with high genetic advance in percent mean (72.44) were estimated for this character. The PCV was higher than GCV indicating presence of environmental influence (Table 4). Such result suggested selection might be effective. Vivek *et al.,* (1999) in chickpea and Tyagi *et al.,* (2000) in cowpea genotypes observed high heritability coupled with genetic advance as a percentage of mean for seed yield per plant.

4.2 Correlation coefficients analysis

4.2.1 Character association in mungbean

Yield is a complex character and associated with several yield contributing characters. Selection for yield may not be effective unless other yield components influencing it directly or indirectly are taken into consideration. When selection pressure is exercise for improvement of any character highly associated with yield, it simultaneously affects a number of other correlated traits. Hence knowledge regarding association of characters with yield and among themselves provides guideline to the plant breeder for making improvement through selection.

Genotypic and phenotypic correlations between pairs of characters are presented in (Table 5). The genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients in most of the cases indicating the association is largely due to genetic reason. The results are discussed character wise as follows:

4.2.2 Days to 50% Flowering

Days to 50% flowering showed highly significant positive correlation with days to 50% maturity and highly significant negative correlation with the number of seeds per pod at both the genotypic and phenotypic level. It showed non-significant positive correlation with plant height, branches per plant, pod bearing peduncle per plant, 100-seed weight and yield per plant for both genotypic and phenotypic levels. Non-significant negative phenotypic and genotypic correlation was also observed with branch length, pods per plant and pod length (Table 5). Arora and Jeena (1999) found positive association of days to 50% flowering with days to maturity. Tyagi *et al.,* (2000) recorded a negative (-0.129) direct effect days to 50% flowering on seed yield per plant.

Table 5. Phenotypic (r_p) and genotypic (r_g) correlation coefficients among different yield contributing characters of mungbean

Characters	Correlations	D50M	PH	BP	BL	PP	PL	SP	PeP	SW	YP
D50F	r_p	0.551**	0.114	0.021	-0.002	-0.217	-0.320	-0.329**	0.068	0.218	0.179
	r_g	0.459**	0.135	0.029	-0.052	-0.227	-0.339	-0.362**	0.069	0.197	0.215
D50M	r_p		-0.172	0.040	-0.307	0.266	-0.189	-0.061	0.097	0.471**	0.266
	r_g		-0.170	0.043	-0.306	0.269	-0.188	-0.071	0.102	0.464**	0.270
PH	r_p			-0.313	0.606**	0.045	-0.178	-0.401*	0.123	0.096	0.161
	r_g			-0.323	0.618**	0.046	-0.179	-0.404*	0.129	0.099	0.162
BP	r_p				-0.020	0.353*	0.096	0.507**	0.510**	0.151	0.047
	r_g				-0.050	0.361*	0.133	0.604**	0.535**	0.155	0.044
BL	r_p					0.210	0.092	-0.035	0.377*	0.223	0.179
	r_g					0.211	0.100	-0.036	0.388*	0.228	0.179
PP	r_p						0.062	0.272	0.542**	0.662**	0.489**
	r_g						0.062	0.281	0.542**	0.662**	0.490**
PL	r_p							0.310	0.042	0.162	0.151
	r_g							0.316	0.036	0.163	0.151
SP	r_p								0.134	0.137	0.049
	r_g								0.158	0.141	0.051
PeP	r_p									0.362*	0.509**
	r_g									0.363*	0.478**
SW	r_p										0.904**
	r_g										0.905**

** indicates significant at 0.01 probability leveland * indicates significant at 0.05 probability level

D50F= Days to 50% flowering, D50M = Days to 50% mature pod, PH = Plant height, BP = Branches per plant, BL = Branch length, PP= Pods per plant, PL = Pod length, SP = Seeds per pod, PeP = Peduncles per plant, SW=100- seed weight, YP= Yield per plant.

4.2.3 Days to 50% maturity

Days to 50% maturity showed positive and highly significant correlation with 100 seed weight at both genotypic and phenotypic level. It showed non-significant positive correlation at both genotypic and phenotypic levels with branches per plant, pods per plant, peduncles per plant and yield per plant. It showed non-significant negative correlation both at genotypic and phenotypic levels with the PH, BL, PL, and SP (Table 5). According to Mahak *et al.,* (2004) days to maturity is a major yield-contributing character in field pea. Kumar *et al.,* (2003) studied on correlation for yield and yield components of pea. The number of days to flowering showed a positive association with number of days to maturity and number of seeds per pod.

4.2.4 Plant height

Plant height showed highly significant positive genotypic and phenotypic correlations with branch length. Positive and non-significant correlation of this trait was found with pods per plant, peduncles per plant and 100 seed weight and yield per plant at both genotypic and phenotypic levels. It showed non-significant negative correlation with branch per plant and pod length at both genotypic and phenotypic levels. It showed significant negative correlations at both phenotypic and genotypic level with seeds per pod (Table 5). Vivek *et al.,* (1999) reported that plant height showed negative correlation with seed yield per plant in chickpea genotypes.

4.2.5 Branches per plant

Branches per plant showed highly significant positive correlation at both the phenotypic and genotypic level with seeds per plant and pod bearing peduncles per plant. This character showed significant positive correlation at both the phenotypic and genotypic levels with pods per plant at 5 % level of significance. It showed non-significant negative correlation with branch length at both genotypic and phenotypic levels. It showed non-significant positive correlation with rest of the characters (Table 5). Kumar *et al.,* (2003) also

found positive correlation of branches per plant at genotypic level. Manoj*et al.,* (2003) in correlation analysis recorded positive correlation of pod yield with number of branches per plant.

4.2.6 Pods per plant

Pods per plant showed highly significant positive correlation with pod bearing peduncles per plant, yield per plant and 100 seed weight both at genotypic and phenotypic levels. It showed non-significant positive correlation with pod length and seeds per pod at both genotypic and phenotypic levels (Table 5). Aroea and Jeena (1999) in *Cicer arietinum* genotypes recorded significant and possitive correlation of with pods per plant. Correlations among the characters indicated that pods per plant are an important character in selection for improved seed yield. Natarajan and Rathinasamy (1999) recorded positive direct effect of pods per plant on yield.

4.2.7 Seeds per pod

Seeds per pod showed positive correlation with peduncles per plant, 100 seed weight and yield per plant both at genotypic and phenotypic levels (Table 5). Yadav (2000) found positive correlation between seed yield and seeds per pod in black gram. Chakraborty and Haque (2000) got the same type of result in lentil. Tiwari *et al.,* (2001) found a significant and positive correlation between seed yield per plant and number of seeds per pod in pea.

4.2.8 Peduncles per plant

Peduncle per plant showed highly significant positive correlation at both genotypic and phenotypic levels with pods per plant and yield per plant. It showed significant positive correlation at both genotypic and phenotypic levels with 100- seed weight (Table 5). Kumar *et al.,* (2003) also found positive correlation of branches per plant at genotypic level. Manoj *et al.,* (2003) in correlation analysis recorded positive correlation of pod yield per plant with number of branches per plant.

4.2.9 100- seed weight

The character 100 seed weight showed highly significant positive correlation with seed yield per plant at both genotypic and phenotypic levels, highly significant positive correlation with 50% maturity, pods per plant at both genotypic and phenotypic levels (Table 5). Vikas *et al*. (1999) recorded positive correlation between seed yield per plant and 100 seed weight.

4.3 Multivariate analysis

4.3.1 Principal Component Analysis

Based on principal component scores (PCA Score 1) and (PCA Score 2) obtained from the principal component analysis, a two-dimensional scatter diagram (Z1-Z2) using principal component score 1 as X-axis and principal component score 2 as Y-axis was constructed, which has been presented in (Figure 2). The positions of the genotypes in the scatter diagram were apparently distributed into five groups, which indicate that considerable diversity exists among the genotypes.

4.3.2 Principal Coordinate Analysis (PCO)

Inter genotypic distances D^2 were 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 genotype 11 and 22 followed by 32 and 27. The lowest distance was observed between genotype 8 and 9. The difference between the highest and the lowest inter genotypic distance indicated the prevalence of variability among the 32 genotypes of mungbean studied.

Intra-cluster distance (Table 9) were calculated from these inter genotypic distances (Singh and Choudhury, 1974). The highest intra-cluster distance was (20.42) observed in cluster III, which was composed of 5 genotypes, followed by cluster IV (18.64) containing 5 genotypes. The intra- cluster

distances in all the five clusters were lower than the inter cluster distances and which indicated that genotypes within the same cluster were closely related and variation was also low.

Table 6. Mean principal components (PC) scores from analysis of variance (ANOVA) of first four PCs of 32 mungbean genotypes

Genotypes	PC1	PC2	PC3	PC4
G1	1.728	0.875	-1.097	1.500
G2	0.079	-1.477	-0.360	0.161
G3	-0.517	-0.689	-1.892	1.439
G4	1.652	1.376	-0.397	1.533
G5	0.597	0.023	-1.406	0.633
G6	-0.128	-2.153	0.527	1.590
G7	-0.724	-1.356	0.932	1.630
G8	-0.479	0.445	-0.666	0.505
G9	-0.466	0.254	-2.093	1.088
G10	2.196	-0.735	-0.687	1.006
G11	4.542	0.486	4.774	-1.160
G12	4.368	1.360	-0.329	0.102
G13	0.639	1.435	-0.626	1.366
G14	-1.373	-0.465	-0.850	-1.604
G15	1.893	-0.604	0.182	-3.050
G16	0.266	-0.712	-1.744	-2.678
G17	-0.010	-0.565	0.761	0.532
G18	-0.863	1.074	0.367	-0.265
G19	-1.185	-0.294	1.962	1.714
G20	-0.868	-1.705	0.008	0.217
G21	2.943	0.262	0.213	-0.616
G22	-3.029	-1.422	2.928	-1.013
G23	-0.175	-0.808	-2.746	-2.299
G24	-1.530	0.161	0.086	-1.819
G25	-1.620	0.948	-0.339	-1.955
G26	-0.298	2.038	-0.075	0.347
G27	-2.581	3.680	1.185	-1.016
G28	-0.653	1.350	-0.846	0.590
G29	-2.229	3.144	0.774	0.203
G30	0.774	-1.975	-0.490	-0.455
G31	-2.166	-0.269	1.007	1.564
G32	-0.780	-3.684	0.935	0.212

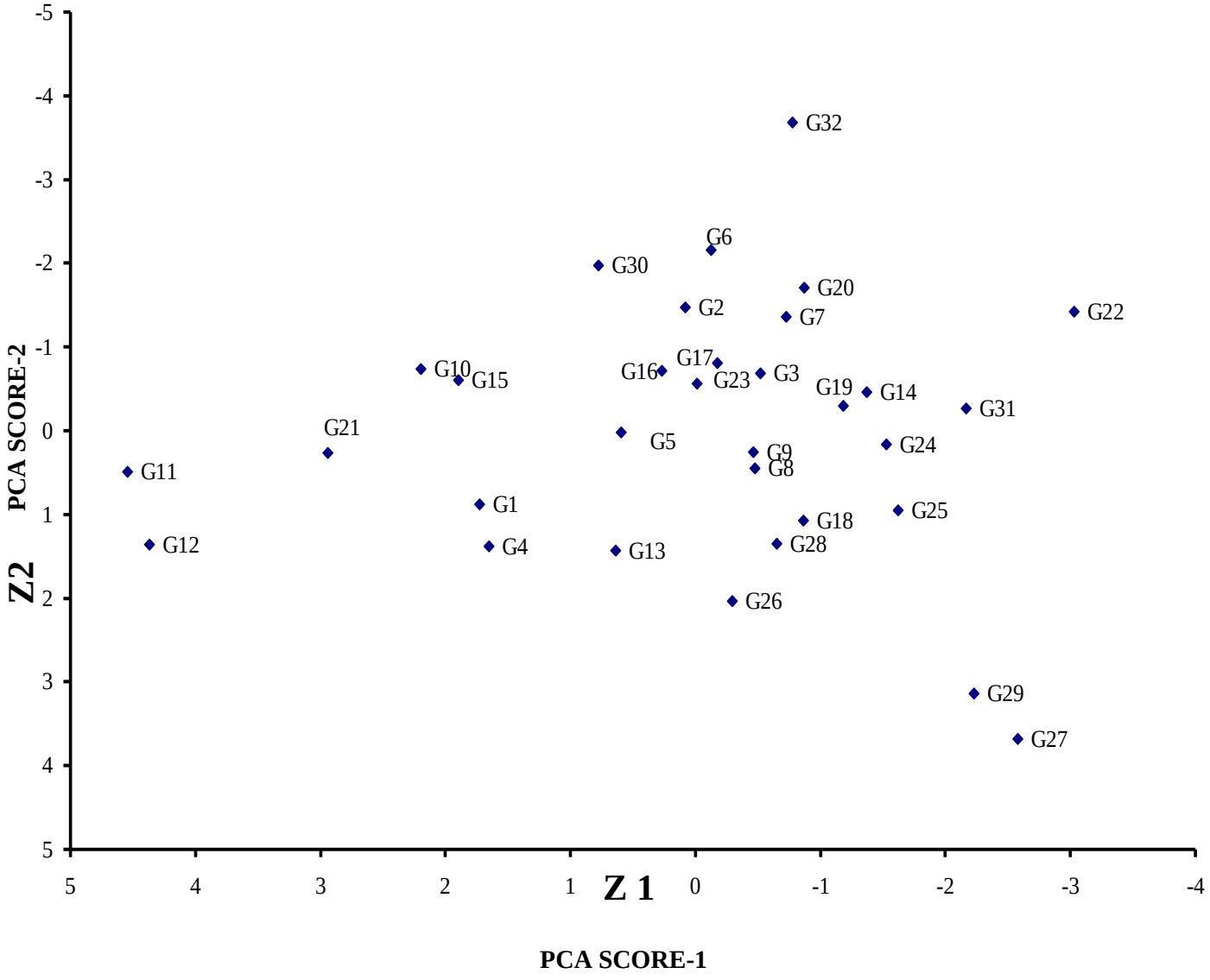

Figure 2. Scatter diagram of 32mungbean genotypes based on their principal component score.

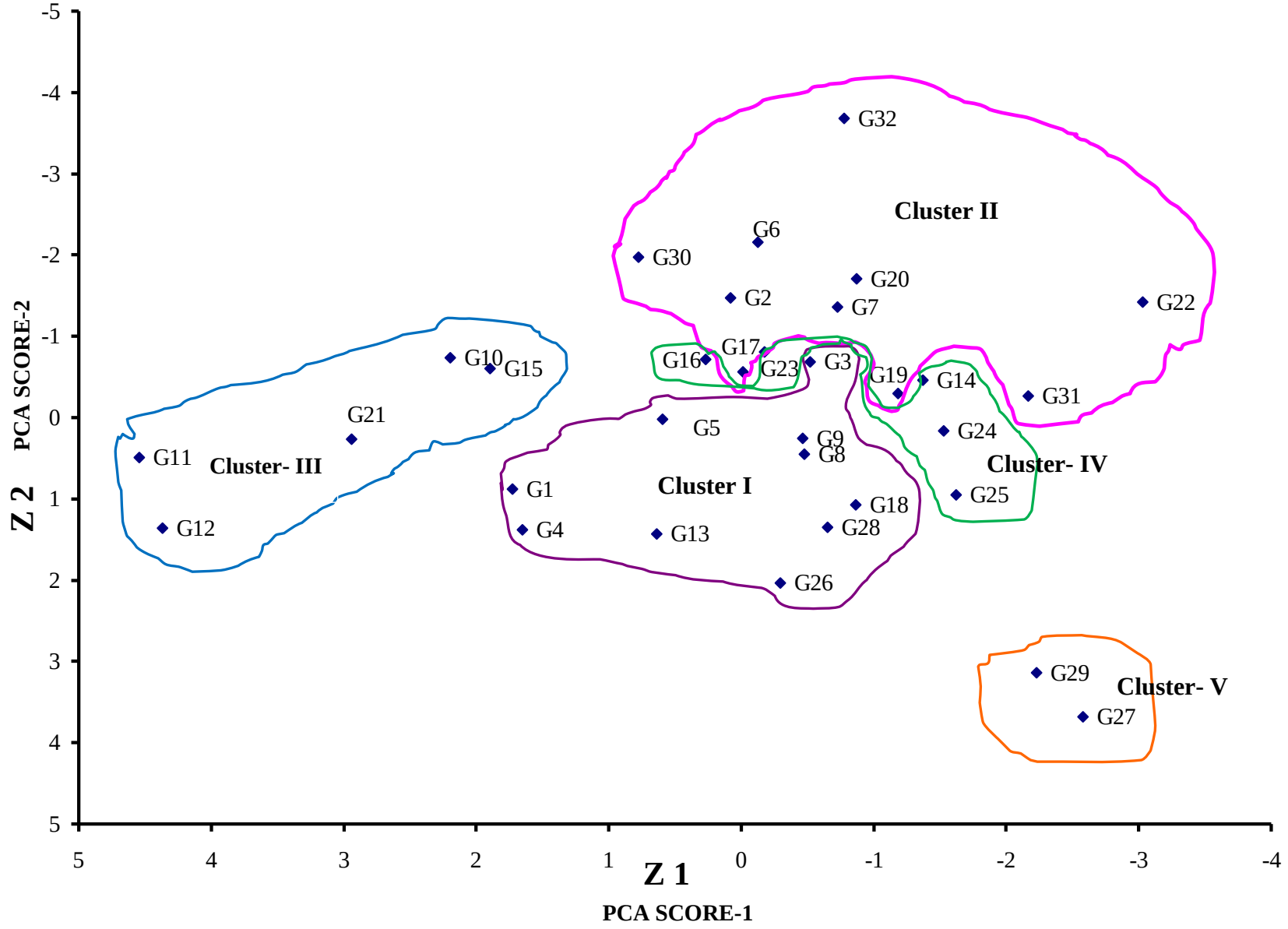

Figure 3. Scatter distribution of 32mungbean genotypes based on their principal component scores superimposed with clusters.

