

**VARIABILITY, INTERRELATIONSHIP AND PATH
ANALYSIS OF AGRONOMIC CHARACTERS IN
MUNGBEAN (*Vigna radiata* L. Wilczek)**

BY

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*This is to certify that thesis entitled, "STUDY ON VARIABILITY, INTERRELATIONSHIP AND CO-PATH ANALYSIS OF SOME AGRONOMIC CHARACTERS IN MUNGBEAN (*Vigna radiata* L. Wilczek)" submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE** in **GENETICS AND PLANT BREEDING**, embodies the result of a piece of bona fide research work carried out by **MD. ROWSHAN ALI**, Registration No. 00935 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.

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***Dedicated To
My
Beloved Parents***

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The Author

LIST OF ABBREVIATED TERMS

FULL NAME	=	ABBREVIATION
Agro-Ecological Zone	=	AEZ
And others	=	<i>et. al.</i>
Bangladesh Agricultural Research Institute	=	BARI
Bangladesh Bureau of Statistics	=	BBS
Centimeter	=	cm
Co-efficient of Variation	=	CV
Days After Sowing	=	DAS
Degree Celsius	=	$^{\circ}\text{C}$
Degrees of freedom	=	d.f
Etcetera	=	etc.
Food and Agriculture Organization	=	FAO
Figure	=	Fig.
Genetic Advance	=	GA
Genotypic Co-efficient of Variation	=	GCV
Genotypic Variance	=	δ_g^2
Gram	=	g
Hectare	=	ha
Heritability in broad sense	=	h^2_b
Journal	=	J.
Kilogram	=	Kg
Meter	=	m
Mean Sum of Square	=	MSS
Millimeter	=	Mm
Muriate of Potash	=	MP
Number	=	No.
Percent	=	%
Phenotypic Co-efficient of Variation	=	PCV
Phenotypic variance	=	δ_p^2
Randomized Complete Block Design	=	RCBD
Sher-e-Bangla Agricultural University	=	SAU
Standard Error	=	SE
Square meter	=	m^2



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**VARIABILITY, INTERRELATIONSHIP AND PATH
ANALYSIS OF AGRONOMIC CHARACTERS IN
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BY

MD. ROWSHAN ALI

ABSTRACTS

The experiment was conducted in a field laboratory at the experimental field of Sher-e Bangla Agricultural University, Dhaka, during March 2008 to June 2008. To evaluate the performance of 45 mungbean genotypes for variability, interrelationship and path analysis. The highest mean value was observed for days to 50% flowering. This character also exhibited the highest range of variation (56.35-29) which indicated that all the genotypes showed wide range of variation in respect of this character. It showed high heritability (59.01%) accompanied with low genetic advance in percentage of mean and the phenotypic variance (15.74) was higher than the genotypic variance (5.48). The significant positive correlation at the 5% level was observed for seeds per pod with branches per plant at genotypic level and the significant positive correlation at the 1% level seed yield per plant with plant height and seeds per pod with branches per plant both at genotypic level. Heritability in broad sense was moderate to high for all the characters studied and it ranged from 37.04% to 59.01% which indicated that selection based on phenotypic expression of any character for breeding could be effective. The genetic advance was very low to moderate. These findings proved that it was indicated of non-additive gene action. The high heritability was being exhibited due to favorable influence of environment rather than genotypes. Thus, the genotypes which performed well in various characters were due to genetic reasons and have a possibility for improvement through selection in the subsequent generations.

A decorative graphic on the left side of the page. It features a thick black vertical line and a thick black horizontal line that intersect. To the left of the vertical line, there are three red squares of varying heights. To the right of the vertical line, there are two red squares. A green vertical bar is positioned to the right of the vertical line, and a green horizontal bar is positioned below the horizontal line. A small white square is located at the intersection of the black lines.

Chapter 1

Introduction

CHAPTER 1 INTRODUCTION

The mungbean (*Vigna radiata* L. Wilczek) is an important crop in our country. Bangladesh grows various types of pulse crops. It is also referred to as grass pea, lentil, mungbean, blackgram, field pea and cowpea are important. Current taxonomy places mungbean in the family Leguminosae, subfamily Papilionidae, the genus *Vigna*. Among the pulse crop, mungbean has a special importance in intensive crop production system of the country for its short growing period (Ahmed *et al.* 1978). Pulses are important crops in Bangladesh. They occupy an area of about 0.47 million ha (>5% of the total cropped area) and contribute about 2% of the total grain production of the country (BBS, 2001). The major pulses grown in Bangladesh are: Khesari (*Lathyrus sativus* L.), Lentil (*Lens culinaris* Medic), Chickpea (*Cicer arietinum* L.), Blackgram (*Vigna mungo* L.), Mungbean (*Vigna radiata* L.) and Fieldpea (*Pisum sativum*). Among these khesari, lentil, chickpea and fieldpea are grown during winter (November-March) and contribute about 82% of total pulses. Blackgram is grown in late summer (August-December). Mungbean is grown both in early summer (February-April) and in late summer.

The crop is potentially useful in improving cropping system as it can be grown as a cash crop due to its rapid growth and early maturing characteristics. It can also fix atmospheric nitrogen through the symbiotic relationship between the host mungbean roots and soil bacteria and thus improve soil fertility. Pulse crops belong to grain legume.

According to FAO (1999) recommendation a minimum intake of pulse by a human should be 80g/day. Where as it is 7.92g in Bangladesh (BBS, 2002). This is because of fact that national production of the pulse is not adequate to meet for national demand. Both the acreage and production of the pulses are decreasing in Bangladesh day by day due to the inception of wheat and Boro rice in our cropping system with irrigation facilities. At present, the area under pulse crop is 0.406 million ha with a production of 0.322 million ton (BBS, 2005), where mungbean is cultivated in the area of 0.108 million ha with production of 0.03 million ton (BBS, 2005). The average yield of mungbean is 0.69 t/ha (BBS, 2005).

Knowingly or unknowingly the people of Bangladesh take pulse as the supplement of animal protein. Though the animal proteins are superior to vegetable protein the protein rice animal products are quite costly and beyond the reach of many of the common people of this country (Gowda and Kaul, 1982). Pulses can supplement the cereals based diet to improve the nutritional value of food. These are also best source of protein for domestic animals. Mungbean is one of the important pulse crops in the country for its high digestibility, good flavor and high protein content. It holds the first position in price, 3rd in protein content and 4th in both acreage and production in Bangladesh (Anonymous, 1999; Sarker *et al.* 1982). Hence from the point of nutritional value, mungbean is perhaps the best of all other pulses (Khan *et al.* 1982). It contains 51% carbohydrate, 26% proteins, 3% mineral and 3% vitamin (Kaul, 1982).

Mungbean originated in South Asia (India, Burma, Thailand etc.). Now it is widely grown in India, Pakistan, Bangladesh, Burma, Thailand, Philippines, China and Indonesia. It is also grown in parts of east and central Africa, The West Indies, USA and Australia (Gowda and Kaul, 1982). In Bangladesh it can be grown in late winter and summer season. Summer mungbean can tolerate a high temperature exceeding 40^oC and grows well in the temperature range of 30-35^oC. There are evidences in India; mungbean gives higher yields under summer planting than winter season (Singh & Yadav, 1978). The crop is also reported to be drought tolerant and can also be cultivated in areas of low rainfall, but also grows well in areas with 750-900 mm (Kay, 1979). So, cultivation of mungbean in the summer season could be an effective effort to increase pulse production in Bangladesh. Such effort may also help to save the foreign exchange for mungbean grain from abroad (Gowda and Kaul, 1982).

Mungbean is a very economical source of quality plant protein food. The seeds can be eaten whole, split and decorticated (dal) or ground as flour (basan), fried dishes, soup, noodles, curry and bean curd. The green pods are used as vegetables and haulms are used as fodder. Husk and split beans are useful as livestock feed. It makes a good cover crop and a soil binder. It is an excellent green manure, easily decomposed when incorporated. Moreover, mungbean can be grown successfully with maize and sugarcane, as intercropping, with a minimum competition with those main crops. Despite numerous

advantages, mungbean production is decreasing. This is mainly because, with the expansion of irrigation facilities, rice area has been increased in good soils, and other crops including mungbean are pushing to marginal lands. Moreover, as a tropical crop, mungbean faces many biotic and abiotic stresses during its growth. The major stresses are low nutrient status of the soil, water stress, water logging, salinity and mungbean yellow mosaic virus (MYMV).

A lot of researches have been done to increase the present yield of grain legumes including mungbean. But so far, no breakthrough has occurred in the yield ceiling of these crops. Researches have shown that as a result of variability, interrelationship and co-path analysis should prove more beneficial. With conceiving the above scheme in mind, the present research works have been undertaken in order to fulfilling the following objectives:

1. To study on variance, heritability, genetic advance and genetic advance in mean performance,
2. To evaluate the performance of 45 mungbean genotypes for yield and yield contributing characters,
3. To find out the degree of interrelationships among different component characters and their towards yield and
4. To study the direct indirect relationship between yield and yield contributing characters.





Chapter 2

Review of Literature

CHAPTER 2

REVIEW OF LITERATURE

For planning a breeding programme, a through knowledge about variability, interrelationship and path coefficient of yield contributing characters are important. Information on genotypic x environmental interaction helps to assess the suitability of growing the same strain in different locations. The genus *Vigna* is pan tropical and now has been broadened to include about 170 species, 120 from Africa, 22 from Indo-Pak sub-continent and Southeast Asia and a few from other parts of the world (Ghafoor *et. al.*, 2001). Only seven species of *Vigna* are cultivated as pulse crops mostly in Asia, Africa and some parts of Latin America (Anishetty and Moss, 1988). It is generally considered that two of these cultivated species are of African origin (sub genus *vigna*) and five are Asiatic origin (sub genus *Ceratotropis*). The Asiatic group consists, mungbean/greengram (*Vigna radiata* L. Wilczek), blackgram (*Vigna mungo* L. Hepper), mothbean (*Vigna aconitifolia* Jack. Marechal), adzukibean (*Vigna angularis* Willd, Ohwi and Ohashi) and ricebean (*Vigna umbellata* Thunb, Ohwi and Ohashi). The sub genus *Ceratotropis* of the genus *Vigna* includes five important Asian pulses; mungbean, blackgram, ricebean, mothbean and adzukibean. Mungbean and blackgram have been the major pulses in Asia since ancient times (Paroda and Thomas, 1988). At present, mungbean cultivation spreads worldwide because it is easily digested as compared to blackgram (Smartt, 1990). The subgenus *Ceratotropis* is considered to have originated in Asia and is called Asian *Vigna*. It forms a discrete group of about seventeen species largely confined to Asia and the Pacific.

Research done over the last several decades on variability, interrelationship and path coefficient analysis in mungbean is insufficient. Literatures concerning the genotype x environmental interactions are also very limited. The available important literature and their findings which are related to the present study are presented in the flowing sections.

2.1. Variability

2.2. Interrelationship

2.3. Path coefficient



2.1. Variability

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

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

Singh and Malhotra (1970) estimated the genetic and environment variability in 75 indigenous and exotic strains of mungbean that appear to differ in eight quantitative characters contributing to yield and found wide genotypic and phenotypic for all the characters. They also concluded that selection based on 100-seed weight, which had the highest genetic variability and very high genetic advance, would be the most effective. Genetic advance was also observed to be high for number of pod, branches and seed yield per plant but these characters had low heritability estimates.

Chowdhury *et al.* (1971) studied genetic variability in 21 varieties of mungbean and found significant differences in the range of variability for all the ten characters studied but number of days to flowering, plant height, and pod length and 100-seed weight gave higher estimates heritability associated with higher genetic gain.

Yohe and Pochlman (1972) studied the genetic variability of 300 strains of mungbean originating from 18 American, Asian, African and Middle Eastern countries and found a wide range of genetic variability for the characters like days to first ripening of pods, plant height, pods/plant, seed number/pod and 1000-seed weight. They also reported that moderately large size, as long as it was not associated with flowering, appeared to be desirable for high yield.

