GENETIC DIVERSITY OF BLACKGRAM *(Vigna mungo* L.)

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GENETIC DIVERSITY OF BLACKGRAM (*Vigna mungo L.)*

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CERTIFICATE

This is to certify that thesis entitled, **"Genetic Diversity And Variety Analysis of Blackgram"** submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE IN GENETICS AND PLANT BREEDING**, embodies the result of a piece of bona fide research work carried out by SUMANA PAUL, Registration No. 10-04197 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: June, 2016
Place: Dhaka, Bangladesh

(Professor Dr. Mohammad Saiful Islam)
Supervisor

DEDICATED
TO
MY BELOVED PARENTS,
HUSBAND & TEACHERS

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GENETIC DIVERSITY OF BLACKGRAM (*Vigna mungo L.*)

By

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ABSTRACT

An experiment was carried out during the Rabi season of 2015-16 at the research field of Sher-e-Bangla Agricultural University, Dhaka to assess the correlation, path coefficient and genetic diversity in 20 morphologically diverse accessions of Blackgram [*Vigna mungo* (L) Hepper]. Analysis of variance indicated significant differences among the genotype for all the traits studied suggesting prevalence of wide range of genetic variability and scope of selection for these traits, except days to 50% flowering. High PCV and GCV were observed for branches per plant, seed yield per plant, pods per plant and plant height. High heritability coupled with high genetic advance was observed for seed yield per plant, branches per plant and plant height indicating preponderance of additive gene action in the inheritance of these traits and selection would be effective. Seed yield per plant exhibited significant and positive correlation with pods per plant and hundred seed weight and insignificant positive correlation with branches per plant, pod length and seeds per pod at both genotypic and phenotypic levels. Through path analysis the direct effects were found to be positive and high for plant height, days to first flowering, pod length and pods per plant. Twenty genotypes were grouped into five clusters. Highest inter-cluster distance was observed between cluster I and III followed by cluster I and V. There was sufficient genetic variability among the genotypes for all the traits under study. Hence selection of these characters simultaneously would bring improvement in yield.

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SOME COMMONLY USED ABREVIATIONS

Full word	Abbreviation
Percent	%
Degree Celsius	^{0}C
At the rate	@
Phenotypic variance	σ^2_p
Genotypic variance	σ^2_g
Environmental variance	σ^2_e
Heritability in broad sense	h^2_b
Agro Ecological Zone	AEZ
Agriculture	Agric.
Agricultural	Agril.
Agronomy	Agron.
Analysis of variance	ANOVA
Bangladesh Agricultural Research Institute	BARI
Bangladesh Bureau of Statistics	BBS
Bangladesh	BD
Centimeter	Cm
Percentage of coefficient of variation	CV%
Cultivars	cv.
Degrees of Freedom	df
And others	*et al.*
Etcetera	etc.
The third generation of a cross between two dissimilar homozygous parents	F_3
Food and Agricultural Organization	FAO
Gram	g
Genotype	G
Genetic Advance	GA
Genotypic coefficient of variation	GCV
Harvest Index	HI
Indian Agricultural Research Institute	IARI
International Center for Agricultural Research in Dry Areas	ICARDA
Journal	J.
Kilogram	kg
Meter	m

SOME COMMONLY USED ABREVIATIONS (*Continued*...)

Full word	Abbreviation
Mean sum of square	MSS
Murate of potash	MP
Ministry of Agriculture	MOA
Square meter	m^2
Phenotypic coefficient of variation	PCV
Randomized complete block design	RCBD
Sher-e-Bnagla Agicultural University	SAU
Triple Super phosphate	TSP

CHAPTER I
INTRODUCTION

Blackgram *(Vigna mungo* L.) Hepper commonly known as blackgram or mash, is a grain legume domesticated from *V. mungo var. sylvestris* (Srivastava Priya *et al.*, 2011).The center of origin of blackgram is in India (Bhosale *et al.*, 2013). Blackgram has been distributed mainly tropical to sub-tropical countries. Blackgram is a self-pollinated crop with low percentage of natural out crossing. It belongs to family fabaceae. It is an important pulse crop of many South Asian countries including Bangladesh, Pakistan, India, Nepal, Thailand, Philippines and Korea (Srivastava Priya *et al.*, 2011).