Table 7. Distribution of 32 mungbean genotypes in different clusters with their percentage accounted for divergence

Cluster number	Number of genotypes	Percent (%)	Name of genotypes	Accession number
I	10	31.25	G1, G3, G4, G5, G8, G9, G13, G18, G26 and G28	BD 6875, BD 6878, BD 6881, BD 6882, BD 6886, BD 6887, BD 6892, BD 6902, BD10026
II	10	31.25	G2, G6, G7, G17, G19, G20, G22, G30, G31 and G32	BD 6876 , BD 6884, BD 6885, BD 6897, BD 6905, BD 6906, BD 6909, BD 10030, BD 10031, BD 10032
III	5	15.63	G10, G11, G12, G15, and G21	BD 6888, BD 6890, BD 6891, BD 6894, BD 6908
IV	5	15.63	G14, G16, G23, G24 and G25	BD 6893, BD 6895, BD 10022, BD 10023, BD 10024
V	2	6.25	G27 and G29	BD 10027, BD 10029

4.3.3 Non-hierarchical Clustering

With the application of co-variance matrix for non-hierarchical clustering, 32 mungbean genotypes were grouped into 5 different clusters (Table 7), Cluster I and II had maximum 10 genotypes (G1, G3, G4, G5, G8, G9, G13, G18, G26 and G28) and (G2, G6, G7, G17, G19, G20, G22, G30, G31 and G32) respectively followed by cluster III and IV which had 5 genotypes each (G10, G11, G12, G15 and G21) and (G14, G16, G23, G24 and G25) respectively, Cluster V comprises with two genotypes (G 27 and G 29).

These results confirmed the clustering pattern of the genotype according to the principal component analysis. Composition of different clusters with their corresponding genotypes and collection site included in each cluster are presented in (Table 10). Results of different multivariate techniques were superimposed in (Figure 3). The clustering pattern obtained coincided with the

apparent grouping patterns performed by PCA. It is clear from the above that the results obtained through PCA were supported by non-hierarchical clustering.

4.3.4 Canonical variate analysis

Canonical variate analysis was done to compute the inter-cluster Mahalanobis's D^2 values. The intra and inter-cluster distance (D^2) values are presented in Table 9. Results indicated that the highest inter-cluster distance was observed between clusters III and V (42.06) followed by I and III (37.59) and III and IV (36.60). The higher inter-cluster distances between these clusters indicate to obtain wide spectrum of variability in the population. However, the highest inter- cluster distance was observed between clusters III and V indicated the genotypes in these clusters were diversed than those of other clusters. The lowest inter-cluster distance was observed between the clusters I and II (18.05), suggesting a close relationship among the genotypes included within these clusters (Figure 4).

The intra-cluster distance varied from 11.39 to 20.42, maximum for cluster III that was composed of 5 genotypes of diverse origin, while the minimum distance was found in cluster V that was composed of 2 genotypes. Statistical distances represent the index of genetic diversity among the cluster. The inter-cluster distances were larger than the intra-cluster distances which indicated wider genetic diversity among the genotypes of different groups.

4.3.5 Cluster mean value

An attempt was made to characterize the individual genotype in respect of their mean values for different characters with a view to get idea that weather genotypes having similar characteristics could be disseminated.

The mean values for all the 13 characters along with the marking of the highest (H) and the lowest (L) for each of the cluster are presented in Table 8. The data revealed that different clusters exhibited different mean values for almost all the characters.

Table 8. Cluster mean values of 13 characters of 32 genotypes in mungbean

Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
DF	34.40	33.80	33.20	32.40	36.50
D50F	37.00	36.40	36.20	35.80	40.50
DM	52.60	46.50	53.40	52.20	54.50
D50M	61.50	55.50	63.60	63.60	64.00
PH	63.19	73.84	74.79	65.40	78.50
BP	4.50	3.90	4.20	3.40	4.00
BL	49.76	56.48	57.30	45.33	49.05
PP	61.00	53.00	84.60	47.00	39.00
PL	6.91	7.17	6.99	6.49	5.90
SP	13.10	12.60	12.80	11.80	11.50
PeP	25.30	20.30	26.60	15.20	16.00
SW	1.95	1.98	4.28	1.84	1.20
YP	16.87	18.90	34.13	19.40	16.17

DF = Days to first flowering, D50F = Days to 50% flowering, DM = Days to first mature pod, D50M = Days to 50% mature pod, PH = Plant height, BP = Branches per plant, BL = Branch length, PP = Pods per plant, PL = Pod length, SP = Seeds per pod, PeP = Peduncles per plant, SW =100- seed weight, YP = Yield per plant

Cluster I constituted 10 genotypes) produced the highest mean for seeds per pod (13.10), branches per plant (4.50). The lowest mean values were observed for plant height (63.19). (Table 11)

Cluster II produced the highest mean for pod length (7.17). But the lowest mean for Days to first mature pod (46.50) and days to 50% mature pod (55.50). That means the genotypes of this cluster were early maturing genotype.(Table 11)

It was observed that cluster III produced the highest mean for branch length (57.30), pods per plant (84.60), peduncles per plant (26.60), 100- seed weight (4.28) and fruit yield per plant(34.13). Second highest for seeds per pod (12.80) and pod length (6.99).(Table 11)

Cluster IV comprising 5 genotypes (G14, G16, G23, G24 and G25) scored the lowest mean for days to first flowering (32.40), days to 50% flowering (35.80),

branches per plant (3.40), branch length (45.33) and peduncles per plant (15.20). But second highest for seed yield per plant (19.40). (Table 8)

Cluster V produced the highest mean for days to first flowering (36.50), days to 50% flowering (40.50), days to first mature pod (54.50), days to 50% mature pod (64) and plant height (78.5) and the lowest mean for pods per plant, pod length, seeds per pod, peduncle per plant, 100- seed weight (1.20) and yield per plant. That means the genotypes of this cluster were late maturing genotypes with higher plant height.(Table 8)

Days for 50% flowering ranged from 35.80 to 40.50 days among all the five clusters (Table 8). Cluster I had mainly moderately late flowering genotype where as it produced the highest mean values for seeds per pod and branches per plant. Cluster II had early maturing genotypes with the highest pod length. The genotypes belonging to the cluster III possess highest mean values for branch length, pods per plant, peduncles per plant, 100 seed weight and fruit yield per plant. Second highest for seeds per pod and pod length. To develop high yielding varieties along with early maturing type these groups can be used in hybridization program. The genotypes belonging to the cluster IV were early flowering and 50% flowering genotype with second highest in seed yield. The genotypes of the cluster V were late maturity type and less seeded types with lowest mean for 100 seed weight.

4.3.6 Cluster Diagram

With the help of D^2 values within and between clusters, an arbitrary cluster diagram (Figure 4) was constructed, which shows the relationship between different genotypes. However, the diagram was not following exact scale. It was apparent from the figure that the genotypes included in cluster I was less diversed from the genotypes of the cluster II and the genotypes belonging to III were far diversed from others and the genotypes in IV and V. Genotypes of cluster I - IV, I -V, II- IV, II - V and IV - V were moderately diverse from each other.

Table 9. Intra and inter cluster distances (D) among 32 mungbean genotypes

Characters	I	II	III	IV	V
I	**16.51**	18.05	37.59	19.15	18.84
II		**16.94**	34.69	19.44	23.45
III			**20.42**	36.60	42.06
IV				**18.64**	18.65
V					**11.39**

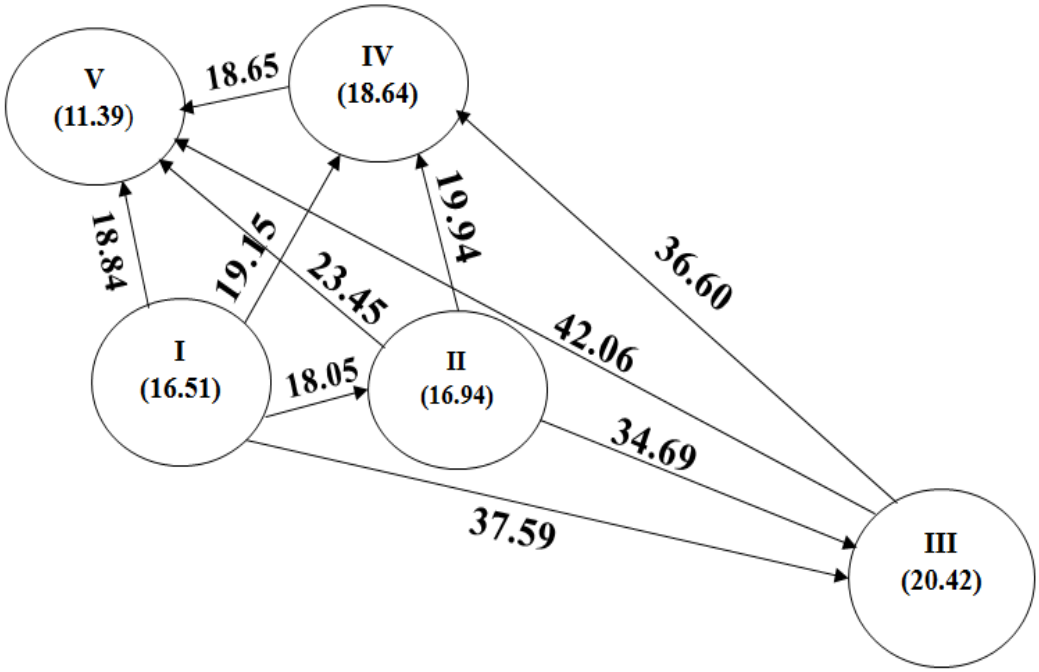

Figure 4. Cluster diagram showing the average intra and inter cluster distances (D = $\sqrt{D^2}$ Values) of 32 mungbean genotypes.

Table 10. Position of 10 prior high yielding genotypes of mungbea considering 11 characters

Genotpes	YP	D50F	D50M	PH	BP	BL	PeP	PP	PL	SP	SW
G13	37.33	M	M	H	M	H	H	H	M	M	H
G14	36.26	H	H	L	H	M	M	H	M	H	M
G17	34.12	M	M	M	L	L	L	H	M	M	M
G12	30.27	M	M	M	H	M	M	M	M	H	L
G18	28.15	M	H	L	L	L	L	L	H	M	H
G19	26.28	L	L	M	M	M	L	L	H	M	L
G23	24.25	H	M	H	M	M	H	H	M	H	L
G28	22.36	H	M	L	H	L	M	M	M	M	L
G7	21.54	L	M	L	H	M	L	M	M	H	L
G16	20.21	L	L	M	M	L	L	L	M	L	L

H= High, M= Medium, L=Low, DF = Days to first flowering, D50F = Days to50% flowering, DM = Days to first mature pod, D50M = Days to 50% mature pod, PH = Plant height, BP = Branches per plant, BL = Branch length, PP= Pods per plant, PL = Pod length, SP = Seeds per pod, PeP = Peduncles per plant, SW=100 seed weight, YP= Yield per plant

4.3.7 Comparison of results based on different multivariate techniques

Results obtained from different multivariate techniques are superimposed in Figure 3 from which it can be concluded that all the techniques gave more or less similar results and one technique supplemented and confirmed the results of the other. The cluster pattern of D^2 analysis through non-hierarchical clustering has taken care simultaneous variation in all the characters studied. However, the distribution of genotypes in different clusters of the D^2 analysis has followed more or less similar trend of the principal component score 1(PC 1) (Z1), principal component score 2 (PC 2) (Z2) of the principal component analysis (PCA). The D^2 and PCA were found to be alternative methods in giving the information regarding the clustering pattern of genotypes. Nevertheless, the canonical variate analysis (CVA) provides the information regarding the contribution of the characters towards divergence of genotypes.

CHAPTER V

SUMMARY AND CONCLUSION

The present experiment was undertaken to study the variability, character association and diversity in 32 genotypes of mungbean based on 13 characters. The salient findings of the present study have been summarized on the basis of the characters studied:

5.1 Univariate analysis

The analysis of variance showed significant differences among the genotypes for all the characters. The minimum duration for days to 50% flowering was recorded 35 days in the genotypes G14, G23, G30and G32 and maximum duration for days to 50% flowering was recorded 41 days in the genotype G 29. The minimum day's required for 50% maturity was recorded 50 days in G32 and maximum 67 days inG12. The genotype G3 produced the shortest (52.60 cm) and genotype G11 produced the tallest (96.13 cm) plant. The maximum branches per plant were found 5 in the genotypes G1, G4, G5, G9, G10, G12 and G13 and minimum branches per plant were found 3 in the genotype G15, G16, G22, G24, G25. Branch length ranged from 36.23 cm to 76.87 cm which was observed in G23 and G11 respectively. The highest number of pod bearing peduncles per plant were observed 41.00 in the G11 and the lowest was 14.00 in G16, G29 and G30. The highest and the lowest number of pods per plant were produced by the G12 (97.00) and G18 (34.00) respectively. The lowest number of seeds per pod was found 9 in G 22 and the highest was 14in G1, G3, G4, G5, G6, G7, G9, G10, G21 and G28. Maximum and minimum of 100 seed weight was found in G11 (5.80) and in G31 (1.20) respectively. The highest seed yield per plant was observed 37.33 in the genotype G11and the lowest seed yield per plant was observed 10.67 in the genotype G22.

The phenotypic variance was higher than genotypic variance in all the characters studied. The phenotypic coefficients of variation were also higher than genotypic coefficients of variation in all the characters studied. Phenotypic coefficients of variation were also close to genotypic coefficients of variation for all the characters. High heritability (>50%) was observed for all characters. High heritability coupled with high genetic advance in percent mean was observed for peduncles per plant, pods per plant, 100 seed weight and yield per plant suggested that effective selection may be done for these characters. Medium heritability coupled with low genetic advance in percent mean was observed in days to 50% flowering, branches per plant.

5.2 Correlation coefficient

Peduncles per plant, seeds per plant showed significant positive correlation with seed yield per plant. Significant positive genotypic and phenotypic correlation was observed by 50 % flowering with days to 50% maturity and negative with seeds per plant. Days to 50% maturity showed significant positive genotypic and phenotypic correlation with 100 seeds weight. Plant height significantly and positively correlated with branch length. Peduncles per plant showed significant positive genotypic and phenotypic correlation with yield. Pods per plant showed significant positive genotypic and phenotypic correlation with 100 seed weight, seed yield per plant and peduncle per plant.

5.3 D^2 Statistics

Genetic diversity of 32 mungbean genotypes based on 13 characters were measured through multivariate analysis. The 40 genotypes fell into five distant clusters. The cluster I and II comprised maximum number (10) of genotypes followed by cluster III and IV (5). The clusters V comprised 2 genotypes. The highest inter-cluster distance (42.06) was observed between the clusters III and cluster IV and highest distant genotypes were G11 and G22 followed by G32 and G27. The lowest inter-cluster distance was observed 18.05between the

clusters I and II, The lowest distance was observed between genotype G8 and G9.The inter-cluster distances were larger than the intra-cluster distances. The intra-cluster distance in the entire 5 clusters was more or less low indicating that the genotypes within the same cluster were less diversed. 50% flowering, peduncles per plant, pods per plant and yield per plant were the important component characters having higher contribution to the genetic divergence.

Based on the results of the study the following conclusions may be drawn:

1. Moderate to high heritability coupled with high genetic advance and high genetic advance in percent mean were observed in peduncles per plant, pods per plant, 100 seed weight, yield per plant. Hence, yield improvement in mungbean would be achieved through selection of these characters.

2. The characters peduncle per plant, pods per plant and 100-seed weight showed positive and significant correlation with seed yield per plant. This result suggested that seed yield per plant can be increased by improving this characters.

3. Days to 50% flowering, branches per plant, branch length, peduncle per plant, pods per plant , seeds per pod and l00 seed weight showed positive direct effect on yield. So yield improvement is associated with these characters.

4. Wide genetic diversity was observed in 32 genotypes of mungbean, which were grouped into five clusters and most diversed genotypes were G11 and G22.

5. The genotypes of cluster III were more diversed from the genotypes of clusters.

6. Plant height, branch length, peduncles per plant, pods per plant and yield per plant were found responsible for maximum diversity. On the other hand, pod length, seeds per pod had least responsibility of both the primary and secondary differentiation of genotypes based on cluster mean.