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

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

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

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

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



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

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

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

Vikas *et al.* (1998) evaluated eighteen mungbean parents (15 females and 3 males) and their 45 F₁ progeny for 12 yield-related traits at 4 sites in India (Simbhaoli, 2 sites in Meerut, and New Delhi) during kharif 1993. The genotypes differed significantly for most of the characters in all the environments. Estimates of components of variation showed that the variability of the material was not influenced by environmental differences. High components of genetic variation, heritability and genetic advance were obtained for plant height, number of clusters per plant, days to 50% flowering, number of pods per plant and biological yield. For these characters, additive gene effects were more

important than non-additive gene effects, indicating the scope for improvement of these characters through selection.

Sharma (1999) studied on genotypic and phenotypic coefficients of variation, heritability derived from data on 9 yield-related traits in 15 mungbean crosses and their six parents grown at Raipur during 1995-96. There was a high degree of genetic variability for all the yield-related traits studied. High heritability and high genetic advance were observed for days to flowering, pods/plant, seeds/plant, 1000seed weight and seed yield the predominance of additive gene effects for this trait.

Islam *et al.* (1999) studied on genetic variation, heritability on 9 yield components in 53 genotypes studied in Joydevpur during 1993. High values for heritability and genetic advance were estimated for plant height, number of pods per plant, seeds per pod, 1000-seed weight and yield per plant.

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

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

first flowering, plant height, number of branches per plant, pod length and 100-seed weight.

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

Khairnar *et al.* (2003) evaluated twenty-two mungbean genotypes for genetic variability in the kharif season of 1997, in Rahuri, Maharashtra, India. A wide range of variability was observed for plant height, clusters per plant, pods per plant, grain yield per plant and 100 grain weight. The estimates of genotypic as well phenotypic coefficients of variation were highest for pods per plant followed by 100-grain weight. High heritability coupled with high genetic advance was observed for clusters per plant, pods per plant, grain yield and 100-grain weight indicating that these characters can be improved by selection.

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

Abraham *et al.* (2007) evaluated genetic variability and heritability analyses for yield and yield components which were conducted for 646 accessions of green gram grown in Coimbatore, Tamil Nadu, India, during the Rabi and kharif of 2002-04. The estimates of phenotypic (PCV) and genetic (GCV) coefficients of variation were higher for single plant yield, number of branches per plant, number of pods per plant, number of clusters

per plant, plant height, and length of branch, indicating greater scope of selection for these traits. Dry matter production and number of clusters per branch revealed wide differences between the estimates of PCV and GCV values, indicating the highly significant effect of environmental factors. The number of days to initial flowering, number of days to 50% flowering, number of days to initial maturity, number of days to full maturity, 100-seed weight, seed length, seed breadth, length of pod, and protein content were less affected by environmental factors, as the difference between the estimates of PCV and GCV was low. The estimates of heritability in the core collection indicated that the number of days to full maturity, number of days to initial maturity, number of days to initial flowering, number of days to 50% flowering, seed length, seed breadth, plant height, length of branch, 100-seed weight, and length of pod were highly heritable. High genetic advance as a percentage of mean was recorded for the number of clusters per branch, length of branch, single plant yield, and number of pods per plant, number of clusters per plant, plant height and number of branches per plant, suggesting the possibility of selection for these traits in the core collection. High genetic advance coupled with high heritability and GCV was observed for length of branch, number of branches per plant, number of clusters per branch, number of clusters per plant, number of pods per plant, single plant yield and plant height indicating the predominance of additive gene action for this traits.

Rao *et al.* (2006) studied sixty genotypes of mungbean (*Vigna radiata*) which were evaluated during 2000 in Guntur, Andhra Pradesh, India for 13 characters to assess genetic variability, heritability and genetic advance. Total dry matter, plant height, number of pods per plant and yield per plant exhibited high variability and heritability coupled with genetic advance, indicating the influence of additive gene action.

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

2.2 Interrelationship

Yohe (1974) conducted an experiment with 5 parents and their F1 and F2 progeny and reported after estimating the phenotypic correlation and heritability that the number of pods/plant had the greatest effect on yield.

Singh *et al.* (1976) studied the correlation and regression coefficient between grain yield and eight plant characters reported that grain weight and branch number/plant were the main factors influencing grain yield.

Bhaumik and Jha (1976) estimated the biometrical relationships in 2 cultivar of mungbean and found positive correlation of seed Yield/plant with 1000-seed weight seed/pod and pods/plant. They also reported negative correlation between seed and plant height.

Ahmed *et al.* (1978) carried out an experiment with seventy strains of mungbean of local, exotic and mutant origin and found significant and positive correlation of yield with number of primary and secondary branches and pods/plant. But the characters like days to first flowering, days to maturity, plant height and seed size showed negative and significant correlation with yield.

Ahmed *et al.* (1981) studied simple, partial and multiple correlation in 70 strains of mungbean and positive significant correlation of yield/plant with number of pods (0.90**) and primary (0.75**) secondary (0.77**) branches/ plant in case simple correlation coefficient. Seed yield/plant also showed negative correlation with plant height, days from sowing to first flowering and to maturity seed size. Partial correlation results revealed that number of pos/plant had the strongest association with seed yield (0.772**). Multiple correlation studies also reveal the highest correlation coefficient between seed yield and number of pods along with days to first flowering. They also concluded that number of pods/plant should serve as the best selection criterion for improving yielding potential in mungbean. Number of primary and secondary branches also proved to be important characters for obtaining higher seed yielding

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

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

Sharma (1995) observed highly significant and positive correlations for number of seeds/plant and 100-seed weight with seed yield in 6 mungbean (*Vigna radiata*) genotypes and their 6 F₁ and 6 F₂ hybrids grown at Jabalpur, Madhya Pradesh in 1985.

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

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

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

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

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

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

Pandey and Singh (2002) studied yield correlations and performance of green gram cultivars ML 552, PS 16, ML 371, LM 1510, PDM 11, Pusa Baishakhi 1, PDM 84-139, PDM 54, ML 374 and ML 574 in rice-wheat cropping system in a field experiment conducted in Meerut, Uttar Pradesh, India during the kharif season of 1998 and summer of 1999. Grain yield had significant positive association with number of seeds per pod and test weight. A 300% cropping intensity can be achieved using the compatible cultivars of rice (Pant Dhan 12 or 10), wheat (UP 2338/PBW 343) and green gram (PS 16).

Dhuppe *et al.* (2005) studies on correlation which were carried out in 35 genotypes (11 parental lines and 24 hybrids) of mungbean, grown in Parbhani, Maharashtra, India, in 1998. Data were recorded for days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number

of pods per plant, number of seeds per plant, 100-seed weight and yield per plant. Grain yield per plant showed positive and significant correlation with days to maturity, number of secondary branches per plant, number of pods per plant and 100-seed weight at genotypic level, whereas secondary branches per plant and 100-seed weight were correlated with grain yield at phenotypic level. L-781 K-H x AKM-9242 were found

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

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

2.3 Path coefficient

Singh and Malhotra (1970) performed an experiment with 75 strains of mungbean to estimate path coefficient and observed that seed yield was influenced by pods/plant, seed/pod and seed size if other yield components were kept constant. However, seed size had a negative indirect effect on yield by affecting the number of seeds/pod and pods/plant.

Bhaumik and Jha (1976) conducted path coefficient analysis in 20 mungbean cultivars and found indirect effect of number of nodes on the main stem and number of the primary branches on the yield through number of seeds/pod and 100-seed weight. They also reported negative correlation of yield with plant height both directly and indirectly.

Singh and Malhotra (1976) performed an experiment with 75 strains of mungbean to estimate path coefficient and observed that seed yield was influenced by pods/plant,

seed/pod and 1000-seedweight if other yield components were kept constant. However, 1000-seedweight had a negative indirect effect on yield by affecting the number of seeds/pod and pod per plant.

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

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

Yaqoob *et al.* (1997) studied ten important agronomic characters for estimation of coefficient of correlation in 30 genotypes/mutants of mungbean grown under rain fed conditions at Dera Ismail Khan in 1991. Path co-efficient analysis revealed positive direct effects of days to 50% flowering, days to maturity, number of branches, 1000-seed weight, dry matter yield and harvest index on grain yield. A negative direct effect of plant height, number of pods and number of clusters on grain yield was observed in this study.

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

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

Rajan *et al.* (2000) were studied path coefficients in 7 parents and F₂ population of their 21 crosses in green gram for 13 characters. Path analysis revealed that pods per plant had the highest positive direct effect on grain yield, followed by hundred grain weight on grain yield. The study revealed that genetic improvement of grain yield is possible by selecting characters having high positive correlation and positive direct effect.

Dhuppe *et al.* (2005) studies on correlation and path analysis which were carried out in 35 genotypes (11 parental lines and 24 hybrids) of mungbean, grown in Parbhani, Maharashtra, India, in 1998. Data were recorded for days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per plant, 100-seed weight and yield per plant. Path analysis revealed that the number of seeds per plant and 100-seed weight were the major yield contributing characters. The performance of Jal-781 x AKM-9504 and Jal-781 K-H x AKM-9242 were found.

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

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



Chapter 3

Materials and Methods



CHAPTER 3 MATERIALS AND METHODS

The present research was conducted to evaluate the various genotypes of a collection of mungbean germplasm and varieties and to determine selection criteria in the experimental field of Genetics and Plant Breeding Department of Sher-e-Bangla Agricultural University, Dhaka, Bangladesh during the period from March to June, 2008 to study on the inter genotypic variability in Mungbean (*Vigna radiata* L. Wilczek). The location of the experiment was 24.7 degree North and 90.50 degree South latitude and longitude respectively and 8.6 meters above from the sea level.

3.1 Materials

The present experimental materials comprised of 45 genotypes of mungbean (Table 1) originated from different places of Bangladesh were used in this experiment. The materials were collected from Genetic Resources Centre at BARI in Gazipur.

3.2 Soil and climate

The land belongs to Agro-ecological region of 'Madhupur Tract' (AEZ 28) of Nodda soil series (Appendix I). The soil was sandy loam in texture having p^H 5.47- 5.63. The climate of the experimental sites was, in general sub-tropical and during 25% of the total period of plant growth in the, the climate of the sites was characterized by dry and high temperature with little rainfall. The mean temperature of the growing period was 23.32° C with average maximum and minimum being 28° C and 20.67° C respectively (AppendixII).

3.3 Experimental design and layout

The study was laid out in Randomized Complete Block Design (RCBD) with three (3) replications. The plant to plant distance was 15 cm and line to line distance was 30 cm. The total land size was 142.60 m². The plot to plot distance was 2.5 m. The genotypes were randomly distributed to each row within each line.

Table 1. Forty five genotypes of mungbean with their sources

Genotype No.	Germplasm/Accession No.	Source	Genotype No.	Germplasm/Accession No.	Source
G1	V2 (BARI-Mung-2)	BARI	G24	BD-6898	BARI
G2	V3 (BARI-Mung-3)	BARI	G25	BD-6900	BARI
G3	V4 (BARI-Mung-4)	BARI	G26	BD-6901	BARI
G4	V5 (BARI-Mung-5)	BARI	G27	BD-6902	BARI
G5	V6 (BARI-Mung-6)	BARI	G28	BD-6903	BARI
G6	BD-6875	BARI	G29	BD-6904	BARI
G7	BD-6876	BARI	G30	BD-6905	BARI
G8	BD-6877	BARI	G31	BD-6907	BARI
G9	BD-6879	BARI	G32	BD-6909	BARI
G10	BD-6880	BARI	G33	BD-6911	BARI
G11	BD-6881	BARI	G34	BD-6912	BARI
G12	BD-6882	BARI	G35	BD-6913	BARI
G13	BD-6884	BARI	G36	BD-6914	BARI
G14	BD-6885	BARI	G37	BD-6918	BARI
G15	BD-6886	BARI	G38	BD-6924	BARI
G16	BD-6888	BARI	G39	BD-6925	BARI
G17	BD-6889	BARI	G40	BD-6926	BARI
G18	BD-6890	BARI	G41	BD-6927	BARI
G19	BD-6891	BARI	G42	BD-6932	BARI
G20	BD-6893	BARI	G43	BD-6933	BARI
G21	BD-6894	BARI	G44	BD-6934	BARI
G22	BD-6895	BARI	G45	BD-6936	BARI
G23	BD-6897	BARI	-	-	-

3.4 Land preparation

The experimental plot was prepared by ploughing with tractor followed by harrowing and laddering by cows. Weeds and stubbles were removed. Manures and fertilizers were applied as per the recommended dose before the final land preparation. Irrigation channels were made around each plot. The final land preparation was done on 06 March 2008.

