GENETIC DIVERGENCE AND PATH ANALYSIS IN MUNGBEAN (*Vigna radiata*)

S.M. SAIEEDUR RAHMAN

DEPARTMENT OF GENETICS AND PLANT BREEDING

SHER-E-BANGLA AGRICULTURAL UNIVERSITY

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GENETIC DIVERGENCE AND PATH ANALYSIS IN MUNGBEAN (*Vigna radiata*)

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S.M. SAIEEDUR RAHMAN
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Approved By:

Prof. Dr. Md. Sarowar Hossain **Supervisor**	**Prof. Dr. Mohammad Saiful Islam** **Co-Supervisor**

Prof. Dr. Jamilur Rahman
Chairman
Examination Committee

Dr. Md. Sarowar Hossain
Professor
Department of Genetics and Plant Breeding
Sher-e-Bangla Agricultural University
Sher-e-Bangla Nagar, Dhaka-1207
E-mail: sarowar2001@rediffmail.com
Cell No. : +88-01552499169

CERTIFICATE

*This is to certify that thesis entitled, "**GENETIC DIVERGENCE AND PATH ANALYSIS IN MUNGBEAN (Vigna radiata)**" submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE** in **Genetics and Plant Breeding**, embodies the result of a piece of bona fide research work carried out by **S.M. SAIEEDUR RAHMAN**, **Registration No. 10-03902** under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.*

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

Dated: December, 2016

Prof. Dr. Md. Sarowar Hossain
Supervisor


Dedicated
To My
Beloved Parents
&
Teachers

LIST OF ABBREVIATE TERMS

FULL WORD	ABBREVIATION
Agriculture	Agric.
Agricultural	Agril.
Agronomy	Agron
Agro-Ecological Zone	AEZ
Analysis of variance	ANOVA
And others	*et al.*
Bangladesh Agricultural Research Institute	BARI
Bangladesh Bureau of Statistics	BBS
Centimeter	cm
Degrees of Freedom	df
Environmental variance	σ^2e
Etcetera	etc.
Food and Agricultural Organization	FAO
Genetic Advance	GA
Genotypic coefficient of variation	GCV
Genotypic variance	σ^2g
Gram	g
Heritability in broad sense	h^2b
Indian Agricultural Research Institute	IARI
Journal	J.
Kilogram	Kg
Mean sum of square	MS
Murate of Potash	MP
Number	No.
Phenotypic variance	σ^2p
Percentage of Coefficient of Variation	CV%
Percentage	%
Phenotypic coefficient of variation	PCV
Randomized Complete Block Design	RCBD
Sher-e-Bangla Agricultural University	SAU
Square meter	m^2
Triple Super Phosphate	TSP

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Dated: December, 2016 *The Author*

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ABSTRACT

In order to investigate the genetic divergence and path analysis of Mungbean (*Vigna radiata*) a study was carried out at Sher-e-Bangla Agricultural University farm,Bangladesh during March to May 2017. The field experiment was laid out in the main field in Randomized Complete Block Design (RCBD) with three replications. 20 genotypes and 6 varieties were used as the experiment.Data were recorded on ten yield and contributing traits. It was observed that significant variation present among all the genotypes used for most of the traits under studied. Days to 50% flower showed Genotypic coefficient of variation (GCV) was lower than phenotypic coefficient of variation. Genotypes G10 required minimum (70) days to mature on the other hand G2,G7,G13 and G21 were needed to maximum days to maturity. The high heritability, the genetic advance,genetic advance in percent of mean was considerable for seeds per pod indicating apparent variation was present in genotypes. The thousand seed weight of G12 had the highest seed weight and the lowest thousand seed weight value was found from G7.The highest yield of genotypes (31.93g) was obtained in G25 whereas, the lowest yield value in G3. The yield per plant showed highly significant and positive correlation with days to 80% maturity,branches per plant,branch length, pods per plant,seeds per plant, seed weight at both genotypic and phenotypic level indicated that the characters were influenced by same gene and simultaneous improvement would be effective. The genotypes were classified under five clusters, cluster I was associated with four genotypes namely G1, G2,G3 and G21. Cluster II was contained in three genotypes namely G10, G20 and G23. Among the five clusters, cluster III composed of six genotypes. The genotypes were G4, G5, G7, G13,G14 and G15. Cluster IV consists of five genotypes G6,G16,G25 and G26. Cluster V constituted with eight genotypes G8,G9,G11,G12,G17,G18,G19 and G22 .Thus, considering the magnitude of phenotypic traits, genetic distance,contribution of character towards divergence, magnitude of cluster mean and agronomic performance the genotype G6,G16,G24,G25,G26 from cluster IV for maximum number of pods in a plant and yield per plant.G2,G3 for early maturity from cluster I. Therefore considering group distance and other agronomic performances for inter genotypic hybridization among genotypes are suggested for future breeding program.

CHAPTER I

INTRODUCTION

Mungbean (*Vigna radiata* L.) is a self-pollinated Leguminous pulse crop, grown principally for its protein rich edible seeds. World mungbean production is estimated 2.5 to 3.0 million MT, harvested from five million hectares. This production of mungbean would constitute about five percent of the world production of all pulses (Poehlman 1991). The major mungbean producing country is India (around 55% of the world hectaragc and 45% of the world production) (Singh and Yadav 1978). Production of mungbean is increasing more rapidly than the production of other pulse species. It is also cultivated in Burma, Thailand, Iran, Pakistan, Vietnam, China and Indonesia. The mungbean is a short day, warm-season crop, grown mainly in Semi-arid to Sub-humid lowland, tropical and subtropical region in the world (Poehlman 1991). Mungbean is playing an important role in our nutrition. Mungbean contains about 24 percent protein, this being about two-third of the protein content of soybean, twice that of wheat and three fold tint of rice. It also contains l.5 % lipids, 62.6% carbohydrate (Poehlman 1991).

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 is planted in three types of multiple cropping systems: (1) Relay cropping, (2) Intercropping and (3) Mixed cropping. In Bangladesh, mungbean is one of the major pulse crops ranking 5^{th} in acreage, 6^{th} in production, 3^{rd} in protein (%) content and l^{st} in respect of price. Mungbean is generally cultivated during early Rabi. It is grown in rabi after rice (January to March) in Summer (April to June) and after Jute (September to November) (Islam 1978). It is grown about 54.44 thousand ha producing 32,737 thousand MT of grain with a mean yield of 843 kg per ha (BBS 2014-15).

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.

An intensive genetic restructuring program is necessary to evolve high yielding varieties of mungbean suitable for Bangladesh agro-climatie condition (Bhadra and Dey 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).

In self-pollinated crops, ecotype differentiation may be the cause of genetic diversity (Viravan *et al.*, 1973). Another possible cause of diversity could be intense natural and human selection for diverse adaptive and gene complexes (Mian and Bahl 1989). Genetic drift and natural forces under diverse environmental conditions within a country could cause considerable diversity than geographical isolation (Murthy and Arunachalam 1966).

The plant breeders are always interested to know the genetic divergence among the types of varieties available due to reasons that crosses between genetically diverse parents are likely to produce high heterotic effect (Ramanujam *et al*., 1974) and crosses involving distantly related parents within the same species produce wide spectrum of variability. 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).

The selection of the best genotypes depends on a number of characters and selection indicates along with the set of coefficients for weighing traits for the gain in economic value. Path coefficient analysis provides such success (Rahman *et al*., 1982), giving the partition of correlation coefficients into direct and indirect effects.

Since mungbean is considerably less improved than its field demand it is necessary to chose genetically diverse parents to achieve heterotic cross for further transgression and also 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:

1) To determine the nature and magnitude of genetic diversity among the genotypes.
2) To determine the direct and indirect associations among the attributes of grain yield.
3) To find out divers germplasm suitable for the utilization in varietal improvement program.

CHAPTER II
REVIEW OF LITERATURE

Genetic divergence and path coefficient analyses are two initial systematic breeding methods for improvement of crops including mungbean. A few literatures on these works in mungbean are available. The literatures available on genetic divergence and path coefficient analysis are 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 *Ceratotropis* distinguished two species *Vigna radiata*, the mungbean, and *Vigna mungo*, the blackgram. The origin and progenitor of mungbean is *V. sublobatus*, according to Verdcourt (1970). The primary centers of origin of mungbean are the mountainous regions of Southwest-Asia, particularly Indian subcontinent (Blixt, 1970).

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 used for classifying the varieties with respect to flowering and fruiting duration.

2.3 Genetic variability and correlation coefficients

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 Mahalanobis 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 (LGG-47l), IV (LGG-450), V (LGG-421) and VI (LGG-427) 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 programmes.

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 morphoeconomic characters like days to flowering, number of primary branches, plant height, pod length, locules/pod, seeds/pod, pods/plant, 100 seed weight, yield/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/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/plant and pods/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).

Principal Component Analysis (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/ha yield potential, synchronous maturity, early flowering at 38 days, seed weight of 60 g/1000 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 alter sowing (DAS). one irrigation at 35 DAS, 2 irrigation, one each at 20 and 35 DAS, and 3 irrigations, one each at 20, 35 and 50 DAS) to mungbean cultivar MH-85-111 grown in sandy loam soil. Among various characters influencing ultimate grain yield, number of branches/plant, number of pods/plant, number of grains/pod, 1000 grain weight and grains/plant, all had positive and significant association with final grain yield. Path analysis revealed that number of branches/plant, number of pods/plant and grain yield/plan was some at the most cordial characters of grain yield of mungbean.

In another report it was mentioned that utilized generalized distance and canonical analysis among 8 genotypes of mungbean and their 15 hybrids. The study yielded 5 clusters among the genotypes and hybrids. Harvest index was identitied as one of the

large source of divergence and clustering patterns were confirmed to a large extent by canonical analysis (Natarajan and Palanisamy, 1990)

Shanmugam and Rangasamy (1982) 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. Each of other clusters contained types from different regions and it failed to indicate any relationship between geographic and genetic divergence. This was in consonance with other findings in green gram (Gupta and Sing 1970, Malhotra *et al*., 1974, Paramasivam 1979 and Boomikumaran 1980). Further suggestion was that same type of materials from same region or same type of mutants distributed in different clusters indicated the presence of wide genetic variability in materials chosen from the same region and good effect in creating variability which results in genetically diversed mutants. They carried out the canonical variate analysis in which first two canonical roots together accounted for 76.60 of the total variability.

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

Correlation studies in agronomic characters of 70 mungbean strains showed that number of pods/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).

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

Sandhu *et al*. (1979) studied correlationship among yield attributes in mungbean and found negative correlation of yield with days to flowering, positive correlation with plant height and branches/plant, highly positive significant correlation with clusters/plants pod length, positive correlation with days to maturity, high positive significant with seed weight, seeds/pod. The correlation study concluded that pods/plant, cluster/plant, weds/pod, pod length and 100 seed weight were important attributes of grain yield.

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

Digby *et al*. (1989) reported that coordinates obtained front PCA is used as input of Principl Coordinate Analysis (PCO) analysis in calculation of distances among the points. Thus PCA is used for graphical representation of the points while FCC to calculate the minimum distance in a straight line between each pair of points.

In another report it was mentioned that the genotypic and phenotypic correlations and path coefficients among twelve quantitative characters of sixty-three genotypes in mungbean. Genotypic correlations were higher than their phenotypic correlations. Seed yield per plant showed positive association with number of clusters per plant, number of pods per plant, number of seeds per pod, 100-seed weight and harvest index. The correlations were quite consistent in nature and magnitude over environments for most of the characters. The path analysis revealed that seed yield per plant was influenced directly by biological yield and harvest index in most of the environments and plant height, number of clusters per plant, number of pods per plant and seed weight in few environments. However, it was directly and negatively influenced by days to flowering and days to maturity. It was indirectly influenced by plant height, number of pods per plant, days to maturity and biological yield via harvest index (Vikas *et al*., 1999).