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CHAPTER I

INTRODUCTION

Mungbean (*Vigna radiata* L.) is a self-pollinated leguminous pulse crop belongs to the family Leguminoseae sub family papilionaceae, grown principally for its protein rich edible seeds. It is one of the important crops well suited to dry areas, mainly under irrigated conditions. The mungbean is a short day, warm season crop, grown mainly in semi-arid to sub-humid lowland, tropical and sub-tropical region in the world (Poehlman, 1991a).It is cultivated traditionally by small landholders throughout tropical, subtropical and temperate tones of Asia including Bangladesh, Pakistan, India, Sri Lanka, Nepal, Thailand, Burma, Iran, Vietnam, Indonesia, China, Korea and Japan. Since mungbean has a short maturity span (60-75 days) it is grown under various cropping systems, hence contributing to the increase income of the small landholders' as well as to the improvement of the soil conditions (Fernandez and Shanmugasundaram, 1988).In the South Asia, mungbean is used to make curry. Daal is the most common dish which is made from various kinds of split legumes with spices. In the Southeast and East Asian countries, it is used to make various kinds of sweet, bean jam, sweetened bean soup, vermicelli, and bean sprout. In Bangladesh it is grown under a wide range of agro-ecological zones of both rainfed and irrigated nature mainly cultivated in the Barisal and Patuakhali district. During 2011-2012, it was cultivated over an area of 91,000acres with 26 thousand tones production (Statistical Year book of Bangladesh, 2012). The average yield is much low than its potential and the yield obtained in other countries. One of the

reasons of low yield is unavailable of high yielding cultivars with better adaptability.

The major mungbean producing country is India (around 55% of the world hectarage and 45% of the world production) (Singh and Yadav, 1978). Production of mungbean is increasing more rapidly than the production of other pulse species. According to FAO (1999) a minimum intake of pulse by a human should be 80gm per head day by day where as it is only 14.19gm in Bangladesh (BBS, 2007). Mungbean is playing an important role in our nutrition. It is a very economical source of quality plant protein food. Mungbeancontains about 23.86 percent protein, this being about two-third of the protein content of soybean, twice that of wheat and three fold that of rice. It also contains 1.5 % lipids. 62.6% CHO, 436% lysine, 75mg methionine, 55mg cystine. (Poehlman, 1991).It offers potential in solving the malnutrition problems in developing nations. The mungbean has easily digestibility coefficient (79%), Biological value (72%) and Nutritional value (32%).

Mungbean can fix atmospheric nitrogen with association of particular soil bacteria and root nodules which are available for use by the plants. According to Morris, *et al.,* 1986, mungbean can be fixed about 86 kg/ha atmospheric nitrogen.Mungbean plant could be used as good fodder after the pods have been picked. Mungbean may be grown as a green manure crop to be ploughed under or as combined cash and soil improvement crops with the residues incorporated into the soil after pods have been harvested. In Bangladesh, mungbean is one of the major pulse crop ranking 5^{th} in acreage, 6^{th} in production, 3^{th} in protein (%)

content and 1st in respect of price. Mungbean is generally cultivated during early Rabi. But it is also grown in rabi after rice (January to March) in Summer (April to June) and after Jute (September to November) (Islam, 1978). 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. 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. The production is declining due to introduction of high yielding varieties of wheat and winter rice. At the present situation, increasing per unit area is the only way to increase production because it is not possible to afford much land to this crop. The low production syndrome results from several factors; (1) low genetic potential in native varieties; (2) yield fluctuations due to drought and floods; (3) losses from disease and insect pest; and (4) poor cultural practices. The per acre productivity of all pulses including mungbean are growing down steadily in Bangladesh.

Genetic diversity is one of the most important criteria for parent selection. Genetic diversity is a prerequisite for an efficient plant breeding program. The availability of transgressive segregants in any breeding program depends upon the diversity of involving parents. The importance of genetic diversity in the improvement of crop has been stressed in both self and cross-pollinated crops. (Griffin &Lindtorm, 1954; Murty and Anand, 1966; Gaur,*et al.* 1978).The quantification of genetic diversity through biometrical procedure (Anderson,

1957; Rao, 1952) has made it possible to choose genetically diverse parents for a successful hybridization program. Genetic diversity is important to know the source of genes for a particular trait within the available germplasms. (Tomooka, 1991). In order to increase the frequency of desired genotypes in breeding progenies, superior parents with high breeding values are needed.

The supreme parents having desired characters could be identified through divergence analysis. Several statistical methods are known for discriminating divergence viz., Mahalanohis's generalized distance (Mahalanobis, 1936), Fishers discriminant analysis, inspection of biometric data and totals of grouped data and Coopers's statistical classification with quadratic forms. Among them Mahalanobis's D^2-statistics based on multivariate analysis appears to be a good index. This technique has been followed by many researchers on a wide range of crops. Based on the above information, the present experiment was conducted to study the available variation, genetic nature and genetic diversity of 32 mungbean genotypes collected from BARI for more promising and necessary study to develop new varieties of mungbean. An intensive genetic restructuring program is necessary to evolve high yielding varieties of mungbean suitable for Bangladesh agro-climatic condition (Bhadra and Dev, 1985). To achieve this breeding goal an understanding of a genetic architecture of the yield determining characters will be helpful in yield improvement (Bhadra and Ali, 1986). A logical way to start any breeding program is to collect precise information on the nature and degree of genetic divergence that would help the plant breeder in

choosing the right type of parents for purposeful hybridization in heterosis breeding (Patel *et al.*, 1989).

Since mungbean is considerably less improved than its field demand it is necessary to choose genetically diverse parents to achieve heterotic cross for further transgression and to identify direct and indirect associations among yield attributes. To generate information on the degree of genetic diversity and coefficient of direct and indirect association among yield contributing characters this study was undertaken with the following objectives:

to study the genetic variability for different quantitative and qualitative characters.

to determine the nature of relationship between yield and yield contributing characters and relative contribution of each character towards seed yield in mungbean through the correlation co-efficient analysis.

to find out diverse germplasm suitable for the utilization in varietal improvement and future hybridization program.

CHAPTER II

REVIEW OF LITERATURE

Genetic divergence analyses is an initial systematic breeding methods for improvement of crops including mungbean. A few literatures of these works in mungbean are available. The literatures available on genetic analysis is summarized below:

2.1 Origin and Distribution

The mungbean is an annual herbaceous legume belonging to the family papilionaceae, includes the genus *vigna*, and subgenus *ceratotropics* distinguished two species (*Vigna radiata)* the mungbean and (*Vigna mungo)* the blackgram. The genus *Vigna* is pan tropical and now has been broadened to include about 170 species, 120 from Africa, 22 from Indo-Pak sub-continent and Southeast Asia and a few from other parts of the world (Ghafoor, *et al.,* 2001). Only seven species of *Vigna* are cultivated as pulse crops mostly in Asia, Africa and some parts of Latin America (Anishetty and Moss, 1988).

It is generally considered that two of these cultivated species are of African origin (sub genus *vigna*) and five are Asiatic origin (sub genus *Ceratotropis*). The Asiatic group consists, mungbean per 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 (Paroda and Thomas, 1988). At present, mungbean cultivation spreads worldwide because it is easily digested as compared to blackgram (Smartt, 1990).

The subgenus *Ceratotropis* is considered to have originated in Asia and is called Asian *Vigna*. It forms a discrete group of about seventeen species

largelyconfined to Asia and the Pacific.The origin and progenitor of mungbean is *Vigna sublobatus* acoording to Verdcourt (1970).The primary centers of origin of mungbean are the mountainous regions of Southwest-Asia, particularly Indian subcontinent.

2.2 Botany

Mungbean is an annual herbaceous plant. It has a tap root system, stems are slender usually branched, and upright in growth and leaves are pinnately compound with three to several leaflets. There are large stipules clasping the stem. The inflorescence is raceme arising from the axil of a leaf. The lowest node at which flower initiation occurs is quite constant under a given set of conditions and is used in classifying the varieties with respect to flowering and fruiting duration.

2.3 Genetic variability

Makeen *et al.,* (2007) studied twenty diverse mung bean 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.

Rohman *et al.,* (2003) studied on phenotypic and genotypic variance, correlation coefficient of variance, heritability conducted for yield and yield components in 82 genotypes of mungbean. High heritability estimates coupled with high genetic advance were observed for seed yield per plant, 100 grain weight, plant height, seed per pod and days to 50% flowering.

Swamy *et al.,* (2002) studied genetic divergence and stability analyses for 12 quantitative traits (number of days to 50% flowering, number of days to

maturity, plant height, number of branches per plant, number of clusters per plant, number of pods per cluster, pod length, number of seeds per pod, 100-seed weight, seed protein content, harvest index and seed yield per plant) in 50 mungbean genotypes. The genotypes were grouped into nine clusters based on Mahalanohis D^2 statistics. Superior genotypes from clusters I (WGG-37 and TARM-2). II (TAP-7), VII (LGG-441), IX (LGG-452), VIII (PDM-89-221), III (LGG471), IV (LGG-450), V (LGG-421) and VI (LGG427) were selected based on genetic divergence and stability for yield and yield components. These genotypes may be used for the selection of genetically divergent and stable segregants for future breeding programs.

In another report it was mentioned that genetic divergence following multivariate analysis from 34 genotypes of green gram grown in summer and pre-kharif season. Ten morpho-economic characters like days to flowering, number of primary branches, plant height, pod length, locules per pod, seeds per pod, pods per plant, 100 seed weight, yield per plant and seed protein content were taken into account. Thirty-four genotypes of green gram fall under eight clusters and four clusters in summer and pre-kharif season, respectively. Some genotypes were clubbed together under the same cluster irrespective of season indicating narrow genetic diversity among them. The genetic divergence was independent of geographical diversity. Greater magnitude of genetic diversity among the population of 34 genotypes could be recorded in summer than pre-kharif season. The character 100-seed weight had the highest contribution towards total divergence followed by seed protein content and yield per plant in summer season whereas in pre-kharif the greatest divergence was due to the seed protein content followed by 100 seed weight and days to flowering. 100 seed weight, seed protein content, days to flowering, yield per plant and pods per plant having maximum contribution towards genetic divergence should form the basis of selection of parents to obtain combinations having high heterotic effects (Moloy Roy *et al.*,2007).

Abrahim *et al.*, (2006) evaluated genetic variability and heritability analyses for yield and yield components which were conducted for 646 accessions of green gram grown in Coimbatore, Tamil Nadu, India during the rabi and kharif of 2002-04. The estimates of phenotypic (PCV) and genetic (GCV) coefficients of variation were higher for single plant yield, number of branches per plant, number of pods per plant, number of clusters per plant, plant height, and length of branch, indicating greater scope of selection for these traits. Dry matter production and number of clusters per branch revealed wide differences between the estimates of PCV and GCV values, indicating the highly significant effect of environmental factors. The number of days to initial flowering, number of days to 50% flowering, number of days to initial maturity, number of days to full maturity, 100-seed weight, seed length, seed breadth, length of pod and protein content were less affected by environmental factors as the difference between the estimates of PCV and GCV was low. The estimates of heritability in the core collection indicated that the number of days to full maturity, number of days to initial maturity, number of days to initial flowering, number of days to 50% flowering, seed length, seed breadth, plant height, length of branch, 100-seed weight, and length of pod were highly heritable. High genetic advance as a percentage of mean was recorded for the number of clusters per branch, length of branch, single plant yield, number of pods per plant, number of clusters per plant, plant height and number of branches per plant, suggesting the possibility of selection for these traits in the core collection.

Days to flowering, 100 seed weight was found to be maximum contributive towards genetic divergence in mungbean (Ramana and Singh, 1987). Pods per plant, seeds per pod and 100 seed weight contributed towards genetic diversity in mungbean (Malik *et al.*, 1985). Ghaderi *et al.*, (1979) found pods per plant, Seeds per pod and 100 seed weight were contributive to genetic diversity in mungbean. Flowering time, maturity, seed density and 100 seed weight were maximum towards genetic diversity in mungbean (Ramanujam *et al.*, 1974).

Upadhyaya *et al.,* (2002) studied phenotypic diversity for morphological and agronomic characteristics in 1956 accessions of chickpea core collection, comprising desi, Kabuli and intermediate types. The Kabuli and intermediate types were not significantly different for growth habit and seed color, while they differed significantly from desi types for both traits. Principal component analysis showed that days to 50% flowering, flowering duration. Apical secondary branches, tertiary branches, 100-seed weight, seed color and seed testa texture were important traits in explaining multivariate polymorphism.

PCA was used as a means of assessing progress toward achieving multiple breeding target of the mungbean breeding program reported by Asian Vegetables Research and Development Center (AVRDC, 1987). A hypothetical ideal mungbean cultivar was defined with the characteristics of 2.5 t per ha yield potential, synchronous maturity, early flowering at 38 days, seed weight of 60 g per l000 seeds, highly resistant to *cercospora* leaf streaks (CLS) and powdery mildew (PM) as compared with elite lines and check lines.

A field experiment was conducted by Jitender Kumar *et al.,* (2002) to study the response of methods of sowing (normal and paired row) and irrigation (controlled flooding and furrow) and irrigation schedules (one irrigation at 20 days after sowing (DAS), one irrigation at 35 DAS. 2 irrigation, one each at 20 and 35 DAS, and 3irrigations, one each at 20, 35 and 50 DAS) to mungbean cultivar M 11-85-111 grown in sandy loam soil. Among various characters influencing ultimate grain yield, number of branches per plant, number of pods per plant, number of grains per pod. 1000 grain weight and grains per plant, all had positive and significant association with final grain yield. Path analysis revealed that number of branches per plant, number of pods per plant and grain yield per plant was some of the most cordial characters of grain yield of mungbean.

Thirty seven diverse genotypes of blackgram and three of mungbean resembling to blackgram, are studied by Ghafoor *et al.,* (2002) to determine the extent of genetic variation based on morphological characters. High variance was

observed for plant height, days to maturity, branches per plant, pods per plant, pod length, seeds per pod, biological yield per plant, grain yield per plant and harvest index (%). First four components of PCA with eigen value >1 contributed 78.7% and 79. 1% of the total variance amongst 40 genotypes during two consecutive years.

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

In another report it was mentioned that utilized generalized distance and canonical analysis in 8 genotypes of mungbean and their 15 hybrids. The study yielded 5 clusters among the genotypes and hybrids. Harvest index was identified as one of the large source of divergence and clustering patterns were confirmed to a large extent by canonical analysis (Natarajan and Palanisamy, 1990).

Shamsuzzaman and Shaikh (1982a) 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 per plant displayed the highest (91.7) and the lowest (31.2) heritability respectively. Number of mature pods per plant showed the highest values for both genetic advance expressed as percentage of the mean.

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 per ha. (35.5%). A considerable variation was also obtained for number for pods per plant (25.9%) and seed yield per plant (24.6%).

Sandhu (1979) studied variability among 435 strains of mungbean for the characters, days to 50% flowering and maturity, plant height, number of branches, pods per p1ant, seeds per pod, 1000-seed weight and grain yield and sufficient variability for all the characters. The phenotypic correlation coefficient of variation was the highest (50.4 for total number of branches per plant. Grain yield per plant, pods per plant and clusters per plant also showed considerable phenotypjc correlation coefficient of variation 34.4, 32.7 and 30.1 percent, respectively.

Ahmad *et al.,* (1997) observed that cluster analyses on the basis of quantitative characters were phenotypically more distinct and exhibited more breeding value. Though cluster analyses grouped together accessions with greater morphological similarity, the cluster did not necessarily include all the accessions per genotypes from the same or nearby sites. Maqbool *et al.,* (1997) reported phylogenetic relationship of 15 genotypes of the genus *Lens* and seven of their interspecific hybrids were determined by morphological (quantitative and qualitative) characters.

Shanmugam and Rangasamy (1982a) observed significant differences among the types of green gram for all the nine characters indicating the presence of high variability among the forty genotypes clustered in sixteen groups. The grouping did not conform to the geographic origin. One cluster contained all types of the genotypes from the same region showing similar genetic architecture among the types of these clusters.

Loganathan *et al.,* (2001a) studied the Genetic diversity using multivariate analysis of 10 quantitative characters (days to first flowering, plant height, number of branches per plant. number of clusters per plant, number of pods per cluster, number of seeds per pod, pod length, 100- seed weight and seed yield per plant) among 42 F3 and eight varietal genotypes of (*Vigna radiata* L). The grouping of material into seven clusters indicated the presence of wide range of genetic diversity among the genotypes. The study indicated no definite relationship between geographic and genetic diversity and geographic diversity

cannot be used as an index of genetic diversity. In general, genetic diversity among the parents was reflected in their progenies. Seed yield per plant contributed maximum, accounting for 41.4% of total divergence. The diverse clusters derived could be used in hybridization program to generate wide range of transgressive segregants in population to develop high yielding green gram varieties with superior yield component traits.

Ghafoor *et al.,* (2000) conducted cluster analysis in mungbean for nine quantitative traits. They observed significant negative correlation of days to maturity with all the characters except branches per plant and suggested that short to medium maturity mungbean cultivars were to be selected for high yield. They identified 44 pure lines on the basis of important agronomic traits that were recommended for testing under wide range of agro-ecological condition in pursuit of best mungbean cultivars.

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

Reddy (1997) evaluated seventy genotypes of greengram from different geographical regions for 10 yield components at Tirupati in 1994. Genotypic and phenotypic variations were highest for branches per plant followed by grain yield per plant and pods per plant. Days to maturity followed by plant height and pod length had the highest heritability and were least influenced by the environment. Clusters per plant, pods per cluster, seeds per pod, 100-seed weight

and grain yield showed high differences in phenotypic and genotypic variation, indicating that the expression of these traits was influenced by environmental components.