3.5 Manure and fertilizer

Mungbean does not generally need nitrogenous fertilizers as its nitrogen need is met by the fixation of atmospheric nitrogen in the root nodules. However, at the time of land preparation and or initial establishment of plant up to the stage of nodule formation a starter dose of 25-50-25 NPK respectively was applied.

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

Table 2. Doses of different fertilizers in field

Fertilizers/ Manures	Dose (Kg)	
	Applied in the plot	Quantity/ha
Urea	2.27	53
TSP	4.00	99
MP	1.70	41
Cowdung	Applied earlier	2.50 ton

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

3.6 Sowing of seeds and intercultural operation

The seeds of 45 mungbean genotypes were sown in the field on 07 March, 2008 at Plant Breeding Field Laboratory of Sher-e-Bangla Agricultural University. Experiment field shown in Plate 1a and Plate 1b.

3.7 Intercultural operation

Necessary Intercultural practices such as weeding, mulching, thinning, gap filling etc. carried out in proper time, precautions were also taken for avoiding disease and insect attracts by regular spraying. i.e. Thinning was done 25 days after sowing and weeding was done twice-the first during thinning and the second after about two months of sowing.

3.8 Harvesting

Different genotypes and varieties matured at different times. So, different genotypes were harvested in different time. The harvesting was completed by 02 June, 2008. Five randomly selected plants were harvested per plot when color of almost all the pods became black and brown. Pods of each plant were kept separately in paper bags and were dried under sunshine. Threshing was done by hand and strict care was taken to avoid mechanical mixture of seeds. Border plants were discarded to avoid border effect.

3.9 Recording of Experimental Data

Data on the following characters were recorded on individual plant basis from the five plants selected at random per plot. For the quantitative characters, out of 08 characters, Days to 50% flowering, Days to maturity were recorded in the field condition and the data on the other characters were recorded in the field Laboratory after harvest.

3.9.1 Days to 50% flowering

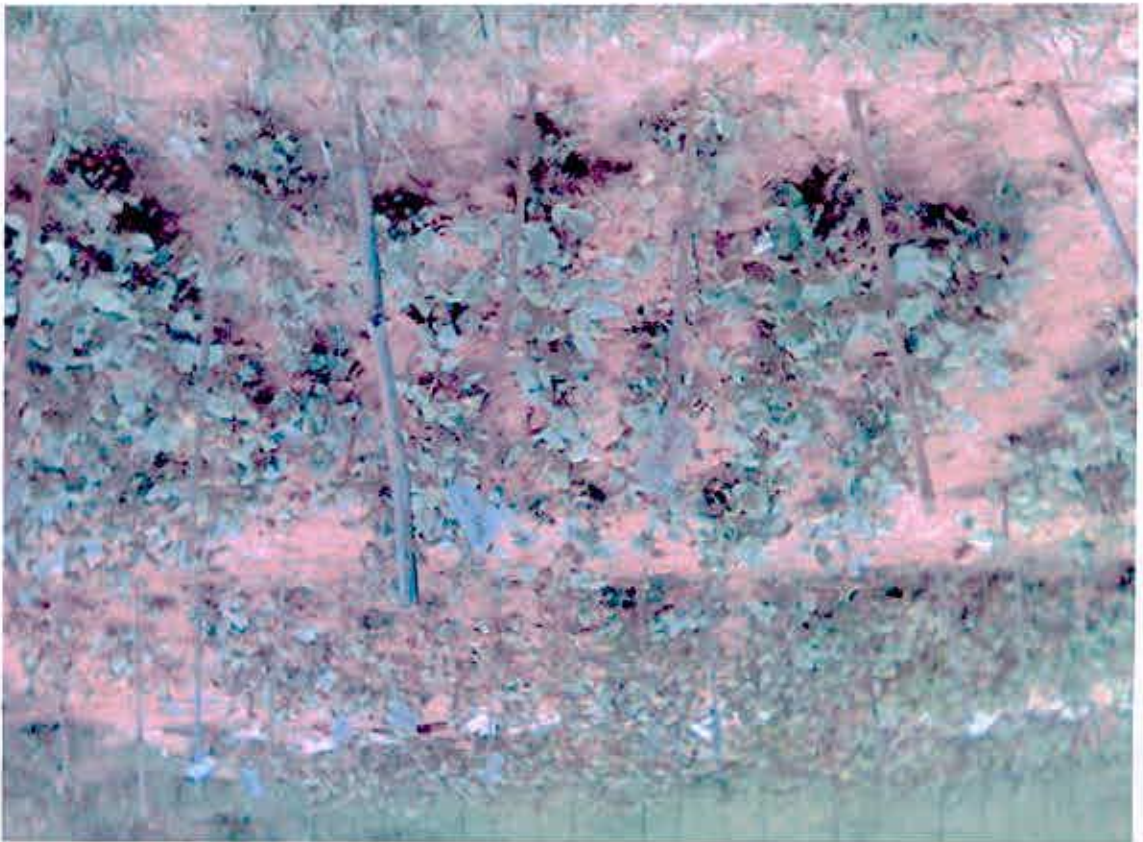
Difference between the dates of sowing to the date of flowering of a plot was counted as days to 50% flowering. Days to 50% flowering was recorded when 50% flowers of a plot were at the flowering stage.



Plate 1b. Field view of the experiment at podding stage



Plate 1a. Field view of the experiment at early stage



3.9.2 Plant height

The height of plant was recorded in centimeter (cm) at harvest in the experimental plots. Data were recorded as the average of 10 plants selected at random from the inner rows of each plot after harvest. The height was measured from the ground level to the tip of the growing point of the main branch.

3.9.3 Number of branches/plant

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

3.9.4 Pod per plant

The total number of pods in individual plants was recorded.

3.9.5 Pod length

Length of pod was measured in cm.

3.9.6 Seed per pod

Total number of seed in each pod within the individual plants was counted.

3.9.7 Seed per plant

Total number of seed in each plant within the individual plants was counted.

3.9.8 1000 seed weight

One thousand seeds were counted randomly from the total seeds of cleaned harvested seeds and then weighted in grams.

3.9.9 Yield/plant

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

3.10 Statistical analysis

3.10.1 Genotypic and phenotypic variance

Genotypic and phenotypic variances were estimated by Johnson *et al.* (1955). Genotypic variance (σ^2_g) was obtained by subtracting Error MS from the Genotype MS and dividing by number of replications as shown below:

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

Where,

GMS = genotypic mean square

EMS = error mean square

r = number of replication

The phenotypic variances (σ^2_p) were by adding genotypic variances (σ^2_g) with error variances (σ^2_e) as given by the following formula:

Phenotypic variance = Genotypic variance + error variance

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

Where,

σ^2_p = phenotypic variance

σ^2_g = genotypic variance

σ^2_e = error variance

3.10.2 Genotypic and phenotypic coefficient of variation

Genotypic and phenotypic coefficients of variation were estimated according to the formula given by Johnson *et al.* (1955).

$$\text{Genotypic coefficient of variation (GCV)} = \frac{\sigma_g}{\bar{x}} \times 100$$

Where,

σ_g = Genotypic standard deviation

\bar{x} = Population mean

$$\text{Phenotypic coefficient of variation (PCV)} = \frac{\sigma_p}{\bar{x}} \times 100$$

Where,

σ_p = Phenotypic standard deviation

\bar{x} = Population mean

3.10.3 Estimation of heritability

Heritability in broad sense was estimated using the given formula suggested by Johnson *et al.* (1955).

$$\text{Heritability (h}^2_{\text{b}}) \% = \frac{\sigma^2_{\text{g}}}{\sigma^2_{\text{p}}} \times 100$$

Where

σ^2_{g} = Genotypic variance

σ^2_{p} = Phenotypic variance

3.10.4 Estimation of genetic advance

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

$$\text{Genetic advance (GA)} = h^2_{\text{b}} K \sigma_p$$

Where,

h^2_{b} = Heritability in broad sense

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

σ_p = Phenotypic standard deviation

3.10.5 Estimation of Genetic advance in Mean Performance

The expected genetic advance in mean performance under selection was estimated using the formula suggested

$$\text{GAMP} = \frac{GA}{\bar{x}} \times 100$$

Where,

GA = Genetic advance

\bar{x} = Population mean

3.10.6 Correlation Coefficient

Genotypic Correlation coefficient was calculated suggested by Miller *et al.* (1955):

$$r_{gxy} = \frac{\sigma^2_{pxy}}{\sqrt{(\sigma^2_{py} \times \sigma^2_{px})}}$$

Phenotypic Correlation coefficient

Phenotypic Correlation coefficient was calculated suggested by Miller *et al.* (1955):

$$r_{psy} = \frac{\sigma^2_{pxy}}{\sqrt{(\sigma^2_{py} \times \sigma^2_{px})}}$$

3.10.7 Path Coefficient analysis (P)

Correlation co-efficient can be partitioned into direct and indirect effect of the component characters on yield.

Thus the effect of different yield contributing characters on yield per plant i.e. path coefficient analysis was done for 9 characters according to the method used by Dewey and Lu (1959).

3.10.8 Calculation of direct effect

The direct effect of different characters with yield was calculated by the formula as follows:

$$A = BC$$

$$\text{i.e. } c = AB^{-1}$$

Where,

C = Direct effect of the characters on yield.

B-1 = Correlation matrix (1, 2... n) of correlation coefficient.

A = Correlation of different characters (1, 2... n) on yield.

3.10.9. Calculation of residual effect

After calculating the direct and indirect effects of the character the residual effect was calculated by the following formula (Singh and Chowdhury, 1985).

$$P_{ry} = \sqrt{1 - \sum P_{iy} \cdot r_{iy}}$$

Where,

r_{iy} = Correlation of the i th character with yield.

P_{iy} = Direct effect of i th character on yield,

P_{ry} = Residual effect.



Chapter 4

Results and Discussion

CHAPTER 4 RESULTS AND DISCUSSION

The results of the present study have been described and discussed under the following sections. With the help of suitable genetic parameters like genetic coefficient of variation, habitability estimates, genetic advance under selection interrelationship and co-efficient analysis. The heritable (genetic) and non-heritable (non-genetic) components were estimated for different characters. Ten characters such as plant height, number of branches per plant, number of pods per plant, length of pod, number of seed per plant, number of seeds per pod, thousand seed weight, days to 50% flowering and seed yield per plant were studied in respect of 45 genotypes. Results of different studies are described in separate section on character basis.

Variability and other biometrical studies

1. Variability and genetic parameter
2. Interrelationship
3. Path co-efficient analysis

4.1 Variability and genetic parameter

The analysis of variance (ANOVA) of the data on different yield components and yield of mungbean are given in (Table 3). The results have been presented and discussed and possible interpretations have been given. The mean values over three replications for the characters of all genotypes are presented in (Table 4); genotypic, phenotypic and environmental variance and genotypic, phenotypic and environmental coefficients of variation, heritability and genetic advances of these characters are presented in (Table 5). Among the genotypes almost all characters showed highly significant variation indicating wide scope of selection for these characters. i.e. the data revealed substantial variability and thus high possibility of improvement in most of the traits. The phenotypic variance was partitioned into genotypic and environmental variances for clear understanding of the pattern of variations.