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.

In another report it was evaluated that fifty-nine mungbean accessions collected from different regions for 11 yields related traits. The results revealed that seed yield per

plant showed positive association with cluster per plant, pods per plant, biological yield per plant and primary branches per plant and harvest index at both phenotypic and genotypic levels. Path-coefficient analysis indicated that an early maturing dwarf plant with high biological yield and harvest index would be suitable for higher seed yield in mungbean (Saxena *et al*., 2007).

Muhammad-Siddique *et al*. (2006) determined the genetic divergence and trait association in mungbean genotypes (01CMGS11, 01CMG512, 01CMG513, 01CMG514. 01CMG516, OlCMG517 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/ha) was recorded for NM-98. Genotypic variance was highest for grain yield followed by l000-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 (89.06%) and number of days to maturity (88.50%). Grain yield (11765.58) and l000-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 between most of the traits.

In another report it was mentioned that sixty-four mungbean lines collected from different sources for yield and yield contributing traits. Wide range of means was observed for all the traits. High heritability coupled with high genetic gain was observed for l00-seed weight, pods per plant, clusters per plant and plant height. All the genotypes irrespective of their place of collection were grouped into eight clusters

each having 37, 09, 0l, 07, 01 and 01 genotypes, respectively. Cluster II showed maximum genetic distance and cluster I showed maximum closeness to all other clusters. Grain yield showed significant positive correlation with pods per plant, clusters, per plant, pod length, seeds per pod and l00-seed weight, while significant negative association with days to 50% flowering. Results suggested that genotypes from the cluster I, II, IV, VI and VI may yield better re-combinations. The l00-seed weight contributed most towards genetic divergence. All the genotypes having bolder seed size grouped in cluster II (Vijay Prakash, 2006).

Asifa-Nazir *et al*. (2005) determined the direct and indirect effects of different genetic parameters in different mungbean lines/cultivars. Twenty mungbean lines/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 l7.01). 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), l00-seed weight (0.48) and seeds per pod (0.77) also had significant phenotypic correlation with seed yield. Plant height (0.l2), 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, l00-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).

Vijaylaxmi and Bhattacharya (2006) evaluated twenty-five mungbean genotypes for the relative efficacy of different phenological days and yield attributing traits for yield determination in mungbean genotypes. Through estimates of correlations, partitioning of correlations into direct and indirect effects through path analysis and regression it was concluded that mungbean seed yield is positively affected by total dry matter yield, per day dry matter production as well as per day dry matter partitioning and negatively by dry matter allocation to pod wall. Amongst traits, maximum and minimum per cent associations were recorded for dry matter partitioning per day of seed filling and 100 seed weight, respectively. The multiple correlations of the traits for mungbean seed yield was estimated 0.988.

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 (Upendra 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 green gram. 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.

In a field experiment conducted by Saxena *et al*. (2002), 59 cultivars of green gram 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 intercluster 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 intercluster distances between them are likely to be more rewarding.

An experiment with fifty genotypes of mungbean conducted by Haritha and Shakar (2002) to study the association and path coefficients of different quantitative characters with grain yield. Highly significant positive correlation of grain yield was observed with harvest index, biological yield/plant, pods/plant and pods/cluster. Path coefficient analysis revealed that clusters/plant exhibited maximum direct effect

followed by pods/cluster and biological yield/plant on grain yield. Hence selection based on these characters would bring an improvement in grain yield in mungbean.

Thirteen genotypes of green gram were studied for seven characters by Venkateswarlu (2001) 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, l00-seed weight and seeds per pod exhibited high indirect effect on seed yield via pods per plant.

Loganatham *et al*. (2001) studied the Genetic diversity using multivariate analysis of 10 quantitative characters (days to first flowering, plant height, number of branches/plant, number of clusters/plant, number of pods/cluster, number of seeds/pod, pod length, 100seed weight and seed yield/plant) among 42 F_3 and eight varietal genotypes of (*Vigna radiata*). 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 programme to generate wide range of transgressive segregants in population to develop high yielding green gram varieties with superior yield component traits.

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 PM 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 pod length, pods, seeds/pod and clusters. Genotypes KMG1, MGG19, WGG47 and PLM292 were recommended for breeding purposes.

In another report it was mentioned that 49 varieties of mungbean (*Vigna radiata*). Seed yield/plant had highly significant and positive correlation with seeds/plant and pods/plant. Path coefficient analysis revealed that seeds/plant and 100 seed weight had the largest positive direct effect on mungbean yield (Sabaghpour *et al*., 1998).

2.4 Path Analysis

Lokesh *et al.* (2003) studied path coefficient analysis for different morphological and quality traits, contributing to grain yield in 79 genotypes including rice bean cv. RBL-6 and mungbean cultivar. High direct and positive effects were recorded for clusters per plant, days to flowering, pods per cluster, 1000-grain weight, pod length, calcium content, starch content, sodium content and phosphorus content on seed yield per plant in that order. The indirect effect of various characters expresses via other characters (mainly clusters per pod and pods per cluster).

In another report it was mentioned that correlation and path analyses for yield and yield components of 19 diverse genotypes of mungbean (*V. radiata*). The genotypic correlation was dominant over 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. All the traits except plant height and number of productive branches per plant had higher magnitude of indirect effects than the direct effects on seed yield per plant. The number of productive branches per plant had a direct significant contribution to seed yield per plant. Thus, it is suggested that greater emphasis should be given to the number of productive branches per plant during selection for the genetic enhancement of the seed yield of mungbean (Anil and Lokendra, 2006).

Mittal *et al.,* (2007) evaluated Correlation and path coefficient analyses of seed yield and its components in 38 diverse lines of mungbean. Seed yield per plant was positively correlated with pods per plant and 100-seed weight but it was negatively correlated with days to flowering, days to maturity and plant height. Path analysis revealed that pods per plant had the maximum positive direct effect on seed yield, followed by 100-seed weight. It is concluded that seed yield in mungbean may be improved by selection for early flowering/maturity, short genotypes with more number of pods having bold seeds.

In another report it was mentioned that genetic variability, correlation and path coefficients for different characters in 60 mungbean genotypes. High estimates of genetic and phenotypic coefficients of variation, heritability and genetic advance were recorded for seed yield per plant, biological yield per plant, number of clusters per plant, and number of pods per plant. The estimates of genotypic correlation revealed

that seed yield had a positive and highly significant association with number of pods per plant, biological yield per plant, and harvest index. Path coefficient analysis indicated that the number of pods per plant, biological yield, and harvest index had maximum direct contribution on seed yield (Rao *et al*., 2006).

Praveen Singh *et al*. (2005) estimated correlation and path coefficients for 9 traits in 9 *Vigna* genotypes (*V. unguiculata* cultivars RC-l9, RC-101 and *Pusa Phalguni*; *V. aconilifolia* cultivars RMO-225 and RMO-257; and *Vigna radiata* cultivars ML-5, Sunaina, Pant M-2 and Pant M-4) inoculated with 5 Rhizobium strains in Ranchi, Jharkhand, India. Correlation analysis showed that grain yield had highly significant and positive correlation with total N content, leghaemoglobin content, nodule fresh weight, 100-seed weight and number of pods per plant. Correlation between grain yield and chlorophyll content was positive but not significant. Path analysis showed that 100-seed weight had the highest direct effect on grain yield. Its indirect effects on grain yield via nodule fresh weight per plant, total N content and number of pods per plant were also positive.

In another report it was mentioned that correlation and path coefficient analyses of 10 characters (days to 50% flowering. days to maturity, plant height, number of branches/pant, number of pods/plant, number of clusters/plant, 1000-seed weight, dry matter yield, grain yield and harvest index) in mungbean (green gram) genotypes. All characters, except days to maturity, plant height and number of branches/plant, had positive direct effects on grain yield in the M1 generation of mungbean. Number of clusters (4.329) showed the highest effect on grain yield, followed by days to 50% flowering and number of pods with the direct path values of 3.755 and 3.445, respectively. The maximum negative effect (-3.444) was observed for number of

branches per plant which also had negative genotypic correlation with grain yield (Obaidullah *et al*., 2006).

Ali and Shaikh (1986) conducted an experiment with 30 local and exotic mungbean varieties and performed the path coefficient analysis with nine characters. They found that seed size had the highest direct contribution to seed yield/plant followed by number of pods/plant, number of seeds/pod and plant height. The direct contribution of days to maturity, number of clusters/plant to yield was negligible whereas pod length, number of primary branches/plant and days to 50% flowering showed negative direct effect. The indirect effect of plant height, number of primary branches/plant and pod length through seed size were appreciable. It was also revealed that the indirect effect of plant height, number of primary branches/plant and number of fruit clusters/plant and number of seeds through number of pods/plant were considerably high.

An experiment with fifty genotypes of mungbean was conducted by Haritha and Sekhar (2002) to study the association and path coefficients of different quantitative characters with grain yield. Highly significant positive correlation of grain yield was observed with harvest index, bio logical yield/plant, pods/plant and pods/cluster. Path coefficient analysis revealed that clusters/plant exhibited maximum direct effect followed by pods/cluster and biological yield/plant on grain yield. Hence selection based on these characters would bring an improvement in grain yield in mungbean.

Correlation and path analysis were carried out by Malik *et al*. (1983) using data on seed yield per plant and 12 related characters in 40 elite genotypes in mungbean. It was observed that yield was positively and significantly correlated with plant height, primary branches/plant, pods/plant, clusters/plant and biological yield. Path analysis

revealed that days to pod initiation, plant height and biological yield had the highest direct positive effect on seed yield per plant. The direct effects of days to flower initiation, days to maturity, clusters/plant, pod length and seeds/pod on seed yield were high and negative.

Path coefficient showed that number of pods/plant had the highest direct effect on grain yield followed by 100 grain weight; plant height had high negative indirect effect via number of pods/plant. Number of branches/plant had negative direct effect. Number of pods/plant and days to flowering had positive indirect effect (Gowda and Pandya, 1975).

A total of 40 green gram cultivars were studied by Kamleshwar Kumar *et al.* (2003) to determine genetic variability, correlation and path coefficient 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. Comparative data on the variance, coefficient of variation, and heritability of the yield and yield components are tabulated.

Variability and character association were studied by Wanjari (1988) in 55 germplasm of black gram. Path analysis showed that days to maturity had higher direct effects on grain yield than other characters. Days to flowering had a negative direct effects and also negative association with yield. They suggested that early flowering and late maturity are the desirable traits to get higher yield, clusters/plant & pod length are also important components to give considerably high direct effects accompanied by positive association with grain yield. The negative direct effect of pods/plant were counterbalanced with the indirect positive effects via cluster per plant, days to

flowering, pod length and 100 seed weight. Thus pods/plant produced in many clusters rather than in a few would be desirable.

Rajan *et al.* (2001) studied the correlation and path coefficients in 7 parents and F_2 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, clusters per plant, pods per plant, seeds per pod, hundred grain weight and harvest index. Number of pods per plant, clusters per plant and harvest index showed high positive correlation on grain yield and also with each other. Path analysis revealed that pods per plant had the highest positive direct effect on grain yield, followed by hundred grain weight on grain yield. The study revealed that genetic improvement of grain yield is possible by selecting characters having high positive correlation and positive direct effect.

In another report it was mentioned that Niazi *et al.* (1999) estimated genotypic correlation and path-coefficients for 8 agronomic characters in 15 elite genotypes of mungbean. All the correlation coefficients were significant, whilst number of filled pods per plant, plant height, number of columns and seeds 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.