Twenty two blackgram genotypes representing a broad based germplasm were analyzed by Ghafoor *et al.,* (2003) using multivariate analyses for two consecutive years. High genetic variance was observed for plant height, maturity, pods, seed weight, biomass, grain yield and harvest index. First four PCs contributed 80.0% of the variation during 1998 and 80.9% during 1999. Five yield contributing traits, i.e. branches, pods, pod length, biomass and grain yield were observed important for first component during both the years. PC2 was more related to maturity rather than reproductive traits. First two PCs which exhibited about 60% of the variance were plotted to observe the relationship between the cultivars. Five genotypes were separated from others during both the years.

Tiwari *et al.,* (1995) evaluated six parents and their 15 F2 progenies during kharif 1981-82. High variability was found in the F2 for days to maturity, clusters per plant, harvest index, pod length and 100-seed weight. Clusters per plant and 100-seed weight had high heritability. In parents, high heritability was found for plant height, seed yield per plant and harvest index and in the F2 for days to maturity, clusters per plant, pod length and 100-seed weight. High heritability estimates were generally associated with low genetic advance.

Reddy *et al.,* (2003) studied thirty-six genotypes of mungbean for genetic variability of seed yield and its contributing characters in summer 2000 at Tirupati, Andhra Pradesh, India. High magnitude of variability was observed for pods per plant and grain yield per plant, while moderate variability was recorded for pods per cluster, clusters per plant, plant height and days to 50% flowering suggesting the possibility of their improvement by selection. High heritability coupled with high genetic advance was observed for pods per plant, grain yield per plant, pods per cluster, clusters per plant, plant height and days to 50% flowering, while high heritability and moderate genetic advance was recorded

for seeds per pod, 100-seed weight and days to maturity suggesting that these traits were controlled by additive gene action.

Loganathan *et al.,* (2001b) studied on Genetic variability in greengram (*Vigna radiata* L.). Fifty genotypes of green gram were used to estimate genetic variability for 10 quantitative characters in Tamil Nadu, India, during rabi 1999. High phenotypic coefficient of variability indicated the favorable effect of environment for number of clusters per plant and seed yield per plant and high genotypic coefficient of variability suggested substantial amount of genetic variability for number of pods per plant and seed yield per plant, high genetic advance, additive gene action and phenotypic selection were effective for number of pods per plant, seed yield per plant and number of seeds per pod. Non-additive gene action, low heritability and low genetic advance were noted for days to first flowering, plant height, number of branches per plant, pod length and 100-seed weight.

Islam *et al*., (1999) studied on genetic variation, heritability on 9 yield components in 53 genotypes studied in Joydebpur 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.

Malhotra and Singh (1971) while working on genetic divergence in blackgram reported narrow range of variability for l00-seed weight and pod length whereas, Shanmugam and Rangaswamy (1982) while analyzing45 genotypes of blackgram reported that yield per plant contributed most to the genetic diversity.

Malik *et al.,* (1985) studied genetic divergence in 12 indigenous varieties of mungbean for six quantitative characters. The study indicated the presence of ample genetic variation among the cultivars irrespective of their origin. They suggested that plant height, days to flowering and grain yield should be considered for selecting genetically divergent lines in mungbean.

Khaimar *et al*., (2003) evaluated twenty-two mung bean genotypes for genetic variability in the kharif season of 1997, in Rahuri, Maharashtra, India. A wide

range of variability was observed for plant height, clusters per plant, pods per plant, grain yield per plant and 100 grain weight. The estimates of genotypic as well phenotypic coefficients of variation were highest for pods per plant followed by 100-grain weight. High heritability coupled with high genetic advance was observed for clusters per plant, pods per plant, grain yield and 100-grain weight indicating that these characters can be improved by selection.

Das and Chakraborty (1998) studied some 22 genotypes of greengram for genetic variability of seed yield and its contributing characters at Nagaon. Plant height, branches per plant, pods per plant, pod length and yield per plant recorded high genotypic coefficients 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 per plant, pods per plant and pod length. It indicates that these traits were mostly controlled by additive gene action. Seeds per pod and yield per plant recorded low heritability coupled with low and high genetic advance, respectively.

Kumar *et al*., (2003b) studied a total of 40 green gram cultivars during the 1998 wet season to determine genetic variability analysis. Data were recorded for days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, pod length, number of seeds per pod, 100-seed weight and grain yield per plant.

Pandey and Singh (2002) studied the genetic variability performance of green gram cultivars ML 552, PS 16, ML 371, LM 1510, PDM 11, Pusa Baishakhi 1, PDM 84-139, PDM 54, ML 374 and ML 574 in rice-wheat cropping system in a field experiment conducted in Meerut, Uttar Pradesh, India during the kharif season of 1998 and summer of 1999. Significant differences among the genotypes were observed in terms of plant height, number of days to 50% flowering and maturity, number of seeds per pod, 100-seed weight, yield and infection by yellow mosaic virus.

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

2.4 Correlation coefficients

Investigation on yield contributing characters with 169 local and exotic mungbean genotypes revealed that mature pods per plant, primary branches per plant and seeds per pod showed significantly positive correlation with yield per plant while maturity, plant height and 100 seed weight were negatively correlated with seed yield (Shamsuzzaman *et al.,* 1983).

Shamsuzzaman and Shaikh (1982a) studied the characters association of 169 local and exotic genotypes of mungbean and observed significant positive correlation of yield per plant with number of primary branches, mature pods per plant and seeds per plant while maturity period, plant height and 1000- seed weight exhibited negatively 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 per plant with number of mature pods per plant.

Correlation studies in agronomic characters of 70 mungbean strains showed that number of pods per plant had strongest association with seed yield. There were negative associations of seed size, plant height and days from sowing, on first flowering and to maturity with seed yield (Ahmed *et al.,* 1981).

Sandhu *et al.,* (1979) studied correlation ship among yield attributes in mungbean and found negative correlation of yield with days to flowering, positive correlation with plant height and branches per plant, highly positive significant correlation with clusters per plants pod length, positive correlation with days to maturity, high positive significant correlation with seed weight,

seeds per pod. The correlation study concluded that pods per plant, cluster per plant, seeds per pod, pod length and 100 seed weight were important attributes of grain yield.

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

Dhuppe *et al*., (2005) studies on correlation which were carried out in 35 genotypes (11 parental lines and 24 hybrids) of mungbean grown in Parbhanj, Maharashtra, India, in 1998. Data were recorded for days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per plant, l00-seed weight and yield per plant. Grain yield per plant showed positive and significant correlation with days to maturity, number of secondary branches per plant, number of pods per plant and 100- seed weight at genotypic level, whereas secondary branches per plant and 100-seed weight were correlated with grain yield at phenotypic level.

In a study of 20 diversed mungbean genotypes, seed yield per plant showed positive correlation with pod and seed yield per plant, seeds per pod and branch number, plant height and seed numbers per pod. Pod length had the greatest positive direct effect on yield as revealed by path coefficient analysis followed by number branches per plant number per plant and plant height (Khan, 1988).

Sirohi and Kumar (2006) studied correlation analysis for yield and yield components which were conducted for 19 diverse genotypes of mungbean (*V. 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.

Kumar *et al.,* (2003) studied on correlation for yield and yield components of pea. The number of days to flowering showed a positive association with number of days to maturity and number of seeds per pod.

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

Yadav (2000) found positive correlation between seed yield and seeds per pod in black gram. Chakraborty and Haque (2000) got the same type of result in lentil. Tiwari *et al.,* (2001) found a significant and positive correlation between seed yield per plant and number of seeds per pod in pea.

In another report it was mentioned that positive significant correlation of yield with branches per plant, positive correlation with plant height, highly negative correlation with days to flowering, highly positive correlation with clusters per plant, pods per plant, pod length and days to maturity, positive correlation with seeds per pod. They suggested that seed weight should be highest priority in selecting genotypes in mungbean (Ali and Shaikh, 1987).

Rohman *et al.,* (2003) studied on correlation coefficient analysis which was conducted for yield and yield components in 82 genotypes of mungbean. Yield was positive and significantly correlated with pod per plant, seed per pod and 100 grain weight, pod per plant, seed per pod and 100 grain weight contributed maximum positive and direct effect on yield indicating these two traits should be given emphasis while selecting high yielding mungbean cultivar for rainfed conditions.

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

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

Bhaumik and Jha (1980) estimated the biometrical relationship in 2 cultivar of mungbean and found positive correlation of seed yield per plant with 1000 seed weight, seed per pod and pods per plant. They also reported negative correlation between seed and plant height.

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

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

Digby *et al.,* (1989) reported that coordinates obtained from PCA is used as input of PCO analysis in calculation of distances among the points. Thus PCA is

used for graphical representation of the points while PCO to calculate the minimum distance in a straight line between each pair of points.

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

Wani *et al.*, (2007) determined the genetic variability among 20 genotypes of green gram (*Vigna radiata*) for quantitative characters and protein content. High heritability, coupled with high genetic advance, was observed for number of pods per plant, number of pods per cluster, plant height and seed yield, suggesting the importance of additive genetic control in the inheritance of these characters. Seed yield exhibited a positive and significant correlation with number of pods per plant followed by number of pods per cluster and pod length. These characters were the major yield-contributing characters. Therefore, the seed yield of green gram may be improved through the direct selection of these characters.

Siddique *et al.*, (2006) determined the genetic divergence and trait association in mungbean genotypes (01CMG511, 01CMG512, 01CMG513, 01CM6514. 01CMCI516. 01CMG517 and 01CMG5518). Analysis of variance indicated highly significant differences for all the traits except grains per pod, which showed non-significant results. Genotype 01CMG515 recorded the lowest number of days to maturity (66), whereas 01CMG518 showed the highest number of days to maturity (76). The highest grain yield (859.26 kg per ha) was recorded for NM-98. Genotypic variance was highest for grain yield followed by 1000-grain weight. The highest value of heritability was recorded for grain yield (99.81%) followed by 1000-grain weight (92.18%), number of days to flowering

(19.06%) and number of days to maturity (88.50%). Grain yield (11765.58) and 1000-grain weight (1568.54) showed the highest genetic advance followed by number of days to flowering (1162.29) and to maturity (655.03). Positive and significant correlation was exhibited by most of the traits.

Yaqoob *et al.,* (1997) studied ten important agronomic characters for estimation of co-efficient of correlation in 30 genotypes per mutants of mungbean grown under rainfed 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.

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

Nazir *et al.,* (2005) determined the direct and indirect effects of different genetic parameters in different mungbean lines per cultivars. Twenty mungbean lines per cultivars were evaluated to exploit yield components to the maximum extent and formulate selection criteria in mungbean. According to the results, high heritability coupled with moderate to high genetic advance was observed for plant height (97.00 and 23.40), seed yield (86.00 and 32.41), harvest index (86.00 and 36.78) and 100-seed weight (74.00 and 17.01). It indicated that additive genes mainly control such characters. Clusters per plant (0.47), pods per plant (0.57), pod length (0.30) and 100-seed weight (0.38) showed positive and significant genotypic correlation with seed yield. Clusters per plant (0.71), pods per plant (0.69), pod length (0.45), 100-seed weight (0.41) and seeds per pod (0.77) also had significant phenotypic correlation with seed yield. Plant height (0.12), clusters per plant (0.47), pods per plant (0.64), pod length (0.33) and harvest index (0.52) showed positive direct effects on seed yield.

In another report it was mentioned that sixty genotypes of mungbean (*Vigna radiata*) for 13 characters to assess genetic variability, heritability, correlation,

genetic advance and genetic diversity. Total dry matter, plant height, number of pods per plant and yield per plant exhibited high variability and heritability coupled with genetic advance, indicating the influence of additive gene action. Correlation studies indicated that the total dry matter, number of pods per plant, number of clusters per plant, number of branches per plant and days to 50% flowering were positive and significantly associated with seed yield, total dry matter and number of pods per plant had direct positive effect on seed yield while plant height had negative effect. The results of multivariate analysis indicated the presence of considerable genetic divergence among the genotypes. The genotypes were grouped into eight clusters. Days to maturity, 100-seed weight, number of pods per plant and total dry matter contributed maximum towards diversity. Crosses can be effective between the genotypes of cluster V and VII followed by cluster I and VII where the maximum inter-cluster distance was exhibited for getting desirable segregants (Rao *et al.*, 2006).

Singh and Pathok (1993) recorded on 11 quantitative traits in 20 (*Vigna radiata)* parents, 90 F1s and 90 F2s. Seed yield was positively correlated with plant height, clusters per plant, number of pods per cluster, number of pods per plant, pod length, seeds per pod and 100-seed weight.

Niazi *et al.,* (1999) evaluated genotypic correlation and path-coefficient analysis for 8 agronomic characters affecting seed yield which was accomplished in 15 elite genotypes of mungbean. All the correlation coefficients were significant, whilst number of tilled pods per plant, plant height, number of columns and seed per pod, and number of clusters per plant revealed a strong positive association with seed yield per plant. Pods per plant emerged as a reliable component that can serve as a selection criterion in breeding high yielding cultivars of mungbean.

Sharma (1995) observed highly significant and positive correlations for number of seeds per plant and 100-seed weight with seed yield in 6 mungbean (*Vigna radiata*) genotypes and their GF1 and GF2 hybrids grown at Jabalpur, Madhya Pradesh in 1985.

In another report it was mentioned that twenty-five diverse genotypes of mungbean to study the variability and character association of eight quantitative characters. The estimates of high heritability with high genetic advance observed for the characters biological yield, days to 50% flowering, number of pods per plant, plant height indicated the presence of additive gene action for these characters. The phenotypic and genotypic coefficients of variation were high for biological yield, number of pods per plant, harvest index, seed yield per plant. The maximum positive and significant phenotypic correlation coefficient (0.825) was observed between the number of pods per plant and seed yield per plant, followed by seed yield per plant with harvest index (0.822), days to 50% flowering and plant height (0,752), number of pods per plant and harvest index (0.670), days to 50% flowering and biological yield (0.663), plant height and biological yield (0.599). Path coefficient analysis showed that number of pods per plant (0.561), harvest index (0.425), 1000 seed weight (0.216), had positive and direct effect towards seed yield, whereas at phenotypic level biological yield (0.195) number of seeds per pod (0.087), days to 50% flowering (0.011) had relatively low direct effect. Therefore, these characters may be selected directly to improve seed yield (Kumar *et al.,* 2005).

A study was conducted by Reddy *et al.,* (2005) to derive information on genotypic and phenotypic correlations, direct and indirect effects of various traits (days to 50% flowering. days to maturity, plant height. branches per plant, pod length. pods per plant. seeds per pod, nodules per plant, clusters per plant, protein content, harvest index, test weight and seed yield per plant) in greengram. The number of seeds per plant was significantly and positively correlated with plant height and number of clusters per plant at both genotypic and phenotypic levels, and significantly and positively associated with the number of seeds per pod, test weight, days to maturity and days to 50% flowering at the genotypic level and with number of pods per plant at the phenotypic level. Path analysis indicated that plant height, days to 50% flowering and test weight recorded the highest direct effect in the desirable direction. Their association with seed yield was significant and positive,

indicating that there exists a true and perfect association between these characters and suggesting that direct selection for these characters will help in isolating early and high yielding genotypes.

Thirteen genotypes of green gram were studied for seven characters by Venkateswarlu (2001a) for association analysis and revealed that pods per plant, days to maturity, plant height, 100-seed weight, seeds per pod and pod length showed significant and positive association with seed yield. Pods per plant and seeds per pod had maximum positive direct effect on seed yield. Days to maturity, clusters per plant, plant height, 100-seed weight and seeds per pod exhibited high indirect effect on seed yield via pods per plant.

In another report it was mentioned that the genetic variation, heritability and characters association 9 yield components in 53 genotypes of mungbean. 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. Yield per plant was significantly and positively correlated with plant height, number of primary branches per plant, number of pods per plant, pod length, number of seeds per pod and 1000-seed weight. Pod length exerted the highest positive direct effect on yield. (Islam*et al.,* 1999).

Manivannan *et al.,* (1998) evaluated thirty green gram (*Vigna radiata*) genotypes for 8 yield components. Genotypes were grouped into 8 clusters based on their genetic diversity. Highest inter-cluster values were observed between clusters VI and VIII, VII and VIII and IV and VII. Plant height contributed most towards divergence followed by length, pods, seeds per pod and clusters. Genotypes KMGI, MGG319, WGG47 and PLM292 were recommended for breeding purposes.

2.5 D^2- Statistic

Nath *et al.,* (2005) estimated the genetic divergence among 19 genotypes of *Vigna* comprising wild and cultivated species following Mahalanohis' D^2 technique and canonical analysis. The genotypes formed three different clusters.

Close correspondence in cluster composition was found between D^2 analysis and canonical analysis. Genotypes belonging to *Vigna radiata*, *V. mungo*. *V. aconitifolia, V. irilobata* and *V. sinensis* [*V. unguiculata*] formed a single cluster. Genotypes of *V. umbellate*, *V. hiniana* [*V. hainiana*] and *V. trichuriensis* formed another cluster. Genotype of *V. minima* formed a third cluster. Wide variability among the germplasms was found. Parental selection in hybridization programs to increase variability in black gram and mungbean is suggested.

Genetic diversity in 39 mutants of mungbean was assessed by Sandhu and Brar *et al.,* (2002) using Mahalanobis' D^2- statistics. The results revealed the existence of a substantial amount of diversity in the mutants isolated from the gamma ray-induced populations of three mungbean cultivars (ML 131, ML 267 and ML 337). The mutants were grouped into eight clusters. Cluster I and VIII were the largest with eight mutants each and cluster VII was the smallest with two mutants. Except for cluster III mutants, all other mutants were derived from two or three cultivars. All the three mutants grouped in cluster III were isolated from a single 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.

