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

BY

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CERTIFICATE

This is to certify that thesis entitled, ***"Genetic variability, correlation and path coefficient analysis of yield and yield contributing 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 bonafide research work carried out by* ***MUMTAZ PARVIN,*** *Registration No.* **07-2612** *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, 2008
Place: Dhaka, Bangladesh

(Prof. Dr. Md. Sarowar Hossain)
Supervisor

LIST OF ABBREVIATED TERMS

FULL NAME	ABBREVIATION
Agro-Ecological Zone	AEZ
And others	*et. al.*
Bangladesh Agricultural Research Institute	BARI
Bangladesh Bureau of Statistics	BBS
Centimeter	cm
Co-efficient of Variation	CV
Days After Sowing	DAS
Degree Celsius	^{o}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^2_g
Gram	g
Hectare	ha
Heritability in broad sense	h^2b
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^2_p
Randomized Complete Block Design	RCBD
Research	Res.
Sher-e-Bangla Agricultural University	SAU
Standard Error	SE
Square meter	m^2
Triple Super Phosphate	TSP
Unites Nations Development Program	UNDP

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SAU, Dhaka

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

BY

MUMTAZ PARVIN

ABSTRACT

Forty genotypes of mungbean (*Vigna radiata L.* Wilzeck.) were studied in a field experiment conducted at the experimental field of Sher-e-Bangla Agricultural University, Dhaka, during February 2008 to May 2008. The objectives of the study were to measure the variability among the genotypes for yield and yield contributing characters, estimate genetic parameters, association among the characters and their contribution to yield. There was a great deal of significant variation for all the characters among the genotypes. Considering genetic parameters high genotypic co-efficient of variation (GCV) was observed for number of primary branches/plant, number of secondary branches/plant whereas pod length and seed per pod showed low GCV. In all cases, phenotypic variances were higher than the genotypic variance. High heritability with low genetic advance in percent of mean was observed for days to 50% flowering which indicated that non-additive gene effects were involved for the expression of this character and selection for such trait might not be rewarding. High heritability with high genetic advance in percent of mean was observed for number of primary branches per plant and secondary branches per plant indicating that this trait was under additive gene control and selection for genetic improvement for this trait would be effective. The results obtained, showed that seed yield per plant had high positive and high significant relation with 1000-seed weight. Correlation studies revealed highest significant association of yield per plant with thousand seed weight at genotypic and phenotypic level. Path coefficient analysis revealed maximum direct contribution towards seed yield per plant thousand seed weight followed by pods per plant. Considering all the characters the G1 (BD-6901), G3 (BD-6903), G11 (BD-6914), G12 (BD-6918), G30 (BD-6886), G37 (BD-6895), G39 (BD-6898) were selected for future breeding programme.

Chapter I

Introduction

CHAPTER I
INTRODUCTION

Bangladesh grows various types of pulse crops. Among them grass pea, lentil, mungbean, blackgram, field pea and cowpea are important. Mungbean *(Vigna radiata* L. Wilczek) belongs to the family Leguminoseae, sub family papilionaceae. Mungbean is an annual food legume. It is one of the important crops well suited to dry areas, mainly under irrigated conditions. It is cultivated traditionally by small landholders throughout tropical, subtropical and temperate zones of Asia including Bangladesh, Pakistan, India, Sri Lanka, Nepal, Thailand, China, Korea and Japan. Since mungbean has a short maturity span (60-75 days) it is grown under various cropping systems, hence contributing to the increase of the small landholders' income as well as to the improvement of the soil conditions (Fernandez and Shanmugasundaram, 1988). In the South Asia, mungbean is used to make daal. Daal is the most common dish which is made from various kinds of split legumes with spices. In the Southeast and East Asian countries, it is used to make various kinds of sweet, bean jam, sweetened bean soup, vermicelli, and bean sprout. In Bangladesh it is grown under a wide range of agro-ecological zones of both rainfed and irrigated nature mainly in the Barisal and Patuakhali district. During 2006-2007, it was cultivated over an area of 65 thousand ha with 40 thousand tones production, and average yield of 1.2-1.4 tones/ha (MOA of Bangladesh, 2007). The average yield is much low than its potential, and the yield obtained in many other countries. One of the reasons of low yield is unavailability of high yielding cultivars with better adaptability.

Most of the cropping patterns are dominated by rice. More than 90 % of the arable land is brought under cultivation, and there is a little scope forincreasing production horizontally (i.e. by bringing more land under cultivation). Recently, Bangladesh achieved self sufficiency in cereal production. Vegetables production trend is also positive for its ready market, high demand and availability of good variety, though fruits production remains static. Production of grain legumes (pulses) and oilseeds declined sharply, mostly for decreasing of cultivation area .The country has to import more than 50% of its requirement for pulses, spending hard currency.

According to FAO (1999) a minimum intake of pulse by a human should be 80gm per head day by day where as it is only 14.19gm in Bangladesh (BBS, 2007). Proximate composition of mungbean are food energy 347 cal, crude protein 23.86%, fat 1.15%, carbohydrate 62.6%, crude fibre 5.27%, ash 3.32%, digestibility 79%, biological co-efficient 72%, lysine 436%, methionine 75mg, cystine 55mg.(Poehlman, 1991).

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.

A lot of research 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. Research have shown that the

ultimate yield components that contribute directly to the grain yield are in order of development , the number pods , average seed number , and average seed size (Adams , 1967). Among these yield components, the most dominant contributor to grain yield is the number of pods per plant or more precisely pods per unit land area in various legumes (Ishag, 1973; Mackenzic, 1975) including mungbean (AVRDC, 1976; Kumari and George, 1982).

Abscission may be of value to the plant in several ways. It can be a process of self-pruning, removing injured, diseased, or senescent parts. It permits the dispersal of seeds and other reproductive structures. It facilitates the recycling of mineral nutrients to the soil. It functions to maintain homeostasis in the plant, keeping in balance leaves and roots, and vegetative and reproductive.

Genetic variability is a prerequisite for a successful breeding programme of any crop species and a critical survey of genetic variability is essential before initiating an improvement programme aiming to develop high yielding varieties. The correlation coefficients between yield components usually show a complex chain of interacting relationship. Path coefficient analysis partitions the components of correlation coefficient into direct and indirect effects and visualizes the relationship in more meaningful way.

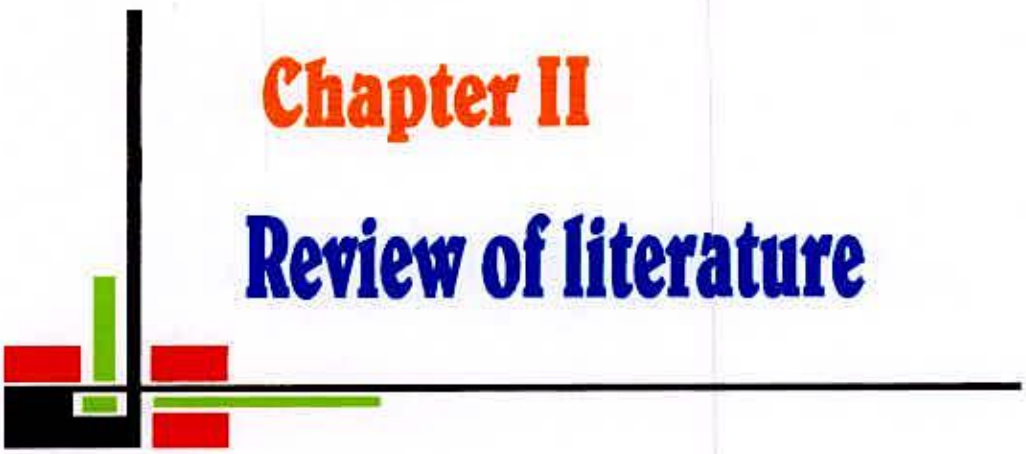
Yield is the complex end product of many factors which jointly or singly influence the seed yield. Mungbean yield is dependent on many important characters as well as on the environmental influence. For yield improvement it is essential to have knowledge on genetic variability of a biological population is an outcome of genetic constitution of the individuals making

up that population in relation to prevailing environment. A survey of genetic variability with the help of suitable parameters such as genotypic co-efficient of variation, heritability and genetic advance are absolutely necessary to start an efficient breeding programme.

The study of character is also essential for ascertaining their contribution towards yield. Direct and indirect effects of yield contributing characters on yield are also important in selecting high yielding genotypes. Path co-efficient analysis is used to detect characters having direct and indirect effects on yield.