2.5 Genetic diversity analysis

Nath *et al*. (2005) estimated the genetic divergence among 19 genotypes of *Vigna* comprising wild and cultivated species following Mahalanobis' 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. mango*, *V. aconitifolia*, *V. trilobula* and *V. sinensis* [*V. unguiculata*] formed a single cluster. Genotypes of *V. umbellara*, *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 programmes 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 gouped into eight clusters. Clusters I and VIII were the largest with eight mutants each and cluster VII was the smallest with two mutants. Except for cluster at mutants, all other mutants were derived from two or three cultivar. 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 1 alone accommodated 30 genotypes. Intercluster 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. lntracluster D^2 value was maximum in cluster III, which has 3 cultivars. The trait seed weight (l00-seed weight) had the highest contribution to genetic divergence.

In another report it was mentioned that 40 genotypes of green gram 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 was 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 to the genetic divergence in the present material (Venkatakrishna *et al.*, 2000).

Some 84 genotypes of mungbean from different geographical regions were grouped into 17 clusters using D^2 analysis. Pods/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 (Roshan 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; KY1945 was recommended for crossing with V3726; brooding efforts should be based on crosses between heterotic groups as determined by cluster analysis; graphics analysis of canonical variates was in agreement with cluster analysis.

In another report it was mentioned that under constraints and statistical properties of resulting groups imposed by hierarchical nature of the grouping into various numbers of classes was not at all clear. So, non heirarchical classification was suggested by them as an alternate approach to optimize some suitability criterion directly from the data matrix. They also suggested that when all the dimensions can be used, squared distance between means as Mahalanobis's D^2 statistics can be computed by PCO. They recommended using canonical variate analysis for discriminatory purposes (Payne and Lane, 1989).

A study on genetic divergence was carried out by Singh and Pathak (1987) using Mahalanobis 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/plant and seed yield/plant. These eight genotypes with four others were recommended for hybridization.

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 time recorded maximum and yield components as pods/plant and seeds/pod had limited influence in genetic divergence was found by Shanmugam and Rangasamy (1982) in forty genotypes in greengram clustered in 16 groups. Yield/plant followed by clusters/plant and pods/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, pod, plant height, and pod length had maximum contribution. Days to flowering, seed size and primary branches/plant was main componems to genetic diversity in mungbean (Malhotra *et al.*, 1974). Days to flowering 100 seed weight was found to be maximum contributive towards genetic divergence in mungbean (Singh and Singh 2003). Pods/plant, seeds/pod and 100 seed weight contributed towards genetic diversity in mungbean (Malik *et al.*, 1985). Ghaderi *et al.* (1979) found pods/plant, seeds/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).

CHAPTER III
MATERIALS AND METHODS

3.1 Experimental Site

The experiment was conducted at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka-1207, during March to May 2017. The location of the site was situated at 23°77’ N latitude and 90°33’ E longitude with an elevation of 8.6 meter from the sea level (Appendix I)

3.2 Climate and Soil

The experimental site was situated in the sub-tropical zone. The soil of the experimental site lies in Agro-ecological region of "Madhupur Tract" (AEZ No. 28). Its top soil was clay loam in texture and olive gray with common fine to medium distinct dark yellowish brown mottles. The pH was 4.47 to 5.63 and organic carbon content was 0.82%. The record of air temperature, humidity and rainfall during the period of experiment were noted from mini weather center of Sher-e-Bangla Agricultural University(Appendix II and III)

3.3 Materials

A total number of 26 genotypes were used in the experiment. The seeds of the genotypes were provided by the Department of Genetics and Plant Breedinng, Sher-e-Bangla Agricultural University. Name of 26 mungbean genotypes are presented in Table 3.1.

Table 3.1 List of 26 mungbean genotypes used in the present study

SL. NO.	GENOTYPES	DESIGNATION
1	G1	BD-6875
2	G2	BD-6876
3	G3	BD-6878
4	G4	BD-6881
5	G5	BD-6882
6	G6	BD-6884
7	G7	BD-6885
8	G8	BD-6886
9	G9	BD-6887
10	G10	BD-6888
11	G11	BD-6890
12	G12	BD-6891
13	G13	BD-6892
14	G14	BD-6893
15	G15	BD-6894
16	G16	BD-6895
17	G17	BD-6897
18	G18	BD-6899
19	G19	BD-6902
20	G20	BD-6905
21	G21	BARI Mung-1
22	G22	BARI Mung-2
23	G23	BARI Mung-3
24	G24	BARI Mung-4
25	G25	BARI Mung-5
26	G26	BARI Mung-6

Source: Department of Genetics and Plant Breeding

3.4 Design and Layout

The experiment was conducted using the Randomized Complete Block Design (RCBD) with 3 replications. The unit plot size was 2.50m X 2.00m with row to row distance 50 cm and plant to plant distance 25cm. Each block consisted of 4 plots, each block consisted of 10 plots and plot to plot distance was 0.5 meter.

3.5 Manure and Fertilizer Application

The unit plots were fertilized with cowdung, urea, TSP and MP @ 10t, 50kg, 85 kg, 35 kg per ha, respectively. The entire cow dung, TSP, MP and half of the urea were 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.

3.6 Seeds Sowing

Seeds of 26 genotypes in three replication in 78 accession lines were sown on 19 March, 2017. The seedlings were emerged five days after seed sowing.

3.7 Data Recorded

Data on germination, flowering and maturity was recorded on whole plant basis. But other following characters were noted on individual plant basis from five randomly selected competitive plants.

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

Days to 80% maturity (D80M): Determined as the days from sowing to 80% mature pod when the pod color change green to black .

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

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

Branch length (BL): length (cm) was measured of longest branch.

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

Pods per plant (PP): Mean number of pods from five randomly selected plants were counted.

Seeds per pod (SPP): Mean number of seeds from ten randomly selected pods were counted.

100 seed weight (SW): One hundred seed weight (g) was taken randomly from the bulk sample of each genotype and adjusted to the l2% moisture content.

Yield per plant (YP): Total weight (g) of seeds per plant (at mature stage) were measured after pod shelling. Plate 1 showing field view of different growth stage of Mungbean plant.

Plate 1. Field view and different growth stage of mungbean plant

3.8Data Analysis

3.8.1 Univariate analysis

The collected data were statistically analyzed. The mean, maximum, minimum and standard deviation (σ_x) 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). The EMS was considered as error variance (σ^2_e). Genotypic variances (σ^2_g) were derived by subtracting EMS from the genotypic MS and dividing by the number of replication as shown below:

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

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:

$\sigma^2_p = \sigma^2_g + \sigma^2_e$

3.8.2 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 coefficient of variation (GCV) $= \frac{\sigma g \times 100}{\bar{X}}$

Where,

σ_g =Genotyplc standard deviation

$\bar{X}$ = Population mean

Similarly,

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

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

Where,

σ_p =Phenotypic standard deviation

$\bar{X}$ =population mean

3.8.3 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).

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

h^2_b =Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_g =Phenotypic variance

3.8.4 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. σ_p

$= K. \frac{\sigma^2_g}{\sigma^2_p} . \sigma_p$

Where,

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

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

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

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

3.8.5 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 were used to compute genotypic and phenotypic correlation between the pairs of the characters as follows:

$$\text{Genotypic correlation} = \frac{\sigma^2_{gxy}}{\sqrt{(\sigma^2_{gx} \times \sigma^2_{gy})}}$$

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,

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

Where,

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

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

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

3.8.6 Estimation of path coefficients

Correlation coefficient were timber partitioned into components of direct and indirect effects by path coefficient analysis originally developed by Wright (1921) and later described by Dewey and Lu (1959).

3.8.7 Multivariate 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.

3.8.8 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).

3.8.9 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.

3.8.10 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.

3.8.11 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.

3.8.12 Computation of average intra-cluster distance

Computation of average lntra-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 foamed. 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.

3.8.13 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.

3.8.14 Computation of average inter-cluster distances

The procedures of calculating inter-cluster distance between cluster II and I and between cluster III 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

The experiment was conducted to study the variability, estimation of genetic parameter, correlation, path coefficient analysis and genetic diversity of Mungbean. The analysis of variances of the data was done on different yield and yield contributing characters. The results of the present study have been presented and discussed in this chapter under the following heading:

4.1 Univariate Analysis in Mung bean

4.1.1 Days to 50% Flower

The phenotypic and genotypic variance was 3.65 and 0.31 for days to 50% flower. Genotypic coefficient of variation (GCV) was lower (1.17) than phenotypic coefficient of variation (4.02) which indicated that little role of environment on the performance of particular character. Heritability in broad sense was 8.52 with low genetic advance (0.34) and genetic advance in percent of mean was 0.71 was considerable for this trait indicating apparent variation for genotype (Table 4.1).

Thus, selection may not be done by considering this trait because low heritability with low genetic advance will not effective. This result also agrees with the findings of Islam (1978) in case of mungbean.

Table 4.1 Genotypic variance, phenotypic variance, genotypic coefficient of variation, phenotypic coefficient of variation, range and mean of yield and yield contributing characters of mungbean genotypes

Traits	GenMS	Min	Max	Mean	CV%	o^2_g	o^2_e	o^2_P	GCV	ECV	PCV	h^2_b	GA	GA (% mean)
Days to 50% Flower	4.27**	45.00	49.33	47.59	3.84	0.31	3.34	3.65	1.17	3.84	4.02	8.52	0.34	0.71
Days to 80% Maturity	84.05**	70.67	87.67	83.60	10.46	2.53	76.46	78.99	1.90	10.46	10.63	3.21	0.59	0.70
Plant Height	62.97**	46.33	60.00	52.67	14.00	2.88	54.35	57.22	3.22	14.00	14.36	5.03	0.78	1.49
Branch Per plant	5.90**	2.77	8.50	5.36	12.28	1.82	0.43	2.26	25.18	12.28	28.02	80.79	2.50	46.63
Branch length	32.55**	39.67	54.00	48.47	11.77	0.02	32.48	32.51	0.31	11.76	11.76	0.07	0.01	0.02
Peduncle per plant	28.54**	12.67	25.67	19.86	15.46	6.37	9.42	15.79	12.71	15.46	20.01	40.34	3.30	16.63
Pods per plant	647.45**	29.33	84.67	51.71	8.90	208.76	21.17	229.93	27.94	8.90	29.32	90.79	28.36	54.85
seed per pod	5.64**	6.07	11.77	8.26	7.41	1.76	0.37	2.13	16.04	7.41	17.67	82.42	2.48	30.01
100 seed weight	3.39**	3.33	7.67	6.41	12.02	0.93	0.59	1.53	15.08	12.02	19.28	61.15	1.56	24.29
yield\plant	65.77**	12.47	31.93	20.99	7.05	21.19	2.19	23.38	21.93	7.05	23.04	90.63	9.03	43.01