It is highly nutritious containing easily digestible and good quality protein (24-26%), carbohydrates (60%), fat (1.5%), minerals, amino acids and vitamins. It forms one of the important constituents in the dietary practices of the local population and is affordable due to lower price than that of other pulses. The biological value improves greatly, when wheat or rice is combined with blackgram because complementation of the essential amino acids such as arginine, leucine, lysine, isoleucine, valine and phenylalanine etc.

It is cultivated under a wide range of agro-ecological zones mainly under rainfed nature. Among pulses, it is the least researched crop and no international centre of CGIAR system has this crop on its mandate (Anon., 1976). Although it has been identified as a potential crop in number of countries, but no systematic research information is available except few reports worldwide, whereas in Bangladesh very little study has been reported.

It is grown as a sole crop or mixed with sorghum, pearl millet and pigeon pea. It is also cultivated as follow-up crop after rice cultivation (Srivastava *et al.*, 2011).

However, its productivity is very low and the major constraints in achieving higher yield of this crop are low yield potential and narrow genetic base of existing cultivars, absence of suitable genotypes for different cropping system, poor harvest index and susceptibility to diseases (Chakraborty *et al.,* 2010 and Srivastava *et al.,* 2011). Lack of suitable varieties and genotypes with adaptation to local condition is among the factors that also affects the production.

The development of new varieties depends largely on the availability of genetic variability in the base material and the extent of variability for the desired character. In addition the assessment of genetic variability for qualitative and quantitative traits of economic importance are prerequisite for any crop-improvement programme. If the variability in among germplasm the population is largely of genetic nature with least environmental influence, the probability of isolating genetically superior genotypes is high. The information about the nature and magnitude of genetic divergence is essential for selection of diverse parents which upon hybridization lead to a wide spectrum of recombination. Mahalanobis's D^2 statistics is a very sensitive tool for measuring genetic divergence of quantitative traits and is also widely used by many breeders for selection of divergent parents. Thus the present investigation was undertaken to measure the genetic diversity among the advance breeding lines.

The knowledge of correlation and path analysis is important to understand the association between the yield and its contributing character to find out guidelines for better selection of quantitative traits. Success of yield improvement largely depends upon the magnitude and nature of genetic variability present in yield contributing traits. Indirect selection can be effective for yield improvement and study of correlation among different economic traits are therefore, essential for an effective selection programme because selection for one or more trait results in correlated response for several other traits and sequence of variation will also be influenced .

However correlation studies measure only mutual association between two traits and it does not imply the cause and effect of relationship. Path analysis is a standardized partial regression analysis, which further permits the partitioning of correlation coefficient into components of direct and indirect effects of independent variable on the dependent variable (Wright, 1921). Genetic diversity is an important factor and also a prerequisite in any hybridization programme. Evaluation of genetic diversity would promote the efficient use of genetic variations in the breeding programme (Paterson *et al*. 1991).

The information about the nature and magnitude of genetic divergence is essential for selection of diverse parents which upon hybridization lead to a wide spectrum of recombination. Mahalanobis's D^2 statistics is a very sensitive tool for measuring genetic divergence of quantitative traits and is also widely used by many breeders for selection of divergent parents. Thus the present investigation was undertaken to measure the genetic diversity among the advance breeding lines. The accurate estimation of genetic diversity can be invaluable in the selection of diverse parental combinations to generate segregating progenies with maximum genetic variability. Furthermore, monitoring the genetic variability within the gene pool of elite breeding material could make crop improvement more efficient by the directed accumulation of favoured alleles.

The average yield of blackgram in Bangladesh is around 883.36 kg ha-1 (BBS, 2010). That's why, the present research was taken with the following objectives:

- To study the variability among the genotypes for different quantitative characters of blackgram;
- To study the interrelationships of yield contributing characters among themselves and with yield; and their direct and indirect effects;

- To estimate diversity among genotypes
- To assess the contribution of different traits towards genetic divergence;
- To find out diverse germplasm suitable for utilization in varietal improvement and further hybridization program .

CHAPTER II
REVIEW OF LITERATURE

The genus *Vigna* comprises about 150 species, of which, mung bean and black gram are the most widely cultivated. Blackgram was classified in the genus *Phaseolus* until Hepper (1956) gave the new name *Vigna mungo* (L.) Hepper for *Phaseolus mungo* (L.). During the past 40 years, the area and production of these crops have shown a positive trend, and are now no more considered as minor crops. However, the productivity has shown a slow progress. To increase the yielding ability with added advantage of stability, crossing programme may be followed by involving wild relatives and land races (Singh and Ahlawat, 2005).