With conceiving the above theme in mind, the present research work has been undertaken in order to fulfilling the following objectives:

1. To assess the variability present in different genotypes .
2. To evaluate the performance of 40 mungbean genotypes for yield and yield contributing characters .
3. To assess the characters association and contribution of characters for yield and yield contributing characters.
4. To screen out the best genotypes for further use in breeding.



Chapter II

Review of literature

CHAPTER II
REVIEW OF LITERATURE

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 aconitofolia* 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.

Identification of superior parents, promising cross combination and suitable breeding methodology are the important pre-requisites for development of high yielding genotypes. The crop has received much attention by the researchers on various aspects of its production and utilization for different consumer uses. Many studies on the abscission, variability, correlation,

heritability and genetic advance have been carried out in many countries of the world. The work so far done in Bangladesh is not adequate and conclusive. Nevertheless, some of the important and informative works and research findings have been reviewed in this chapter under the following headings:

2.1 Variability

2.2 Correlation coefficient

2.3 Path coefficient

2.1 Variability:

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

Abrahim *et al.* (2006) evaluated genetic variability and heritability analyses for yield and yield components which were conducted for 646 accessions of green gram grown in Coimbatore, Tamil Nadu, India, during the rabi and kharif of 2002-04. The estimates of phenotypic (PCV) and genetic (GCV) coefficients of variation were higher for single plant yield, number of branches per plant, number of pods per plant, number of clusters per plant, plant height, and length of branch, indicating greater scope of selection for these traits. Dry matter production and number of clusters per branch

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

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

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.

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

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

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

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.

Venkateswarlu (2001) were assessed genotypic coefficents 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.

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

Sharma (1999) studied on genotypic and phenotypic coefficients of variation, heritability derived from data on 9 yield-related traits in 15 mung bean 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.

Vikas *et al.* (1998) evaluated eighteen mung bean 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.

Das and Chakraborty (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.

Reddy (1997) evaluated seventy genotypes of green gram from different geographical regions for 10 yield components at Tirupati in 1994. Genotypic and phenotypic variation were 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 heritabilities 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.

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

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

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

Sandhu (1979) studied variability among 435 strains of mun gbean for the characters, days to 50% flowering and maturity, plant height,number of branches, pods/plant, pod /plant, seed/pod,1000-seed weight and grain grain yield and sufficient variability for all the characters. The phenotypic

coefficient of variation was the highest (50.4 for total number of branches/plant. Grain yield/plant, pods/plant and clusters/plant also showed considerable phenotypic coefficient of variation (34.4, 32.7 and 30.1 percent, respectively.

2.2 Correlation coefficient:

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

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

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

Dhuppe *et al.* (2005) studies on correlation which were carried out in 35 genotypes (11 parental lines and 24 hybrids) of mung bean, grown in

Parbhani, Maharashtra, India, in 1998. Data were recorded for days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per plant, 100-seed weight and yield per plant. Grain yield per plant showed positive and significant correlation with days to maturity, number of secondary branches per plant, number of pods per plant and 100-seed weight at genotypic level, whereas secondary branches per plant and 100-seed weight were correlated with grain yield at phenotypic level. l-781 K-H x AKM-9242 were found .

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

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

Rajan *et al.* (2000) were studied the correlation 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, 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.

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

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

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

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

Sharma (1995) observed highly significant and positive correlations for number of seeds/plant and 100-seed weight with seed yield in 6 mung bean (*Vigna radiata*) genotypes and their 6 F_1 and 6 F_2 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 and Pathok (1993) recorded on 11 quantitative traits in 20 *Vigna radiata* parents, 90 F_1s and 90 F_2s. Seed yield was positively correlated with plant height, clusters/plant, number of pods/cluster, number of pods/plant, pod length, seeds/pod and 100-seed weight.

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

reported the height and 1000-seed weight exhibited negative correlated with seed yield.They also reported the heighest 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.

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.

2.3 Path coefficient:

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

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

effects on seed yield per plant. The number of productive branches per plant had a direct significant contribution to seed yield per plant.

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

Dhuppe *et al.* (2005) studies on correlation and path analysis which were carried 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.

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

Sharma *et al.* (1999) studied on correlation coefficients is derived from data on 9 yield-related traits in 15 mung bean crosses and their six parents grown at Raipur during 1995-96.Phenotypic and genotypic path analysis revealed

that seeds/plant had the highest positive direct effect on grain yield followed by 1000 seed weight, plant height and pods/plant..

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

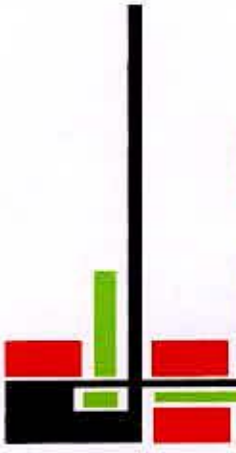
Yaqoob *et al.* (1997) studied ten important agronomic characters for estimation of co-efficient of correlation in 30 genotypes/mutants of mung bean grown under rainfed conditions at Dera Ismail Khan in 1991. Path co-efficient analysis revealed positive direct effects of days to 50% flowering, days to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

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

Bhaumik and Jha (1980) conducted path coefficient analysis in 20 mungbean cultivars and found indirect effect of number of nodes on the

main stem and number of primary branches on the yield through the number of pods/plant and that of pod length was through number of seeds/pod and 1000-seed weight. They also reported negative correlation of yield with plant height both directly and indirectly.

Singh and Malhotra (1976) performed an experiment with 75 strains of 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.



Chapter III

Materials and Methods

CHAPTER III
MATERIALS AND METHODS

A field experiment was conducted in the experimental field of Genetics and Plant Breeding Field Laboratory of Sher-e Bangla Agricultural University, Dhaka, Bangladesh during the period from last week of February 2007 to First week of May 2008 to study on the inter genotypic variability and genetic divergence in Mungbean *(Vigna radiata* L. Wilczek) .The materials and methods of this experiment are presented in this chapter under the following headings

3.1 Site of experiment:

The experiment was conducted at the field laboratory of the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka during the period from February 2008 to May 2008. The experimental site was at 90022" E longitude and 23041" N latitude at an altitude of 8.6 meters above the sea level.

3.2 Materials:

A total of forty genotypes (40) 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.

3.3 Soil and climate:

The land belongs to Agro-ecological region of 'Madhupur Tract' (AEZ 28) of Nodda soil series. The soil was sandy loam in texture having pH 5.47-5.63. The mean temperature of the growing period was 24.36◦ C with average maximum and minimum being 30◦ C and 18.67◦ C respectively.

Table 1. List of mungbean genotypes with their sources

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

3.4 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 15cm and line to line distance was 30 cm. The total land size was 126.75 m^2. The plot to plot distance was 2.5 m. The genotypes were randomly distributed to each row within each line. Field of the experiment is presented in the Plate no. 1 and A single mungbean plant is presented in Plate no.2.

3.5 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 26 February 2008.

3.6 Manure and fertilizer:

Due to its ability of nitrogen fixation from the atmosphere lentil require less nitrogen application. But for initial establishment of plant up to the stage of nodule formation a starter dose of 20-40-20 NPK respectively was applied. 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.

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.