Sinha *et al.,* (1999) estimated the genetic divergence using Mahalanobis's D^2 statistic. Altogether 8 clusters were formed. Cluster I alone accommodated 30 genotypes. Inter-cluster distance was maximum (471.66) between cluster VII and VIII followed by clusters IV and VIII. There was no strict relationship between geographical distribution and genetic divergence. However, there was a tendency to be grouped in a cluster for cultivars belonging to a zone. Intra-cluster D^2 value was maximum in cluster III, which has 3 cultivars. The trait seed weight (100-seed weight) had the highest contribution to genetic divergence.

In another report it was mentioned that 40 genotypes of greengram through D^2 analysis and revealed a wide genetic variability among the genotypes. There was no relationship between geographic and genetic diversity as genotypes chosen

from same eco-geographical region were found in different clusters as well as in the same clusters. The maximum inter-cluster distance was observed between clusters I and XIV and as followed by clusters VIII and IX, clusters III and IX and clusters I and IX indicating wide divergence among these clusters. The variance of cluster means revealed that number of pods per plant, days to maturity, days to flowering and plant height were the main characters contributing 10 the genetic divergence in the present material (Kishore *et al.,* 2000).

Some 84 genotypes of mungbean from different geographical regions were grouped into 17 clusters using D^2 analysis. Pods per plant contributed most to cluster differentiation. Genetic diversity was independent of geographic origin and parentage. Glutamate oxaloacetate transaminase (aspartate aminotransferase) activity was high in high-yielding clusters. The present study suggests the importance of biochemical divergence in relation to morphological divergence (Lal *et al.,* 1998).

Miranda *et al.,* (1999) studied thirty mungbean lines using canonical variate and cluster analysis for yield components. D^2- statistics of Mahalanobis' generalized distance identified 9 heterotic groups. The genotypes Ouro Verde and KY-8 were the most similar, while KY1945 and V3726 were the most dissimilar: KY 1945 was recommended for crossing with V3726; breeding efforts should be based on crosses between heterotic groups as determined by cluster analysis, graphics analysis of canonical varieties was in agreement with cluster analysis.

A study on genetic divergence was carried out by Singh and Pathak (1987) using Mahalanohis' D^2- statistics in 20 genotypes of mungbean of diverse origin with 112 quantitative traits including yield per plant. The genotypes were grouped into six clusters; the members of all clusters were geographically unrelated. Cluster 2 with eight genotypes had the maximum values for pods per plant and seed yield per plant. These eight genotypes with four others were recommended for hybridization.

Manivannan (2002) analyzed 33 mungbean genotypes derived from ten crosses to determine genetic diversity using multivariate analysis. The genotypes were grouped into seven clusters. Among the characters studied, 100-seed weight and powdery mildew reaction contributed them towards the total divergence. Based on the performance they suggested seven genotypes to be included in the hybridization program.

Ramanujam *et al.,* (1974) explained that in mungbean flowering time, maturity, seed density and 100 seed weight contributed maximum toward genetic diversity from a study of D^2 analysis. They suggested that in general there was fair agreement between the extent of heterosis and genetic divergence between the parents. Seed density, maturity time, seed size and flowering lime recorded maximum and yield components as pods per plant and seeds per pod had limited influence in genetic divergence was found by Shanmugam and Rangasamy, (1982a) in forty genotypes in greengram clustered in 16 groups. Yield per plant followed by clusters per plant and pods per cluster contributed maximum towards genetic divergence. Natarajan *et al.,* (1988) studied 45 greengram genotypes which was clustered into 4 groups and suggested that seed weight followed by days to flowering contributed maximum towards genetic diversity. Seed size and pod length contributed maximum towards genetic divergence in mungbean reported by Gupta and Singh. (1970). Thulasidass. (1984) classified 30 mungbean genotypes into 7 clusters and reported that 100 seed weight, pods per plant, plant height, and pod length had maximum contribution. Days to flowering, seed size and primary branches per plant was main components to genetic diversity in mungbean (Malhotra *et al.,* 1974).

In a field experiment conducted by Saxena *et al.,* (2002) 59 cultivars of greengram were grouped into sixteen clusters utilizing data on a set of twelve characters related to yield and its contributing characters (days to maturity, plant height. number of primary branches per plant, height of first fruiting internode, cluster per plant, number of pods per plant, number of pods per cluster, 100-seed weight, biological yield per plant, seed yield per plant and harvest index). Major

clusters in divergence analysis contained cultivars of heterogeneous origin, indicating no parallelism between genetic and geographic diversity. The cluster pairs exhibiting very high inter cluster distances were cluster IX and XIV, cluster IX and XII, cluster VII and X. cluster V and XII, and cluster V and XIV. Days to maturity, followed by plant height, seed yield, height of first fruiting internode, biological yield and number of clusters per plant showed high percent contribution towards genetic divergence. Therefore, crosses between members of clusters having high cluster means for important characters coupled with high inter cluster distances between them are likely to be more rewarding.

Mishra and Rao (1990) reported thirteen clusters in a comparative study of D^2 and meteroglyph analyses of 117 chickpea genotypes. Cluster I had the maximum number of genotypes. Meteroglyph analysis did not show similar type of clustering as observed in D^2 analysis, but canonical analysis showed similar type of clustering.

Tawar *et al.,* (1988) conducted genetic divergence using D^2 analyses in 34 genotypes of mungbean and these were grouped in five clusters. Variability observed in the parents was related to genetic diversity of the parents selected under study. First canonical root contributed 88% of the total variation. Inclusion of such genotype from distinct clusters and their implication in mungbean breeding program as suggested by Singh *et al.,* (1991) examined the organization of diversity for morphological and agronomic characters in 306 landraces of cultivated common bean (*Phaseolus vulgaris* L.) by analyzing data for multivariate statistical analyses and observed genetic variance within and between groups. Kumar and Arora (1992) presented observation of 40 genotypes of chickpea collected from various geographical regions for 18 character s including seed yield, Multivariate analyses revealed 10 clusters. No definite relationship was established between genetic diversity and geographical distribution. Maximum hybrid vigor was observed among most diverse genotypes.

CHAPTER III

MATERIALS AND METHODS

A field experiment was conducted at the experimental field of Genetics and Plant Breeding department of Sher-e Bangla Agricultural University, Dhaka Bangladesh during March 2015 to July 2015 to study on the inter genotypic variability, genetic divergence and path coefficient in Mungbean (*Vigna radiata* L.).The materials and methods of this experiment are presented in this chapter under these following headings:

3.1 Site of experiment:

The research work was conducted at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka- 1207. The experimental site was at $90^0 22'$ E longitude and $23^0 41'$ N latitude at an altitude of 8.6 meters above the sea level.

3.2 Soil and Climate of the experimental Site

The experimental area was under the sub-tropical monsoon climate zone, which is characterized by heavy rainfall, high humidity, high temperature and relatively long day during the *Kharif* season while hardly rainfall, low humidity, low temperature and short day during the Rabi season. Rabi season is favorable for mungbean cultivation but it also be cultivated as summer crops in kharif-1 season. The land belongs to agro-ecological region of 'Madhupur Tract' (AEZ 28) of Nodda soil series. The soil was sandy loam in texture having pH 5.47-5.63. The mean temperature of the growing period was 26.43°C with average maximum and minimum being 36°C and 20.54°C respectively. Details of the meteorological data in respect of temperature, rainfall, relative humidity, total sunshine and soil temperature during the period of experiment were collected from the weather station, Dhaka, Bangladesh.

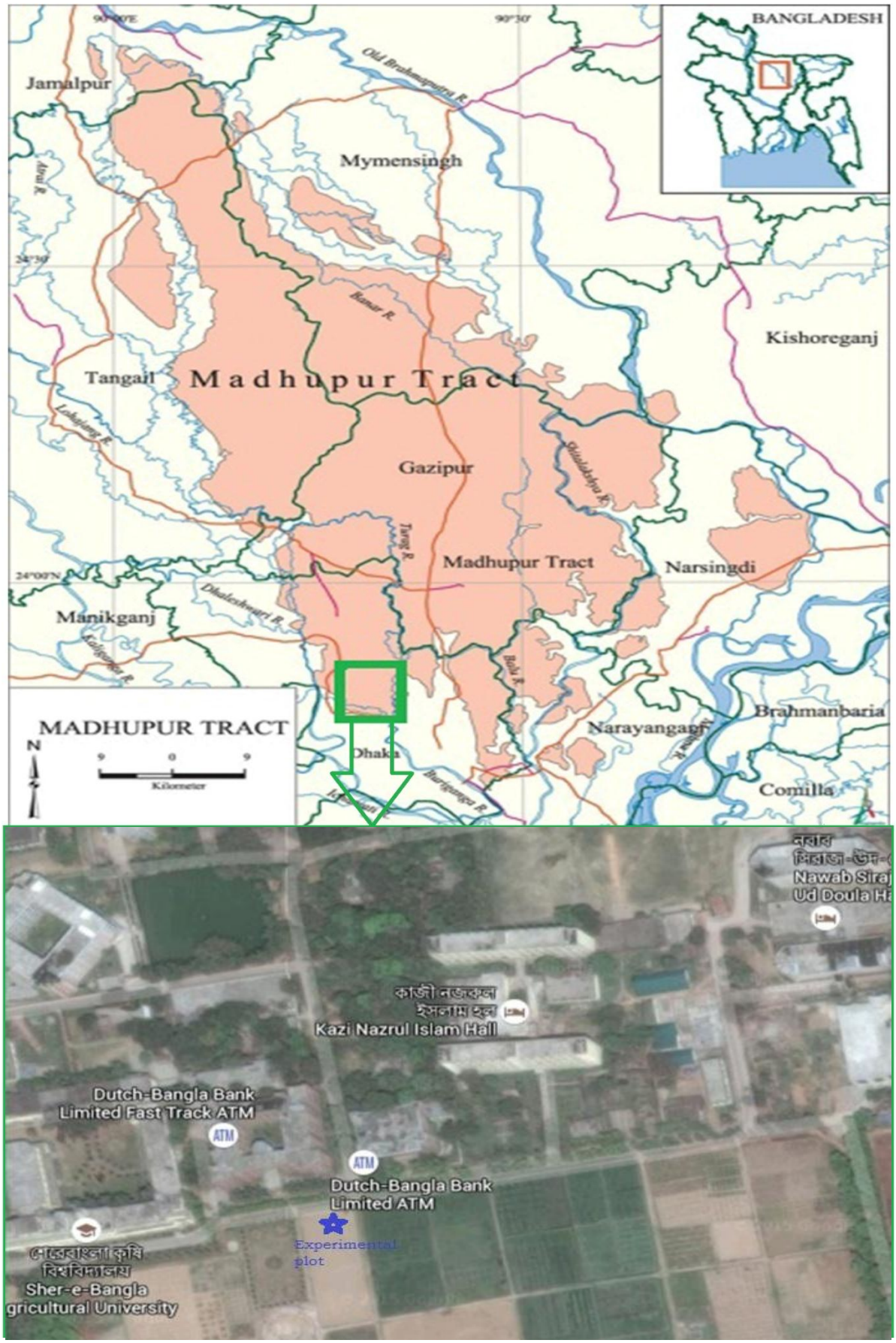

Figure 1. Location of the experimental site

3.3Genetic materials used for the experiment

Thirty two (32) genotypes were used in the study. The seeds of 32 accession lines were collected from Plant Genetic Resources Center (PGRC) of Bangladesh Agricultural Research Institute (BARI). Descriptions of the genotypes are given in (Table 1).

Table 1. The code, accession name and source of collection of the 32 genotypes of mungbean used in the experiment

Sl No.	Code	Accession number	Source of Collection
1	G1	BD-6875	BARI
2	G2	BD-6876	BARI
3	G3	BD-6878	BARI
4	G4	BD-6881	BARI
5	G5	BD-6882	BARI
6	G6	BD-6884	BARI
7	G7	BD-6885	BARI
8	G8	BD-6886	BARI
9	G9	BD-6887	BARI
10	G10	BD-6888	BARI
11	G11	BD-6890	BARI
12	G12	BD-6891	BARI
13	G13	BD-6892	BARI
14	G14	BD-6893	BARI
15	G15	BD-6894	BARI

Table 1. Continued

Sl No.	Code	Accession number	Source of Collection
16	G16	BD-6895	BARI
17	G17	BD-6897	BARI
18	G18	BD-6902	BARI
19	G19	BD-6905	BARI
20	G20	BD-6906	BARI
21	G21	BD-6908	BARI
22	G22	BD-6909	BARI
23	G23	BD-10022	BARI
24	G24	BD-10023	BARI
25	G25	BD-10024	BARI
26	G26	BD-10026	BARI
27	G27	BD-10027	BARI
28	G28	BD-10028	BARI
29	G29	BD-10029	BARI
30	G30	BD-10030	BARI
31	G31	BD-10031	BARI
32	G32	BD-10032	BARI

3.4 Design and layout of the experiment

The experiment was laid out in Randomized Complete Block Design (RCBD) with 3 replications. The field was divided into 3 blocks then the blocks were further sub-divided into 4 plots each of which was (2 m × 3 m) where genotypes were randomly assigned. Total land size was 120 m^2. The individual block size was 2m ×12m. Block to Block distance was 70 cm, plant to plant distance was 20 cm and row to row distance was 40 cm. The genotypes were distributed to each row with each block randomly.

3.5 Preparation of the experimental field

The selected field for growing mungbean was first opened with power tiller and was exposed to the sun for a week. Then the land was prepared to obtain good tilth by several ploughing, cross ploughing and laddering. Subsequent operations were done with harrow, spade and hammer. Weeds and stubbles were removed, larger clods were broken into small particles and finally attained into a desirable tilth to ensure proper growing conditions. The plot was partitioned into the unit plots according to the experimental design as mentioned earlier. Recommended doses of well decomposed cowdung, manure and chemical fertilizers were applied and mixed well with the soil each plot. Proper irrigation and drainage channels were also prepared around the plots. Each unit plot was prepared keeping 5 cm height from the drains. The bed soil was made friable and the surface of the bed was leveled.

3.6 Manure and fertilizer application:

Due to its ability of nitrogen fixation from the atmosphere mungbean requires less nitrogen than other pulse crops. But for initial establishment of plant up to the stage of nodule formation a starter dose of 20-40-20 NPK respectively was applied. The unit plots were fertilized with cow dung, urea, TSP and MP @ 10 ton, 50 kg, 85 kg, 35 kg per ha respectively. The entire cow dung, TSP, MP and half of the urea was applied at the time of final land preparation. The remaining

half of urea was applied as top dressing in two installments. First top dressing was done at 20 days after and second at 35 days after sowing.

In this study fertilizer was applied as per the recommendation of Bangladesh Agricultural Research Institute (BARI). The following doses of fertilizers and manures were applied to the plot for mungbean cultivation.

Table 2. Doses of different fertilizers used in the experimental field

Fertilizers/ manures	Doses (kg)	
	Applied in the plot	Quantity/ ha
Urea	2.01	47
TSP	3.50	88
MP	1.50	36
Cow dung	20	2.00 ton

3.7 Seed sowing

Seeds of 32 accession were sown on 23 March, 2015. The seedlings were emerged 4-5 days after seed sowing.

3. 8 Intercu1tural operations

The growing seedlings were always kept under care observation. After sowing the seeds, the following intercu1tural operations were accomplished for their better growth and development

3.8.1 Irrigation

A shallow irrigation was applied in the experimental field just after sowing the seeds. Here after the crop was irrigated when needed depending on the moisture status of the soil and requirement of plants.

3.8.2 Weeding and mulching

Weeding and mulching were necessary to keep the plots free from weeds, easy aeration and for conserving soil moisture. When the plants were well established, the soil around the base of plants was pulverized.

3.8.3 Top dressing

The remaining doses of Urea were applied as top dressing in two equal installments. First top dressing was done at 20 DAS and second at 35 DAS.

3.8.4 Plant protection measures

The established plants were affected by aphids. Diazinon 60EC (l5cc per 10 liter) was applied against aphids and other insects. Few plants found to be infected by yellow mosaic were uprooted and destroyed.

3.9 Harvesting

Different genotypes matured at different times. The harvesting was completed by 30 May 2015. Ten plants from each plot were randomly selected to collect data and these were harvested by uprooting. Border plants were discarded to avoid border effect.

3.10 Data collection

In order to study the genetic divergence among the genotypes, the data were collected in respects of 13 parameters. Data on germination, flowering and maturity was recorded on whole plant basis. The other following parameters were noted on individual plant basis from five randomly selected competitive plants.

3.10.1 Days to first flowering (DF): Determined as the days from sowing to first begun to flower of the plant.

3.10.2 Days to 50% flowering (D50F): Determined as the days from sowing to 50% of plants had begun to flower.

3.10.3 Days to first mature pod (DM): Determined as the days from sowing to first mature pod when the pod color change from green to black.

3.10.4 Days to 50% mature pod (D50M): Determined as the days from sowing to 50% mature pod when the pod color change green to black

3.10.5 Branches per plant (BP): Count only pod-bearing branches whose origin was in the leaf axils on the main stem.

3.10.6 Branch length (BL): length (in cm) of longest branch from main stem to the branch top.

3.10.7 Plant height (PH): The length of the main stem from the ground level to the tip, what was measured in centimeter (cm).