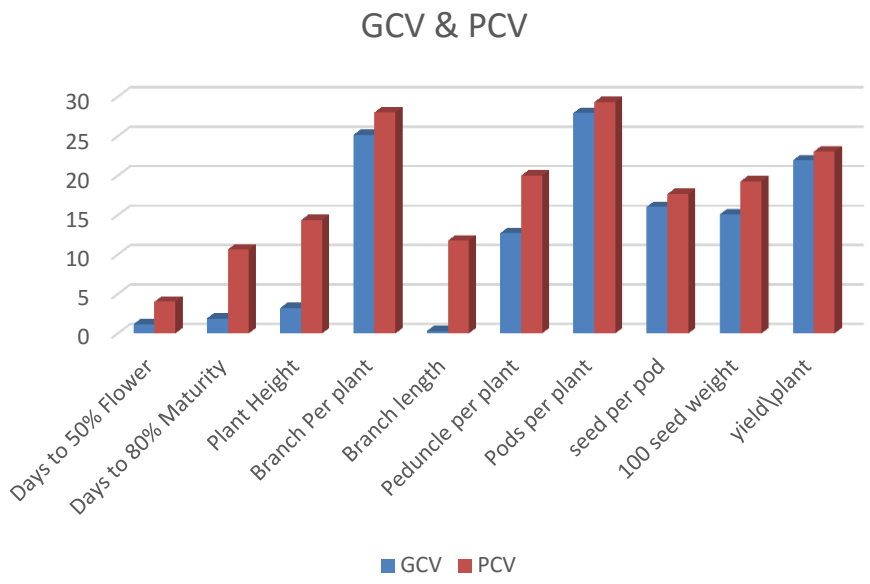

Figure 1. Estimates of genotypic coefficient of variation, phenotypic coefficientof variation for 10 traits of 26 mungbean genotypes

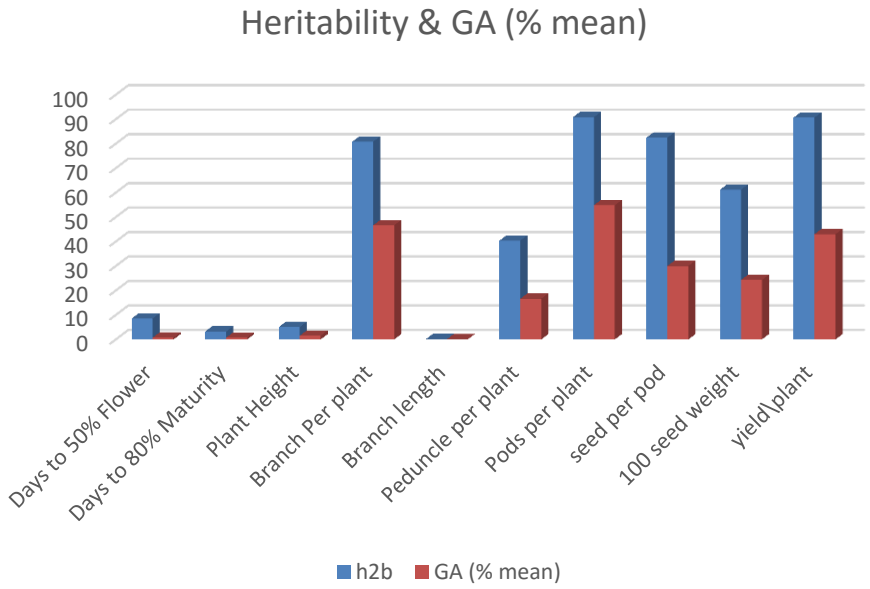

Figure 2. Estimates of heritability and genetic advance for 10 characters of 26 mungbean genotypes

4.1.2Days to 80% maturity

The days to 80% maturity varied significantly among the genotypes studied and ranged from 70 to 87 days with the mean value of 83.67. The highest days to maturity (87 day) were recorded from G2, G7, G13, and G21 which was significantly different from other accessions. The shortest days to 80% maturity (70 day) were recorded from G10 (Appendix). Considerable differences between genotypic (2.53) and phenotypic (78.99) variance as well as genotypic (1.90) and phenotypic (10.46) coefficient of variation indicating considerable environmental effect in the expression of the character of maturity (Table 4.1).

4.1.3 Plant height (cm)

The genotypic and phenotypic variances for plant height were 2.88 and 57.22 respectively. The GCV and PCV were 3.22 and 14.36, respectively (Table 4.1). Difference was observed between genotypic and phenotypic variance as well as genotypic and phenotypic co-efficient of variation indicating environmental influences on this trait. The heritability in broad sense for plant height was low (5.03) with genetic advance (0.78) and genetic advance in percent of mean (1.49) was considerable for this trait indicating little variation was due to genotypes. So selection based on this in trait would be ineffective. This result also has agreement with the findings of Bhadra and Ali (1986).

4.1.4 Branches per plant (no.)

The mean for branches per plant was 5.36. The genotypic variance (1.82) was moderately low than phenotypic variance (2.26) as well as GCV (25.18) was lower than PCV (28.02) indicating environmental influence on the expression of this trait. The heritability (h^2b) for this character was high (80.79) (Table 4.1). The genetic

advance (2.50) and genetic advance in percent of mean (46.63) was considerable for this trait indicating apparent variation was due to genotypes. Malhotra (1974) got the high genetic advance and genetic advance percent of mean was considerable for this trait indicating apparent variation. So, selection based on this trait would be effective. This result also has the agreement with the findings of Harith and Sekhar (2002).

4.1.5 Branch length (cm)

Branch length varied significantly among the 26 genotypes and ranged from 39.67 cm to 54.00 cm with the mean value of 48.47(Table 4.1). Longest branch was recorded from G19 (54.00 cm) while the shortest fruit (39.67) was recorded from G15 which was significantly different from other genotypes. These findings agree with the results of Lokesh *et al* (2003). Differences between genotypic (0.02) and phenotypic (32.51) variance as well as genotypic (0.31%) and phenotypic (11.76) coefficient of variation were observed and indicating environmental effect upon the expression of the character of fruit length (Table 4.1).

4.1.6 Peduncle per plant (no.)

The genotypic variance was (6.37) and phenotypic variance was (15.79) for peduncle per plants. The GCV and PCV were (12.71 and (20.01), respectively. It indicated that there was very low environmental influence on the expression of the traits (Table 4.1). The genetic advance (3.30) and heritability (h^2b) was medium (40.54) and genetic advance in percent of mean (16.63) was considerable for this trait indicating apparent variation was due to genotypes. So selection based on this trait would be effective. This result also has the agreement with the findings of Ghaderi *et al. (*1979).

4.1.7 Pods per plant (no.)

The genotypic variance was 208.76 and phenotypic variance was 229.93.The GCV(27.94) and PCV (29.32) were found for pods per plant. This indicated very much influenced on the expression of this trait. The heritability (h^2b) was very high (90.79) indicating the selection of the character would be effective for further breeding purpose (Table 4.1). Malhotra (1974) observed significant variation among the genotypes of mungbean in respect of number of fruits per plant. The genetic advance and genetic advance in percent of mean was considerable for this trait indicating variation was due to genotypes. So selection based on this trait would be effective. This result also has the agreement with the findings of Asifa-Nazir (2005) in mungbean.

4.1.8 Seed per pod (no.)

The genotypic and phenotypic variances were found 1.76 and 2.13, respectively. The GCV and PCV were found 16.04 and 17.67, respectively. This indicated that this trait was lowering genetically controlled. The heritability was also very high (82.42) (Table 4.1) The genetic advance (2.48), genetic advance in percent of mean (30.01) was considerable for this trait indicating apparent variation was due to genotypes. Gowda and Pandva (1975) also reported wide variability in mungbean.

4.1.9 100 seed weight (g)

100 seed weight varied significantly among the genotypes and ranged from 3.33 g to 7.67 g (Table 4.1). The thousand seed weightof G12 had the highest seed weight (7.67 g) followed by G5, G9, G24 and G25. On the contrary, the lowest thousand seed weight (3.33 g) was recorded from G7. The variation of fruit weight could be due to the genetical, physiological, nutritional or environmental influence. Khan (1988) reported similar results in respect of single fruit weight in mungbean.

4.1.10 Yield per plant

Among the 26 mungbean genotypes studied, yield per plant varied significantly (Table 4.1). The maximum yield of genotypes (31.93g) was obtained in G25, which was statistically different from other accessions. Whereas, the minimum yield of genotypes (12.47) was obtained in G3. Slight differences between genotypic (21.19) and phenotypic (23.38) variance as well as genotypic (21.93) and phenotypic (23.04) coefficient of variation were observed and indicating slightly environmental effect upon the expression of the character of yield of plant (Table 4.1). This finding was supported by Ali and Shaikh (1986).

Plate 2. Seed of 26 genotype with Mungbean pod (G1-G26 chronologically)

		
G16	G17	G18
		
G19	G20	G21
		
G22	G23	G24
		
G25		G26

Plate 2. Cont'd

4.2 Correlation Co-efficient

Yield is a character which depends upon several interdependent quantitative characters. Selection for yield may not be effective unless the directly or indirectly influences of other yield components are taken into consideration. When selection pressure is exercised for improvement of any character highly associated with yield, it simultaneously affects a number of other correlated traits. Hence knowledge regarding association of character with yield and among themselves provides guidelines to the plant breeder for making improvement through selection provide a clear understanding about the contribution in respect of establishing the association by genetic and non genetic factors.

4.2.1 Days to first 50% flowering

The character showed highly significant and negative correlation with days to 80% maturity,plant height, branches per plant, branch length,peduncle per plant, pod per plant and seed per plant phenotypic and genotypic level (Table 4.2 and 4.3). Seed weight was significantly positively correlated at genotypic (0.091) and phenotypic (0.0.078) level. Positiveinsignificant correlated was found with yield (0.024) at genotypic level, negative insignificant correlation was found with yield (-0.020) at phenotypic level.

4.2.2 Days to 80% maturity

Days to 80%maturity showed highly significant and negative correlation with plant heightat genotypic level (-1.000) indicated that if days to 80% maturity increases plant height would be highly decreased (Table 4.2 and 4.3). Highly significant positive correlation were found with branches per plant,branch length,pod per

plant,seed per plant and seed weight at both genotypic and phenotypic level. Ahmed *et al.* (1981) reported the similar result.

Table 4.2 Coefficients of genotypic correlation among different yield components

	D50F	D80M	PH	BPP	BL	PPP	PP	SPP	SW	YP
D50F		-1.000**	-1.000**	-0.214**	-1.000**	-0.316**	-0.255**	-0.136**	0.091*	0.024
D80M			-1.000**	0.840**	1.000**	0.105**	0.832**	0.661**	0.729**	0.913**
PH				-1.000**	-1.000**	-1.000**	1.000**	-1.000**	-1.000**	-1.000**
BPP					0.970**	-0.104**	0.982**	0.925**	0.092*	0.969**
BL						-0.949**	0.221**	0.817**	1.000**	0.779**
PPP							-0.102**	-0.061**	-0.278**	-0.182**
PP								0.984**	0.170**	0.938**
SPP									0.276**	0.941**
SW										0.152**

Table 4.3 Coefficients of phenotypic correlation among different yield components

	D50F	D80M	PH	BPP	BL	PPP	PP	SPP	SW	YP
D50F		-0.272**	-0.112**	-0.103**	-0.007	-0.146**	-0.129**	-0.082*	0.078	-0.020
D80M			0.010	0.240**	0.314**	-0.010	0.290**	0.251**	0.158**	0.309**
PH				-0.088**	0.230**	-0.275**	0.052	-0.073	-0.112**	0.012
BPP					0.152**	-0.035	0.923**	0.864**	0.051	0.917**
BL						-0.053	0.040	0.125**	0.139**	0.149**
PPP							-0.091*	-0.015	-0.209**	-0.116**
PP								0.940**	0.149**	0.915**
SPP									0.237**	0.909**
SW										0.111**

D50F = Days to first 50% flowering, D80M = Days to 80% maturity, PH = Plant height, BPP = Branches per plant, BL = Branch length, PPP = Peduncle per plant, PP = Pod per plant, SPP = Seed per pod, YP = Yield per plot