Various reports indicate that many desirable traits having great potential for *Vigna* improvement are available in wild or related species. However, most of these species remain unutilized due to complications such as crossing barriers and linkage drag (Singh *et al.,* 2010). The literature pertaining to the various aspects of present investigation has been reviewed under the following heads:

2.1 Genetic variability

Shah and Patel (1981) noticed higher GCV, heritability and genetic advance for plant height, moderate heritability and genetic advance for numbers of clusters per plant and pods per plant while, low heritability was reported for seed yield in black gram genotypes.

Ramakrishna and Jairaj (1981) noticed high GCV and heritability associated with high genetic gain (84%) for plant height. They also reported low genetic advance for 100-seed weight fairly high heritability for seed yield for blackgram.

Patel and Shah (1982) noticed high GCV, heritability coupled with high genetic advance for plant height in greengram. Whereas, high heritability estimates with low

genetic advance was observed for number of pods per cluster, seeds per pod and 100-seed weight.

Mishra (1983) while working on variability, heritability and genetic advance in 18 varieties of black gram having diverse origin observed that heritability estimates were high for 100 seed weight and plant height and moderate for pods per plant. Plant height, pods per plant and clusters per plant had high-predicted genetic advance accompanied by high variability and moderate heritability.

Kumar and Reddy (1986) revealed variability for plant height, primary branches, clusters per plant and pods per plant, from a study on 28 F_3 progenies indicating additive gene action. Pods per plant, pod length, seeds per pod, 100-seed weight and seed yield per plant recorded low to moderate heritability.

Singh *et al*. (1987) while working on 48 crosses of F_1 and F_2 of wheat reported high heritability for plant height in F_1 and F_2 and number of seeds per pod in F_2. Estimates were higher in F_2 for all traits than F_1. Estimates of genetic advance were similar to heritability in both the generations.

Ramprasad *et al.* (1989) reported high heritability, genotypic variance and genetic advance in percent of mean for seed yield per plant, pods per plant and clusters per plant from the data on seven yield components in F_2 crosses of 14 lines.

Sirohi *et al.* (1994) carried out studies on genetic variability, heritability and genetic advance in 56 blackgram genotypes. The estimates of heritability and genetic advance were high for 100-seed weight, seed yield per plant and plant height.

Byregouda *et al*. (1997) evaluated 18 blackgram genotypes of diverse origin for PCV, GCV, heritability and genetic advance. Sufficient variability was recorded in the material for grain yield per plant, pods per plant, branches per plant and plant height. High heritability values associated with high genetic advance were obtained for grain yield per plant and pods per plant. High heritability in conjugation with medium genetic advance was obtained for 100-seed weight and branches per plant.

Katna and Verma (2001) analysed genetic variability, correlation and path coefficient for 11 traits of 41 blackgram cultivars grown under monocropping and intercropping conditions. High genetic variability and low genetic coefficient of variation (GCV) and genetic advance were recorded for all the traits.

Bhareti *et al.* (2011) studied genetic variability and association analysis of advanced lines and cultivars following intervarietal and interspecific crosses in blackgram. High heritability estimates suggested that large amount of phenotypic variance was attributable to the genetic variance.

Pradhan and Misra (2005) evaluated 30 black gram genotypes and revealed that all the genotypes varied significantly for the 11 characters indicating high genetic variation. High heritability and high genetic advance for characters like seed yield per plant, pods per plant and pod yield per plant indicated the role of additive gene action, emphasizing the importance of these traits for selection.

Bisht *et al.* (2005); assessed diversity in morphological characters of 206 accessions of 14 wild Vigna species from India and found that within species variation was higher in *V. mungo* var. silvestris populations and *V. umbellata* showed more similarity to *V. dalzelliana* than *V. bourneae* and *V. minima* in the angularis-umbellata (adzuki bean group). They revealed that the cultigens of the nonspecific wild species were more robust in growth, with large vegetative parts and often of erect growth with three to five-fold increase in seed size and seed weight.

Reena Mehra *et al*. (2016) conducted an experiment to assess the variability in 75 morphologically diverse accessions of blackgram [*Vigna mungo* (L) Hepper]. and reported that plant height, pods per plant, seeds per plant and 100-seed weight exhibited significant and positive correlation with seed yield both at genotypic and phenotypic level.