3.10.8 Peduncles per plant (PeP): Number of peduncles having at least one fully grown pod at first harvest including both main stem and branches.

3.10.9 Pods per plant (PP): The pods per plant was calculated from the five randomly selected plants.

3.10.10 Pod length (PL): Mean length (in cm) of pods from ten randomly selected mature pods.

3.10.11 Seeds per pod (SP): It was the mean number of seeds from ten randomly selected pods.

3.10.12 100 seed weight (SW): One hundred seed weight (g) was taken randomly from the bulk sample of each genotype and adjusted to the 12% moisture content and measured the weight by an electrical balance.

3.10.13 Yield per plant (YP): Total weight of seeds per plant (at mature stage) after pod shelling was measured in gram.

3.11Data analysis

3.11.1 Univariate analysis

The collected data were statistically analyzed. The mean, maximum, minimum and standard deviation for each character have been calculated and analysis of variance for each of the character was performed. The mean square (MS) at error and phenotypic variances were estimated as per Johnson, *et al.* (1995).

$$\sigma^2_g = \frac{GMS - EMS}{r}$$

Where,

GMS and EMS are the genotypic and error mean square and r is the number of replication.

The phenotypic variances (σ^2_p), were derived by adding genotypic variances with the error variances (σ^2_e), as given by the following formula,$\sigma^2_p = \sigma^2_g + \sigma^2_e$

3.11.2 Estimation of genotypic and phenotypic co-efficient of variation

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

Genotypic co-efficient of variation (GCV) = $\frac{\sigma_g \times 100}{\bar{X}}$

Where,

σ_g= Genotypic standard deviation

$\bar{X}$ = Population mean

Similarly,

The phenotypic co-efficient of variation was calculated from the formula:

Phenotypic co-efficient variation (PCV) = $\frac{\sigma_p \times 100}{\bar{X}}$

Where,

σ_p=Phenotypic standard deviation

$\bar{X}$= Population mean

3.11.3 Estimation of genetic advance

The expected genetic advance for different characters under selection was estimated using the formula suggested by Lush (1949) and Johnson, *et al.*, (1955).

Genetic advance (GA) = K. $h^2.\sigma_p$

Where,

K = Selection differential, the value of which is 2.06 at 5% selection,

σ_p= Phenotypic standard deviation estimating from Genetic advance in percentage of mean

3.11.4 Estimation of heritability

Broad sense heritability was estimated (defined by Lush. 1949) by the following formula suggested by Hanson, *et al.*, (1956) and Johnson, *et al,* (1955).

$$h^2_b\% = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where,

h^2_b= Heritability in broad sense, σ^2_g= Genotypic variance, σ^2_p= Phenotypic variance.

3.11.5 Genetic advance in percent mean

Genetic advance as percentage of mean was calculated from the following formula:

$$\text{Genetic advance (\% of mean)} = \frac{\text{Genetic advance}}{\text{Population mean}} \times 100$$

3.11.6 Estimation of genotypic and phenotypic Correlation co-efficient

For calculating the genotypic and phenotypic correlation coefficient for all possible combination the formula suggested by Johnson, *et al.,* (1955) and Hanson, *et al.*, (1956) were adopted.

The genotypic covariance components between two traits and of the phenotypic covariance component were derived in the same way as for the corresponding variance components. The covariance components are used to compute genotypic and phenotypie correlation between the pairs of the characters as follows:

Genotypic correlation = $\frac{\sigma^2_{gxy}}{\sqrt{\sigma^2_{gx}+\sigma^2_{gy}}}$

Where,

σ^2_{gxy}= Genotypic covariance between the traits x and y.

σ^2_{gx}= Genotypic variance of the trait x

σ^2_{gy}= Genotypic variance of the trait y thus,

Phenotypic correlation (rph_{xy}) = $\frac{\sigma^2_{phxy}}{\sqrt{\sigma^2_{phx}+\sigma^2_{phy}}}$

Where,

σ^2_{phxy}= Phenotypic covariance between the traits x and y.

σ^2_{phx}= Phenotypic variance of the trait x

σ^2_{phy}= Phenotypic variance of the trait y thus,

3.11.7 Multivanate analysis (D^2 Statistics)

Mean data for each character was subjected to multivariate analysis methods viz, principal component analysis (PCA), principal coordinate analysis (PCO), canonical variate analysis (CVA) and cluster analysis (CLSA) using GENSTAT 4.2 program.

3.11.8 Principal component analysis (PCA)

Principal component analysis is one of the multivariate techniques to know the interrelationships among several characters and can be done from the sum of squares and product matrix for the characters. Principal components were computed from the correlation matrix and genotypic scores obtained for the first

component and succeeding components with latent roots greater than unity (Jager, *et al.,* 1983).

3.11.9 Principal coordinate analysis (PCO)

Principal coordinate analysis is equivalent to PCA but it is used to calculate inter-unit distances. Through the use of all dimensions of p it gives the minimum distances between each pair of n points using similarity matrix (Digby *et al.,* 1989). Inter-distances between genotypes were studied by PCO.

3.11.10 Canonical variate analysis (CVA)

The canonical variate analysis is based upon the roots and vectors of W-IB, where W is the pooled within groups covariance matrix and B is the among groups covariance matrix. It provides two-dimensional plots that helped in separating different populations involved.

3.11.11 Cluster analysis (CLSA)

Genotypes were divided into groups on the basis of a data set into some number of mutually exclusive groups. The clustering was done using non-hierarchical classification. In GENSTAT, the algorithm is used to search for optical values of the chosen criterion. The optimal values of the criteria followed by some initial classification of the genotypes into required number of groups, the algorithm repeatedly transfers genotypes from one group to another so long as such transfer improved the value of the criterion. When no further transfer can be found to improve the criterion, the algorithm switches to second stage that examine the effect of two genotypes of different classes and so on.

3.11.12 Computation of average intra-cluster distance

Computation of average Intra-cluster distance for each cluster was calculated by taking possible D^2 values within the members of a cluster obtained from the PCO after the clusters are formed. The formula utilized was $\sum D^2/n$, where $\sum D^2$ is the sum of distances between all possible combinations (n) of the genotypes

included in a cluster. The square root of the average D^2 values represents the distance (D) within cluster.

3.11.13 Cluster diagram

It was drawn using the values between and within clusters distances, which presents a momentary idea of the pattern of diversity among the genotypes included in a cluster.

3.11.14 Computation of average inter-cluster distances

The procedures of calculating inter-cluster distance between cluster II and I and between cluster Ill and I and between I and IV, between II and IV and so on. The clusters were taken one by one and their distances from other clusters were calculated.

CHAPTER IV

RESULTS AND DISCUSSION

In the present investigation 32 genotypes of mungbean were studied. The results presented here provide some information on genetic variability, correlation and D^2- statistic. Mean values for different characters, mean squares from analysis of variance, genotypic and phenotypic co-efficient of variation, heritability; genetic advance and partitioning of genotypic correlation into direct and indirect effect and multivariate analysis are presented in Table 3 to 11. The results obtained from this study are presented and discussed under the following headings:

4.1 Univariate analysis

4.1.1 Analysis of variance and genetic parameters

The analysis of variance (Table 3) indicated the existence of significant variability for all the characters studied. The mean, range, genotypic, phenotypic and environmental variance, genotypic, phenotypic and environmental coefficients of variation, heritability estimates, genetic advance and genetic advance in percent mean are presented in (Table 4). The results are discussed character wise as follows:

4.1.2 Days to 50% flowering

The analysis of variance showed that the genotypes varied significantly for 50 % flowering. The minimum and maximum duration for 50% flowering was observed in the genotypes G14, G23, G30, G32 (35 days) and G29 (41 days), respectively (Appendix III). The estimates of GCV (3.29) and PCV (4.51) were moderate with very little difference, heritability (53.15) of this trait was moderate and GA% was low (4.94) but genetic advance (1.81) was also low (Table 4). It reveals non-additive gene action and high heritability was exhibited due to influence of favorable environment rather than genotypes, so selection may not be rewarded. But Mohar *et al.,* (1999) reported that days to 50% flowering showed higher estimates of heritability along with genetic advance.

4.1.3 Days to 50% maturity

The mean square due to genotypes differed significantly for days to maturity. The mean for this character was 60.44, which ranged from 50 - 67. The minimum days required for 50% maturity was in G32 (50 days) and maximum days were for G12 (67 days) (Appendix III). The phenotypic variance (18.64) was a little higher than genotypic variance (15.25). The genotypic (6.46) and phenotypic (7.14) coefficient of variation were moderate with a little difference indicates that environment have a little effect on the expression of this character. High heritability (81.82) was obtained due to this low environmental influence but genetic advance in percent of mean was medium (12.04) (Table 4). Such results indicated that selection based on this trait might be effective. Chakraborty and Haque (2000) found high heritability and low genetic advance in lentil for this trait.

4.1.4 Plant height

The average height of plant was 69.63 cm. The genotype G3 had the shortest (52.60) and genotype G11 produced the tallest (96.13) plant. (Appendix III). Phenotypic variance (80.00) was considerably higher than the genotypic variance (75.36). The phenotypic coefficient of variation (12.85) and genotypic coefficient of variation (12.47) were close to each other indicating negligible influence of environment on this trait. A high heritability (94.19) along with moderate genetic advance (17.36) and genetic advance in percent of mean (24.93) indicated that selection for this trait would be rewarding (Table 4). High heritability and low genetic advance in percent of mean for plant height was also found by Chaudhary and Sharma (2003), Ramesh *et al.*, (2002), Sureja and Sharma (2000), Tyag *et al.*, 2000).

Table 3. Analysis of variance for different morphological plant characters of 32 mungbean genotypes

Sources of variation	d.f	Mean sum squares					
		DF	D50F	DM	D50M	PH	BP
Replication	2	29.656	23.156	17.281**	4.906	9.834	1.531
Genotypes	31	6.408**	5.658**	41.371**	49.149**	230.72**	1.149
Error	62	2.237	1.285	6.701	3.390	4.646	0.370

** indicates significant at 0.01 probability level.

Table 3. Continued

Sources of variation	d.f	Mean sum squares						
		BL	PP	PL	SP	PeP	SW	YP
Replication	2	17.086**	0.500	0.793	10.53	3.406**	0.020	0.948
Genotypes	31	180.595**	1033.50**	1.312	4.424	130.207**	3.631**	158.53**
Error	62	12.900	7.210	0.052	0.725	3.116	0.020	0.475

** indicates significant at 0.01 probability level.

DF = Days to first flowering, D50F = Days to 50% flowering, DM = Days to first mature pod, D50M = Days to 50% mature pod, PH = Plant height, BP = Branches per plant, BL = Branch length, PP= Pods per plant, PL = Pod length, SP = Seeds per pod, PeP = Peduncles per plant, SW=100 seed weight, YP= Yield per plant

Table 4. Genetic component of variation for yield and yield contributing characters in mungbean

SL. No.	Characters	Minimum	Maximum	Mean	Phenotypic variance (δ^2p)	Genotypic variance (δ^2g)	PCV (%)	GCV (%)	Heritability (%)	GA	GA (%)
1	DF	30.00	37.00	33.84	3.63	1.39	5.63	3.48	38.33	1.50	4.44
2	D50F	35.00	41.00	36.72	2.74	1.46	4.51	3.29	53.15	1.81	4.94
3	DM	42.00	55.00	50.88	18.26	11.56	8.40	6.68	63.30	5.57	10.95
4	D50M	50.00	67.00	60.44	18.64	15.25	7.14	6.46	81.82	7.28	12.04
5	PH	52.60	96.13	69.63	80.00	75.36	12.85	12.47	94.19	17.36	24.93
6	BP	3.00	5.00	4.06	0.63	0.26	19.54	12.55	41.24	0.67	16.60
7	BL	36.23	76.87	52.30	68.80	55.90	15.86	14.30	81.25	13.88	26.54
8	PP	34.00	97.00	58.63	349.31	342.10	31.88	31.55	97.94	37.71	64.31
9	PL	5.03	8.10	6.87	0.47	0.42	10.00	9.43	88.98	1.26	18.33
10	SP	9.00	14.00	12.59	1.96	1.23	11.11	8.82	62.97	1.82	14.42
11	PeP	14.00	41.00	21.78	45.48	42.36	30.96	29.88	93.15	12.94	59.41
12	SW	1.20	5.00	2.26	1.22	1.20	48.95	48.55	98.37	2.24	99.18
13	YP	10.67	37.33	20.55	53.16	52.68	35.48	35.32	99.11	14.89	72.44

DF= Days to first flowering, D50F= Days to 50% flowering, DM= Days to first mature pod, D50M= Days to 50% mature pod, PH= Plant height, BP= Branches per plant, BL= Branch length, PP= Pods per plant, PL= Pod length, SP= Seeds per pod, PeP= Peduncles per plant, SW=100 seed weight, YP= Yield per plant,PCV= Phenotypic coefficient of variations, GCV= Genotypic coefficient of variations, GA= Genetic advance, GA (%)= Genetic advance in percent mean

4.1.5 Branches per plant

The maximum branches per plant were found (5) in the genotypes G1, G4, G5, G9, G10, G12 and G13 and minimum branches per plant were found (3) in the genotype G15, G16, G22, G24, G25 (Appendix III). The phenotypic variance (0.63) was slightly higher than genotypic variance (0.26) and the PCV (19.54) was also a little greater than GCV (12.55) indicating the role of environment on the expression of this trait which was low other than high heritability (41.24) of the trait. The genetic advance was also low (0.67) with moderate genetic advance in percent of mean (16.60) for this trait (Table 4).

4.1.6 Branch length

Based on the branch length there was significant variations among the genotypes. Branch length ranged from 36.23 cm to 76.87 cm which was observed in G23 and G11, respectively. Average value for branch length was 52.30 cm. (Appendix III). Phenotypic variance (68.80) was higher than the genotypic variance (55.90). The Phenotypic and genotypic coefficient of variations were 15.86 and 14.30, respectively, which differed each other indicating favorable influence of environment on this trait. Heritability of this trait was high (81.25) but genetic advance was low (13.88) along with moderate genetic advance as a percentage of mean (26.54) (Table 4). The high heritability was exhibited due to influence of favorable environment that means selection may not be effective. Ramesh *et al.*, (2002) found moderate to high heritability coupled with high genetic advance as a percentage of mean for branch length in cowpea.

4.1.7 Peduncles per plant

Significant differences among the genotypes were observed due to pod bearing peduncles per plant. The highest number of pod bearing peduncles per plant was 41.00, produced by the G11 and the lowest number of pod bearing peduncles per plant was 14.00, produced by G16, G29 and G30 and mean of this character was 21.78 (Appendix III). The phenotypic variance (45.48) was

slightly higher than genotypic variance (42.36). Moderate genotypic coefficient of variation (29.88) and phenotypic coefficient of variation (30.96) were found for this trait with a non-significant difference which indicated that there were little environmental effect on the expression of character. The heritability was very higher (93.15) together with high genetic advance (12.94) and genetic advance in percent of mean (59.41) indicating the selection for this character would be effective (Table 4). Devendra *et al.*, (1998) in pea, Arora and Jeena (1999) in chickpea. Yadav and Dahiya (2000) in blackgram found high heritability for this character and it indicates pod bearing peduncles per plant was an important character for selection with restriction and improvement of seed yield.

4.1.8 Pods per plant

The highest and the lowest number of pods per plant were produced by the G12 (97.00) and G18 (34.00) respectively and mean of this character was 58.63 (Appendix III). The phenotypic and genotypic variance was high and the difference between the phenotypic variance (349.31) and the genotypic variance (342.10) was not significant. Moderate genotypic coefficient of variation (31.55) and phenotypic coefficient of variation (31.88) were found for this trait with a non-significant difference which indicated that there was little environmental effect on the expression of the character. This character showed high heritability (97.94) along with high genetic advance (37.71) and high genetic advance in percent of mean (64.31) might indicate that the heritability was due to additive gene effect and phenotypic selection might be effective (Table 4).

4.1.9 Seeds per pod

The variation among the genotypes for seeds per pod was not significant. The mean of all the genotypes for this character was 12.59, which ranged from 9 to 14. The lowest number of seeds per pod was found (9) in G22 and the highest was found (14) in G1, G3, G4, G5, G6, G7, G9, G10, G21 and G28 (Appendix III). The genotypic variance (1.23) and phenotypic variance (1.96) were low for

this trait. The estimates of genotypic coefficient of variation (8.82) and phenotypic coefficient of variation (11.11) were moderate with little difference. Therefore, it can be concluded that there was an environmental influence for expression of this character. Moderate heritability (62.97) and low genetic advance (1.82) and genetic advance in percent of mean (14.42) were also observed for the trait concerned (Table 4).

4.1.10 100- seed weight

Significant differences among the genotypes were observed due to 100 seed weight. Maximum number of 100 seed weight was found in G11 (5.80) and minimum in G31 (1.20) with a mean value of 2.26 (Appendix III). Little influence of environment upon this trait was reported due to difference between the estimation of GCV (48.55) and PCV (48.95). High heritability (98.37) and high genetic advance in percent of mean (99.18) was found for this trait (Table 4). Thus suggesting phenotypic selection for 100 seed weight would be rewarding. Gupta *et al.,* (1998) in pea and Vivek *et al.,* (1999) observed high heritability coupled with genetic advance as a percentage of mean was for 100-seed weight in chickpea.