4.1.1 Plant height (cm)

The mean square due to genotype from the analysis of variance was found statistically significant at 1% level of probability for plant height (32.19**) indicating genotypic differences present among the genotypes used under the present study (Table 3). From the mean value it was found that the tallest genotype was G2 (37.67cm) while the shortest genotype was G13 (22.67cm) in (Table 4). The phenotypic variance (20.30) was considerably higher than the genotypic variance (5.94) and the phenotypic and genotypic co-efficient of variations were 14.87% and 8.04%, respectively (Table 5). The result indicated the existence of inherent variability among the population with possibility of high potential for selection. Highest phenotypic and genotypic variances and genotypic and phenotypic co-efficient of variations for plant height were also observed by Makeen *et al.* (2007), Abraham *et al.* (2007), Rao *et al.* (2006), Vikas *et al.* (1998) and Reddy *et al.* (2003) in their study. Plant height showed high heritability (54.09%) together with low genetic advance (5.02%) and genetic advance in percentage of mean (16.57) which indicate high heritability coupled with high genetic advance was observed in plant height, indicating the importance of additive gene effect for the expression of these character reported by Makeen *et al.* (2007), Abraham *et al.* (2007) Reddy *et al.* (2003), Das *et al.* (1998). Non-additive gene action, low heritability and low genetic advance were noted for plant height was reported by Loganathan *et al.* (2001).

4.1.2 Number of branches per plant

Analysis of variance of the data for number of primary branches/plant showed highly statistically significant difference among the genotype (Table 3). Maximum number of branches/plant was recorded in genotype G38 (6.00) (Table 4). On the other hand the minimum number of branches/plant was recorded in the genotypes G22 (4.00) which was followed respectively by G19, G21, G23, G34, and G43. The phenotypic variance (0.51) was higher than the genotypic variance (0.07) indicated less environmental influence on this characters (Table 5) and genotypic co-efficient (5.33%) and phenotypic co-efficient of variation (14.39%) which indicate that the genotype had high variability (Table 5). Number of branches/plant showed very high heritability (37.04%) coupled with low genetic advance (0.54%) and high genetic advance in percentage of mean (10.98). These findings revealed that it was indicative of non-additive gene action. High genetic

Table 3. Analysis of variance of the data of nine important characters in respect of 45 *Vigna radiata* L.Wilczek

Source of variance	df	Plant Height (cm)	No. of Branch Per Plant	No. of Pod Per Plant	Pod Length (cm)	No. of Seed Per Plant	No. of Seed Per Pod	1000 Seed Weight (gm)	Days to 50% Flowering	Yield Per Plant (gm)
Replication	2	229.62**	0.81	25.16**	0.89	7.34**	3144.90*	6.96**	2.50	1.09
Genotypes	44	32.19**	0.66	24.67**	0.67	2.66	1298.46*	5.80**	26.71**	3.89*
Error	88	14.36	0.44	9.55	0.37	1.38	857.47	2.80	10.26	2.17

**Significant at 5% level and * Significant at 1% level; df = degree of freedom

Table 4: Mean performance of 9 important characters in respect of 45 *Vigna radiata* L.Wilczek genotypes

Genotype Acc. No./name	Plant height (cm)	Branch per plant	Pods per plant	Pod length (cm)	Seed per pod	Seed per plant	1000 seed weight (gm)	Days to 50% flowering	Yield per plant (gm)
G1 V2 (BARI-Mung-2)	31.00	4.67	33.67	5.80	10.33	175.33	22.95	39.14	22.98
G2 V3 (BARI-Mung-3)	37.67	5.00	31.33	5.83	10.33	220.33	22.55	47.90	22.49
G3 V4 (BARI-Mung-4)	36.00	4.67	32.33	5.63	9.33	183.00	22.91	40.09	24.03
G4 V5 (BARI-Mung-5)	32.00	4.67	32.67	5.67	10.33	141.33	22.02	35.68	22.98
G5 V6 (BARI-Mung-6)	31.00	5.67	27.33	5.80	10.33	182.00	22.73	45.23	21.95
G6 BD-6875	30.33	4.67	26.33	5.37	11.67	172.67	23.76	46.28	23.27
G7 BD-6876	27.67	5.00	25.00	5.60	11.33	161.67	24.82	38.68	22.69
G8 BD-6877	26.00	4.67	25.00	5.50	10.00	163.33	26.27	42.48	22.87
G9 BD-6879	27.67	5.33	34.67	5.50	11.00	183.33	25.28	44.50	23.48
G10 BD-6880	29.67	5.33	30.00	5.50	10.33	179.67	28.14	42.14	24.42
G11 BD-6881	26.33	5.00	25.33	5.33	9.00	207.33	25.85	35.58	23.02
G12 BD-6882	29.00	4.67	27.33	5.60	8.67	147.67	24.28	40.33	24.45
G13 BD-6884	22.67	5.33	26.67	4.80	8.33	151.00	22.84	42.76	21.60
G14 BD-6885	27.33	4.67	33.33	4.70	7.00	166.33	26.42	45.73	22.73
G15 BD-6886	30.00	4.67	30.33	5.80	11.33	161.67	23.73	39.99	24.12
G16 BD-6888	28.00	5.00	30.33	5.47	10.67	188.67	22.34	38.23	25.25

Table 4: (Cont'd)

Genotype Acc. No./name	Plant height (cm)	Branch per plant	Pods per plant	Pod length (cm)	Seed per pod	Seed per plant	1000 seed weight (gm)	Days to 50% flowering	Yield per plant (gm)
G17 BD-6889	26.67	5.67	32.67	5.07	11.67	184.00	22.95	41.41	22.65
G18 BD-6890	29.00	5.00	29.67	4.33	10.00	126.33	23.87	37.75	22.94
G19 BD-6891	28.33	4.33	32.00	5.27	11.33	179.33	25.12	43.79	22.12
G20 BD-6893	27.33	4.67	26.67	5.43	11.00	176.00	22.64	44.51	24.10
G21 BD-6894	32.67	4.33	27.67	4.87	8.67	154.00	24.47	43.64	23.74
G22 BD-6895	28.00	4.00	35.33	4.90	11.33	172.00	23.69	39.45	21.89
G23 BD-6897	27.00	4.33	29.00	4.30	11.00	174.67	24.60	43.29	22.40
G24 BD-6898	36.00	5.67	30.67	5.60	10.33	187.00	24.20	39.46	24.12
G25 BD-6900	32.67	5.67	30.67	5.93	11.00	173.33	22.66	39.47	25.39
G26 BD-6901	32.67	5.67	32.00	5.10	10.33	185.00	24.03	42.84	23.26
G27 BD-6902	29.33	5.33	27.67	5.40	10.00	194.33	23.86	42.92	24.49
G28 BD-6903	30.33	5.67	31.33	5.60	10.67	156.00	23.33	39.40	23.56
G29 BD-6904	28.33	5.33	28.33	6.27	10.67	144.67	23.57	41.44	22.85
G30 BD-6905	34.33	5.33	25.67	4.77	10.00	160.00	26.10	40.91	23.30
G31 BD-6907	28.00	5.00	32.00	6.53	10.33	180.00	23.59	39.57	24.63
G32 BD-6909	27.00	5.33	30.33	5.10	10.00	201.00	22.89	40.96	25.24



Table 4: (Cont'd)

Genotype Acc. No./name	Plant height (cm)	Branch per plant	Pods per plant	Pod length (cm)	Seed per pod	Seed per plant	1000 seed weight (gm)	Days to 50% flowering	Yield per plant (gm)
G33 BD-6911	29.33	4.67	32.33	5.23	10.00	167.33	21.70	39.30	25.78
G34 BD-6912	29.33	4.33	26.33	5.43	10.00	160.67	21.79	45.00	23.41
G35 BD-6913	30.33	5.00	26.67	5.00	10.33	138.00	22.68	43.05	23.13
G36 BD-6914	30.67	5.33	25.33	6.07	10.33	163.33	23.26	37.98	25.51
G37 BD-6918	29.33	4.33	28.00	4.97	8.67	206.33	22.47	41.06	22.27
G38 BD-6924	32.00	6.00	33.33	5.27	10.33	163.67	21.64	37.22	21.34
G39 BD-6925	30.00	5.00	30.00	5.67	10.00	184.00	24.62	43.23	23.20
G40 BD-6926	31.33	4.67	29.67	6.03	10.33	193.33	23.92	41.58	23.06
G41 BD-6927	32.67	5.00	30.33	5.53	10.67	189.33	24.06	42.43	24.75
G42 BD-6932	31.33	4.67	29.33	5.00	9.00	131.67	25.28	46.03	25.25
G43 BD-6933	35.33	4.33	25.00	4.63	9.67	149.33	25.15	43.16	24.82
G44 BD-6934	34.00	4.67	27.67	5.33	9.33	163.33	24.91	48.34	22.45
G45 BD-6936	31.67	5.00	29.00	5.23	10.67	137.00	23.45	42.38	22.09
MEAN	0.29	4.96	29.47	5.37	10.17	170.67	23.81	41.66	23.42
SE	0.42	0.06	0.33	0.06	0.12	2.77	0.17	0.34	0.14
% CV	12.51	13.31	10.48	11.37	11.54	17.16	7.02	7.69	6.29

Table 5: Estimation of genetic parameters, heritability and genetic advance & genetic advance in percentage of mean for yield and yield contributing characters of 45 *Vigna radiata* L. Wilzeck

Genetic parameter Character	σ^2_g	σ^2_e	σ^2_p	GCV (%)	PCV (%)	h^2b (%)	GA (%)	GAMP (%)
PH	5.94	14.36	20.30	8.04	14.87	54.09	5.02	16.57
NBPP	0.07	0.44	0.51	5.33	14.39	37.04	0.54	10.98
NPPP	5.04	9.55	14.59	7.61	12.96	58.77	4.62	15.69
PL	0.10	0.37	0.47	5.89	12.77	46.13	0.65	12.13
NSPP	0.43	1.38	1.81	6.44	13.23	48.74	1.35	13.28
NSPD	147.00	857.47	1004.47	7.10	18.57	38.25	24.97	14.63
TSWT	1.00	2.80	3.80	4.20	8.18	51.29	2.06	8.65
DFF	5.48	10.26	15.74	5.61	9.52	59.01	4.82	11.57
YLD	0.57	2.17	2.74	3.22	7.07	45.61	2.57	6.64

Where, σ^2_g = genotypic variance, σ^2_e = environmental variance, σ^2_p = phenotypic variance GCV = genotypic coefficient of variation, PCV = phenotypic coefficient of variation, h^2b = heritability in broad sense, GA = genetic advance, GAMP = Genetic advance in Mean Performance

Advance coupled with high heritability in number of branches per plant was reported by Abraham *et al.* (2007). Non-additive gene action, low heritability and low genetic advance were noted for number of branches per plant was reported by Loganathan *et al.* (2001). Number of branches displayed the highest (91.7) heritability was observed by Shamsuzzaman and Shaikh (1982). The number of branches per plant is shown in Plate2.

4.1.3 Days to 50% flowering

From the (Table 3) there were highly significant variations among the genotypes (26.71**) for days to 50% flowering. The days to 50% flowering was observed highest (48.34) in G45 which was followed by G2 (47.90) (Table 4). The lowest value found in G11 (35.58) which was followed by G4 (35.68) (Table 4). Genotypic and phenotypic variance of days to 50% flowering was observed 15.74 and 5.48, respectively with high differences between them indicated large environmental influences on these character for their phenotypic expression and values of GCV and PCV were 5.61% and 9.52%, respectively which indicated moderate variability present among the genotypes for this character (Table 5). Reddy *et al.* (2003), Kumar *et al.* (2003), Vikas *et al.* (1998) recorded highest variability for days to 50% flowering. Days to 50% flowering showed high heritability (59.01%) with genetic advance (4.82%) and genetic advance in percentage of mean (11.57%) revealing that the character is governed by non-additive genes and heterosis indicated the expression of this character was influenced by the environment. Abraham *et al.* (2007) observed in days of 50% flowering was highly heritable. High heritability estimates coupled with high genetic advance were observed for days to 50% flowering were reported by Reddy *et al.* (2003), Vikas *et al.* (1998).