2.2 Correlation coefficient

Rao *et al*. (2006) studied 12 genotypes of bean for 7 different characters under 4 environments and found that the seed yield was positively and significantly associated with days to maturity and pods per plant.

Sarkar *et al.* (2006) evaluated 7 diverse genotypes of blackgram to assess the variability, correlation coefficient and path coefficient analysis of 8 yield components. They observed a strong association of seed yield per plant with clusters per plant, pods per plant and seeds per pod.

Shafique *et al*. (2011) reported positive significant correlation between numbers of pods per plant and dry pod length, grain yield and number of seeds per plant and 100-seeds weight and biological yield.

Correlation coefficient analysis revealed that genotypic correlation coefficients were in general superior in magnitude to their corresponding phenotypic correlation coefficients. Days to maturity showed highly significant positive genotypic correlation with days to 50% flowering, whereas days to 50% flowering had negative genotypic and phenotypic correlation with grain yield per plant suggesting that caution should be exercised not to lose yield while breeding for earliness (Bhareti *et al.*, 2011).

Correlation coefficient was performed by Reena Mehra *et al*. (2016) and revealed that the degree of association was highest between seeds per plant and seed yield per plant followed by pods per plant, biological yield per plant, plant height and 100 seed weight. Correlation studies indicated that seed yield per plant showed significant positive correlation with seeds per plant, pods per plant, biological yield per plant, plant height and 100- seed weight.

2.3 Path analysis

Path coefficient analysis at the genetic level revealed the importance of number of pods per plant, number of seeds per pod and 100-seed weight due to the high significant direct effects of these traits on grain yield (Katna and Verma, 2001).

Pervin *et al.* (2007) observed a wide range of variability in 24 lines of blackgram for 5 yield and yield contributing characters.

Path coefficient analysis revealed that highest positive direct effect was shown by seeds per plant followed by biological yield per plant on the seed yield both at phenotypic and genotypic levels in blackgram genotypes (Reena Mehra *et al*., 2016).

2.4 Genetic Diversity

Ghafoor and Ahmad (2005) evaluated a broad based germplasm of genotypes using multivariate analyses. They observed high genetic variance for plant height, maturity, pods, seed weight, biomass, grain yield and harvest index and suggested that the genetic base of cultivated blackgram should be broadened by involving diverse parents in the breeding programme.

Ghafoor *et al*. (2001); evaluated 484 accessions of blackgram for qualitative and quantitative traits for cluster and principal component analysis and found a wide range of diversity for most of the traits along with some accessions with unique characters that could help to identify landraces to be used in hybridization programme.

Vaithiyalingan (2004) studied 24 diverse strains of blackgram collected from different geographic regions to analyze the extent of genetic divergence. They found that seed yield, dry matter production, 100-seed weight and pod length were the important contributors to genetic divergence.

Ali *et al.* (2008) estimated genetic divergence from 31 genotypes of black gram for seven morpho-economic characters (plant height, branches per plant, pods per plant,

pod length, seeds per pod, 100-seed weight and seed yield per plant) and found that seed yield per plant was highest contributor towards total divergence.

Ghafoor and Arshad (2008) selected 37 pure lines at random from a broad based germplasm and evaluated for quantitative traits to investigate the impact of selection on diversity in relationship to agronomic performance.

Elangaimannan *et al*. (2008) collected 55 genotypes from various sources and grouped into seven clusters following Mahalanobis D^2 statistics. Cluster I was the largest (34 genotypes) followed by clusters IV (eight), II (Six), V (four) and remaining three are monogenotypic clusters (III, VI and VII). The maximum intra-cluster distance was observed in custer I suggesting that genotypes having diverse genetic architecture. The inter-cluster distance was high between clusters II and VI there by indicating wide range of variation among the clusters. The percent contribution towards genetic diversity was high in number of pods per plant (26.12%). Based on cluster mean and per se performance, seven genotypes were selected for hybridization.

Chauhan *et al.* (2008) studied genetic diversity in 210 true breeding lines along with three checks of urdbean on the basis of yield and related traits by employing nonhierarchical Euclidean cluster analysis. The 210 genotypes were grouped into 9 different clusters that showed considerable differences in intra cluster group means of 12 characters and genotypes having distinctly different mean performance for various characters.