4.1.11 Yield per plant

The genotypes varied significantly for seed yield per plant. The highest seed yield per plant was observed in the genotype G11 (37.33). The lowest seed yield per plant was observed in the genotype G22 (10.67) (Appendix III). The phenotypic variance (53.16) differed slightly from genotypic variance (52.68) for this trait. Moderate genotypic (35.32) and phenotypic (35.48) coefficient of variation and high heritability (99.11) along with high genetic advance in percent mean (72.44) were estimated for this character. The PCV was higher than GCV indicating presence of environmental influence (Table 4). Such result suggested selection might be effective. Vivek *et al.,* (1999) in chickpea and Tyagi *et al.,* (2000) in cowpea genotypes observed high heritability coupled with genetic advance as a percentage of mean for seed yield per plant.

4.2 Correlation coefficients analysis

4.2.1 Character association in mungbean

Yield is a complex character and associated with several yield contributing characters. Selection for yield may not be effective unless other yield components influencing it directly or indirectly are taken into consideration. When selection pressure is exercise for improvement of any character highly associated with yield, it simultaneously affects a number of other correlated traits. Hence knowledge regarding association of characters with yield and among themselves provides guideline to the plant breeder for making improvement through selection.

Genotypic and phenotypic correlations between pairs of characters are presented in (Table 5). The genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients in most of the cases indicating the association is largely due to genetic reason. The results are discussed character wise as follows:

4.2.2 Days to 50% Flowering

Days to 50% flowering showed highly significant positive correlation with days to 50% maturity and highly significant negative correlation with the number of seeds per pod at both the genotypic and phenotypic level. It showed non-significant positive correlation with plant height, branches per plant, pod bearing peduncle per plant, 100-seed weight and yield per plant for both genotypic and phenotypic levels. Non-significant negative phenotypic and genotypic correlation was also observed with branch length, pods per plant and pod length (Table 5). Arora and Jeena (1999) found positive association of days to 50% flowering with days to maturity. Tyagi *et al.,* (2000) recorded a negative (-0.129) direct effect days to 50% flowering on seed yield per plant.

Table 5. Phenotypic (r_p) and genotypic (r_g) correlation coefficients among different yield contributing characters of mungbean

Characters	Correlations	D50M	PH	BP	BL	PP	PL	SP	PeP	SW	YP
D50F	r_p	0.551**	0.114	0.021	-0.002	-0.217	-0.320	-0.329**	0.068	0.218	0.179
	r_g	0.459**	0.135	0.029	-0.052	-0.227	-0.339	-0.362**	0.069	0.197	0.215
D50M	r_p		-0.172	0.040	-0.307	0.266	-0.189	-0.061	0.097	0.471**	0.266
	r_g		-0.170	0.043	-0.306	0.269	-0.188	-0.071	0.102	0.464**	0.270
PH	r_p			-0.313	0.606**	0.045	-0.178	-0.401*	0.123	0.096	0.161
	r_g			-0.323	0.618**	0.046	-0.179	-0.404*	0.129	0.099	0.162
BP	r_p				-0.020	0.353*	0.096	0.507**	0.510**	0.151	0.047
	r_g				-0.050	0.361*	0.133	0.604**	0.535**	0.155	0.044
BL	r_p					0.210	0.092	-0.035	0.377*	0.223	0.179
	r_g					0.211	0.100	-0.036	0.388*	0.228	0.179
PP	r_p						0.062	0.272	0.542**	0.662**	0.489**
	r_g						0.062	0.281	0.542**	0.662**	0.490**
PL	r_p							0.310	0.042	0.162	0.151
	r_g							0.316	0.036	0.163	0.151
SP	r_p								0.134	0.137	0.049
	r_g								0.158	0.141	0.051
PeP	r_p									0.362*	0.509**
	r_g									0.363*	0.478**
SW	r_p										0.904**
	r_g										0.905**

** indicates significant at 0.01 probability leveland * indicates significant at 0.05 probability level

D50F= Days to 50% flowering, D50M = Days to 50% mature pod, PH = Plant height, BP = Branches per plant, BL = Branch length, PP= Pods per plant, PL = Pod length, SP = Seeds per pod, PeP = Peduncles per plant, SW=100- seed weight, YP= Yield per plant.

4.2.3 Days to 50% maturity

Days to 50% maturity showed positive and highly significant correlation with 100 seed weight at both genotypic and phenotypic level. It showed non-significant positive correlation at both genotypic and phenotypic levels with branches per plant, pods per plant, peduncles per plant and yield per plant. It showed non-significant negative correlation both at genotypic and phenotypic levels with the PH, BL, PL, and SP (Table 5). According to Mahak *et al.,* (2004) days to maturity is a major yield-contributing character in field pea. Kumar *et al.,* (2003) studied on correlation for yield and yield components of pea. The number of days to flowering showed a positive association with number of days to maturity and number of seeds per pod.

4.2.4 Plant height

Plant height showed highly significant positive genotypic and phenotypic correlations with branch length. Positive and non-significant correlation of this trait was found with pods per plant, peduncles per plant and 100 seed weight and yield per plant at both genotypic and phenotypic levels. It showed non-significant negative correlation with branch per plant and pod length at both genotypic and phenotypic levels. It showed significant negative correlations at both phenotypic and genotypic level with seeds per pod (Table 5). Vivek *et al.,* (1999) reported that plant height showed negative correlation with seed yield per plant in chickpea genotypes.

4.2.5 Branches per plant

Branches per plant showed highly significant positive correlation at both the phenotypic and genotypic level with seeds per plant and pod bearing peduncles per plant. This character showed significant positive correlation at both the phenotypic and genotypic levels with pods per plant at 5 % level of significance. It showed non-significant negative correlation with branch length at both genotypic and phenotypic levels. It showed non-significant positive correlation with rest of the characters (Table 5). Kumar *et al.,* (2003) also

found positive correlation of branches per plant at genotypic level. Manoj*et al.,* (2003) in correlation analysis recorded positive correlation of pod yield with number of branches per plant.

4.2.6 Pods per plant

Pods per plant showed highly significant positive correlation with pod bearing peduncles per plant, yield per plant and 100 seed weight both at genotypic and phenotypic levels. It showed non-significant positive correlation with pod length and seeds per pod at both genotypic and phenotypic levels (Table 5). Aroea and Jeena (1999) in *Cicer arietinum* genotypes recorded significant and possitive correlation of with pods per plant. Correlations among the characters indicated that pods per plant are an important character in selection for improved seed yield. Natarajan and Rathinasamy (1999) recorded positive direct effect of pods per plant on yield.

4.2.7 Seeds per pod

Seeds per pod showed positive correlation with peduncles per plant, 100 seed weight and yield per plant both at genotypic and phenotypic levels (Table 5). Yadav (2000) found positive correlation between seed yield and seeds per pod in black gram. Chakraborty and Haque (2000) got the same type of result in lentil. Tiwari *et al.,* (2001) found a significant and positive correlation between seed yield per plant and number of seeds per pod in pea.

4.2.8 Peduncles per plant

Peduncle per plant showed highly significant positive correlation at both genotypic and phenotypic levels with pods per plant and yield per plant. It showed significant positive correlation at both genotypic and phenotypic levels with 100- seed weight (Table 5). Kumar *et al.,* (2003) also found positive correlation of branches per plant at genotypic level. Manoj *et al.,* (2003) in correlation analysis recorded positive correlation of pod yield per plant with number of branches per plant.

4.2.9 100- seed weight

The character 100 seed weight showed highly significant positive correlation with seed yield per plant at both genotypic and phenotypic levels, highly significant positive correlation with 50% maturity, pods per plant at both genotypic and phenotypic levels (Table 5). Vikas *et al*. (1999) recorded positive correlation between seed yield per plant and 100 seed weight.

4.3 Multivariate analysis

4.3.1 Principal Component Analysis

Based on principal component scores (PCA Score 1) and (PCA Score 2) obtained from the principal component analysis, a two-dimensional scatter diagram (Z1-Z2) using principal component score 1 as X-axis and principal component score 2 as Y-axis was constructed, which has been presented in (Figure 2). The positions of the genotypes in the scatter diagram were apparently distributed into five groups, which indicate that considerable diversity exists among the genotypes.

4.3.2 Principal Coordinate Analysis (PCO)

Inter genotypic distances D^2 were 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 genotype 11 and 22 followed by 32 and 27. The lowest distance was observed between genotype 8 and 9. The difference between the highest and the lowest inter genotypic distance indicated the prevalence of variability among the 32 genotypes of mungbean studied.

Intra-cluster distance (Table 9) were calculated from these inter genotypic distances (Singh and Choudhury, 1974). The highest intra-cluster distance was (20.42) observed in cluster III, which was composed of 5 genotypes, followed by cluster IV (18.64) containing 5 genotypes. The intra- cluster

distances in all the five clusters were lower than the inter cluster distances and which indicated that genotypes within the same cluster were closely related and variation was also low.

Table 6. Mean principal components (PC) scores from analysis of variance (ANOVA) of first four PCs of 32 mungbean genotypes

Genotypes	PC1	PC2	PC3	PC4
G1	1.728	0.875	-1.097	1.500
G2	0.079	-1.477	-0.360	0.161
G3	-0.517	-0.689	-1.892	1.439
G4	1.652	1.376	-0.397	1.533
G5	0.597	0.023	-1.406	0.633
G6	-0.128	-2.153	0.527	1.590
G7	-0.724	-1.356	0.932	1.630
G8	-0.479	0.445	-0.666	0.505
G9	-0.466	0.254	-2.093	1.088
G10	2.196	-0.735	-0.687	1.006
G11	4.542	0.486	4.774	-1.160
G12	4.368	1.360	-0.329	0.102
G13	0.639	1.435	-0.626	1.366
G14	-1.373	-0.465	-0.850	-1.604
G15	1.893	-0.604	0.182	-3.050
G16	0.266	-0.712	-1.744	-2.678
G17	-0.010	-0.565	0.761	0.532
G18	-0.863	1.074	0.367	-0.265
G19	-1.185	-0.294	1.962	1.714
G20	-0.868	-1.705	0.008	0.217
G21	2.943	0.262	0.213	-0.616
G22	-3.029	-1.422	2.928	-1.013
G23	-0.175	-0.808	-2.746	-2.299
G24	-1.530	0.161	0.086	-1.819
G25	-1.620	0.948	-0.339	-1.955
G26	-0.298	2.038	-0.075	0.347
G27	-2.581	3.680	1.185	-1.016
G28	-0.653	1.350	-0.846	0.590
G29	-2.229	3.144	0.774	0.203
G30	0.774	-1.975	-0.490	-0.455
G31	-2.166	-0.269	1.007	1.564
G32	-0.780	-3.684	0.935	0.212

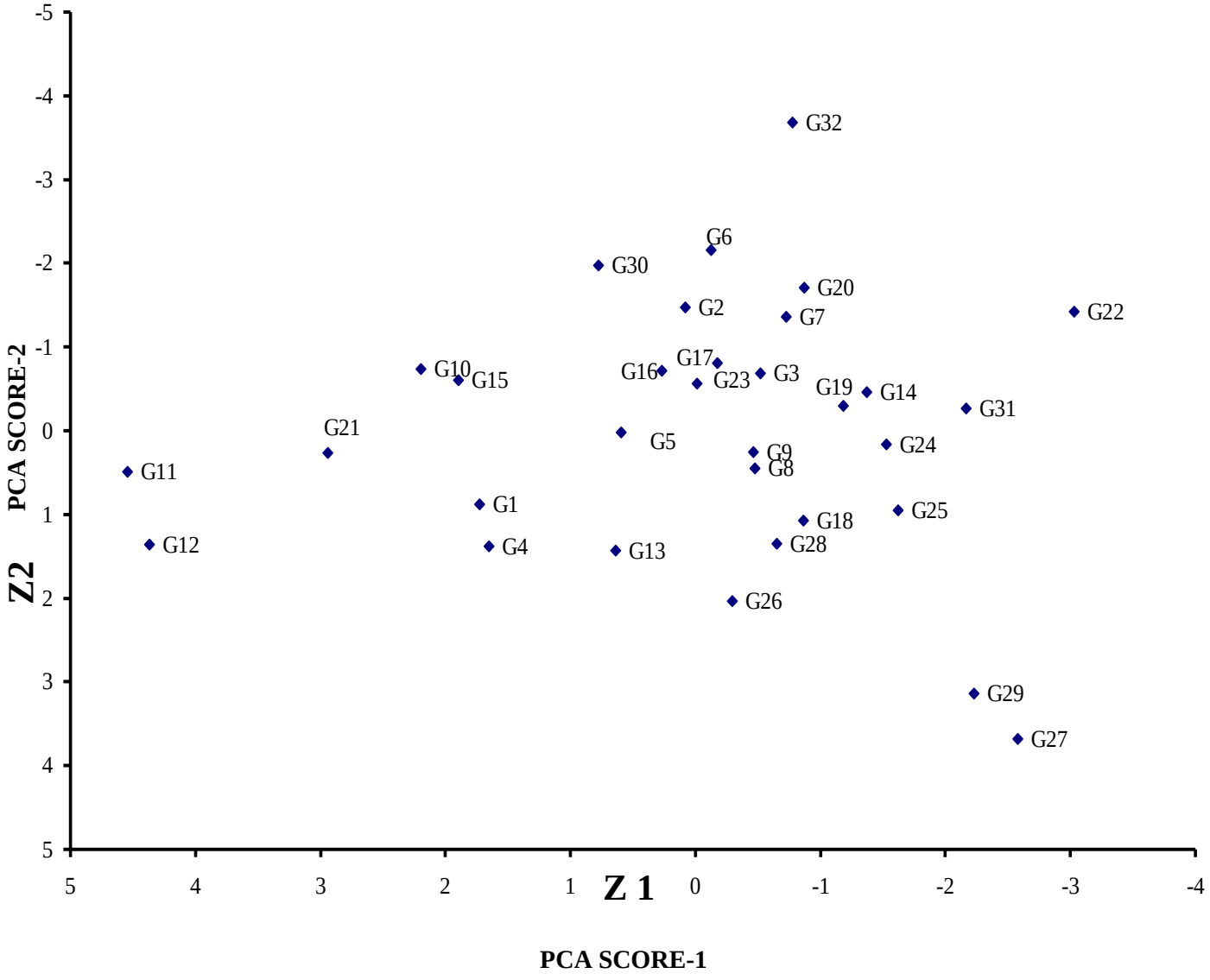

Figure 2. Scatter diagram of 32mungbean genotypes based on their principal component score.

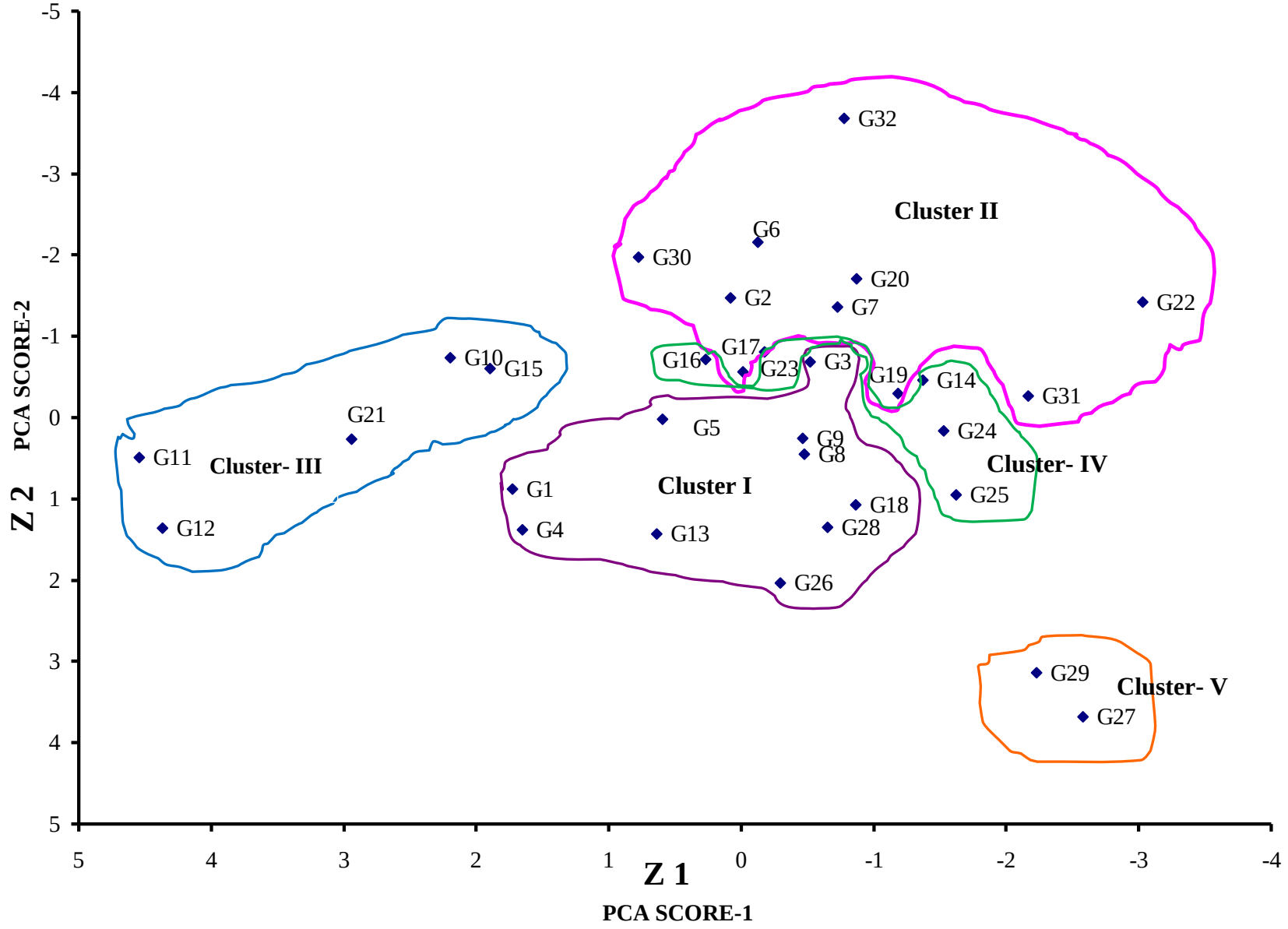

Figure 3. Scatter distribution of 32mungbean genotypes based on their principal component scores superimposed with clusters.