4.1.4 Pod per plant:

The mean square value due to genotype from the analysis of variance was found statistically significant difference (24.67**%) at 1% level of probability for number of pod/plant among the genotypes used as experimental material under the present experiment (Table 3). From the mean value it was found that the highest number of pod/plant was recorded for the genotype G22 (35.33) which was followed by the genotype G9 (34.67) and both G8 and G43 (25.00) was found the minimum number of



Plate 2.Branching habit of G38 genotype of mungbean

pod/plant which was followed by the genotype G36 (25.33) (Table4). The phenotypic variance (14.59%) was considerably higher than the genotypic variance (5.04) and the phenotypic and genotypic co-efficient of variations were 12.96% and 7.61%, respectively (Table 5). Abraham *et al.* (2007) was observed highest phenotypic coefficient of variation (PCV) and genotypic coefficient of variation for pod per plant. High heritability coupled with high genetic advance was observed for pods per plant by Reddy *et al.* (2003), Venkateswarlu *et al.* (2001), Vikas *et al.* (1998), Rahman (1982). Number of pod/plant showed low heritability (58.77%) coupled with very low genetic advance (4.62%) and low genetic advance in percentage of mean (15.69). These findings revealed that it is indicative of non-additive gene action. High heritability coupled with high genetic advance was observed in pods per plant was reported by Makeen *et al.* (2007), Abraham *et al.* (2007), Rao *et al.* (2006), Reddy *et al.* (2003), Khairnar *et al.* (2003), Loganathan *et al.* (2001), Islam *et al.* (1999), Sharma (1999), Vikas *et al.* (1998), Das *et al.* (1998).

4.1.5 Number of seeds per plant

Maximum number of seed per pod was recorded in genotype G37 (206.33) and which was followed G32 (201.00) and the minimum (126.33) was recorded in the genotypes G18 and which was followed G42 (131.67) and it was also statistically different from other genotypes (Table 4). The phenotypic variance (1.81%) was considerably higher than the genotypic variance (0.43%) and the phenotypic and genotypic co-efficient of variations were 13.23% and 6.44%, respectively (Table 5). The heritability in broad sense (h^2_b) of this trait was high (48.74%) and low genetic advance (1.35%) and low genetic advance in percentage of mean (13.28%). These results indicated additive genes involvements in the expression of the character and this with many scope of improvement by direct selection. The heritability in broad sense (h^2_b) of this trait was high (38.25%) and high genetic advance (24.97%) and low genetic advance in percentage of mean (14.63%). These results indicated additive genes involve in the expression of the character and it has enormous opportunity to improve this character by phenotypic selection. High heritability estimates coupled with high genetic advance were observed for seed/pod reported by Reddy *et al.* (2003).

4.1.6 Pod Length (cm)

From the (Table 4) there were no significant variations among the genotypes for the pod length because pod lengths are about similar. The phenotypic variance (0.47) was considerably higher than the genotypic variance (0.10) and the phenotypic and genotypic co-efficient of variations were 12.77% and 5.89%, respectively (Table 5). Pod length recorded high genotypic coefficients of variation suggesting the possibility by Das *et al.* (1998). Length of pod/plant showed very high heritability (46.13%) connected with very low genetic advance (0.65%) and genetic advance in percentage of mean (12.13%) which findings exposed the action of additive gene effect on the expression of this character as well as a scope of improvement through selection. Length of pod were highly heritable found Abraham *et al.* (2007), Tiwari *et al.* (1995). Non-additive gene action, low heritability and low genetic advance were noted for pod length. High heritability associated with high genetic advance over mean was observed for pod length was reported by Das *et al.* (1998). Pods in different genotypes are shown in Plate 3a, Plate 3b and Plate 3c.

4.1.7 Seed per pod

From the (Table 4) there were no significant variations among the genotypes for the number of seeds per pod because number of seeds per pod was about similar. The value of the analysis of variance of the data for the number of seed per pod showed highly significant difference (1298.46*) at 0.05 level among the genotypes of mungbean used in the present experiment (Table 3). The difference in magnitudes in between genotypic (1004.47) and phenotypic variances (147.00) and the phenotypic and genotypic co-efficient of variations were 18.57% and 7.10%, respectively (Table 5)

Pandey and Singh (2002) was observed highest difference value for seed per pod. The heritability in broad sense (h^2_b) of this trait was high (38.25%) and high genetic advance (24.97%) and low genetic advance in percentage of mean (14.63%). These results indicated additive genes involvements in the expression of the character and this with many scope of improvement by direct selection. High heritability estimated coupled with high genetic advance were observed for seed/pod reported by Reddy *et al.* (2003). Pods appearance in different genotypes are shown in Plate 4a, Plate 4b and Plate 4c.