Plate 1: Field view of the experimental field

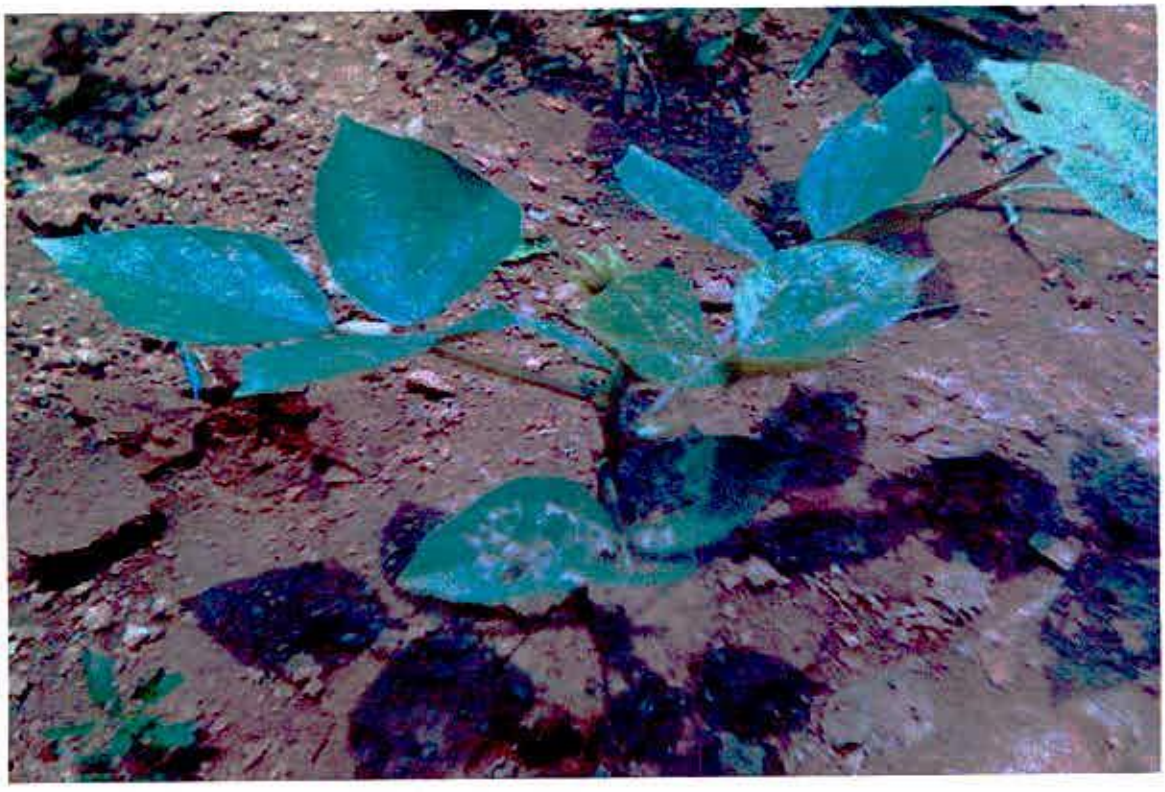


Plate 2: A single mungbean plant in the experimental field

Table: 2 Doses of different fertilizers in field

Fertilizers/ Manures	Dose (Kg)	
	Applied in the plot	Quantity/ha
Urea	2.01	47
TSP	3.56	88
MP	1.51	36
Cow dung	Applied earlier	2.00 ton

3.7 Sowing of seeds and intercultural operation:

The seeds of 40 mungbean genotypes were sown in the field on 25 February 2008. Intercultural practices were done uniformly for all the genotypes. Thinning was done 25 days after sowing and wedding was done twice-the first during thinning and the second after about two months of sowing.

3.8 Harvesting:

Different genotypes matured at different times. The harvesting was completed by 14 may 2008. Ten plants from each plot were randomly selected to collect data and these were harvested by uprooting. Border plants were discarded to avoid border effect.

3. 9 Recording of Experimental Data:

Data on the following characters were recorded on individual plant basis from 10 randomly selected plants per genotypes in each replicate. For the quantitative characters, out of 10 characters, Days to 50% flowering, Abscission %, Days to maturity were recorded in the field condition and the

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. A mungbean plant with flowers is presented in Plate no. 3.

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 primary branches/plant

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

3.9.4 Number of secondary branches/plant

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

3.9. 5 Percentage of Abscission

Abscission parameters were recorded from ten randomly selected plants. Flowers that opened everyday were counted in the morning. The flower count until the plants almost stopped flowering. At maturity, the matured pods, seeds per pods, and 1000gm seed weight were recorded from the same plants that were to collect abscission data.

The abscission percentage will be computed as follows –

$$\text{Abscission (\%)} = \frac{\text{Total open flower} - \text{total matured pod} \times 100}{\text{Total open flower}}$$

Total open flower

3.9.6 Pod per plant: The total number of pods in individual plants was recorded. A mungbean plant with some mature pod is presented in Plate no.4.

3.9.7 Pod length: length of pod was measured in cm.

3.9.8 Seed per pod: Total number of seed in each pod within the individual plants was counted.

3.9.9. 1000 seed weight

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

3.9.10 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. Formula of the percentage of abscission:

Reproductive abscission is a possible limiting yield factor in mungbean, *Vigna radiata* (L.) Wilzeck).

The abscission percentage will be computed as follows –

$$\text{Abscission (\%)} = \frac{\text{Total open flower} - \text{total matured pod}}{\text{Total open flower}} \times 100$$

All the collected data of the present study were used for statistical analyses. For each character, analysis of variance (ANOVA), Mean, Range were calculated by computer sing MSTATE software, the mean values were separated by DMRT then analyzed for genotypic and phenotypic variance, genotypic and phenotypic coefficient of variation,

Plate 3:A mungbean plant with flower

Plate 4: A mungbean plant with some mature and green pod

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

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

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

3.10.3 Genotypic and Phenotypic coefficient of variation

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

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

Where,

σ_g = Genotypic standard deviation

$\bar{x}$ = Population mean

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

Where, σ_p = Phenotypic standard deviation

$\bar{x}$ = Population mean

3.10.4. Estimation of Heritability

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

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

Where, σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

3.10.5 Estimation of Genetic advance

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

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

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

3.10.6 Correlation Coefficient

Genotypic Correlation coefficient was calculated suggested by Miller *et al.* (1955): $r_{gxy} = \frac{\sigma^2_{gxy}}{\sqrt{(\sigma^2_{gy} \times \sigma^2_{gx})}}$

Phenotypic Correlation coefficient

Phenotypic Correlation coefficient was calculated suggested by Miller *et al.* (1955): $r_{pxy} = \frac{\sigma^2_{pxy}}{\sqrt{(\sigma^2_{py} \times \sigma^2_{px})}}$

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).

3.10.8Calculation of direct effect:

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

$A = BC$

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

Where,

C = Direct effect of the characters on yield .

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

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

3.10.9. Calculation of residual effect:

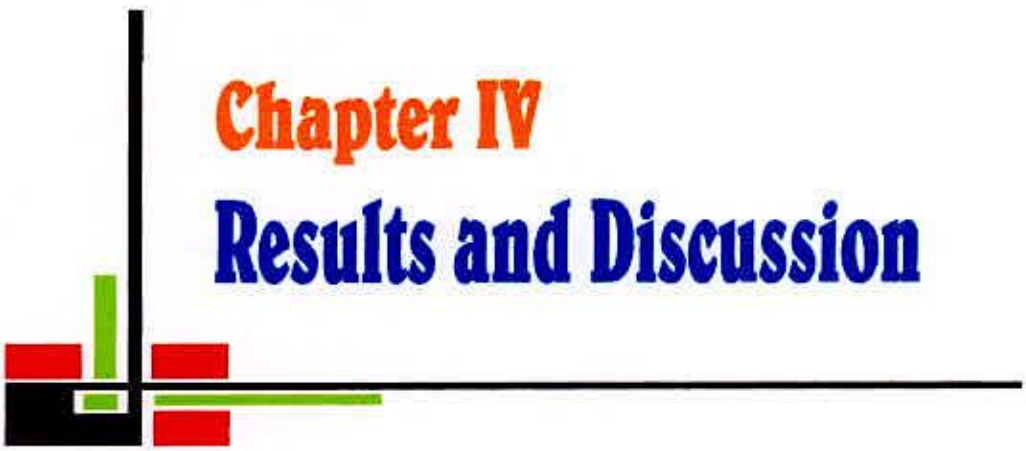
After calculating the direct and indirect effects of the character the residual effect was calculated by the following formula (Singh and Chowdhury, 1985).

$Pry = \sqrt{1 - \sum Piy.riy}$

Where, ry = Correlation of the ith character with yield.

Piy = Direct effect of ith character on yield

Pry = Residual effect.



Chapter IV

Results and Discussion

CHAPTER IV
RESULTS AND DISCUSSION

This chapter comprises the presentation and discussion of the findings obtained from the study. The study was carried out to find out the phenotypic and genotypic variability, co-efficient of variation, heritability, genetic advance, correlation, path coefficient analysis among different genotypes to estimate the direct and indirect effect of yield contributing traits on yield. The heritable (genetic) and non-heritable (non-genetic) components were estimated for different characters. Ten characters such as plant height, number of primary branches per plant, number of secondary branches per plant, days to 50% flowering, percentage of abscission, number of pods per plant, length of pod, number of seeds per pod, thousand seed weight and seed yield per plant were studied in respect of 40 genotypes.