Table 7. Distribution of 32 mungbean genotypes in different clusters with their percentage accounted for divergence

Cluster number	Number of genotypes	Percent (%)	Name of genotypes	Accession number
I	10	31.25	G1, G3, G4, G5, G8, G9, G13, G18, G26 and G28	BD 6875, BD 6878, BD 6881, BD 6882, BD 6886, BD 6887, BD 6892, BD 6902, BD10026
II	10	31.25	G2, G6, G7, G17, G19, G20, G22, G30, G31 and G32	BD 6876 , BD 6884, BD 6885, BD 6897, BD 6905, BD 6906, BD 6909, BD 10030, BD 10031, BD 10032
III	5	15.63	G10, G11, G12, G15, and G21	BD 6888, BD 6890, BD 6891, BD 6894, BD 6908
IV	5	15.63	G14, G16, G23, G24 and G25	BD 6893, BD 6895, BD 10022, BD 10023, BD 10024
V	2	6.25	G27 and G29	BD 10027, BD 10029

4.3.3 Non-hierarchical Clustering

With the application of co-variance matrix for non-hierarchical clustering, 32 mungbean genotypes were grouped into 5 different clusters (Table 7), Cluster I and II had maximum 10 genotypes (G1, G3, G4, G5, G8, G9, G13, G18, G26 and G28) and (G2, G6, G7, G17, G19, G20, G22, G30, G31 and G32) respectively followed by cluster III and IV which had 5 genotypes each (G10, G11, G12, G15 and G21) and (G14, G16, G23, G24 and G25) respectively, Cluster V comprises with two genotypes (G 27 and G 29).

These results confirmed the clustering pattern of the genotype according to the principal component analysis. Composition of different clusters with their corresponding genotypes and collection site included in each cluster are presented in (Table 10). Results of different multivariate techniques were superimposed in (Figure 3). The clustering pattern obtained coincided with the

apparent grouping patterns performed by PCA. It is clear from the above that the results obtained through PCA were supported by non-hierarchical clustering.

4.3.4 Canonical variate analysis

Canonical variate analysis was done to compute the inter-cluster Mahalanobis's D^2 values. The intra and inter-cluster distance (D^2) values are presented in Table 9. Results indicated that the highest inter-cluster distance was observed between clusters III and V (42.06) followed by I and III (37.59) and III and IV (36.60). The higher inter-cluster distances between these clusters indicate to obtain wide spectrum of variability in the population. However, the highest inter- cluster distance was observed between clusters III and V indicated the genotypes in these clusters were diversed than those of other clusters. The lowest inter-cluster distance was observed between the clusters I and II (18.05), suggesting a close relationship among the genotypes included within these clusters (Figure 4).

The intra-cluster distance varied from 11.39 to 20.42, maximum for cluster III that was composed of 5 genotypes of diverse origin, while the minimum distance was found in cluster V that was composed of 2 genotypes. Statistical distances represent the index of genetic diversity among the cluster. The inter-cluster distances were larger than the intra-cluster distances which indicated wider genetic diversity among the genotypes of different groups.

4.3.5 Cluster mean value

An attempt was made to characterize the individual genotype in respect of their mean values for different characters with a view to get idea that weather genotypes having similar characteristics could be disseminated.

The mean values for all the 13 characters along with the marking of the highest (H) and the lowest (L) for each of the cluster are presented in Table 8. The data revealed that different clusters exhibited different mean values for almost all the characters.

Table 8. Cluster mean values of 13 characters of 32 genotypes in mungbean

Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
DF	34.40	33.80	33.20	32.40	36.50
D50F	37.00	36.40	36.20	35.80	40.50
DM	52.60	46.50	53.40	52.20	54.50
D50M	61.50	55.50	63.60	63.60	64.00
PH	63.19	73.84	74.79	65.40	78.50
BP	4.50	3.90	4.20	3.40	4.00
BL	49.76	56.48	57.30	45.33	49.05
PP	61.00	53.00	84.60	47.00	39.00
PL	6.91	7.17	6.99	6.49	5.90
SP	13.10	12.60	12.80	11.80	11.50
PeP	25.30	20.30	26.60	15.20	16.00
SW	1.95	1.98	4.28	1.84	1.20
YP	16.87	18.90	34.13	19.40	16.17

DF = Days to first flowering, D50F = Days to 50% flowering, DM = Days to first mature pod, D50M = Days to 50% mature pod, PH = Plant height, BP = Branches per plant, BL = Branch length, PP = Pods per plant, PL = Pod length, SP = Seeds per pod, PeP = Peduncles per plant, SW =100- seed weight, YP = Yield per plant

Cluster I constituted 10 genotypes) produced the highest mean for seeds per pod (13.10), branches per plant (4.50). The lowest mean values were observed for plant height (63.19). (Table 11)

Cluster II produced the highest mean for pod length (7.17). But the lowest mean for Days to first mature pod (46.50) and days to 50% mature pod (55.50). That means the genotypes of this cluster were early maturing genotype.(Table 11)

It was observed that cluster III produced the highest mean for branch length (57.30), pods per plant (84.60), peduncles per plant (26.60), 100- seed weight (4.28) and fruit yield per plant(34.13). Second highest for seeds per pod (12.80) and pod length (6.99).(Table 11)

Cluster IV comprising 5 genotypes (G14, G16, G23, G24 and G25) scored the lowest mean for days to first flowering (32.40), days to 50% flowering (35.80),

branches per plant (3.40), branch length (45.33) and peduncles per plant (15.20). But second highest for seed yield per plant (19.40). (Table 8)

Cluster V produced the highest mean for days to first flowering (36.50), days to 50% flowering (40.50), days to first mature pod (54.50), days to 50% mature pod (64) and plant height (78.5) and the lowest mean for pods per plant, pod length, seeds per pod, peduncle per plant, 100- seed weight (1.20) and yield per plant. That means the genotypes of this cluster were late maturing genotypes with higher plant height.(Table 8)

Days for 50% flowering ranged from 35.80 to 40.50 days among all the five clusters (Table 8). Cluster I had mainly moderately late flowering genotype where as it produced the highest mean values for seeds per pod and branches per plant. Cluster II had early maturing genotypes with the highest pod length. The genotypes belonging to the cluster III possess highest mean values for branch length, pods per plant, peduncles per plant, 100 seed weight and fruit yield per plant. Second highest for seeds per pod and pod length. To develop high yielding varieties along with early maturing type these groups can be used in hybridization program. The genotypes belonging to the cluster IV were early flowering and 50% flowering genotype with second highest in seed yield. The genotypes of the cluster V were late maturity type and less seeded types with lowest mean for 100 seed weight.

4.3.6 Cluster Diagram

With the help of D^2 values within and between clusters, an arbitrary cluster diagram (Figure 4) was constructed, which shows the relationship between different genotypes. However, the diagram was not following exact scale. It was apparent from the figure that the genotypes included in cluster I was less diversed from the genotypes of the cluster II and the genotypes belonging to III were far diversed from others and the genotypes in IV and V. Genotypes of cluster I - IV, I -V, II- IV, II - V and IV - V were moderately diverse from each other.

Table 9. Intra and inter cluster distances (D) among 32 mungbean genotypes

Characters	I	II	III	IV	V
I	**16.51**	18.05	37.59	19.15	18.84
II		**16.94**	34.69	19.44	23.45
III			**20.42**	36.60	42.06
IV				**18.64**	18.65
V					**11.39**

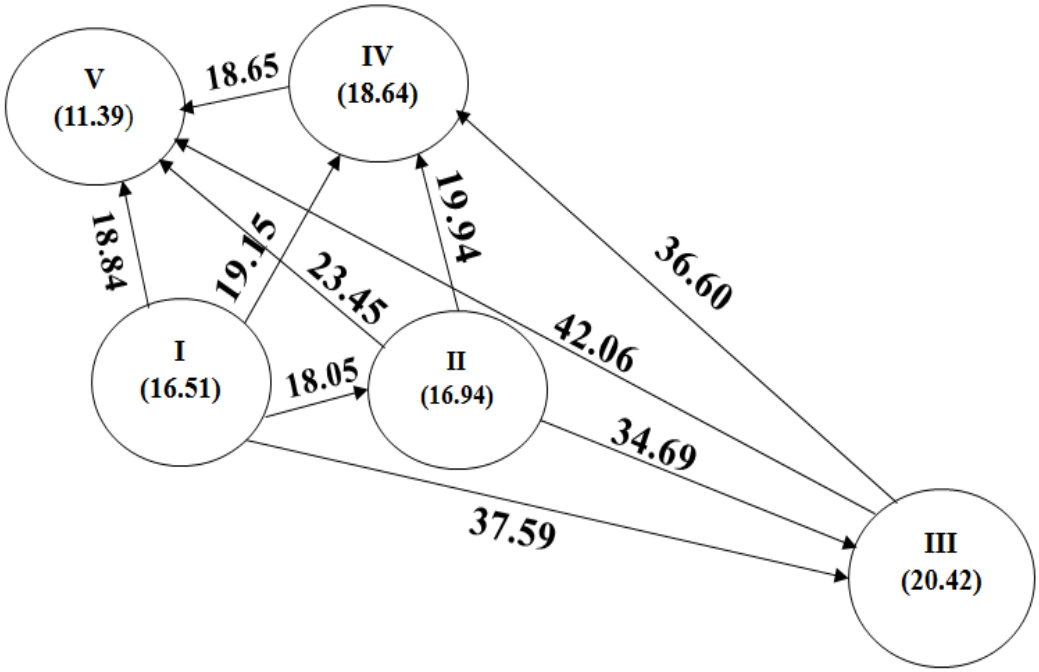

Figure 4. Cluster diagram showing the average intra and inter cluster distances (D = $\sqrt{D^2}$ Values) of 32 mungbean genotypes.

Table 10. Position of 10 prior high yielding genotypes of mungbea considering 11 characters

Genotpes	YP	D50F	D50M	PH	BP	BL	PeP	PP	PL	SP	SW
G13	37.33	M	M	H	M	H	H	H	M	M	H
G14	36.26	H	H	L	H	M	M	H	M	H	M
G17	34.12	M	M	M	L	L	L	H	M	M	M
G12	30.27	M	M	M	H	M	M	M	M	H	L
G18	28.15	M	H	L	L	L	L	L	H	M	H
G19	26.28	L	L	M	M	M	L	L	H	M	L
G23	24.25	H	M	H	M	M	H	H	M	H	L
G28	22.36	H	M	L	H	L	M	M	M	M	L
G7	21.54	L	M	L	H	M	L	M	M	H	L
G16	20.21	L	L	M	M	L	L	L	M	L	L

H= High, M= Medium, L=Low, DF = Days to first flowering, D50F = Days to50% flowering, DM = Days to first mature pod, D50M = Days to 50% mature pod, PH = Plant height, BP = Branches per plant, BL = Branch length, PP= Pods per plant, PL = Pod length, SP = Seeds per pod, PeP = Peduncles per plant, SW=100 seed weight, YP= Yield per plant

4.3.7 Comparison of results based on different multivariate techniques

Results obtained from different multivariate techniques are superimposed in Figure 3 from which it can be concluded that all the techniques gave more or less similar results and one technique supplemented and confirmed the results of the other. The cluster pattern of D^2 analysis through non-hierarchical clustering has taken care simultaneous variation in all the characters studied. However, the distribution of genotypes in different clusters of the D^2 analysis has followed more or less similar trend of the principal component score 1(PC 1) (Z1), principal component score 2 (PC 2) (Z2) of the principal component analysis (PCA). The D^2 and PCA were found to be alternative methods in giving the information regarding the clustering pattern of genotypes. Nevertheless, the canonical variate analysis (CVA) provides the information regarding the contribution of the characters towards divergence of genotypes.

CHAPTER V

SUMMARY AND CONCLUSION

The present experiment was undertaken to study the variability, character association and diversity in 32 genotypes of mungbean based on 13 characters. The salient findings of the present study have been summarized on the basis of the characters studied:

5.1 Univariate analysis

The analysis of variance showed significant differences among the genotypes for all the characters. The minimum duration for days to 50% flowering was recorded 35 days in the genotypes G14, G23, G30and G32 and maximum duration for days to 50% flowering was recorded 41 days in the genotype G 29. The minimum day's required for 50% maturity was recorded 50 days in G32 and maximum 67 days inG12. The genotype G3 produced the shortest (52.60 cm) and genotype G11 produced the tallest (96.13 cm) plant. The maximum branches per plant were found 5 in the genotypes G1, G4, G5, G9, G10, G12 and G13 and minimum branches per plant were found 3 in the genotype G15, G16, G22, G24, G25. Branch length ranged from 36.23 cm to 76.87 cm which was observed in G23 and G11 respectively. The highest number of pod bearing peduncles per plant were observed 41.00 in the G11 and the lowest was 14.00 in G16, G29 and G30. The highest and the lowest number of pods per plant were produced by the G12 (97.00) and G18 (34.00) respectively. The lowest number of seeds per pod was found 9 in G 22 and the highest was 14in G1, G3, G4, G5, G6, G7, G9, G10, G21 and G28. Maximum and minimum of 100 seed weight was found in G11 (5.80) and in G31 (1.20) respectively. The highest seed yield per plant was observed 37.33 in the genotype G11and the lowest seed yield per plant was observed 10.67 in the genotype G22.

The phenotypic variance was higher than genotypic variance in all the characters studied. The phenotypic coefficients of variation were also higher than genotypic coefficients of variation in all the characters studied. Phenotypic coefficients of variation were also close to genotypic coefficients of variation for all the characters. High heritability (>50%) was observed for all characters. High heritability coupled with high genetic advance in percent mean was observed for peduncles per plant, pods per plant, 100 seed weight and yield per plant suggested that effective selection may be done for these characters. Medium heritability coupled with low genetic advance in percent mean was observed in days to 50% flowering, branches per plant.

5.2 Correlation coefficient

Peduncles per plant, seeds per plant showed significant positive correlation with seed yield per plant. Significant positive genotypic and phenotypic correlation was observed by 50 % flowering with days to 50% maturity and negative with seeds per plant. Days to 50% maturity showed significant positive genotypic and phenotypic correlation with 100 seeds weight. Plant height significantly and positively correlated with branch length. Peduncles per plant showed significant positive genotypic and phenotypic correlation with yield. Pods per plant showed significant positive genotypic and phenotypic correlation with 100 seed weight, seed yield per plant and peduncle per plant.

5.3 D^2 Statistics

Genetic diversity of 32 mungbean genotypes based on 13 characters were measured through multivariate analysis. The 40 genotypes fell into five distant clusters. The cluster I and II comprised maximum number (10) of genotypes followed by cluster III and IV (5). The clusters V comprised 2 genotypes. The highest inter-cluster distance (42.06) was observed between the clusters III and cluster IV and highest distant genotypes were G11 and G22 followed by G32 and G27. The lowest inter-cluster distance was observed 18.05between the

clusters I and II, The lowest distance was observed between genotype G8 and G9.The inter-cluster distances were larger than the intra-cluster distances. The intra-cluster distance in the entire 5 clusters was more or less low indicating that the genotypes within the same cluster were less diversed. 50% flowering, peduncles per plant, pods per plant and yield per plant were the important component characters having higher contribution to the genetic divergence.

Based on the results of the study the following conclusions may be drawn:

1. Moderate to high heritability coupled with high genetic advance and high genetic advance in percent mean were observed in peduncles per plant, pods per plant, 100 seed weight, yield per plant. Hence, yield improvement in mungbean would be achieved through selection of these characters.

2. The characters peduncle per plant, pods per plant and 100-seed weight showed positive and significant correlation with seed yield per plant. This result suggested that seed yield per plant can be increased by improving this characters.

3. Days to 50% flowering, branches per plant, branch length, peduncle per plant, pods per plant , seeds per pod and l00 seed weight showed positive direct effect on yield. So yield improvement is associated with these characters.

4. Wide genetic diversity was observed in 32 genotypes of mungbean, which were grouped into five clusters and most diversed genotypes were G11 and G22.

5. The genotypes of cluster III were more diversed from the genotypes of clusters.

6. Plant height, branch length, peduncles per plant, pods per plant and yield per plant were found responsible for maximum diversity. On the other hand, pod length, seeds per pod had least responsibility of both the primary and secondary differentiation of genotypes based on cluster mean.

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