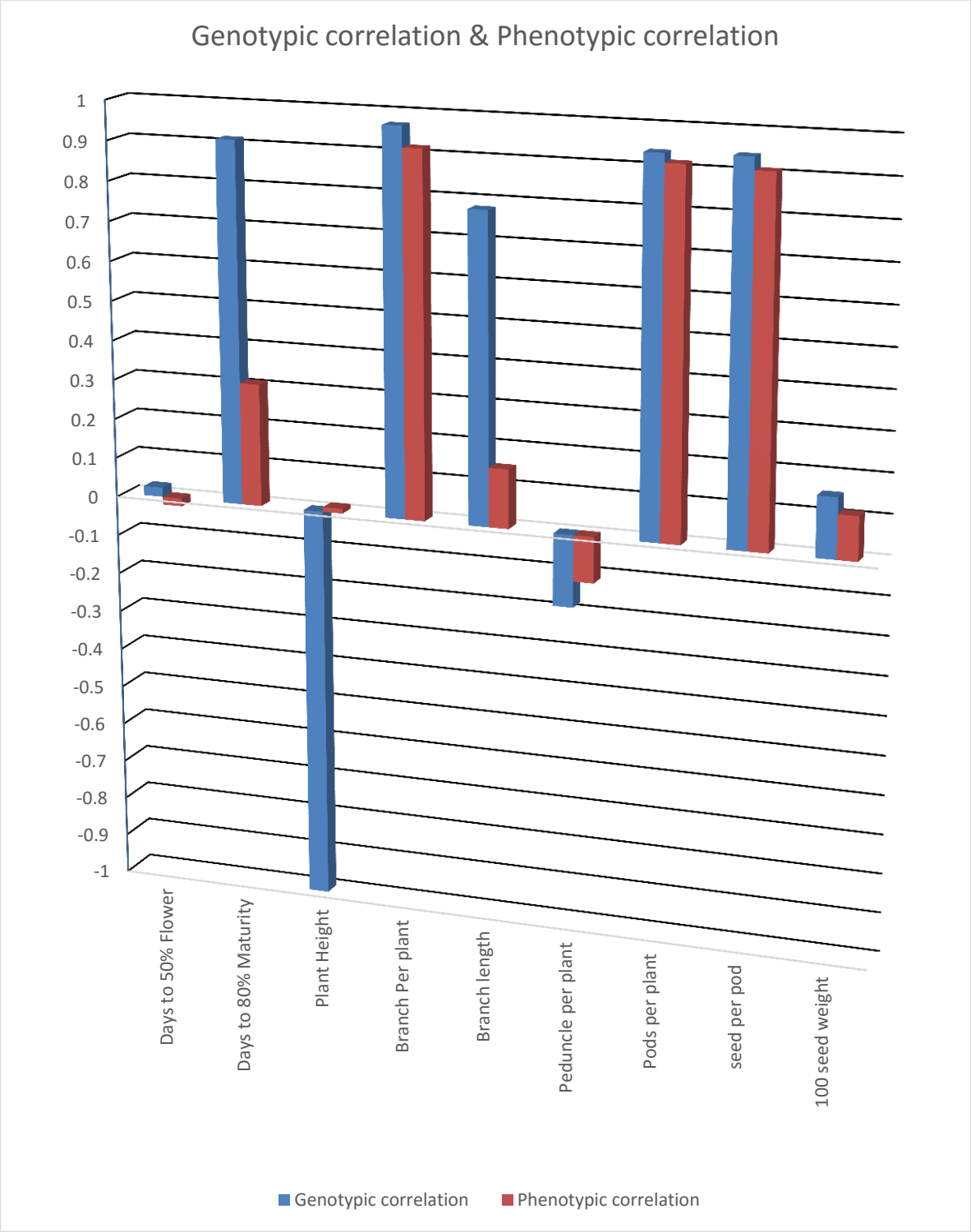

Figure 3.Coefficients of genotypic and phenotypic correlation among different yield components

4.2.3. Plant height (cm)

Negative and highly significant correlation was found with branches per plant,peduncle per plant,seed per plant at both genotypic and phenotypic level indicating if these traits increased yield per plant may be decreased. It also showed highly significant positive correlation with pod per plant at both genotypic (1.000) and phenotypic (0.052) level (Table 4.2 and 4.3). Ali and Shaikh (1986) reported that yield was strongly correlated with fruit breadth in mungbean.Ali and Shaikh*etal.* (1987) also found fruit breadth was positively correlated with fruit weight.

4.2.4. Branches per plant (no.)

Highly positive significant correlation was found with branch length,pod per plant,seed per plant and yield per plant at both genotypic (0.970, 0.982, 0.925, 0.969) and phenotypic (0.152, 0.923,0.846, 0.917) level indicating if these characters may be increased yield will be increase (Table 4.2 and 4.3). It also showed negative and insignificant correlation with peduncle per plant at both genotypic and phenotypic level.

4.2.5. Branch length (cm)

The character showed highly significant and positive correlation with days 80% maturity,plant height,branches per plant at both genotypic (1.000,1.000,.970) and phenotypic (0.314,0.230,0.152) level. Days to 50% flowering was negatively correlated at genotypic (-1.000) and phenotypic (-0.007) level indicating correlation with these traits indicated that number of fruit per plant would be increased if these parameter increased.

4.2.6 Peduncle per plant (no.)

Peduncle per plant showed negative and highly significant correlation with days to 50% flowering (-0.316),plant height (-1.000), branches per plant (-0.104),branch length (-0.949) yield per plant (-0.182) both genotypic and phenotypic level indicating if these traits increased peduncle per plant would be highly decreased (Table 4.2 and 4.3). Gupta and Singh (1970) reported that yield was strongly correlated with fruit length in mungbean. Mian and Bahl (1989) studied *vigna radiate* cultivars and observed that yield per hectare can be improved through selection of fruit length.

4.2.7 Pods per plant

The character showed highly significant and positive correlation with days to 80% maturity (0.832),plant height (1.000),branches per plant (0.982), branch length (0.221)at genotypic level. Number of pod per plant was positively correlated at genotypic and phenotypic level which indicated that number of pod per plant would be increased if these parameter increased.

4.2.8 Seed per pod

Seed per pod showed negative and highly significant correlation with days to 50% flowering (-0.316 and -0.082),plant height (-1.000 and -0.073), peduncle per plant (-0.274 and -0.015) at both genotypic and phenotypic level(Table 4.2and 4.3)indicating if these traits increased seed per podwould be highly decreased. Gupta and Singh (1970) reported that yield was strongly correlated with peduncle per plant in mungbean.

4.2.9 Seed weight (g)

Seed weight showed highly significant positive correlation with days to 50% flowering(0.091 and 0.078),days to 80% maturity (0.729 and 0.158),branches per

plant (0.092 and 0.051),branch length (1.000 and0.149) and seed per plant (0.276 and 0.237)at both genotypic and phenotypic level (Table 4.2 and 4.3) indicated that if these trail were increased,then the seed weight also increased. But it showed negative and significant correlation with plant height (-1.000 and -0.112) and peduncle per plant (-0.274 and -0.209) at both genotypic and phenotypic level which indicated that if these characters increased seed weight would be decreased. Bhadra and Dev *et al.*(1985) reported that yield is strongly correlated with fruit weight in mungbean. Anil sirohi and Lokendra Kumar(2006) also found fruit weight has positive high correlation with yield.

4.2.10Yield per plant

The character showed highly significant and positive correlation with days to 80% maturity (0.913 and 0.309),branches per plant (0.969 and 0.917),branch length (0.779 and 0.149),pod per plant (0.938 and 0.915),seed per plant (0.941 and 0.909),seed weight (0.152 and 0.111) at both genotypic and phenotypic level.Peduncle per plant was highly significantly negatively correlated at genotypic and phenotypic level indicating that if peduncles per plant increase then yield will be decreased.

4.3 Path analysis

Association of character determined by correlation co-efficient may not provide an exactpicture of the relative importance of direct and indirect influence of each of yield components on seed yield per hector. In order to find out a clear picture of the inter-relationship between yield per plant and other yield attributes, direct and indirect effects were worked out using path analysis at phenotypic level which also measured the relative importance of each component. Estimation of direct and indirect phenotypic and genotypic effect of path coefficient analysis of mungbean is presented in Table 4.4.

4.3.1 Days to 50% flowering

Days to 50% flowering showed a positive direct genotypic effect (0.035) on yield (Table 4.4). This character showed highest negative indirect effect through days of first femaleflowering (-0.093). It also showed negative indirect character via peduncle per plant (-0.019).Days to 80% maturity (0.077),branch per plant (0.042),branch length (0.071),pod per plant (0.076),seed weight (0.016) and significant with seed per plant (0.079)showed positive effect for genotypic effect which were contributed to result insignificant positive phenotypic correlation with yield per plant (0.025) showing in Table 4.4 also found similar result in cucumber for their trait.

4.3.2 Days to 80% maturity

The character showed a positive direct phenotypic effect (0.108) on yield (Table 4.4). Days to 80% maturity showed negative indirect effect on plant height (-0.090) and peduncle per plant(-0.017). It showed positive indirect effect to first 50% flowering(0.032),branch per plant (0.046),branch length (0.071),seed weight (0.014)and significant with pod per plant (0.081) ,seed per plant (0.082) which finallyproduced a positive significant genotypic direct correlation with yield (0.901) showing inTable 4.4.

Table 4.4 Path coefficient analysis showing direct and indirect effects of different characters on yield of Mungbean

Characters	Direct effect	Indirect effect									Genotypic correlation with yield
		D50F	D80M	PH	BPP	BL	PPP	PP	SPP	SW	
D50F	0.035		0.032	0.017	-0.015	0.005	0.006	-0.032	-0.020	-0.004	0.025
D80M	0.108	0.077		0.083*	0.107**	0.084*	0.083*	0.141**	0.137**	0.081*	0.901**
PH	-0.062	-0.093*	-0.090*		-0.080*	-0.104**	-0.087*	-0.124**	-0.076	-0.277**	-0.993**
BPP	0.209	0.042	0.046	0.045		0.048	-0.002	0.287**	0.247**	0.045	0.968**
BL	0.121	0.071	0.071	0.077	0.093*		0.068	0.080*	0.089*	0.067	0.737**
PPP	-0.056	-0.019	-0.017	-0.020	-0.002	-0.014		-0.048	-0.003	-0.006	-0.185**
PP	0.183	0.076	0.081*	0.079*	0.185**	0.078	0.080*		0.191**	-0.008	0.946**
SPP	0.325	0.079*	0.082*	0.079*	-0.151**	0.080*	0.075	0.301**		0.064	0.934**
SW	-0.059	0.016	0.014	0.011	0.011	0.016	0.019	0.052	0.072		0.152**

4.3.3 Plant height

Plant height showed negative and insignificant direct phenotypic effect (-0.062) on yield (Table 4.4). The character showed highest positive indirect effect via daysto80%maturity(0.083) followed by branch length (0.071),pod per plant (0.079),seed per plant (0.079),seed weight (0.011).The negative indirect effect via peduncle plant (-0.020) which finally produced a negative and significant genotypic correlation with yield (-0.993) showing in Table 4.4.

4.3.4 Branches per plant

Branch per plant showed positive and insignificant direct phenotypiceffect (0.209) on yield (Table 4.4). The character showed highest positive indirect effect via pod per plant (0.185) followed by days to 80% maturity (0.107),branch length (0.093),seed weight (0.011).It showed negative significant indirect effect via days to 50% flower (-0.015),Plant height (-0.080),peduncle per plant (-0.002) and seed per plant (-0.151) finally produced a positive significant genotypic correlation with yield (0.968) showing in Table 4.4.

4.3.5 Branch length

Branch length showed positive direct phenotypic effect (0.121) on yield. Theshowed highest positive indirect effect via days to 80% maturity (0.084) followed by days to 50% flower (0.005),branches per plant (0.048),pod per plant (0.078),seed per plant(0.080),seed weight (0.016). It also showed the negative indirect effect via plant height (-0.104) and peduncle per plant (-0.014) through which finally produced a direct positive significant genotypic correlation with yield (0.737) showing in Table 4.4.