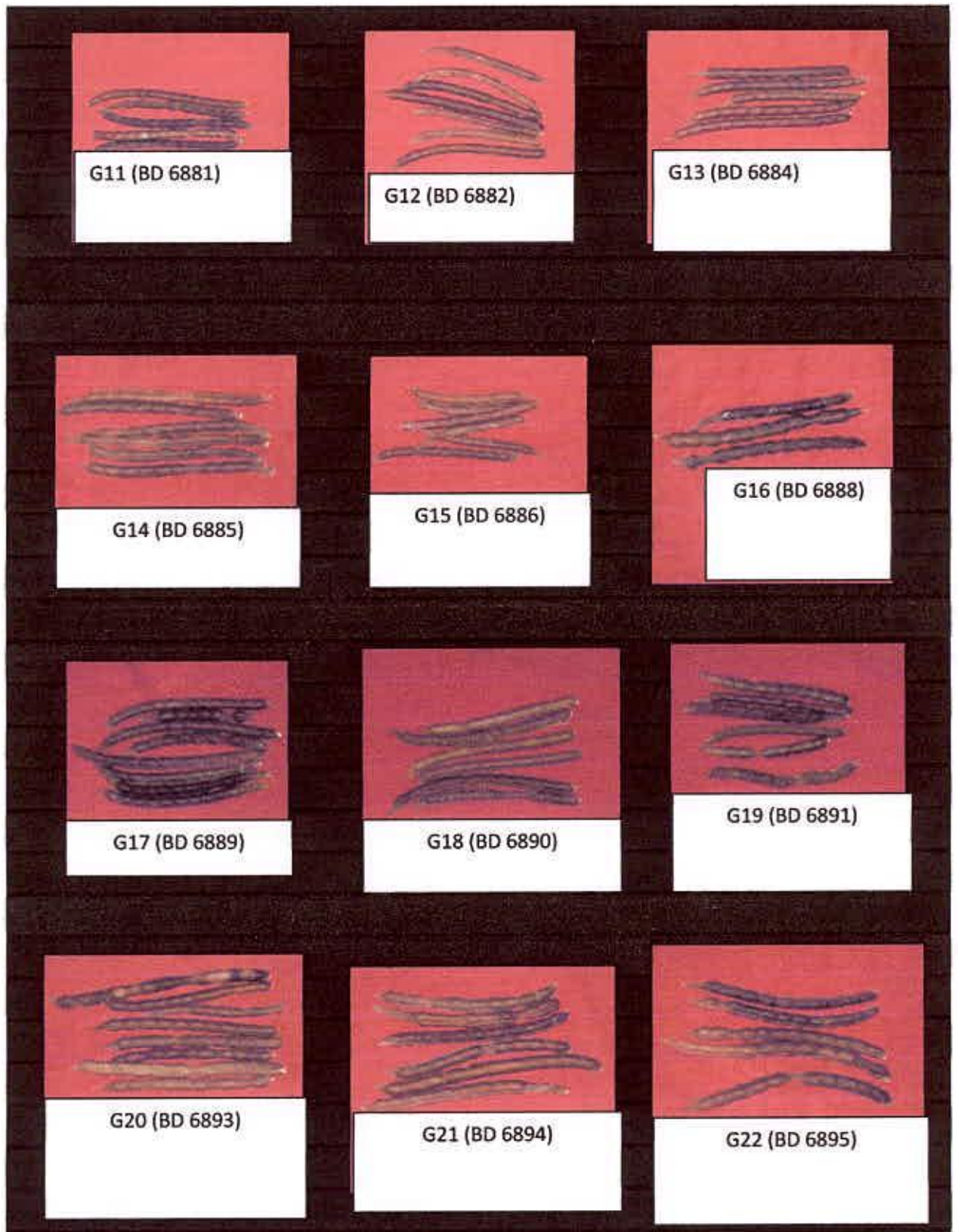


Plate 3a. Pod appearance in different genotypes in mungbean



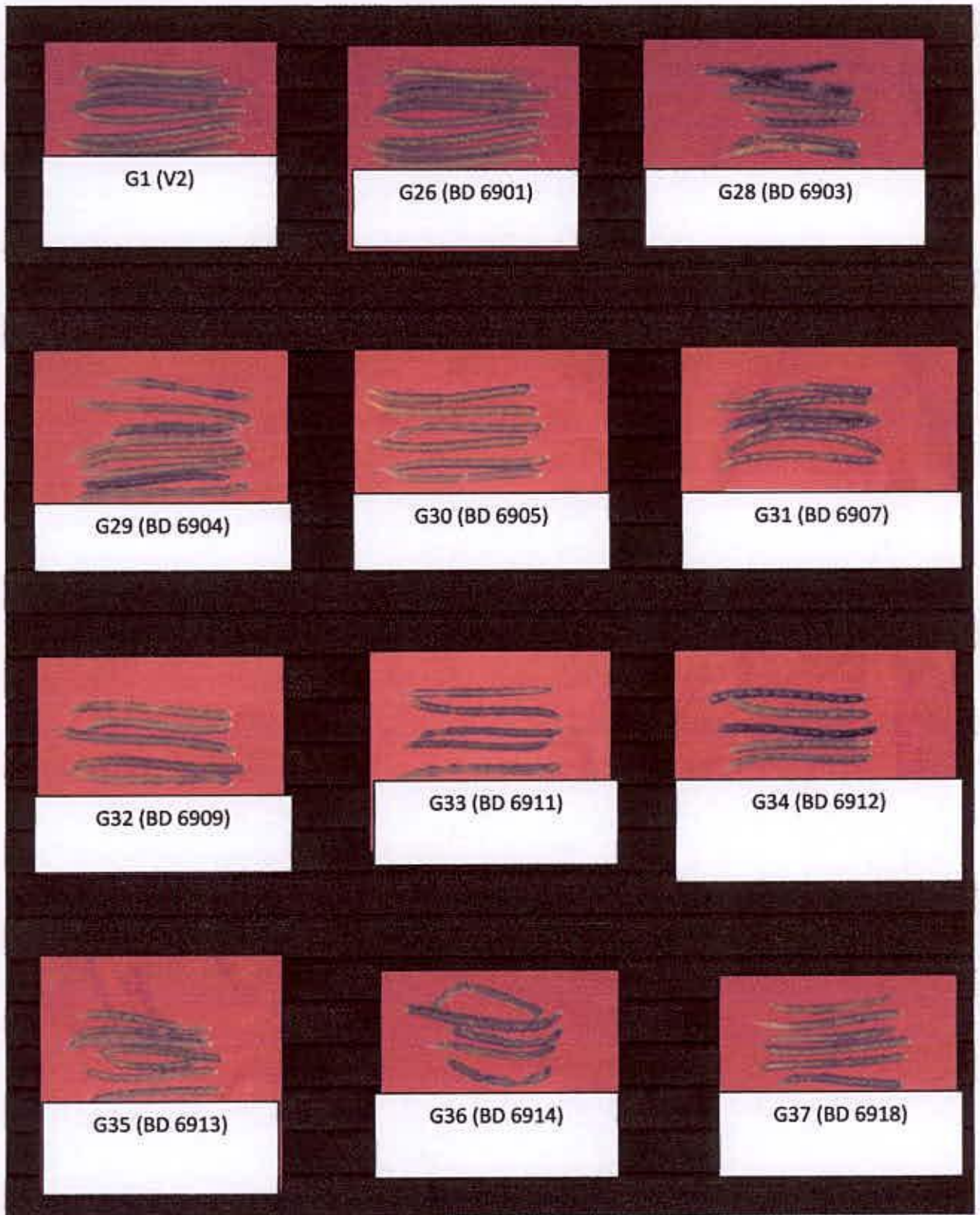


Plate 3b. Pod appearance in different genotypes in mungbean



Plate 3c. Pod appearance in different genotypes in mungbean



Plate 4a. Seed appearance in different genotypes



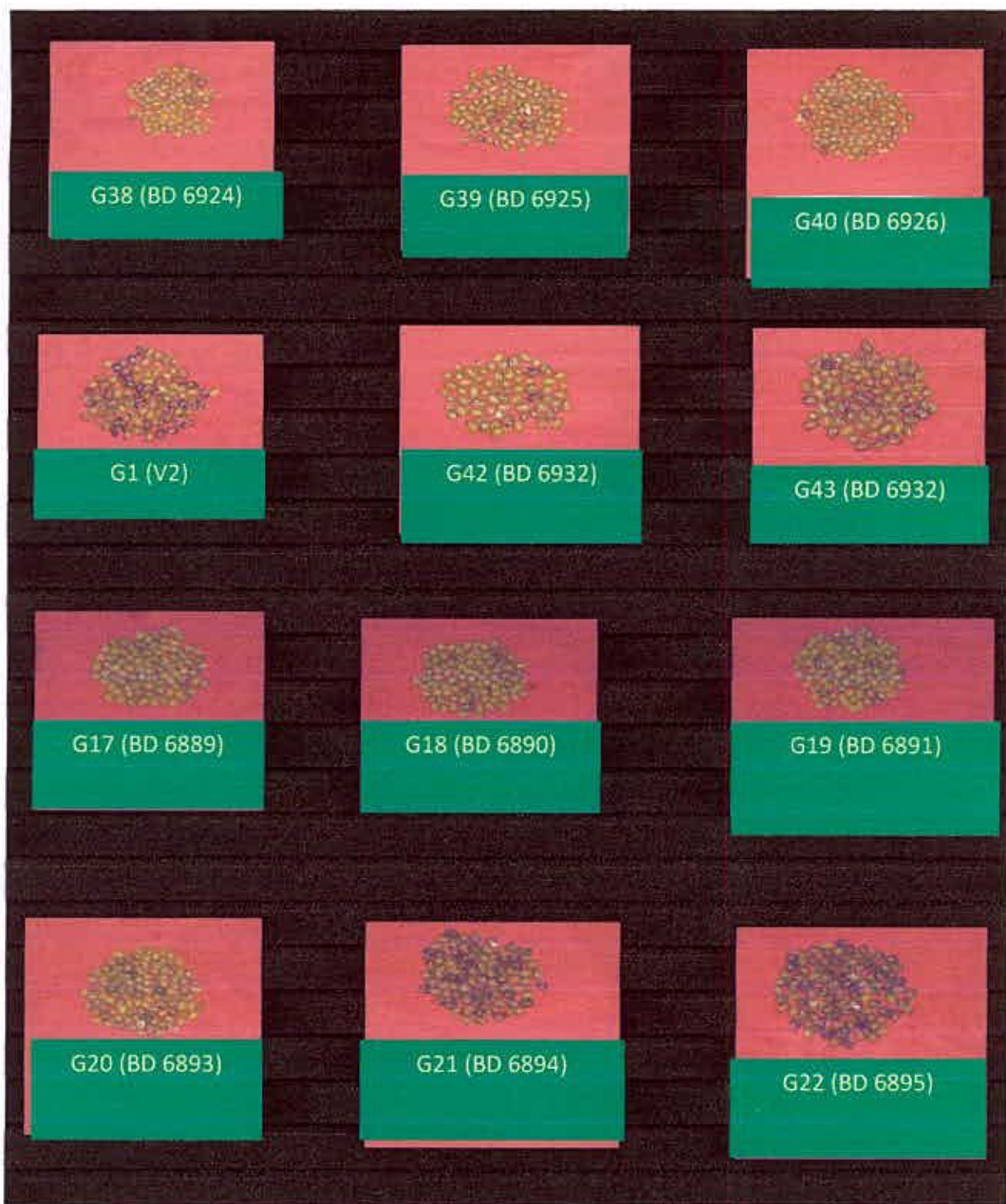


Plate 4b. Seed appearance in different genotypes



Plate 4c. Seed appearance in different genotypes



4.1.8 1000 Seed Weight (g)

The mean square due to genotype from the analysis of variance was found statistically significant at 1% level of probability and that was (5.80**) for 1000 seed weight indicating genotypic differences among the genotypes used under the present experiment (Table 3). From the mean value it was found that the highest 1000 seed weight was recorded in the genotype G10 (28.14g) which was followed by G14 (26.42g) while the lowest 1000 seed weight (21.64g) was in the G38 which was followed by G33 (21.70g) (Table 4). The phenotypic variance (3.80) was higher than the genotypic variance (1.00) and the phenotypic and genotypic co-efficient of variations were 8.18% and 4.20%, respectively for 1000 seed weight of mungbean genotypes (Table 5). Similar result was found by Sandhu *et al.* (1979). Very high heritability (51.29%) associated with low genetic advance (2.06%) and genetic advance in percentage of mean (8.65%) was calculated in respect of 1000 seed weight of *Brassica* genotypes. These findings exposed the action of additive gene effect on the expression of this character as well as a scope of improvement through selection. High values for heritability and genetic advance were estimated 1000-seed weight reported by Islam *et al.* (1999), Sharma (1999) and Sandhu *et al.* (1979).

4.1.9 Yield/Plant (g)

In the present experiment, the genotype mean square for seed yield per plant was found significant 3.89* (Table 3). The seed yield per plant was recorded highest in the G33 (25.78) which was followed by G16 (25.25) and the lowest mean value (21.34) was in G38 which was followed G13 (21.60) (Table 4). The phenotypic variance (2.74) was higher than the genotypic variance (0.57) and the phenotypic and genotypic co-efficient of variations were 7.07% and 13.22%, respectively for yield per plant of mungbean genotypes (Table 5). Rao *et al.* (2006) yield per plant exhibited high variability and heritability coupled with genetic advance, indicating the influence of additive gene action. High phenotypic coefficient of variability indicated the favourable effect of environment for number of clusters per plant and seed yield per plant, and high genotypic coefficient of variability suggested substantial amount of genetic variability for seed yield per plant was reported by Loganathan *et al.* (2001), Das *et al.* (1998). High heritability (45.61%) coupled with low genetic advance (2.57%) and genetic advance in percentage of mean (6.64) was recorded in respect of yield/plant. These findings revealed that it is indicative

of non-additive gene action. The high heritability is being exhibited due to favorable influence of environment rather than genotypes and selection for such traits may not be rewarding. High heritability estimates coupled with high genetic advance were observed for yield/plant Rao *et al.* (2006), Reddy *et al.* (2003), Sharma (1999).

4.2 Interrelationship

The results of simple correlation co-efficient between pair of characters in 45 genotypes for *Vigna radiata* L. Wilzeck are presented in (Table 6) and correlation matrix between pairs of characters in 45 mungbean genotypes (Figure 1). It was evident that in majority to the cases, the genotypic correlation co-efficient was higher than the corresponding phenotypic correlation co-efficient. This indicated a strong inherent association between the characters studied and suppressive effect of the environment modified the phenotypic expression of these characters by reducing phenotypic correlation values. In few cases, however, phenotypic correlation co-efficient was same with or higher than their corresponding genotypic correlation co-efficient suggesting that both environmental and genotypic correlation in these cases act in the same direction and finally maximize their expression at phenotypic level. Seed yield per plant had highest significant positive correlation with plant height ($G = 0.959^{**}$) which indicated that, if plant height increase, seed yield per plant also increase (Table 7). Number of seed per pod had also significant positive correlation with plant length ($G = 0.385^*$) at genotypic level (Table 6). Plant length had insignificant positive correlation with seed per plant ($G = 0.294$) at genotypic level (Table 6).

On the other hand, number of branch per plant had shown highest negative significant correlation with 1000 seed weight ($G = -0.652^{**}$) which indicated 1000 seed weight was increased with decreasing the number of branch per plant . For this why, ultimately yield per plant was decreased.

4.2.1 Plant height (cm)

Plant height showed significant positive correlation with yield per plant ($G = 0.959^{**}$) and was followed 50% flowering ($G=0.660^{**}$) at genotypic level (Table 6). On the other hand, plant height showed significant negative correlation with number of pods per plant ($G= -0.550^{**}$) at 1% genotypic level. Plant height also showed insignificant positive correlation with number of branch per plant ($G=.236$) genotypic level. On

Table 6. Genotypic and phenotypic correlation coefficient between yield and component characters in *Vigna radiata* L.Wilczek

Character	Correlation	No of Branch Per Plant	No. of Pod Per Plant	Pod Length (cm)	No. of Seed Per Plant	No. of Seed Per Pod	1000 Seed Weight (gm)	Days to 50% Flowering	Yield per plant (gm)
Plant Height (cm)	G	0.236	-0.550**	-0.080	-0.061	0.065	-0.007	0.660**	0.959**
	P	0.069	-0.045	0.172	0.025	-0.113	-0.041	0.006	0.060
No of Branch Per Plant	G		0.959**	0.198	0.102	0.399*	-0.652**	-0.377*	-0.112
	P		-0.021	0.184	0.111	0.055	0.078	-0.134	0.067
No. of Pod Per Plant	G				0.510**	0.067	-0.065	-0.191	-0.466**
	P			0.029	0.133	0.214	-0.020	-0.008	0.049
Pod Length (cm)	G				0.294	0.385*	-0.337*	-0.383*	0.674**
	P				0.291	0.207	-0.142	-0.043	0.056
No. of Seed Per Plant	G					0.060	-0.334*	-0.329*	-0.029
	P					0.125	-0.146	-0.018	0.003
No. of Seed Per Pod	G						-0.172	0.229	0.161
	P						0.023	0.002	-0.005
1000 Seed Weight (gm)	G							0.437**	-0.083
	P							0.089	0.048
Days to 50% Flowering	G								-0.297
	P								-0.080