Neelavathi and Govindarasu (2010) studied 74 diverse genotypes of blackgram under rice fallow condition for yield and its component traits. They observed high genotypic variability for branches per plant, clusters per plant, pods per plant, biological yield and seed yield along with high heritability and high genetic advance, suggesting effective improvement of these characters through a simple selection programme. They grouped genotypes into five clusters by Mahalanobis D^2 analysis and based on cluster mean values, genotypes OBG 4 and KKB 98001 were found to be suitable parents for hybridization programme. They also concluded that characters viz., pods

per plant, 100-seed weight and biological yield contributed maximum for genetic divergence.

Senapati and Misha (2010) conducted a study on mutant and parental cultivars and divided them into twelve genetic diverse clusters. The average seed yield of seven clusters was found to be higher than parental cluster. They concluded that 100-seed weight, days to flowering and pods per plant were found to be major contributors to genetic divergence.

Majumder *et al.* (2011) analyzed 155 genotypes comprising commercial cultivars and landraces for genetic diversity and grouped them into 8 clusters indicating improved yield potential by hybridization and selection of superior genotypes in segregating generations.

Ghafoor and Arshad (2011) crossed six cultivars of blackgram selected from genetically diverse groups and revealed that the source of variation was attributed to both the factors, i.e. hybrids and generations representing high proportions of the total sum of squares. Two factors gave eigen values greater than unity and these contributed 77% of the total variability.

Shafique *et al*. (2011) evaluated 34 blackgram cultivars through morphological traits and observed considerable amount of genetic diversity among the cultivars.

Reena Mehra *et al*. (2016) studied on 75 blackgram and found seventeen clusters using D^2 analysis and maximum 13 genotypes were found in cluster thirteen. Clustering pattern revealed that genetic diversity was directly related to geographic diversity. Among the genotypes studied RBU 38, CBG 757, NDU 5-3, COBG 761, TPU 05-13, KKB 20055, KPU 07-06, RUG 1, PU 06-20 and VBG 04-008 had potential for higher yield based on the genetic merit of yield factors, and are selected for further study for eventual release as varieties for farmers. Additionally, These genotypes also can be used in genetic enhancement program to generate transgressive segregants since they were genetically diverse lines.

CHAPTER III
MATERIALS AND METHODS

This chapter deals with the information on the subject of materials and methods that were used in conducting the experiment. It consists of a short explanation of locations of the experimental site, soil characteristics, climate, materials used in the experiment, layout and design of the experiment, land preparation, manuring and fertilizing, transplanting of seedlings, intercultural practices, harvesting, data recording procedure and statistical analysis etc., which are presented as follows:

3.1 Experimental site

The experiment was conducted at the experimental field of Sher-e-Bangla Agricultural University, Dhaka-1207 during December 2015 to April 2016. The location of the experimental site was situated at $23^0$74' N latitude and $90^0$35' E longitude with an elevation of 8.6 meter from the sea level.

3.2Soil and Climate

The experimental site was situated in the subtropical zone. The soil of the experimental site belongs to the Agro-ecological zone of "The Modhupur Tract" (AEZ-28). The soil was clay loam in texture and olive gray with common fine to medium distinct dark yellowish brown mottles. The p^H ranges from 5.47 to 5.63 and organic carbon content is 0.82% (Appendix II). The records of air temperature, humidity and rainfall during the period of experiment were noted from the Bangladesh Meteorological Department, Agargaon, Dhaka (Appendix III).

3.3 Experimental materials

The healthy seeds of twenty blackgram varieties collected from the Dept. of Genetics and Plant Breeding, Sher-E-Bnalga Agricultural University, Dhaka-1207 which were used as experimental materials. The materials used in this experiment is shown in Table 1.

Table 1.The code accession name and sources of collection of the 20 blackgram genotypes used in the experiment.

Sl.No.	Code	Accession number
1	G1	BD 6814
2	G2	BD 6831
3	G3	BD 6833
4	G4	BD 6836
5	G5	BD 6838
6	G6	BD 6839
7	G7	BD 6840
8	G8	BD 6841
9	G9	BD 6841
10	G10	BD 6848
11	G11	BD 6855
12	G12	BD 6856
13	G13	BD 6857
14	G14	BD 6859
15	G15	BD 6860
16	G16	BD 6861
17	G17	BD 6863
18	G18	BD 6865
19	G19	BD 6866
20	G20	BD 6867

Source: Bangladesh Agricultural Research Institute.