4.1 Variability

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 are presented in Table 5; heritability and genetic advances of these characters are presented in Table 6. Among the genotypes almost all characters showed highly significant variation indicating wide scope of selection for these characters. The data revealed substantial variability and thus high possibility of improvement in most of the traits. The phenotypic variance was

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 (34.559**) 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 G10 (33.04 cm) and the genotypes G30 and G7 were statistically about similar (33.00 and 32.95) which was statistically different with other genotypes while the shortest genotype was G14 (19.20cm) which was followed by G19 (21.13 cm) (Table 4).The phenotypic variance (16.50) was considerably higher than the genotypic variance (9.03) and the phenotypic and genotypic co-efficient of variations were 14.04 % and 10.39 %, 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), Abrahim *et al.* (2006), Rao *et al.* (2006), Vikas *et al.* (1998) and Reddy *et al.* (2003) in their study.

4.1.2 Number of Primary Branches/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 primary branches/plant was recorded in genotype G28 (6.90) (Table 4).On the other hand the minimum number of primary branches/plant was recorded in the genotypes G13 (1.33) which was

Table 3. Analysis of variance of the data of 10 important characters in respect of 40 *Vigna radiata*

Source of variance	df	Plant height	Primary branch	Secondary branch	Days to 50% flowering	% abscission	Pods/plant	Pod length(cm)	Seeds/pod	1000 seed weight (g)	Yield /plant (g)
Replication	2	8.379	3.543**	0.001	4.608**	43.814	7.722	0.576	0.269	28.277	1.923
Genotypes	39	34.559**	5.167**	1.550**	46.366**	70.173**	44.674**	1.112	134.100*	274.059**	12.511**
Error	78	7.467	0.242	0.242	0.643	20.522	18.329	0.862	0.787	11.116	1.253

*Indicates significant at the 0.05 df=Degrees of freedom

**Indicates significant at the 0.01 level

Table 4: Mean performance of 10 important characters in respect of 40 *Vigna radiata* L.Wilczek genotypes

Genotype	Acc. No.\name	Plant height	Primary branch/plantt	Secondary branch/plant	50% Flowering	% Abscission	Pods /plant	Pod length (cm)	Seed/pod	1000-seed weight (g)	Yield/plant(g)
G1	BD-6901	25.72c-h	4.00i-n	0.87jk	42.00f-h	23.86j-l	34.00b-g	6.81	9.95ab	37.13k-m	12.55c-g
G2	BD-6902	32.59a-c	5.25c-f	1.47g-k	39.00k	25.48h-l	34.67a-g	6.76	9.02a-e	37.20k-m	11.30e-h
G3	BD-6903	32.49a-c	5.38c-f	1.53g-k	45.00c	24.67j-l	33.33b-g	7.21	10.07a	39.88h-m	13.82a-d
G4	BD-6904	31.94a-d	4.47f-k	1.23h-k	39.00k	30.46a-k	33.00b-g	7.18	10.07a	37.87j-m	12.59c-g
G5	BD-6905	32.70ab	3.70k-o	2.60a-d	35.33l	28.42c-k	38.67a-e	6.62	8.60a-e	40.54h-m	13.14b-g
G6	BD-6907	32.35a-c	2.70p-s	3.37a	35.67l	37.29a-c	33.00b-g	8.48	9.17a-e	34.10m-o	11.53e-h
G7	BD-6909	32.95a	4.47f-k	3.00ab	40.67h-j	36.10a-e	39.67a-d	7.17	9.34a-e	34.48m-o	12.93b-g
G8	BD-6911	28.37a-f	2.50p-s	1.33g-k	39.00k	33.83a-i	36.33a-f	5.95	9.09a-e	30.50n-p	10.09h-j
G9	BD-6912	30.24a-e	5.23c-f	3.20a	35.00l	31.86a-k	38.57a-e	6.34	7.99de	25.89p-r	8.63j
G10	BD-6913	33.04a	2.80o-s	1.17h-k	47.67b	31.38a-k	34.67a-g	7.08	9.36a-e	28.93o-q	9.19ij
G11	BD-6914	28.85a-f	2.60p-s	1.20h-k	35.00l	18.20l	37.90a-e	7.94	9.37a-e	56.33bc	15.61a
G12	BD-6918	27.11e-g	2.57p-s	1.07i-k	43.00d-f	27.26c-k	36.97a-f	6.64	9.62a-d	52.67cd	15.56a
G13	BD-6924	22.30g-i	1.33t	0.78jk	39.00k	34.64a-g	38.67a-e	5.91	7.75e	40.59h-m	12.17c-h
G14	BD-6925	19.20i	4.07h-m	1.50g-k	34.67l	34.16a-h	41.67ab	6.35	8.02c-e	36.33l-n	12.13c-h
G15	BD-6926	26.30e-g	5.83bc	1.77d-j	39.67jk	34.07a-h	40.33a-c	6.63	8.69a-e	35.17mn	12.05c-h
G16	BD-6927	29.61a-e	3.45l-p	1.57f-k	40.33i-k	27.53d-k	40.67a-c	7.18	8.52a-e	47.02d-g	14.95ab
G17	BD-6932	28.03a-f	3.27m-r	1.57f-k	36.00l	34.87a-g	39.67a-d	6.90	8.23b-e	45.89c-i	14.17a-c
G18	BD-6933	26.80d-g	2.40q-s	0.73k	35.67l	28.28c-k	39.13a-e	7.51	8.04c-e	36.33l-n	11.83d-h
G19	BD-6934	21.13hi	3.07n-r	2.10b-h	35.33l	24.90i-l	41.13ab	7.53	9.81a-c	63.63a	15.95a
G20	BD-6936	25.47e-h	2.33rs	0.87jk	36.00l	28.94b-k	40.80a-c	7.13	7.97de	42.87f-k	12.91b-g
G21	BD-6875	30.75a-e	4.93c-i	3.27a	42.00f-h	32.77a-j	37.00a-f	7.67	9.19a-c	26.47p-r	9.04j

Table 4: (Continuied)

Genotype	Acc. No.\name	Plant height	Primary branch/plant	Secondary branch/plant	50% Flowering	% Abscission	Pods /plant	Pod length	Seed/pod	1000-seed weight	Yield/plant
G22	BD-6876	28.52a-f	4.27g-l	1.30g-k	40.00i-k	36.60a-d	39.00a-e	6.16	8.98a-e	25.93p-r	9.02j
G23	BD-6877	23.55f-i	6.33ab	1.00jk	33.33m	38.70a	41.00ab	6.65	8.25b-e	35.80l-n	12.10c-h
G24	BD-6879	29.36a-e	2.70p-s	1.23h-k	42.33e-g	23.22kl	30.67e-g	6.74	9.14a-e	47.50d-f	12.99b-g
G25	BD-6880	32.67ab	3.67k-o	1.33g-k	47.67b	35.49a-f	35.33a-g	6.74	8.32a-e	23.33qr	8.43j
G26	BD-6881	29.93a-e	4.10h-m	1.67d-k	40.00i-k	33.90a-i	37.67a-e	7.42	9.35a-e	22.12r	8.06j
G27	BD-6882	32.54a-c	5.00c-h	2.73a-c	44.33cd	28.93b-k	28.70fg	7.19	8.52a-e	43.97f-j	11.75d-h
G28	BD-6884	27.53a-g	6.90a	2.50a-f	35.67l	35.88a-e	27.33g	7.40	9.44a-e	40.74g-m	11.06g-i
G29	BD-6885	29.80a-e	5.63b-d	1.47g-k	39.67jk	37.78ab	31.33d-g	7.34	9.83a-c	40.32h-m	12.37c-g
G30	BD-6886	33.00a	4.83d-j	1.73d-j	50.33a	23.15kl	36.07a-f	7.15	9.47a-e	35.99l-n	13.34b-f
G31	BD-6888	32.50a-c	2.80o-s	2.00c-i	39.67jk	29.98a-k	33.33b-g	7.81	9.72a-d	39.67i-m	13.32b-f
G32	BD-6889	30.06a-e	3.40l-p	1.67d-k	41.00g-j	25.85g-l	30.67e-g	7.15	9.55a-e	46.22e-h	13.40b-e
G33	BD-6890	29.32a-e	3.90j-n	1.00jk	41.33g-i	32.53a-j	35.67a-g	6.39	8.99a-e	35.03m-o	11.13f-i
G34	BD-6891	27.88a-f	4.67e-j	1.58e-k	39.00k	26.51f-l	39.00a-e	5.72	8.66a-e	35.70l-n	12.03c-h
G35	BD-6893	27.33b-g	5.70b-d	2.27b-g	43.00d-f	28.64b-k	36.80a-f	7.09	8.71a-e	34.85m-o	11.91d-h
G36	BD-6894	29.78a-e	5.60b-e	2.50a-f	35.67l	32.52a-j	32.13c-g	7.01	9.55a-e	54.25bc	13.92a-d
G37	BD-6895	32.27a-d	5.07c-g	1.50g-k	42.00f-h	29.22b-k	37.17a-f	7.19	9.72a-d	59.93ab	15.72a
G38	BD-6897	28.00a-f	3.35l-q	1.17h-k	42.00f-h	35.35a-f	39.33a-e	6.32	8.09c-e	41.84f-l	12.99b-g
G39	BD-6898	26.79d-g	4.97c-h	2.53a-e	43.67c-e	30.90a-k	43.17a	6.15	9.47a-e	51.50c-e	14.89ab
G40	BD-6900	28.35a-f	2.10st	2.00c-i	40.00i-k	25.06h-l	30.67e-g	5.78	9.90ab	43.23f-k	12.83b-g
LSD(0.05)		4.442	0.80	0.799	1.303	7.364	6.959	NS	1.442	5.42	1.82
CV%		9.45	12.21	28.34	2.01	14.86	11.77	13.44	9.82	8.40	9.07