4.3.6 Peduncle per plant

Peduncle per plant showed positive direct negative phenotypic effect (-0.056) on yield (Table 4.4). The character showed highest positive and significant indirect effect via days to 80% maturity (0.083) followed by days to 50% maturity(0.006),branch length (0.068),pod per plant (0.080) seed per plant (0.301),seed weight (0.052).The character also produced negative indirect effect on yield through plant height (-0.087).The cumulative effect produced a highly significant negative genotypic correlation with yield (-0.185) showing in Table 4.4.

4.3.7 Pod per plant

Pod per plant showed positive direct phenotypic effect (0.183) on yield (Table 4.4). Thecharacter showed highest positive indirect effect via branch per plant (0.287) followed by days to 80% maturity (0.141),branch length (0.080), seed per plant (0.301), seed weight (0.052). It showed the negative indirect effect via plant height (-0.0124),peduncle per plant (-0.048) throughwhich finally produced a negative insignificant genotypic correlation with yield (0.0.946) showing in Table 4.4. Ahmed *et al.* (1981) also found negative direct phenotypic effect of fruit weighton yield in mungbean.

4.3.8 Seed per plant

Seed per plant showed positive direct genotypic effect (0.325) on yield (Table 4.4). Thecharacter showed highest positive direct genotypic effect on branch per plant (0.247)followed by days to maturity (0.137),branch length (0.089),pods per plant (0.191),seed weight (0.072). The character also produced negative indirect genotypic effect on yield through days to 50% flower (0.020), plant height (0.076),peduncle per plant (-0.003), which finally produced a positive phenotypic significant yield (0.934) showing in Table 4.4.

4.3.9 Seed weight

The character showed negative direct phenotypic effect (-0.059) on yield (Table 4.4) and highest positive indirect effect on days to maturity (0.081) followed by branch per plant (0.045),branch length (0.067),seed per plant (0.064). The negative indirect charactervia plant height (-0.277), days to 50% flowering (-0.004),peduncle per plant (-0.006),pod per plant (-0.008) which finally produced a positive significant genotypic correlation with yield (0.152) showing in Table 4.4.

4.4 Multivariate analysis in Mungbean

By using GENSTAT software program genetic divergence in mungbean was analyzed.Genetic diversity analysis involved several steps i.e., estimation of distance between then genotypes, Clusters and analysis of inter-Cluster distance. Therefore, more than onemultivariate technique was required to represent the results more clearly and it was obviousfrom the results of many researchers.

4.4.1 Construction of scatter diagram

In multivariate analysis, Cluster analysis refers to methods used to divide up objects intosimilar groups, or more precisely, groups whose members are all close to one another on various dimensions being measured. Depending on the values of principal component scores 2 and 1 obtained from the principal component analysis, a two dimensional scatter diagram (Z1- Z2) using component score 1 as X-axis and component score 2 as Y-axis was constructed, which has been presented in Figure 3 The position of the genotypes in the scatter diagram was apparently distributed into five groups, which indicated that there existed considerable diversity among the genotypes.

4.4.2 Principal component analysis

From the correlation matrix from genotype scores obtained from first components andsucceeding components with latent roots greater than the unity principal components were computed. Contribution of different morphological characters towards divergence were discussed from the latent the vectors of the first two principal components. The principal component analysis yielded given values of each principal component axes with the first axes totally accounting for the variation among the genotypes, while two of these with Eigen values above unity accounted for 47.248% (Table 4.5). The first three principal axes accounted for 66.83% of the total variation among the 10 characters describing 26 mungbean genotypes. Based on principal component axes I and II, a two dimensional chart (Z1 - Z2) of the cultivars are presented in Figure 4. The scatter diagram revealed that apparently there were mainly five clusters. The genotypes were distantly located from each other.

Table 4.5 Eigen values and percent variation for 10 principal component analysis in 26 mungbean genotypes

Parameters	Eigen values	Percent variation	Cumulative % of Percent variation
Days to 50% Flower	**3.9446**	**39.45**	39.45
Days to 80% Maturity	**1.4262**	**14.26**	53.71
Plant Height	**1.3120**	**13.12**	66.83
Branch Per plant	**1.0528**	**10.53**	77.36
Branch length	**0.8694**	**8.69**	86.05
Peduncle per plant	**0.6502**	**6.50**	92.55
Pods per plant	**0.5535**	**5.54**	98.09
seed per pod	**0.1038**	**1.04**	99.13
100 seed weight	**0.0633**	**0.63**	99.76
yield\plant	**0.0241**	**0.24**	100

Table 4.6 Principal Component(PC) scores of twenty six genotypes of mungbean

Genotype number	PC1	PC2
G1	21.231	-3.116
G2	19.298	-5.838
G3	25.311	10.21
G4	1.148	-0.451
G5	-12.039	1.534
G6	-23.316	1.233
G7	-6.401	-2.986
G8	0.964	-2.302
G9	2.281	-3.906
G10	14.29	11.51
G11	6.167	-3.612
G12	8.846	-4.054
G13	-4.471	-3.795
G14	-2.092	-0.7
G15	1.295	1.581
G16	-21.386	0.956
G17	5.063	-3.353
G18	7.07	-3.102
G19	6.722	-3.95
G20	0.577	11.149
G21	20.962	-6.286
G22	1.57	-2.582
G23	9.495	10.42
G24	-22.029	-0.725
G25	-35.1	1.169
G26	-25.453	0.993

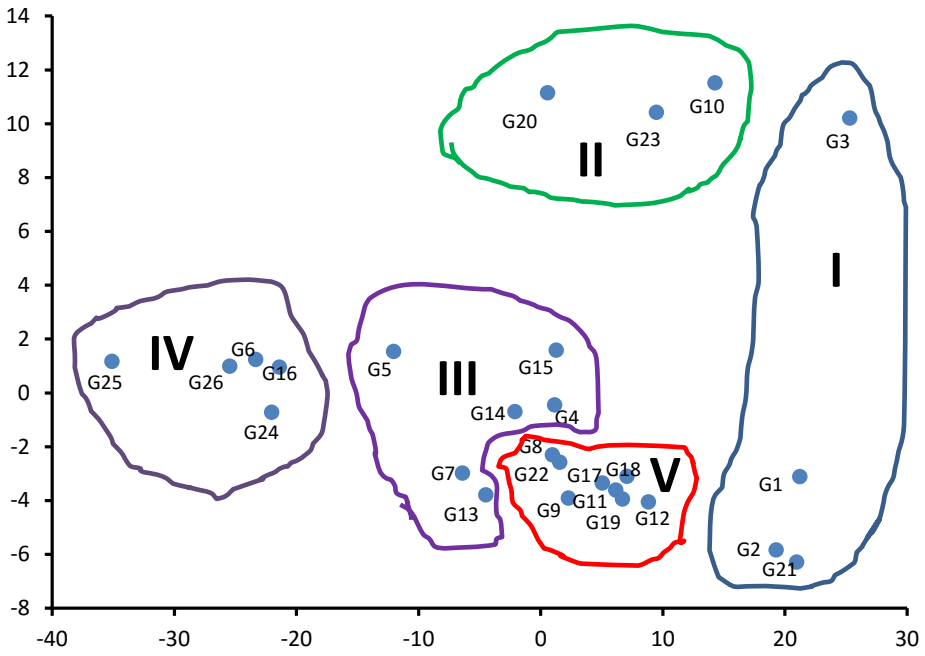

Figure 4. Scatter diagram of 26 mungbean genotypes based on their principal component scores

Researchers were used the comparison of different multivariate techniques in classifying some variety or line of crops. It was marked that three methods gave similar results. But factorial discriminate and Mahalanobis's D^2 distance methods required collecting data plant by plant, while the PCA method required taking data by plots.

Out of five clusters, cluster I was associated with four genotypes namely G1, G2, G3 and G21 (Figure 4). From the clustering mean values (Table 4.9), it was observed that cluster I produced the highest mean for 80% maturity (82.75) followed by days to 50% maturity (47.5), branch length and pod per plant similar findings were mentioned by Khan (1988).The lowest mean value was for the branch per plant cluster I (3.26).Cluster II was associated with three genotypes namely G10, G20 and G23 (Table 4.7).

Table 4.7 Distribution of genotypes in different clusters

Cluster	Number of population	Genotypes
I	4	G1, G2, G3 andG21
II	3	G10, G20 and G23
III	6	G4,G5, G7, G13, G14 and G15
IV	5	G6, G16, G24, G25 and G26
V	8	G8, G9, G11, G12, G17, G18, G19 and G22

Table 4.8 Intra (Bold) and inter cluster distances (D^2) for 26 genotypes of mungbean

1	2	3	4	5	
0.35965	6.514	9.329	15.355	4.722	1
	0.487633	8.646	11.176	2.153	2
		0.426292	7.722	7.332	3
			0.33348	11.384	4
				0.370996	5

These genotypes produced the highest mean fordays to 80% maturity (71.67),plant height (52.89), days to 50% flower (48.55), branch length (46.89),pods per plant (45.22). Similar findings were mentioned by Boomikumaran (1980). The lowest mean value for cluster II (5.05) was the branch length (Table 4.9).

Among the five clusters, cluster III composed of six genotypes. The genotypes were G4, G5, G7, G13,G14 and G15 (Table 4.7). In cluster III the highest mean is for days to 80% maturity (85.78),pods per plant (55.22),plant height (53.72),days to 50% flower (47.28).Similar findings werementioned by Islam (1978) the lowest mean value for cluster III (5.35) was the branch per plant (Table 4.9). Cluster IV consists of five genotypes G6,G16, G25 and G26 (Table 4.7). From the clustering meanvalues it was observed that cluster IV produced the highest mean days to 80% maturity (85.73), plant height (52.8) and for days to 50% flowering (47.6). Thelowest mean value for cluster IV (7.51) was the branch per plant.

Cluster V constituted with eight genotypes G8,G9,G11,G12,G17,G18, G19 and G22 (Figure4). In cluster-V the highest mean for days to 80% maturity (85.54) followed by plant height (52.42), branch length length (51.42)and pods per plant (46.63)flowering. However, the lowest mean value for cluster V (5.19) was the branch per plant (Table 4.9). Lokesh *et al.* (2003) found five clusters in 15 mungbean genotypes where four genotypes were in cluster I, cluster- II was associated with three genotypes, cluster III composed of threegenotypes, cluster IV consists of one genotypes and cluster V constituted with four genotypes

Table 4.9 Cluster mean values of ten different characters of 26 genotypes

Parameters	I	II	III	IV	V
Days to 50% Flower	47.5	48.55	47.28	47.6	47.5
Days to 80% Maturity	82.75	71.67	85.78	85.73	85.54
Plant Height (cm)	51.25	52.89	53.72	52.8	52.42
Branch Per plant (no.)	3.26	5.05	5.35	7.51	5.19
Branch length (cm)	47.34	46.89	46	48.6	51.42
Peduncle per plant (no.)	19.75	21.11	18.94	19.33	20.46
Pods per plant (no.)	31.33	45.22	55.22	75.8	46.63
seed per pod (no.)	6.45	7.82	8.05	10.63	8
100 seed weight (g)	6.25	5.89	5.89	6.8	6.83
yield\plant (g)	13.98	19.08	21.7	28.29	20.12

4.4.3 Principal coordinate analysis

Inter-genotypic distances as obtained by Principal Coordinate analysis for selectivecombination showed the distances among the cluster (Figure 5). By using these intergenotypic distances intra-Cluster genotypic distances were calculated (Table 12) as suggested by Chowdhury *et al.* (1993) that, cluster III which (32.17) composed of five genotypes showed the maximum intra cluster distances and cluster IV and cluster V showed the lowest intra-cluster distance (0.000) which are composed of one genotype. The coordinates obtained from the Principal Component analysis (PCA) were used as input at Principal Coordinate Analysis.PCO was use to calculate distances among the points reported by Digby *et al.* (1989). PCA were used for the graphical representation of the points while PCO was to calculate the minimum distance straight line between each pair of points.