**Significant at 1% level of probability, * Significant at 5% level of probability g=Genotypic, p=Phenotypic

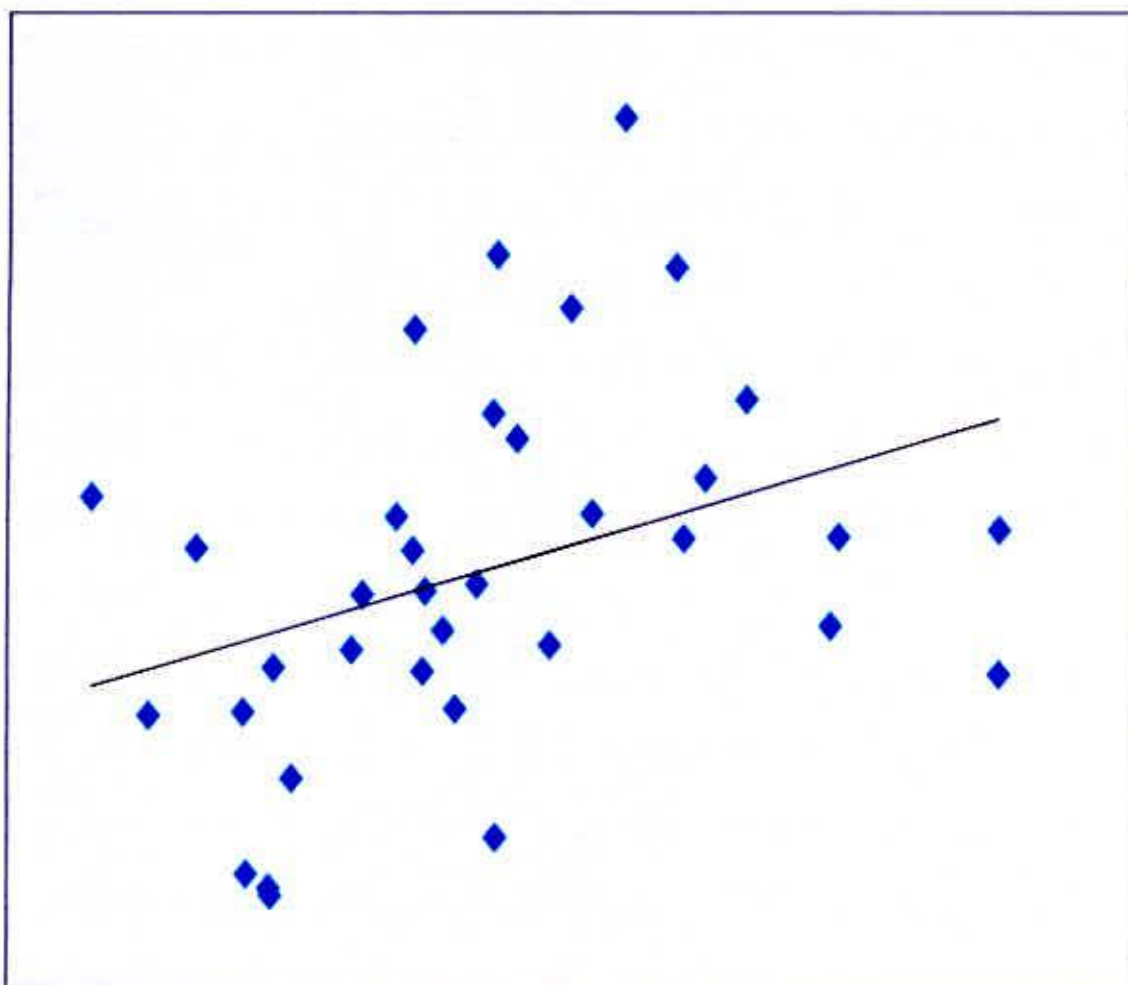


Figure 1. Correlation matrix between pair of characters in 45 mungbean genotypes



Makeen *et al.* (2007), Islam *et al.* (1999), Niazi *et al.* (1999) indicated that plant height had significant positive correlation with seed yield.

4.2.2 Number of branches per plant

This trait showed highly significant positive correlation with number of pod per plant ($G = 0.959^{**}$) at genotypic level (Table 6). On the other hand, number of branches showed highly significant negative correlation with 1000 seed weight ($G = -0.652^{**}$) at 1% genotypic level (Table 6). Significantly positive correlation was found with seed per pod ($G = 0.399^*$) at 5% genotypic level and significant negative correlation was found with 50% flowering ($G = -0.377^*$) at 5% genotypic level. Islam *et al.* (1999) studied yield per plant was significantly and positively correlated with number of primary branches per plant.

4.2.3 Pod per plant

Pods per plant showed significant positive correlation with seed per plant ($G = 0.510^{**}$) at genotypic level (Table-6). Pods per plant also showed significant negative correlation with yield per plant ($G = -0.466^{**}$) at genotypic level (Table-6). It was showed insignificant positive correlation with seed per pod ($P = 0.214$) at phenotypic level.

4.2.4 Pod length (cm)

Pod length showed significant highly positive correlation with yield per plant ($G = 0.674^{**}$) at genotypic level. It was also showed significant positive correlation with number of seed per pod ($G = 0.385^*$) at genotypic level. It was showed significant negative correlation with 50% flowering ($G = -0.383^*$) at genotypic level and followed by 1000 seed weight ($G = -0.337^*$) at genotypic. It was also showed insignificant positive correlation with number of seed per plant ($P = 0.291$) at genotypic level and followed by seed per plant ($G = -0.337^*$) at phenotypic. Similar result was reported by Islam *et al.* (1999), Singh *et al.* (1993). Rahman (1982) was found positively correlation for pod length with 1000-seed weight.

4.2.5 Seed per plant

Seeds per pod showed significant only correlation with 1000 seed weight ($G = -0.334^*$) and followed by 50% flowering ($G = -.329^*$) at genotypic level. Similar results were obtained by Rajan *et al.* (2000), Islam *et al.* (1999) in respect to seeds per plant.

4.2.6 Seed per pod

Seeds per pod showed insignificant only positive correlation with 50% flowering ($G = 0.229$) and non-significant negative correlation with 1000 seed weight ($P = -0.172$) at genotypic level. Similar results were obtained by Rajan *et al.* (2000), Islam *et al.* (1999).

4.2.7 Thousand seed weight (g)

Thousand seed weight showed significant positive correlation with 50% flowering ($G = 0.437^{**}$) at genotypic level. Similar result were obtained by Islam *et al.* (1999), Sharma (1999), Yaqoob *et al.* (1997). Shamsuzzaman and Shaikh (1982) reported 1000-seed weight exhibited negative correlated with seed yield.

4.2.8 Days to 50% flowering

Days to 50% flowering showed highly insignificant negative association with yield per plant ($G = -0.297$) at genotypic level. Rao *et al.* (2006), Yaqoob *et al.* (1997) reported that days to 50% flowering were positive and significantly associated with seed yield. Rahman (1982) obtained positive correlation of days to 50% flowering with days to maturity.



4.3 Path co-efficient

The total correlation coefficient were analyzed further by path co-efficient method to determine the direct and indirect effects of the nine characters on 50% flowering, plant height, branch, pod length, seed per pod, seed per plant, pods per plant, 1000 seed weight and yield per plant. The direct and indirect effects of different characters on yield are present in Table 7.

Path co-efficient analysis proved that, plant length had the highest direct positive effect (0.780) on seed yield followed by plant height (0.508), 1000 seed weight (0.321), number of branch per plant (0.162) and seed per plant (0.004) which indicating true relationship between them and direct selection for this trait would be rewarding for yield improvement (Figure 2).

4.3.1 Plant height (cm)

Plant height (0.508) had positive direct effect on branch per plant (0.038), number of pod per plant (0.205), seed per plant (0.001) and had high positive direct effect (0.508) on yield per plant (0.959**) and positive indirect effect through plant length (-0.063), seeds per pod (-0.008), 1000 seed weight (-0.002) days to 50% flowering (-0.018) (Table 7). Maximum direct effect on seed yield was observed in plant height reported by Makeen *et al.* (2007), Sharma (1999). Rao *et al.* (2006) and Yaqoob *et al.* (1997) found plant height showed negative direct effect on seed yield.

4.3.2 Number of branches per plant

Number of branches per plant (0.162) had positive direct effect on plant height (0.120), pod length (0.154), seed per plant (0.001) and days to 50% flowering (0.065). On the other hand positive indirect effect (0.162) was found on viz. pod per plant (-0.357), seed per pod (-0.047), 1000 seed weight (-0.209), and seed yield per plant (-0.112). Bhaumik and Jha (1980) found indirect effect of primary branches on the yield.

4.3.3 Pod per plant

Pod per plant (-0.373) showed negative direct effect on branches per plant (0.155), plant length (0.024), seed per plant (0.002) and 50% flowering (0.033). On the other hand, Pod

Table 7. Direct (Diagonal) and indirect effect of some yield contributing characters on *Vigna radiata* L. Wilczek

Character	PH (cm)	NBPP	NPPP	PL (cm)	NSPP	NSPD	TSWT (g)	DFP	Yield (g)
PH (cm)	0.508	0.038	0.205	-0.063	0.001	-0.008	-0.002	-0.018	0.959 **
NBPP	0.120	0.162	-0.357*	0.154	0.001	-0.047	-0.209	0.065	-0.112
NPPP	-0.279	0.155	-0.373	0.024	0.002	-0.008	-0.021	0.033	-0.466**
PL(cm)	-0.041	0.032	-0.012	0.780	0.001	-0.045	-0.108	0.066	0.674**
NSPP	-0.031	0.017	-0.190	0.230	0.004	-0.007	-0.107	0.057	-0.029
NSPD	0.033	0.064	-0.025	0.300	0.000	-0.117	-0.055	-0.040	0.161
TSWT(g)	-0.003	-0.105	0.024	-0.263	-0.001	0.020	0.321	-0.075	-0.083
DFP	0.052	-0.061	0.071	-0.299	-0.001	-0.027	0.140	-0.172	-0.297

Residual Effect (R) = 0.148

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

PH = Plant height (cm), NBPP=No. of branches/plant, NPPP= No. of Pod per Plant, PL=Pod length (cm), NSPP= No. of Seed /Plant, NSPD= No. of Seed/Pod, TSW= Thousand seed wt. (g), SYPP=Seed yield per plant, DFP = Days to 50% flowering (days).

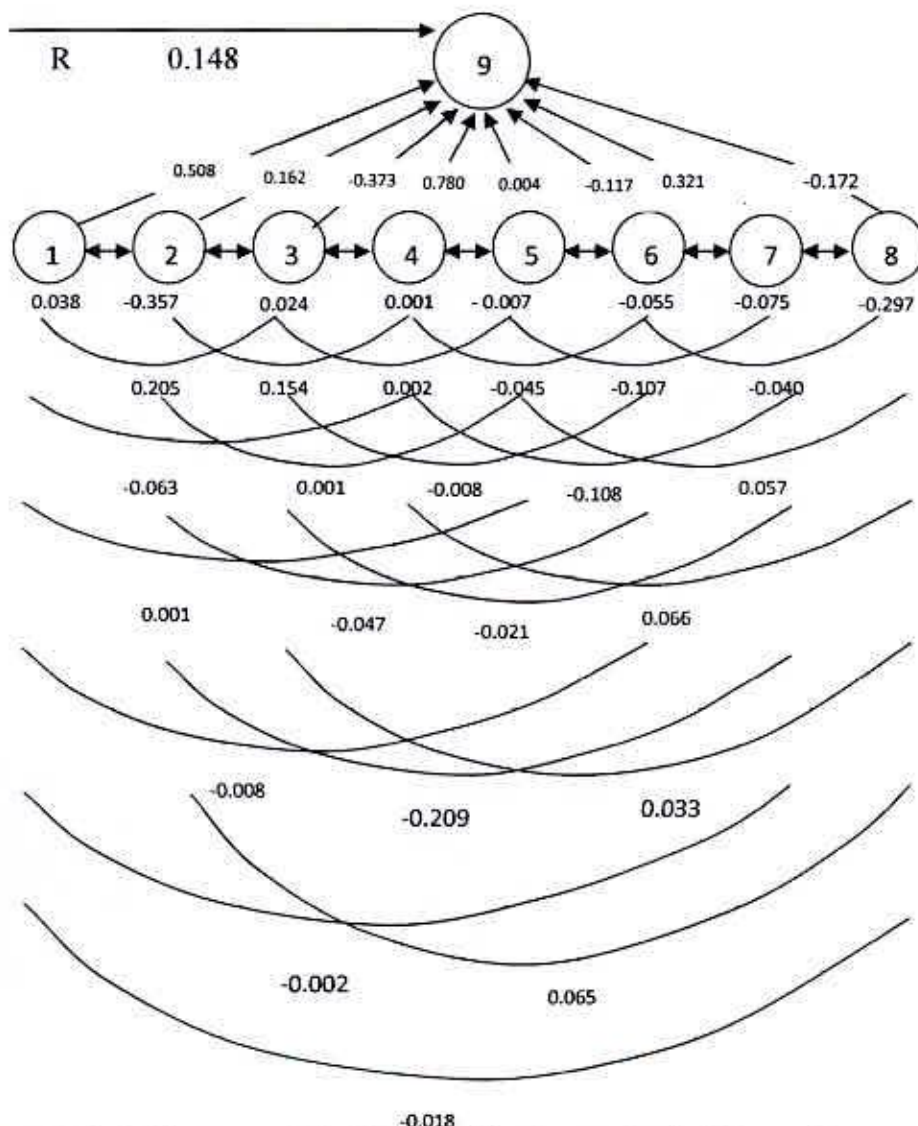


Figure 2. Path diagram of 9 yield contributing traits in 45 mungbean genotypes

1 = days to 50% flowering, 2 = plant height, 3=branch, 4 = pods/plant, 5= pod length, 6 = seed/pod, 7= seed/plant, 8=1000 seed weight, 8 = yield/plant

R= residual effect.

per plant (-0.373) showed negative indirect effects through plant height (-0.279), seed per pod (-0.008), 1000 seed weight (-0.021) and had highest negative indirect effect on yield per plant (-0.466) (Table 7). Makeen *et al.* (2007), Rao *et al.* (2006), Rajan *et al.* (2000), Sharma (1999), Singh and Malhotra (1976) found maximum positive direct effect on seed yield was observed in pods per plant.