Note: Means separated by uncommon letters in order of alphabetic preferences are significantly different from each other at p=0.05

Table 5: Estimation of genetic parameters for yield and yield contributing characters of 40 genotypes of *Vigna radiata* L. Wilzeck

Genetic parameters → Characters ↓	σ^2_g	σ^2_p	σ^2_e	GCV (%)	PCV (%)	ECV (%)
Plant height (cm)	9.03	16.50	7.47	10.39	14.04	9.45
No. of Primary branches/plant	1.04	1.88	0.24	31.77	34.03	12.21
No. of secondary branches/plant	0.44	0.68	0.24	38.08	47.47	28.34
Days to 50% flowering	15.24	15.88	0.64	9.79	9.99	2.01
Percentage of abscission	16.55	37.07	20.52	13.35	19.98	14.86
Pod/plant	8.78	27.11	18.33	8.15	14.32	11.77
Pod length (cm)	0.08	0.95	0.86	4.18	14.07	13.44
No. of seed/pod	0.18	0.97	0.79	4.75	10.91	9.82
1000 seed wt. (gm)	87.65	98.76	11.12	23.59	25.04	8.40
Yield/plant	3.75	5.01	1.25	15.71	18.14	9.07

followed by G40 (2.10).The phenotypic variance (1.88) was slightly higher than the genotypic variance (1.04) indicating less environmental influence on this characters (Table 5) and relatively moderate genotypic co-efficient (31.77%) and phenotypic co-efficient of variation (34.03%) which indicated that genotype had high variability (Table 5). Kumar *et al.* (2003) found significant differences for number of primary branches per plant.

4.1.3 Number of Secondary Branches/Plant

In the present experiment analysis of variance of the data for number of secondary branches/plant showed highly significant difference among the genotypes included in the present experiment. The mean squares value (1.550**) regarding to number of secondary branches/plant (Table 3) indicated the presence of variability among the genotypes. Highest number of secondary branches/plant was recorded in genotype G6 (3.37) which was followed by G21 (3.267), G9 (3.20) (Table 4).The lowest mean was observed in G18 (0.73) which was statistically different with other genotypes (Table 4). Number of secondary branches per plant showed low values and little differences between genotypic (0.44) and phenotypic (0.68) variance indicating that they had some short of interaction with environment and relatively high GCV (38.08%) and PCV (47.47%) (Table 5) .

4.1.4 Days to 50% Flowering

From the (Table 3) There were highly significant variations among the genotypes (46.366**) for days to 50% flowering (Table 3). The days to 50% flowering was observed highest (50.33) in G30 which was followed by G25 (47.67) and G10 (47.67) both were similar. The lowest value found in G23

(33.33) which was followed by G14 (34.67) (Table 4). Genotypic and phenotypic variance of days to 50% flowering was observed 15.24 and 15.88, respectively with high differences between them indicating large environmental influences on these character for their phenotypic expression and values of GCV and PCV were 9.79% and 9.99%, respectively which indicate 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.

4.1.5 Percentage of Abscission :

From the (Table 3) there were highly significant variations among the genotypes (70.173**) for the percentage of abscission. The higest percentage of abscission was recorded G23 (38.70) among the genotypes while the lowest abscission was G11 (18.20) which was followed by G30 (23.15) (Table 4)

Genotypic and phenotypic variance of percentage of abscission was observed 16.55 and 37.07, respectively with high differences between them indicating large environmental influences on these characters for their phenotypic expression and values of GCV and PCV were 13.35% and 19.98% (Table 5). Ahmed *et al.* (1993) reported for reproductive abscission.

4.1.6 Pod per plant:

The mean square value due to genotype from the analysis of variance was found statistically significant difference (44.674%) 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 G39 (43.17) which was followed by the genotype G14 (41.67) and G19 (41.13) while the

minimum number (27.33) was recorded for the genotype G28 (Table 4). The phenotypic variance (27.11) was considerably higher than the genotypic variance (8.78) and the phenotypic and genotypic co-efficient of variations were 14.32% and 8.15%, respectively (Table 5). Abrahim *et al.* (2006) 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). A comparative photograph of pod per plant has been presented in Plate No. 5.

4.1.7 Pod Length (cm)

From the Table 4 there were no significant variations among the genotypes for the pod length because pod lengths were about similar. The phenotypic variance (0.95) was considerably higher than the genotypic variance (0.08) and the phenotypic and genotypic co-efficient of variations were 14.07% and 4.18%, respectively (Table 5). Pod length recorded high genotypic coefficients of variation suggesting the possibility by Das *et al.* (1998).

4.1.8 Number of Seeds per pod:

The value of the analysis of variance of the data for the number of seed per pod showed highly significant difference (134.100**) at 0.05 level among the genotypes of *Mungbean* used in the present experiment (Table 3). Maximum number of seed per pod was recorded in genotype G3 (10.07) and G4 (10.07) both were similar and the minimum (7.753) was recorded in the genotypes G13 which was statistically different from other genotypes(Table 4).The difference in magnitudes in between genotypic (0.18) and phenotypic variances (0.79)

A.Highest pod G (39)

B.Lowest pod in G (28)

Plate no. 5 Photograph showing variation for pod per plant between G 39 and G 28 of (*Vigna radiata* (L.) Wilzeck) genotypes.

and the phenotypic and genotypic co-efficient of variations were 10.91% and 4.75%, respectively (Table 5) .Pandey *et al.* (2002) was observed highest difference value for seed per pod.

4.1.9 1000 Seed Weight (g)

The mean square due to genotype from the analysis of variance was found statistically significant at 1% level of probability 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 G19 (63.63g) which was followed by G37 (59.93 g) while the lowest 1000 seed weight (22.12g) was in the G26 (Table 4). The phenotypic variance (98.76) was higher than the genotypic variance (87.65) and the phenotypic and genotypic co-efficient of variations were 25.04% and 23.59%, respectively for 1000 seed weight of mungbean genotypes (Table 5). Sandhu *et al.* (1979) was found similar result. A comparative photograph of pod and seed of different genotypes are presented in Plate No.6.

4.1.10 Yield/Plant (g)

In the present experiment, the genotype mean square for seed yield per plant was found significant 12.511** (Table 3). The seed yield per plant was recorded highest in the G19 (15.95) which was statistically similar with the genotypes G37 (15.72) and G11 (15.61) and the lowest mean value (8.057) was in G26 (Table 4). The phenotypic variance (5.01) was higher than the genotypic variance (3.75) and the phenotypic and genotypic co-efficient of variations were 18.14% and 15.71%, respectively for yield per plant of mungbean genotypes

Plate 6: Photograph showing variation for different type of pod (A) and seed (B) of (*Vigna radiata* (L.) Wilczek) 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).

4.2 Heritability and Genetic Advance

Findings of the heritability, genetic advance and genetic advance in percentage of mean of individual character are discussed in this part of the thesis and the results related to this character are presented in Table 6

4.2.1 Plant Height (cm)

Plant height showed high heritability (54.74%) together with low genetic advance (4.58%) and genetic advance in percentage of mean (15.83) which indicated, High heritability 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), Abrahim *et al.* (2006) Reddy *et al.* (2003), Rohman *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).