3.4 Methods

The following precise methods have been followed to carry out the experiment:

3.4.1 Land preparation

The experimental plot was prepared by several ploughing and cross ploughing followed by laddering and harrowing with tractor and power tiller to bring about good tilth. Weeds and other stubbles were removed carefully from the experimental plot and leveled properly.

3.4.2 Application of manure and fertilizer

The crop was fertilized as the rate of 10 tons of cowdung, 100 kg urea, 150 kg triple super phosphate (TSP), 80 kg murate of potash (MP), 180 kg gypsum, 3kg zinc oxide and 1 kg boron per hectare. The half amount of urea, total amount of cowdung, TSP, MP, gypsum, zinc oxide and boron was applied during final land preparation. The rest amount of urea was applied as top dressing after 25 days of sowing.

3.4.3 Experimental design and layout

Field lay out was done after final land preparation. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. Total experimental area was 216 m^2. Each replication size was 12 m x 9 m, and the distance between replications was 1 m. The spacing between row was 30 cm. Seeds were sown in line in the experimental plots on 09 December 2015. The seeds were placed at about 1.5 cm depth in the soil. After sowing the seeds were covered with soil carefully so that no clods were on the seeds. An experimental plot was shown in Plate 1.

3.4.4 Intercultural operations

Intercultural operations, such as weeding, thinning, irrigation, pest management, etc. were done uniformly in all the plots. Irrigation was given with cane after sowing of seeds to bring proper moisture condition of the soil to ensure uniform germination of the seeds. A good drainage system was maintained for immediate release of rainwater from the experimental plot during the growing period. Thinning was done for maintaining a distance of 10 cm from plant to plant in rows of 30 cm apart. Weeding was done when necessary. Insect was managed through spraying insecticides.

3.4.5 Crop harvesting

The crop was harvested in different dates according to maturity. Harvesting was started on 20th March 2016. When 80% of the plants showed maturity symptoms the crop was assessed to attain maturity. The harvesting wad done by my supervision .15 plants were selected at randomly from each replication. The plants were harvested then they were tagged properly. Data were recorded on different parameters from these plants.

Plate 1. Photograph showing of 20 Blackgram genotypes experiment field

3.4.6 Data collection

Ten characters were taken into consideration for studying different genetic parameters, association and genetic diversity. Data were recorded on ten selected plants for each genotype from each replication on the following parameters. The details of data recording are given below on individual plant basis.

Total plant height (cm): Total length of a plant was measured from main root tip to the tip of the main shoot at the time of maturity.

Plant height (cm): Total length of a plant from ground level to the tip of the main shoot was measured in cm at the time of maturity.

Branches per plant: Total numbers of branches emerging from the main stem were counted for each plant.

Days to first flowering: Total number of days taken from the date of sowing to the five percent blooming of the plants in each plot.

Days to fifty percent flowering: Total number of days taken from the date of sowing to the fifty percent blooming of the plants in each plot.

Pods per plant: Total numbers of pods per plant were counted at the time of maturity.

Pod length (cm): Length of five randomly selected pods per plant was measured in cm.

Number of seeds per pod: Total numbers of seeds per pod were estimated by dividing the total number of seeds by the total number of pods harvested.

Days to maturity: Total number of days taken from the date of sowing to the eighty percent maturity of plants in each plot.

100 seed weight: Weight of randomly counted hundred seeds of each genotypes was recorded. It was measured in gram (g).

Seed yield per plant (g): Plants were harvested at maturity in the field and total weight of the seeds produce by selected plants was recorded in grams.

3.4.7 Statistical analysis

Mean data of the characters were used for statistical analyze like analysis of variance (ANOVA), mean, range were calculated by using MSTATC software program. Genotypic and phenotypic variance was estimated by the formula used by Johnson *et al*. (1955). Heritability and genetic advance were measured using the formula given by Singh and Chaudhary (1985) and Allard (1960). Genotypic and phenotypic coefficient of variation were calculated by the formula of Burton (1952). Genotypic and phenotypic correlation coefficient was obtained using the formula suggested by Miller et al. (1958), Johnson et al. (1955) and Hanson et al. (1956); path coefficient analysis was done following the method outlined by Dewey and Lu (1959). Multivariate analysis viz., principal component analysis (PCA), principal coordinate analysis (PCO), cluster analysis (CA) and canonical vector analysis (CVA) were done by using GENSTAT 5.13 and Microsoft excel 2007 software.