4.4.4 Canonical variate analysis

Mahalanobis's analysis was used to compute the inter-cluster. Figure 5 indicated the intra and inter-cluster distance (D^2) values. The inter-cluster distances were higher than the intra-cluster distances suggesting wider genetic diversity among the genotypes of different groups. Results indicated that the highest inter-cluster distance was observed between cluster I and cluster IV (15.335) followed by between cluster IV to cluster V (11.384), cluster II to cluster I V (11.176), cluster III to cluster IV (7.722), and cluster I to cluster III (9.329) (Figure 5). The lowest intercluster distances was observed between the cluster II to cluster V (2.153), followed by clusterI to cluster IV (4.722) and cluster I to cluster II (6.514) (Figure 5). Inter-cluster distances were larger than the intra-cluster distances suggesting wider genetic diversity among the genotypes of different groups (Figure 4).Islam *et al*. (1999) was carried out an

experiment on mungbean and obtained larger inter-cluster distances than the intra-cluster distances in a multivariate analysis.

Table 4.10 Ten highest and ten lowest inter genotypic distance among the twenty six genotypes of mungbean

10 highest inter genotypic distances			
Sl	Genotypes	Genotypes	Values
1	G25	G3	1.7835
2	G26	G3	1.5901
3	G25	G21	1.5759
4	G25	G2	1.5616
5	G6	G3	1.5265
6	G25	G1	1.5168
7	G24	G3	1.5095
8	G16	G3	1.4525
9	G26	G21	1.3762
10	G24	G21	1.3646
10 lowest inter genotypic distances			
Sl	Genotypes	Genotypes	Values
1	G15	G14	0.1843
2	G26	G6	0.1901
3	G9	G8	0.2033
4	G21	G2	0.2069
5	G14	G8	0.2244
6	G14	G4	0.2276
7	G16	G6	0.2293
8	G20	G8	0.2380
9	G19	G11	0.2480
10	G17	G11	0.2631

Table 4.11 Nearest and farthest clusters of 26 mungbean genotypes

Cluster	Nearest with D^2 values	Farthest with D^2 values
I	V (4.722)	IV (15.355)
II	V (2.153)	IV (11.176)
III	V (7.332)	I (9.329)
IV	III (7.722)	I (15.355)
V	II (2.153)	IV (11.384)

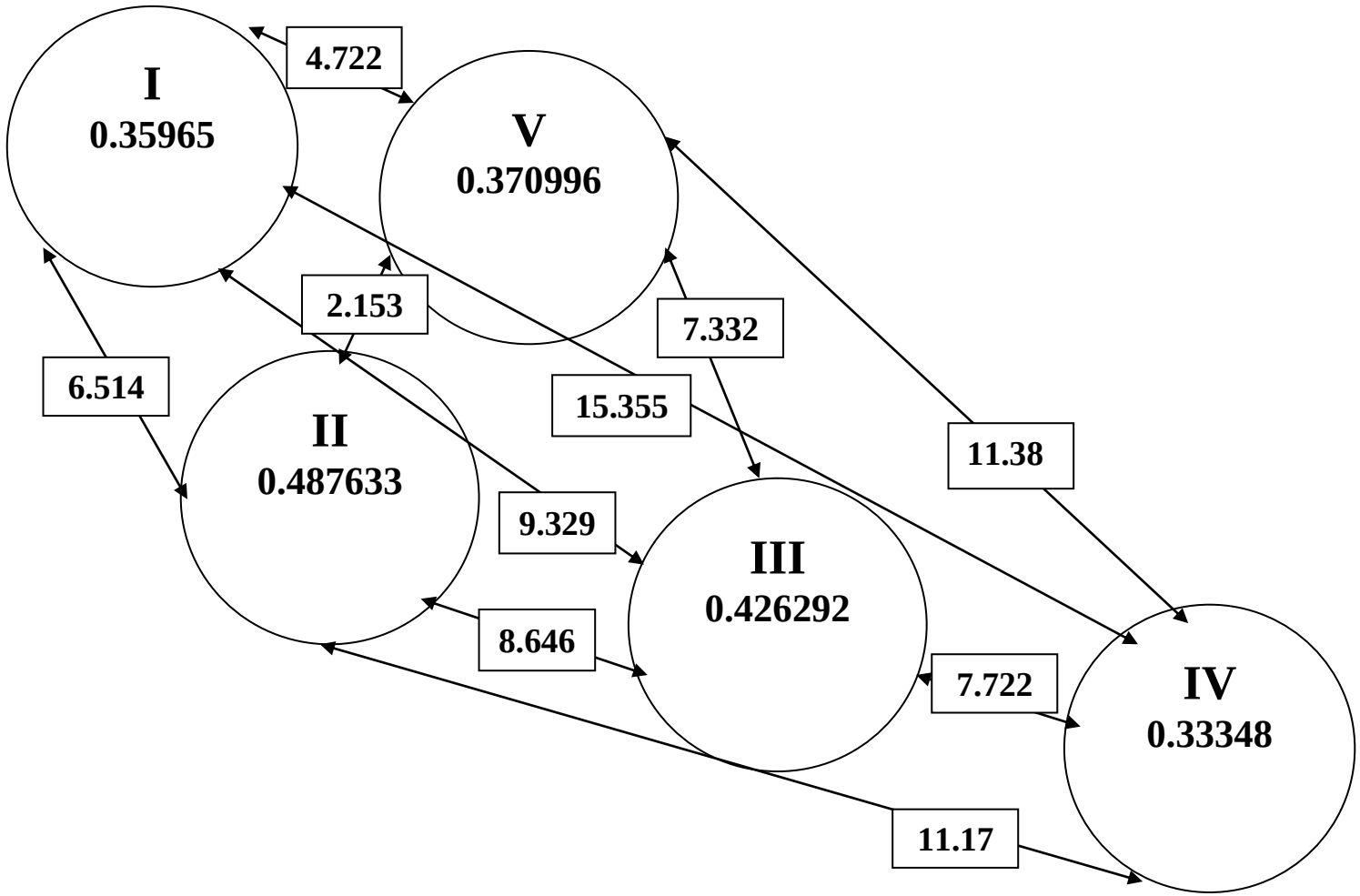

Figure 5. Cluster diagram showing the average intra and inter cluster distancesvalues of 26 mungbean genotypes

However the maximum inter-Cluster distance was observed between cluster I and cluster IV maintaining more distances than other clusters, and the lowest inter -cluster distance found between the cluster II to cluster V, maintaining less distance than other cluster.Genotypes from the cluster I and cluster IV, if involved in hybridization might produce a wide spectrum of this segregating population, as genetic variation was very distinct among groups.Results obtained from different multivariate techniques were superimposed in Figure from which it might be concluded that all the techniques gave more or less similar results and one technique supplemented and confirmed the results of another one. The clustering revealed that genotype originating from the same places did not form a single Cluster because of direct selection pressure. It has been observed that geographic diversity is not always related to genetic diversity. The free cluster of the genotypes suggested dependence on directional selection pressure applied for realizing maximum yield in different region. The nicely evolved homeostatic devices would favor constant associated characters. This would suggest that it was not necessary to choose diverse parents for diverse geographic regions.

4.5 Selection of parents for future hybridization

The most important thing in a breeding programme is the selection of genetically diverse parents. Thus, considering the magnitude of morphological character, genetic distance,contribution of character towards divergence, magnitude of cluster mean and agronomic performance the genotype G6,G16,G24,G25,G26 from cluster IV for maximum number of fruit in a plant and yield per plantG2,G3 for early maturity from cluster I. Therefore considering group distance and other agronomic performances for inter genotypic crosses among genotypes are suggested for future breeding programme.

CHAPTER V
SUMMARY AND CONCLUSION

The experiment was conducted at the Sher-e-Bangla Agricultural University farm,Bangladesh during March 2017 to May 2017 to study on Genetic divergence and Path analysis of Mungbean (*Vigna radiata).* The field experiment was laid out in the main field in Randomized Complete Block Design (RCBD) with three replications. It was observed that significant variation exist among all the genotypes used for most of the characters studied. Days to 50% flower showed Genotypic coefficient of variation (GCV) was lower than phenotypic coefficient of variation which indicated that little role of environment on the expression of the traits. The highest days to maturity (87 day) were recorded from G2, G7, G13, and G21 which was significantly different from other accessions. The shortest days to 80% Maturity (70 day) were recorded from G10. Considerable differences between genotypic and phenotypic variance heritability in broad sense for plant height was low with genetic advance and genetic advance in percent of mean was considerable for this trait indicating little variation was due to genotypes. So selection based on this in trait would be ineffective. Branch length varied significantly among the 26 genotypes and ranged from 39.67 cm to 54.00 cm with the mean value of 48.47.

Longest branch was recorded from G19 while the shortest fruit was recorded from G15 which was significantly different from other genotypes. Peduncle per plants showed that the difference between PCV and GCV was little,it indicated that there was very low environmental influence on the expression of the traits. The GCV(27.94) and PCV (29.32) were found for pods per plant. This indicated very much influenced on the expression of this trait.The high heritability,the genetic

advance,genetic advance in percent of mean was considerable for seeds per pod indicating apparent variation was due to genotypes.100 seed weight varied significantly among the genotypes and ranged from 3.33 g to 7.67 g. The thousand seed weight of G12 had the highest seed weight and the lowest thousand seed weight was recorded from G7.The maximum yield of genotypes (31.93g) was obtained in G25 whereas, the minimum yield of genotypes was obtained in G3.

Days to 50% flower showed significant and negative correlation with days to 80% maturity ,plant height, branch per plant, branch length,peduncle per plant,pod per plant,seed per plant phenotypic and genotypic level. Days to 80% maturity showed significant and negative correlation with plant height at genotypic level indicated that if days to 80% maturity increases plant height would be highly decreased.Negative and highly significant correlation was found with branch per plant,peduncle per plant, seed per plant at both genotypic and phenotypic level indicating if these traits increases yield per plant may decrease.

The branch length showed highly significant and positive correlation with days 80% maturity,plant height,branch per plant at both genotypic and phenotypic level indicated that the traits were governed by same gene and simultaneous improvement would be effective. Peduncle per plant showed negative and highly significant correlation with days to 50% flowering,plant height, branch per plant,branch length, yield per plant and days to 50% flowering,plant height, branch per plant, branch length, yield per plant at both genotypic and phenotypic level.

The yield per plant showed highly significant and positive correlation with days to 805 maturity (0.913 and 0.309),branch per plant (0.969 and 0.917),branch length (0.779 and 0.149),pod per plant (0.938 and 0.915),seed per plant (0.941 and

0.909),seed weight (0.152 and 0.111) at both genotypic and phenotypic level indicated that the traits were governed by same gene and simultaneous improvement would be effective.