4.2.2 Number of Primary Branches/Plant

Number of primary branches/plant showed very high heritability (87.13%) coupled with low genetic advance (2.46%) and high genetic advance in

Table 6: Heritability and genetic advance &genetic advance inpercentage of mean for yield and yield contributing characters of 40 (*Vigna radiata (L) Wilczek*). genotypes

Genetic parameters → Characters ↓	Heritability	Genetic advance 5%	GA in percent of means 5%
Plant height (cm)	54.74	4.58	15.83
No. of primary branches/plant	87.13	2.46	61.08
No. of secondary branches/ plant	64.35	1.09	62.93
Days to 50% flowering	95.96	7.88	19.75
% Abscission	44.64	5.60	18.37
Pod/plant	32.39	3.47	9.55
Pod length (cm)	8.82	0.18	02.56
No. of seed/pod	18.99	0.39	4.27
1000 seed wt. (gm)	88.74	18.17	45.77
Yield/plant (cm)	74.98	3.46	28.01

percentage of mean (61.08). These findings revealed that it was indicative of non-additive gene action. But high genetic advance coupled with high heritability in number of branches per plant was reported by Abrahim *et al.* (2006). 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).

4.2.3 Number of Secondary Branches/Plant

High heritability (64.35%) coupled with low genetic advance (1.09%) and high genetic advance in percentage of mean (62.93%) was calculated in respect of number of secondary branches/plant. High genetic advance coupled with high heritability in number of branches per plant was reported by Abrahim *et al.* (2006). 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).

4.2.4 Days to 50% Flowering

Days of 50% flowering showed very high heritability (95.96%) with genetic advance (7.88%) and genetic advance in percentage of mean (19.75%) revealing that the character was governed by non-additive genes and heterosis breeding may be useful and also indicated that the character was least influenced by the environmental effects. Garard-Abrahim *et al.* (2006) observed in days of 50% flowering was highly heritable. High heritability estimates

coupled with high genetic advance were observed for days to 50% flowering was reported by Rohman *et al.* (2003), Reddy *et al.* (2003), Vikas *et al.* (1998).

4.2.5 Percentage of Abscission:

The magnitude of heritability in broad sense (h^2b) of this character was low (44.64%) and low genetic advance (5.60%) and low genetic advance in percentage of mean (18.37%). These findings revealed that it was indicative of non-additive gene action. The high heritability was being exhibited due to favorable influence of environment rather than genotypes and selection for such traits may not be rewarding.

4.2.6 Number of Pod/Plant

Number of pod/plant showed low heritability (32.39%) coupled with very low genetic advance (3.47%) and low genetic advance in percentage of mean (9.55). These findings revealed that it was 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), Abrahim *et al.* (2006), Rao *et al.* (2006), Reddy *et al.* (2003), Khairnar *et al.* (2003), Loganathan *et al.* (2001), Islam *et al.* (1999), Sharma *et al.* (1999), Vikas *et al.* (1998), Das *et al.* (1998).

4.2.7 Pod length (cm)

Length of pod/plant showed very low heritability (8.82%) connected with very low genetic advance (0.18%) and genetic advance in percentage of mean (2.56%) which findings exposed the action of non-additive gene effect on the expression of this character as well as a scope of improvement through selection. Length of pod were highly heritable was reported by Abrahim *et al.* (2006), 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).

4.2.8 Number of Seed/pod

The heritability in broad sense (h^2b) of this trait was low (18.99%) and very low genetic advance (0.39%) and low genetic advance in percentage of mean (4.27%). These results indicated non-additive genes involvements in the expression of the character and this with limited scope of improvement by direct selection. High heritability estimates coupled with high genetic advance were observed for seed/pod reported by Rohman *et al.* (2003), Reddy *et al.* (2003).

4.2.9 1000 Seed Weight (g)

Very high heritability (88.74%) associated with low genetic advance (18.17%) and genetic advance in percentage of mean (45.77%) was calculated in respect of 1000 seed weight of *Mungbean* 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 *et al.* (1999), Sandhu *et al.* (1979).

4.2.10 Yield/Plant (g)

High heritability (74.98%) coupled with low genetic advance (3.46%) and genetic advance in percentage of mean (28.01) 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), Rohman *et al.* (2003), Reddy *et al.* (2003), Sharma *et al.* (1999).

4.3 Correlation co-efficient:

Genotypic and phenotypic correlation co-efficient between pairs of characters for (*Vigna radiate (L.*) Wilzeck).is presented in table 7. It was evident that in majority to the case, the genotypic correlation co-efficient were 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 were 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 Thousand seed weight (G = 0.934 and P = 0.882) which indicating that, if thousand seed weight increase, seed yield per plant also increase. Yield per plant had also significant positive correlation with seed per pod (G = 0.380) at genotypic level. Insignificant positive correlation was found with seed per pod (P = 0.237) at phenotypic level (Table 7). Again, seed yield per plant had highest significant negative correlation with the percentage of abscission (G = - 0.542, P = - 0.411) which indicating that, if the percentage of abscission was increases then yield per plant was decreases. Insignificant negative correlation was found with plant height (G = - 0.250) at genotypic level and secondary branch (P= -0.125) at phenotypic level.

Table 7. Genotypic and phenotypic correlation coefficient between yield and component characters in (*Vigna radiata (L.)*Wilczek)

Characters		Plant height	Primary branch	Secondary branch	% abscission	Pods/plant	Pod length	Seeds/pod	1000 seed weight	Yield per plant
Days to 50% flowering	g	0.534**	0.031	-0.102	-0.227	-0.305	-0.133	0.462**	-0.186	-0.120
	p	0.370*	0.029	-0.087	-0.170	-0.167	-0.059	0.178	-0.166	-0.096
Plant height (cm)	g		0.193	0.434**	-0.138	-0.627**	0.830**	0.259	-0.268	-0.250
	p		0.068	0.204	-0.046	-0.333*	0.156	0.419**	-0.164	-0.105
Primary branches	g			0.400*	0.290	-0.203	0.048	0.291	-0.141	-0.151
	p			0.288	0.198	-0.038	0.061	0.043	-0.121	-0.115
Secondary branches	g				0.187	-0.151	0.583**	0.236	-0.072	-0.104
	p				0.156	-0.147	0.182	0.056	-0.065	-0.125
% Abscission	g					0.205	-0.262	-0.611**	-0.533**	-0.542**
	p					0.081	-0.040	-0.181	-0.378*	-0.411**
Pods/plant	g						-0.490**	-0.730**	-0.015	0.082
	p						-0.188	-0.373*	0.010	0.192
Pod length (cm)	g							0.939**	0.341	0.317*
	p							0.154	0.059	0.077
Seeds/pod	g								0.417**	0.380*
	p								0.210	0.237
1000 seed weight	g									0.934**
	p									0.882**

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

4.3.1 Days to 50% flowering

Days to 50% flowering showed highly significant positive association with plant height (G = 0.534), seeds per pod at (G = 0.462) genotypic level (Table 7). The result revealed that if days to 50% flowering is increased, then plant height and seed per pod also increased. Days to 50% flowering showed highly insignificant negative association with plant height (G = 0.305) at genotypic level. On the other hand, if days to 50% flowering increased, then number of pod per plant decreased. 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 .

4.3.2 Plant height:

Plant height showed significant positive correlation with pod length (G = 0.830.) and was followed secondary branch (G=0.434) at genotypic level and seed per pod (P=0.419) at the phenotypic level. On the other plant height showed significant negative correlation with number of pods per plant (G = - 0.627) at 1% genotypic level and (P=0.333) at 5% phenotypic level (Table 5). Insignificant positive correlation was found high in seed per pod (G=0.259) and Insignificant negative correlation was found high in 1000 seed weight (G=-0.268) at genotypic level. Makeen *et al.* (2007), Islam *et al.* (1999), Niazi *et al.* (1999) indicated that plant height had significant positive correlation with seed yield.

4.3.3 Number of primary branches per plant:

This trait showed highly significant positive correlation with secondary branch (G = 0.400) at genotypic level (Table 7). Insignificant positive correlation was found with seed per pod (G =0.291) at genotypic level and the followed by % abscission (G=0.290). Islam *et al.* (1999) studied yield

per plant was significantly and positively correlated with number of primary branches per plant.

4.3.4 Number of secondary branches per plant:

Number of secondary branches per plant had significant positive correlation with pod length (G = 0.583) at genotypic level. This trait had insignificant positive correlation seed per pod (G = 0.236) (Table 7). Secondary branches per plant positive correlated with grain yield at phenotypic level observed by Dhuppe *et al.* (2005).

4.3.5 Percentage of abscission:

Percentage of abscission showed highly significant negative correlation with seed per pod (G = - 0.611) at genotypic level. and followed by 1000 seed weight (G = -0.533) at genotypic level and P=-0.378 at phenotypic level. This trait also showed insignificant positive correlation only with pods per plant (G = 0.205, P = 0.081) (Table 7).Ahmed result reported by Ahmed *et al.* (1993).