3.4.7.1 Estimation of genotypic and phenotypic variances

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

$$\text{Genotypic variance } (\sigma^2_g) = \frac{GMS - EMS}{r}$$

Where,

GMS = Genotypic mean sum of square
EMS = Error mean sum of square
r = number of replications

Phenotypic variance (σ^2_p) = σ^2_g + σ^2_e

Where,

σ^2_g = Genotypic variance

EMS = Error mean sum of square

σ^2_e = Error variance

3.4.7.2 Estimation of genotypic and phenotypic co-efficient of variation

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

Genotypic co-efficient of variation (GCV %) = $\sqrt{\frac{\sigma^2_g}{\bar{x}}} \times 100$

Where,

σ^2_g = Genotypic variance

$\bar{x}$ = Population mean

Similarly, the phenotypic co-efficient of variation was calculated from the following formula.

Phenotypic co-efficient variation (PCV) = $\sqrt{\frac{\sigma^2_{ph}}{\bar{x}}} \times 100$

Where,

σ^2_p= Phenotypic variance

$\bar{x}$ = Population mean

PCV and GCV were classified as suggested by Shivasubramanian and Menon (1973) as follows:

0-10% = low
10-20% = Moderate
20% and above = high

3.4.7.3 Estimation of heritability

Broad sense heritability was estimated (Lush, 1943) by the following formula, suggested by Johnson *et al.* (1955).

Heritability, $h^2_b\% = \frac{\sigma^2 g}{\sigma^2 p} \times 100$

Where,

h^2_b = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

Heritability percentage was categorized as demonstrated by Robinson *et al.* (1949).

0-30% = Low
30-60% = Moderate
60% and above = High

3.4.7.4 Estimation of genetic advance

The expected genetic advance for different characters under selection was estimated using the formula suggested by Lush (1943) and Johnson *et al.* (1955).

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

Or Genetic advance, $GA = K. \frac{\sigma^2 g}{\sigma^2 p}. \sigma_p$

Where,

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

σ_p = Phenotypic standard deviation

h^2_b= Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

3.4.7.5 Estimation of genetic advance mean's percentage

Genetic advance as percentage of mean was calculated from the following formula as proposed by Comstock and Robinson (1952):

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

The advance as percent mean was categorized into low, moderate and high By Johnson *et al.* (1955) and is as follows:

0-10% = Low
10- 20% = Moderate
20 and above = High

3.4.7.6 Estimation of genotypic and phenotypic correlation co-efficient

The calculation of genotypic and phenotypic correlation co-efficient for all possible combinations through the formula suggested by Miller *et al.* (1958), Johnson *et al.* (1955) and Hanson *et al.* (1956) were adopted. The genotypic co-variance component between two traits and have the phenotypic co-variance component were derived in the same way as for the corresponding variance components. The co-variance components were used to compute genotypic and phenotypic correlation between the pairs of characters as follows.

Genotypic correlation, $r_{gxy} = \frac{GCOVxy}{\sqrt{GVx.GVy}} = \frac{\sigma_{gxy}}{\sqrt{(\sigma^2_{gx} . \sigma^2_{gy})}}$

Where,

Genotypic co-variance between the traits x and y

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

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

Phenotypic correlation $(r_{pxy}) = \frac{PCOVxy}{\sqrt{PVx.PVy}} = \frac{\sigma_{pxy}}{\sqrt{(\sigma^2_{px} . \sigma^2_{py})}}$

Where,

σ_{pxy} = Phenotypic covariance between the trait x and y

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

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

3.4.7.7 Estimation of path co-efficient

Path analysis was done according to the procedure employed by Dewey and Lu (1959) also quoted in Singh and Chaudhary (1985), using genotypic correlation coefficient values. In path analysis, correlation coefficients between yield and yield contributing characters were partitioned into direct and indirect effects on yield per plant.