4.3.4 Pod length (cm)

Pod length (0.780) showed highest positive direct effect on branches per plant (0.032), seed per plant (0.001) and 50% flowering (0.066) and had highest positive direct effect on yield per plant (0.674). On the other hand, Pod length showed positive indirect effects (0.780) through plant height (-0.041), Pod per plant (-0.012), seed per pod (-0.045) and 1000 seed weight (-0.021) (Table 8). Bhaumik and Jha (1980) found the same result.

4.3.5 Seed per plant

Seed per plant showed positive direct effect (0.004) on branches per plant (0.017), pod length (0.230) and 50% flowering (0.057). On the other hand, Seed per plant showed positive indirect effects (0.004) through Pod per plant (-0.190), seed per pod (-0.007), 1000 seed weight (-0.107) and yield per plant (-0.029) (Table 7).

4.3.6 Seed per pod

Seed per pod showed negative direct effect (-0.117) on plant height (0.033), branches per plant (0.064), pod length (0.300) and yield per plant (0.161). On the other hand, Seed per pod showed negative indirect effects (-0.117) through seed per plant (-0.025), 1000 seed weight (-0.055), and 50% flowering (-0.040), and pod per plant (-0.025) (Table 8). Rahman (1982) found number of seeds/pod (-0.800) had negative direct contribution to yield.

4.3.7 Thousand seed weight (gm)

Thousand seed weight had positive direct effect (0.321) on pod per plant (0.024) and seed per pod (0.020) and yield per plant (0.161). On the other hand, thousand seed weight positive indirect effects (0.321) through plant height (-0.003), branches per plant (-0.105), seed per plant (-0.001), pod length (-0.263), and 50% flowering (-0.075) (Table 7). Singh

and Malhotra (1976) observed 1000-seedweight had a negative indirect effect on yield by affecting the number of seeds/pod. Singh and Malhotra (1976) observed 1000-seedweight had a negative indirect effect on yield by affecting the number of seeds/pod.

4.3.8 Days to 50% flowering

Days to 50% flowering had negative direct effect (-0.172) on plant height (0.052), number of pod per plant (0.071), 1000 seed weight (0.140). Days to 50% flowering had negative indirect effect (-0.172) on yield per plant (-0.297), branch per plant (-0.061), seed per pod (-0.001) and seed per plant (-0.027) (Table7). Yaqoob *et al.* (1997), Rahman (1982) observed positive direct effect of days to 50% flowering on seed yield.



Chapter 5

Summary and Conclusion



CHAPTER 5 SUMMARY AND CONCLUSION

An experiment was conducted in a randomized block design with three replication with a view to determine the variability in respect of yield and interrelationship among the characters and their path analysis of 45 genotypes of *Vigna radiata* L. Wilzeck at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka, during March 2008 to April 2008. Data on Plant height (cm), branches/plant, days to 50% flowering, no. of pod /plant, 1000 seed wt. (g), no. of seed/pod, no of seed per plant, Pod length (cm), yield/ plant (g) were recorded. There was play a great role of significant variation for all the characters among the genotypes and varieties. The highest mean value was observed for days to 50% flowering. This character also exhibited the highest range of variation (56.35-29) indicated that all the genotypes showed wide range of variation in respect of this character. It showed high heritability (59.01%) accompanied with low genetic advance in percentage of mean and the phenotypic variance (15.74) was higher than the genotypic variance (5.48). However, these differences were in case of plant height, pod per plant, 1000- seed weight indicating greater influence on environment for the expression of these characters. These entire characters showed moderate to high phenotypic and genotypic co-efficient of variation among these characters, days to 50% flowering, branches per plant, pod length, seed per pod, and yield per plant showed least difference between phenotypic and genotypic variance, which indicated additive gene action for the expression of this characters.. Among the characters the highest genotypic co-efficient of variation was recorded no. of Plant height (8.04), no. of branches/plant (7.61) followed by 1000-seed weight (23.59), yield/plant (15.7), plant height (10.39).

Heritability in broad sense was moderate to high for all the characters studied and it ranged from 37.04% to 59.01% which indicated that selection based on phenotypic expression of any character for breeding could be effective. The genetic advance was very low to moderate. These findings proved that it was indicative of non-additive gene action. The high heritability was being exhibited due to favorable influence of environment rather than genotypes. Thus, the genotypes which performed well in various characters

were due to genetic reasons and have a possibility for improvement through selection in the subsequent generations.

The significant positive correlation at the 5% level was observed for seed per pod with branches per plant at genotypic level and the significant positive correlation at the 1% level seed yield per plant with plant height and seed per pod with branch per plant both at genotypic level. The significant negative correlation at the 1% level was observed for 50% flowering with plant length genotypic (-0.383) level. A high degree of significant positive association were observed for seed yield per plant vs. plant height (highest value 0.959) and plant length, 50% flowering vs. plant height and 1000 seed weight, seed per pod vs. branch per plant (highest value 0.959). Strong negative significant correlations were found between 1000 seed weight vs. branch per plant, pod per plant vs. plant height, seed yield per plant vs. pod per plant, pod length vs. thousand seed weight and 50% flowering, seed per plant vs. thousand seed weight and 50% flowering and 50% flowering vs. branch per plant. Thousand seed weight and yield per plant; pod per plant vs. pod length and seed per pod. The highest insignificant positive correlation was observed for seed per plant vs. pod length, branch per plant vs. plant height, pod per plant vs. seed per pod, pod length vs. seed per pod and 50% flowering vs. seed per pod. The highest insignificant negative correlation was observed for days to 50% flowering vs. seed yield per plant at genotypic level.

The character plant height had maximum positive direct effect on yield per plant. Pod per plant had maximum negative direct effect on yield per plant. The residual effect was medium. Plant height, number of branch per plant, 1000-seed weight, pod length, 50% flowering and yield per plant, are the characters for the improvement of yield of the crop and can be used as selection criteria in future breeding programme.

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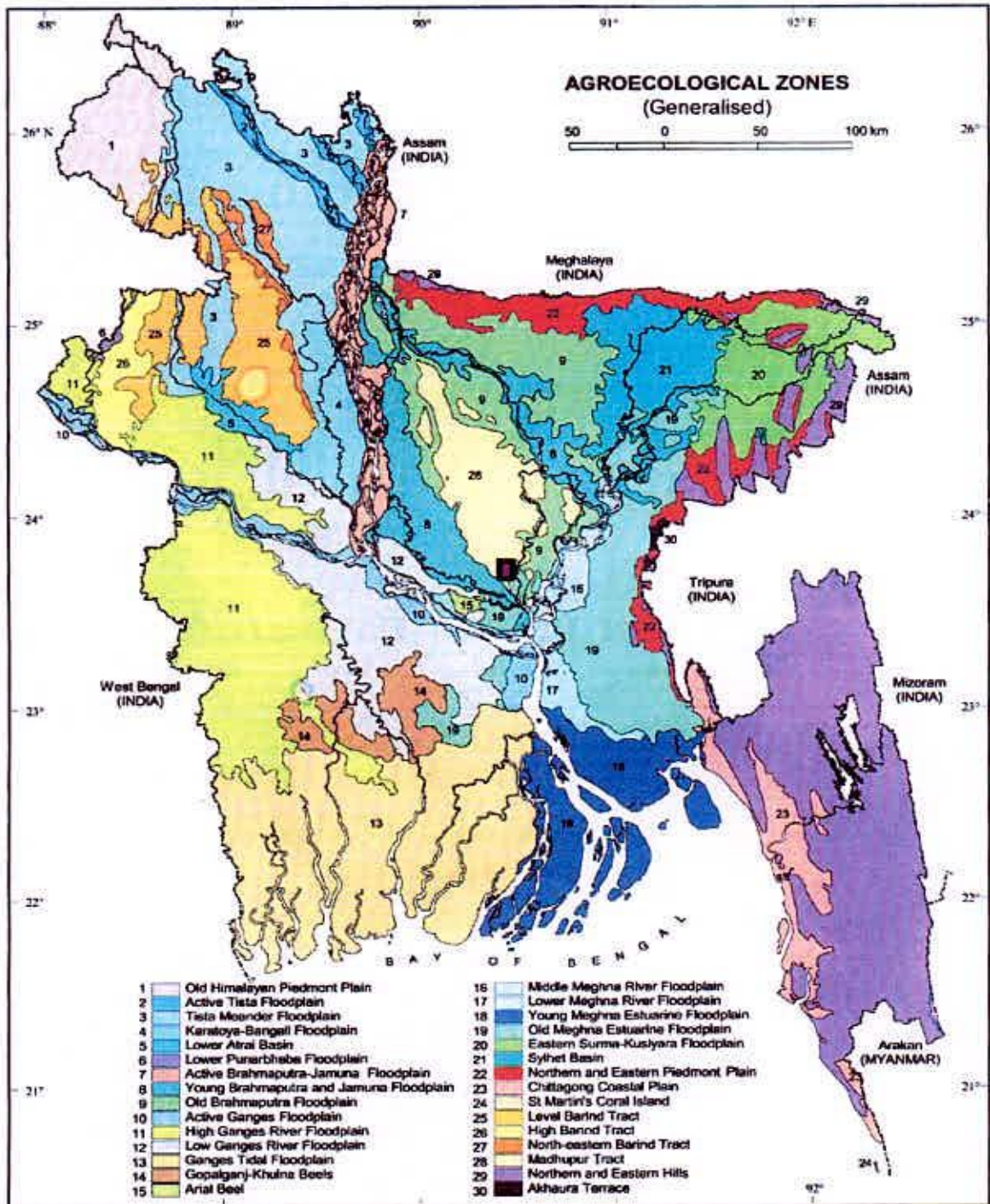
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APPENDICES

Appendix I. Map showing the experimental site under study



THE EXPERIMENTAL SITE UNDER STUDY



APPENDIX II. Monthly record of air temperature, relative humidity and rainfall of experimental site during the period from November 2007 to May 2008

Month	Year	Air temperature (°c)		Relative Humidity (%) at 12 p.m.	Rainfall (mm)
		Maximum	Minimum		
November	2007	29.07	18.80	65.13	0
December	2007	27.07	15.65	63.80	3
January	2008	24.76	13.46	69.53	0
February	2008	31.26	19.42	51.27	0
March	2008	33.20	22.00	46.13	0
April	2008	33.74	23.81	61.40	185
May	2008	33.66	24.95	46.27	180

Source: Bangladesh Meteorological Department (Climate Division) Agargaon, Dhaka1212.