4.3.6 Pods per plant:

Pods per plant showed significant negative correlation with seed per pod (G = -0.730, P = -0.373) at genotypic and phenotypic level and followed by pod length (G=-0.490) at genotypic level. Pods per plant exhibited significant and positive correlation with seed yield per plant reported by Makeen *et al.* (2007), Sirohi *et al.* (2006), Rao *et al.* (2006), Rohman *et al.* (2003), Rajan *et al.* (2000), Islam *et al.* (1999).

4.3.7 Pod length:

Pod length showed significant highly positive correlation with seed per pod (G = 0.939) at genotypic level .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.

4.3.8 Seeds per pod:

Seeds per pod showed significant only positive correlation with 1000 seed weight (G = 0.417) and non-significant positive correlation with 1000 seed weight (P = - 0.431) at phenotypic level and seed yield per plant (G = 0.380, P = 0.237). Similar, result were obtained by Rohman *et al.* (2003), Rajan *et al.* (2000), Islam *et al.* (1999).

4.3.9 Thousand seed weight:

Hundred seed weight showed most highly significant positive correlation with yield per plant (G = 0.934, P=0.882) at genotypic and phenotypic level. Similar result were obtained by Islam *et al.* (1999, Sharma *et al.* (1999)), Yaqoob *et al.* (1997). Shamsuzzaman and Shaikh (1982) reported 1000-seed weight exhibited negative correlated with seed yield.

4.4 Path co-efficient:

Path coefficient analysis was done with days to 50% flowering, plant height, primary branch, secondary branch , percentage abscission, pod length, seed per pod, pods per plant, 1000 seed weight and yield per plant. The direct and indirect effects of different characters on yield are present in Table 8. Path co-efficient analysis revealed that, 1000 seed weight had the highest direct positive effect (0.899) on seed yield followed by pod per plant (0.219), pod length (0.069), plant height (0.055), 50% flowering (0.053) and seed per pod (0.052) which indicating true relationship between them and direct selection for this trait will be rewarding for yield improvement.

4.4.1 Days to 50% flowering:

Days to 50% flowering had positive direct effect (0.053) on yield per plant. Days to 50% flowering had positive indirect effect on plant height (0.029),

primary branch (0.001), Secondary branch (0.009), % abscission (0.007) and seed per pod (0.024). Negative indirect effect were found via pod per plant (- 0.067), pod length (-0.009) and thousand seed weight (- 0.167) (Table 8). Yaqoob *et al.* (1997), Rahman (1982) observed positive direct effect of days to 50% flowering on seed yield.

4.4.2 Plant height (cm):

Path analysis revealed that plant height had positive direct effect (0.055) on yield per plant and positive indirect effect through days to 50% flowering (0.028), number of primary branches per plant (0.006), % abscission (0.004), pod length (0.058), seeds per pod (0.013) (Table 8). On the other hand, plant height showed negative indirect effect on yield per plant via number of secondary branches per plant (- 0.037), pod per plant (- 0.137) and thousand seed weight (-0.241)Maximum direct effect on seed yield was observed in plant height reported by Makeen *et al.* (2007), Sirohi *et al.* (2006), Sharma *et al.* (1999). Rao *et al.* (2006), Yaqoob *et al.* (1997) found plant height showed negative direct effect on seed yield.

4.4.3 Primary branches per plant:

Number of primary branches per plant had the highest positive direct effect on yield per plant (0.0533). This trait had positive indirect effect on days to 50% flowering (0.002), plant height (0.011), pod length (0.003), seed per pod (0.015). On the other hand negative indirect effect was found on number of secondary branches per plant (-0.034), % abscission (-0.009), pod plant (-0.044), thousand seed weight (-0.127) (Table 8). Bhaumik and Jha (1980) found indirect effect of primary branches on the yield.

Table 8. Partitioning of genotypic correlation coefficients into Direct (bold faced) and indirect effect of some yield contributing characters on (*Vigna radiata* (L.)Wilczek) by path analysis.

Characters	DFF	PH	PB	SB	PA	PP	PL	SP	TSW	SYPP
DFF	**0.053**	0.029	0.001	0.009	0.007	-0.067	-0.009	0.024	-0.167	-0.120
PH	0.028	**0.055**	0.006	-0.037	0.004	-0.137	0.058	0.013	-0.241	-0.250
PB	0.002	0.011	**0.033**	-0.034	-0.009	-0.044	0.003	0.015	-0.127	-0.151
SB	-0.005	0.024	0.013	**-0.084**	-0.006	-0.033	0.041	0.012	-0.065	-0.104
PA	-0.012	-0.008	0.009	-0.016	**-0.032**	0.045	-0.018	-0.032	-0.479	-0.542**
PP	-0.016	-0.034	-0.007	0.013	0.007	**0.219**	-0.034	-0.038	-0.014	0.082
PL	0.007	0.045	0.002	-0.049	0.008	-0.107	**0.069**	0.049	0.307	0.317*
SP	0.025	0.014	0.010	-0.020	0.020	-0.160	0.065	**0.052**	0.375	0.380*
TSW	-0.010	-0.015	-0.005	0.006	0.017	-0.003	0.024	0.022	**0.899**	0.934**

Residual effect (R): 0.315

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

DFF = Days to 50% flowering (days), PH = Plant height (cm), PB = Primary branches plant/plant, SB = Secondary branches/plant, PA = Percentage of abscission, PP = Pod per Plant, PL = Pod length (cm), SP= Seed /pod, TSW= Thousand seed wt. (g), SYPP = Seed yield per plant

4.4.4 Secondary branches per plant:

Number of secondary branches per plant had negative direct effect (-0.084) on yield per plant and positive indirect effect on plant height (0.024), pod length (0.041) and seed per pod (0.012). On the other hand this trait showed negative indirect effect on days to 50% flowering (- 0.005), number of primary branches per plant (0.173), % abscission (-0.006), pod per plant (-0.033), and length of pod (- 0.065) (Table 8).

4.4.5 Percentage of abscission:

Percentage of abscission showed negative direct (-0.032) effect on yield per plant and positive indirect effects through number of primary branches per plant (0.009) pod per plant (0.045). Percentage of abscission had negative indirect effect on days to 50% flowering (-0.012), plant height (-0.008), secondary branch (-0.016), pod length (-0.018), seed per pod (-0.032) and thousand seed weight (-0.479) (Table 8). Similar result reported by Ahmed *et al.* (1993)

4.4.6 Pod per plant:

Pod per plant showed positive direct (0.219) effect on yield per plant and positive indirect effects through secondary branches per plant (0.219). Pod per plant had negative indirect effect on all other characters. (Table 8). Makeen *et al.* (2007), Rao *et al.* (2006), Rajan *et al.* (2000), Sharma *et al.* (1999) found maximum positive direct effect on seed yield was observed in pods per plant.

4.4.7 Pod length:

Path analysis revealed that pod length had direct positive effect (0.069) on yield per plant. This trait had also indirect positive effect on plant height (0.045), primary branches per plant (0.002), percentage of abscission (0.008) seed per pod (0.049) and 1000 seed weight (0.307). On the other hand pod length

showed indirect negative effect on days to 50% flowering (-0.007), secondary branch (-0.049) and pod per plant (-0.107) (Table 8). Bhaumik and Jha (1980) found the same result.

4.4.8 Seed per pod:

Seeds per pod had positive direct effect (0.052) on yield per plant and negative indirect effect on secondary branch (-0.020) and pods per plant (-0.160). On the other hand this trait showed positive indirect effect on all other parameters (Table 8). Rahman (1982) found number of seeds/pod (-0.800) had negative direct contribution to yield.

4.4.9 Thousand seed weight:

Thousand seed weight had high positive direct effect on yield per plant (0.899) and positive indirect effect on secondary branch per plant (0.006), percentage of abscission (0.017), pod length (0.024) and seed per pod (0.022). Thousand seed weight had negative indirect effect on days to 50% flowering (-0.010), plant height (-0.015), primary branch (-0.005) and pods per plant (-0.003) (Table 8). Singh and Malhotra (1976) observed 1000-seedweight had a negative indirect effect on yield by affecting the number of seeds/pod.