Days to 80% maturity showed negative indirect effect on plant height and peduncle per plant. It showed positive indirect effect to first 50% flowering, branch per plant, branch length ,seed weight and significant with pod per plant ,seed per plant which finally produced a positive significant genotypic direct correlation with yield .Plant height showed negative and insignificant direct phenotypic effect on yield. The character showed highest positive indirect effect via days to 80%maturity followed by branch length,pod per plant, seed per plant,seed weight.The negative indirect effect via peduncle plant, which was finally produced a negative and significant genotypic correlation with yield.The character showed negative direct phenotypic effect on yield and highest positive indirect effect on days to maturity followed by branch per plant ,branch length ,seed per plant . The negative indirect character via plant height (-0.277), days to 50% flowering,peduncle per plant,pod per plant which finally produced a positive significant genotypic correlation with yield.

Out of five clusters, cluster I was associated with four genotypes namely G1, G2,G3 and G21. From the clustering mean values,it was observed that cluster I produced the highest mean for 80% maturity followed by days to 50% maturity , branch length and pod per plant .The lowest mean value was for the branch per plant cluster I .Cluster II was associated with three genotypes namely G10, G20 and G23 .These genotypes produced the highest mean for days to 80% maturity ,plant height, days to 50% flower, branch length,pods per plant .The lowest mean value for cluster II was the branch length . Among the five clusters, cluster III composed of six genotypes. The

genotypes were G4, G5, G7, G13, G14 and G15. In cluster III the highest mean is for days to 80% maturity, pods per plant, plant height, days to 50% flower. The lowest mean value for cluster III was the branch per plant, Cluster IV consists of five genotypes G6, G16, G25 and G26. From the clustering mean values it was observed that cluster IV produced the highest mean days to 80% maturity, plant height (52.8) and for days to 50% flowering. The lowest mean value for cluster IV (7.51) was the branch per plant. Cluster V constituted with eight genotypes G8, G9, G11, G12, G17, G18, G19 and G22. In cluster-V the highest mean for days to 80% maturity followed by plant height, branch length and pods per plant flowering. However, the lowest mean value for cluster V was the branch per plant. Thus, considering the magnitude of morphological character, genetic distance, contribution of character towards divergence, magnitude of cluster mean and agronomic performance the genotype G6,G16,G24,G25,G26 from cluster IV for maximum number of fruit in a plant and yield per plant.G2,G3 for early maturity from cluster I. Therefore considering group distance and other agronomic performances for inter genotypic crosses among genotypes are suggested for future breeding program.

CHAPTER VI
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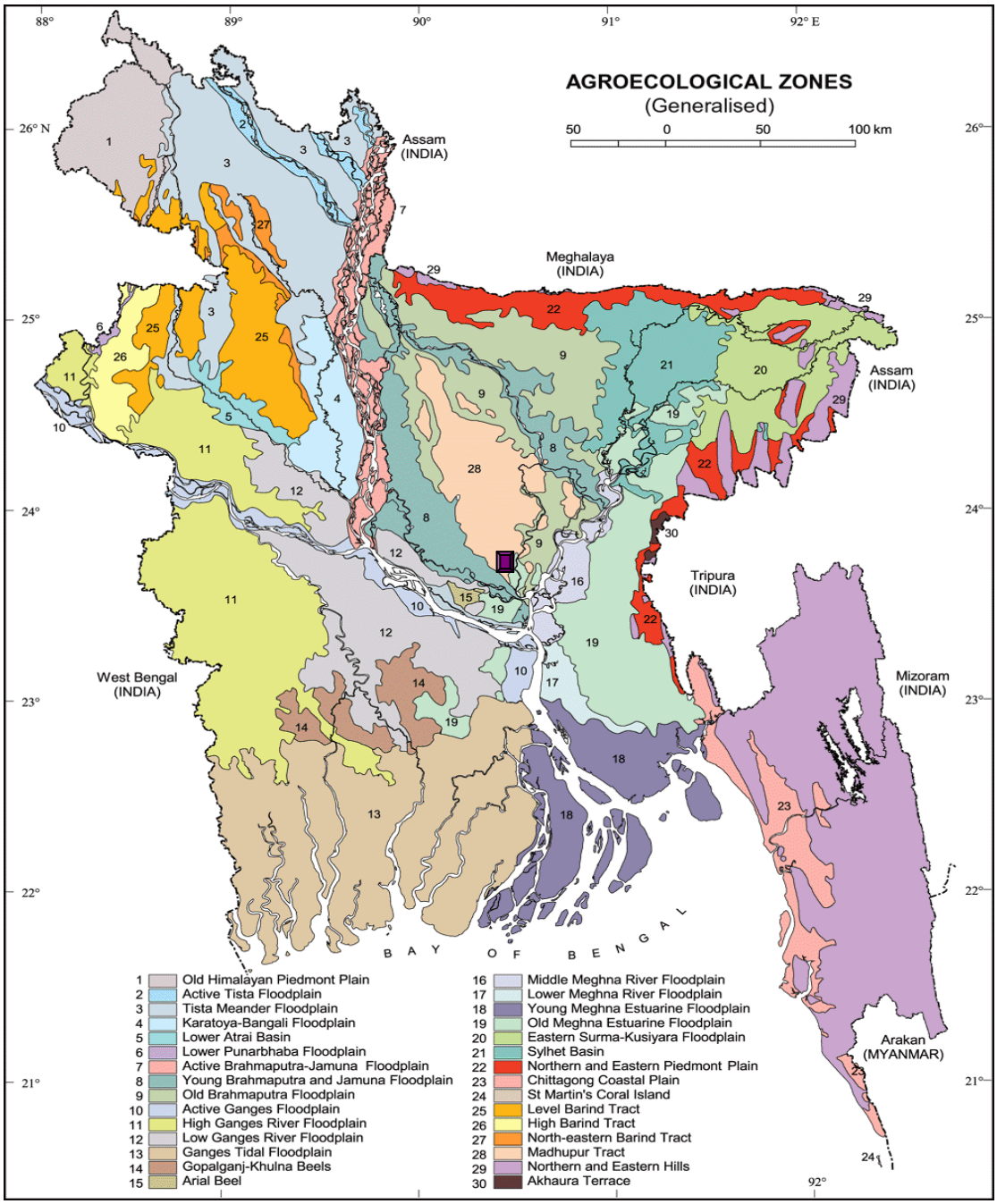
APPENDICES

Appendix I. Map showing the experimental site under the study



The experimental site under study

Appendix II. Monthly average Temperature, relative humidity and total rainfall and sunshine of the experimental site during the period from March to May, 2017.

Month	Air temperature (°C)		Relative humidity (%)	Rainfall (mm) (total)	Sunshine (h)
	Maximum	Minimum			
February, 2017	34.8	18.0	77	227	5.8
March, 2017	32.3	16.3	69	0	7.9
April, 2017	29.0	13.0	79	0	3.9
May, 2017	28.1	11.1	72	1	5.7

Source: Bangladesh Meteorological Department (Climate and Weather Division), Agargoan, Dhaka - 1212

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

A. Physical composition of the soil

Soil separates	%
Sand	36.90
Silt	26.40
Clay	36.66
Texture class	Clay loam

B. Chemical composition of the soil

Sl. No.	Soil characteristics	Analytical data
1	Organic carbon (%)	0.82
2	Total N (kg/ha)	1790.00
3	Total S (ppm)	225.00
4	Total P (ppm)	840.00
5	Available N (kg/ha)	54.00
6	Available P (kg/ha)	69.00
7	Exchangeable K (kg/ha)	89.50
8	Available S (ppm)	16.00
9	pH (1:2.5 soil to water)	5.55
10	CEC	11.23

Source: Central Library, Sher-e-Bangla Agricultural University, Dhaka.

Appendix IV. Mean performance of various growth parameter and yield componentsof 26 genotypes of mungbean

Genotypes	D50F	D80M	PH	BPP	BL	PPP	PP	SPP	SW	Y\P(g)
1	48.33	85.00	51.00	3.83	46.67	17.00	31.33	6.43	6.67	14.47
2	47.67	87.67	51.33	3.27	48.00	21.67	33.33	6.73	5.67	13.87
3	47.67	71.33	52.33	2.77	44.67	16.33	29.33	6.07	6.00	12.47
4	48.67	84.67	55.67	4.67	47.33	18.33	50.67	7.93	5.00	20.00
5	46.67	84.67	53.67	5.77	44.67	20.67	63.67	8.67	7.33	23.00
6	47.67	85.67	51.67	7.27	46.33	23.33	74.33	10.50	6.33	26.27
7	46.00	87.33	57.00	5.50	49.67	22.00	57.33	8.37	3.33	23.00
8	45.00	85.33	51.00	5.50	50.00	18.00	51.33	8.10	6.67	18.00
9	48.00	86.00	46.33	5.00	52.00	19.33	50.00	8.00	7.67	18.23
10	48.33	70.67	50.67	4.33	45.33	21.67	39.00	7.67	6.67	19.00
11	46.00	85.00	52.00	5.83	52.67	18.33	44.33	7.80	6.00	23.00
12	48.00	85.67	49.67	4.00	51.00	24.67	42.67	8.67	7.67	19.83
13	49.33	87.00	48.33	5.67	51.33	12.67	55.33	7.50	7.00	23.33
14	45.00	86.33	54.33	5.17	43.33	19.33	54.00	7.87	6.00	19.77
15	48.00	84.67	53.33	5.33	39.67	20.67	50.33	7.97	6.67	21.10
16	48.00	85.67	52.00	6.93	46.67	19.33	72.33	10.10	7.33	26.00
17	48.67	86.00	58.67	5.00	51.00	20.67	45.67	7.90	7.00	21.87
18	49.00	86.00	60.00	4.33	50.00	15.33	43.67	8.13	7.33	21.13
19	48.00	85.00	49.67	5.67	54.00	21.67	45.00	7.90	5.67	19.27
20	48.33	72.00	54.67	5.00	49.00	19.67	53.33	8.50	7.00	17.90
21	46.33	87.00	50.33	3.17	50.00	24.00	31.33	6.57	6.67	15.10
22	47.33	85.33	52.00	6.17	50.67	25.67	50.33	7.47	6.67	19.67
23	49.00	72.33	53.33	5.83	46.33	22.00	43.33	7.30	4.00	20.33
24	47.33	86.33	55.33	7.17	50.67	14.67	72.00	10.30	7.33	28.13
25	46.33	85.33	54.00	8.50	51.67	18.67	84.67	11.77	7.33	31.93
26	48.67	85.67	51.00	7.67	47.67	20.67	75.67	10.50	5.67	29.13
Min	**45.00**	**70.67**	**46.33**	**2.77**	**39.67**	**12.67**	**29.33**	**6.07**	**3.33**	**12.47**
Max	**49.33**	**87.67**	**60.00**	**8.50**	**54.00**	**25.67**	**84.67**	**11.77**	**7.67**	**31.93**
Average	**47.59**	**83.60**	**52.67**	**5.36**	**48.47**	**19.86**	**51.71**	**8.26**	**6.41**	**20.99**

Appendix V. Min-Max-SE-Mean-LSD of various growth parameter and yield components of 26 genotypes of mungbean

	Minimum	Maximum	Mean	CV(%)	SE	$LSD_{0.05}$
Days to 50% Flower	45.00	49.33	47.59	3.84	1.49	2.38
Days to 80% Maturity	70.67	87.67	83.60	10.46	7.14	3.27
Plant Height	46.33	60.00	52.67	14.00	6.02	2.06
Branch Per plant	2.77	8.50	5.36	12.28	0.54	2.09
Branch length	39.67	54.00	48.47	11.77	4.66	12.06
Peduncle per plant	12.67	25.67	19.86	15.46	2.51	9.75
Pods per plant	29.33	84.67	51.71	8.90	3.76	14.62
seed per pod	6.07	11.77	8.26	7.41	0.50	1.95
100 seed weight	3.33	7.67	6.41	12.02	0.63	2.45
yield\plant	12.47	31.93	20.99	7.05	1.21	4.70