The residual effect observed in path analysis was high (0.315) indicating that the character under study contributed 69% of the seed yield per plant. It is suggested that there are some other factors/characters those contributed 0.315% to the seed yield per plant. (Figure 1)

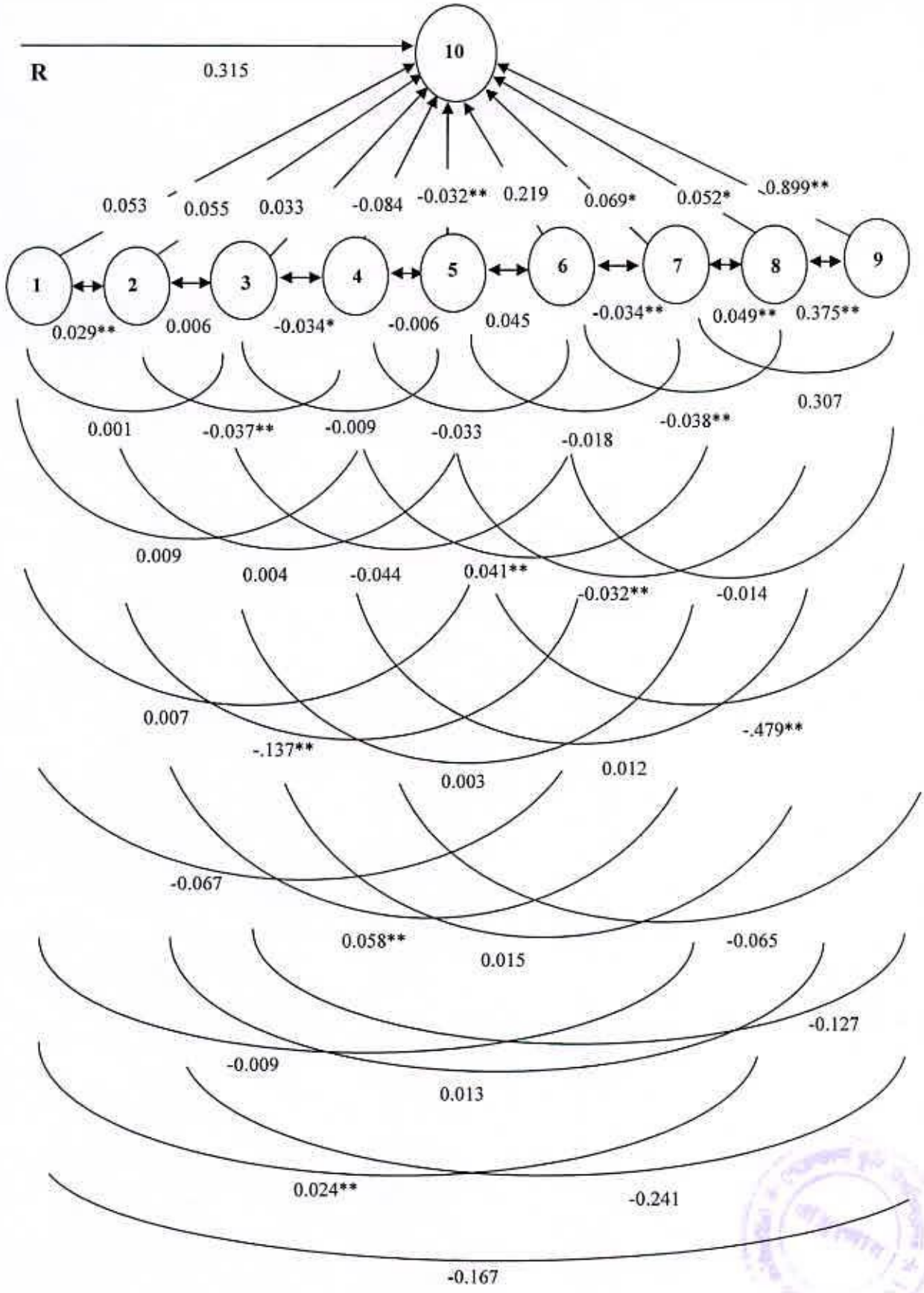


Fig. 1. Path diagram of 10 yield contributing traits in 40 mungbean genotypes

1 = days to 50% flowering, 2 = plant height, 3=Primary branch, 4= Secondary branch, 5 = % abscission, 6 = pods/plant, 7 = pod length, 8 = seed/pod, 9 = 1000 seed weight, 10 = yield/plant
R= residual effect.

Chapter V

Summary and Conclusion

CHAPTER V
SUMMARY AND CONCLUSION

The experiment was conducted with a view to the relation of abscission percentage on yield and determine the variability in respect of yield and some yield contributing characters, the degrees of association among the characters and their direct and indirect effects of 40 genotypes of (*Vigna radiata* L.Wilzcek) at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka, during February 2008 to May 2008. Seeds were sown in the field in Randomized Complete Block Design (RCBD) with three replications. Data on plant height (cm), no. of primary branches/plant, no. of secondary branches/plant, days to 50% flowering, percentage of abscisson, no. of pod /plant, 1000 seed wt. (g), no. of seed/pod, pod length (cm), yield/ plant (g) were recorded. There was a great deal of significant variation for all the characters among the genotypes.

The highest mean value was observed for thousand seed weight. This character also exhibited the highest range of variation indicating that all the genotypes showed wide range of variation in respect of this character. It showed high heritability (88.74%) accompanied with low genetic advance in percentage of mean and the phenotypic variance (98.76) was higher than the genotypic variance (87.65). However, these differences were in case of plant height, percentage of abscission, pod per plant, 1000- seed weight indicating greater influence of environment for the expression of these characters. Among these characters, days to 50% flowering, primary branches per plant, secondary branches per plant, pod length, seed per pod, yield per plant showed least difference between phenotypic and genotypic variance, which indicated additive gene action for the expression of this characters. All these characters showed moderate to high phenotypic and

genotypic co-efficient of variation except for days to 50% flowering. Among the characters the highest genotypic co-efficient of variation was recorded in primary branches per plant (31.77), no. of secondary branches/plant (38.08) followed by 1000-seed weight (g) (23.59), yield/plant (g) (15.7), percentage of abscission (13.35) and plant height (10.39).

Heritability in broad sense was low to high for all the characters studied and it ranged from 8.82 % to 95.96 % 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 revealed 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.

Correlation revealed the significant positive association at the 5% level was observed for seed yield per plant with pod length and seed per pod at genotypic level and the significant positive correlation at the 1% level seed yield per plant with 1000-seed weight both genotypic and phenotypic level. The significant negative correlation at the 1% level was observed for seed yield per plant with the percentage of abscission both genotypic (-0.542) and phenotypic level (-0.411). A high degree of significant positive association were observed for days to 50% flowering vs. plant height and seed per pod, plant height vs. secondary branches and pod length, secondary branch vs. pod length, pod length vs. seed per pod (highest value 0.939) and seed per pod vs. thousand seed weight. Strong negative significant

correlations were found between plant height vs. percentage of abscission vs. seed per pod, 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 pod length vs. 1000-seed weight at genotypic level and The highest insignificant negative correlation was observed for days to 50% flowering vs. pods per plant at genotypic level.

Path analysis revealed that the character 1000- seed weight had maximum positive direct effect on yield per plant followed by pod per plant. Secondary branches per plant had maximum negative direct effect on yield per plant. The residual effect was moderate large. Thousand seed weight, percentage of abscission, pod length, yield per plant, secondary branch per plant are the characters for the improvement of yield of the crop and can be used as selection criteria in future breeding programme. Considering all the characters G1 (BD-6901), G3 (BD-6903), G11 (BD-6914), G12 (BD-6918), G30 (BD-6886), G37 (BD-6895), G39 (BD-6898) were selected for future breeding programme.

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APPENDICES

APPENDIX I. 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

* Monthly average
** Monthly total
Source: Bangladesh Meteorological Department (Climate Division) Agargoan, Dhaka-1212.

APPENDIX: II Analysis of Variance of 10 important characters in respect of 40 *Vigna radiata* genotypes

Source of variance	df	Days to 50% flowering	Plant height	Primary branch	Secondary branch	% abscission	Pods/plant	Pod length	Seeds/pod	1000 seed weight	Yield per plant
Replication	2	4.608**	8.379	3.543**	0.001	43.814	7.722	0.576	0.269	28.277	1.923
Genotypes	39	46.366**	34.559**	5.167**	1.550**	70.173**	44.674**	1.112	134.100*	274.059**	12.511**
Error	78	0.643	7.467	0.242	0.242	20.522	18.329	0.862	0.787	11.116	1.253

* indicates significant at the 0.05 level
** indicates significant at the 0.01 level
df =Degrees of freedom

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