3.4.7.8 Multivariate analysis

The genetic diversity among the genotypes was assessed by Mahalanobis's (1936) general distance (D^2) statistic and its auxiliary analyses. The parents selection in hybridization program based on Mahalanobis's D^2 statistic is more reliable as requisite knowledge of parents in respect of a mass of characteristics is available prior to crossing. Rao (1952) suggested that the quantification of genetic diversity through biometrical procedures had made it possible to choose

genetically diverse parents for a hybridization program. Multivariate analysis viz. Principal Component analysis, Principal Coordinate analysis, Cluster analysis and Canonical Vector analysis (CVA), which quantify the differences among several quantitative traits, are efficient method of evaluating genetic diversity. These are as follows:

3.4.7.8.1 Principal component analysis (PCA)

Principal Component analysis, one of the multivariate techniques, is used to examine the inter-relationships among several characters and can be done from the sum of squares and products matrix for the characters. Thus, PCA finds linear combinations of a set variate that maximize the variation contained within them, thereby displaying most of the original variability in a smaller number of dimensions. Therefore, Principles components were computed from the correlation matrix and genotypes scores obtained for first components (which has the property of accounting for maximum variance) and succeeding components with latent roots greater than unity. Contribution of the different morphological characters towards divergence is discussed from the latent vectors of the first two principal components.

3.4.7.8.2 Principal Coordinate analysis (PCO)

Principal Coordinate analysis is equivalent to PCA but it is used to calculate inter unit distances. Through the use of all dimension of p it gives the minimum distance between each pair of the n points using similarity matrix (Digby *et al.*, 1989).

3.4.7.8.3 Cluster analysis (CA)

Cluster analysis divides the genotypes of a data set into some number of mutually exclusive groups. Clustering was done using non-hierarchical classification. In GENSTAT, the algorithm is used to search for optimal values of chosen criterion proceeds as follows. Starting from some initial

classification of the genotypes into required number of groups, the algorithm repeatedly transferred genotypes from one group to another so long as such transfer improved the value of the criterion. When no further transfer can be found to improve the criterion, the algorithm switches to a second stage which examines the effect of swooping two genotypes of different classes and so on.

3.4.7.8.4 Canonical vector analysis (CVA)

Canonical vector analysis (CVA) finds linear combination of original variability's that maximize the ratio of between group to within group variation, thereby giving functions of the original variables that can be used to discriminate between the groups. Thus, in this analysis a series of orthogonal transformations sequentially maximizing of the ratio of among groups to the within group variations. The canonical vector are based upon the roots and vectors of WB, where W is the pooled within groups co-variance matrix and B is the among groups co-variance matrix.

3.4.7.8.5 Calculation of D^2 values

The Mahalanobis's distance (D^2) values were calculated from transformed uncorrelated means of characters according to Rao (1952), and Singh and Chaudhury (1985). The D^2 values were estimated for all possible combinations between genotypes. In simpler form D^2 statistic is defined by the formula:

$$D^2 = \sum_{i}^{x} d_i^2 = \sum_{i}^{x} (Y_i^j - Y_j^k) \qquad (j \neq k)$$

Where,

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

x = Number of characters.

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

3.4.7.8.6 Computation of average intra-cluster distances

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

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

Where,

D_i^2 = the sum of distances between all possible combinations (n) of genotypes included in a cluster

n= Number of all possible combinations between the populations in cluster

3.4.7.8.7 Computation of average inter-cluster distances

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

Average inter-cluster distance= $\frac{\sum D_{ij}^2}{n_i \times n_j}$

Where,

$\sum D_{ij}^2$ = The sum of distances between all possible

Combinations of the populations in cluster i and j

n_i= Number of populations in cluster i

n_j= Number of populations in cluster j

3.4.7.8.8 Cluster diagram

Using the values of intra and inter-cluster distances (D = $\sqrt{D^2}$), a cluster diagram was drawn as suggested by Singh and Chuadhury (1985). It gives a brief idea of the pattern of diversity among the genotypes included in a cluster.

CHAPTER IV
RESULTS AND DISCUSSIONS

The findings of the present experiments of genetic analysis like variability, correlation coefficients, path analysis and diversity 20 blackgram genotypes carried out during Rabi season 2015-16 are presented in the following sections.

4.1 Nature of variation and association among seed yield and related traits

The development of an effective plant breeding programme is dependent upon the existence of genetic variability, careful management of this genetic variability, techniques to be employed and clear understanding of extent and nature of genetic variability, which is important for effective selection. Selection which is the basis of any breeding programme operates on heritable variation which is genetic in nature. A wide range of genetic variability present in any crop species provide a better chance of selecting the desired types (Vavilov, 1951). Most of the traits of interest to plant breeder are quantitative in nature which exhibit continuous variation. The continuous variation comprises of heritable and non heritable components (Fisher, 1918). As it is difficult to assess genotypic components directly in the field, it is possible only through the assessment of phenotypic expression, which appears as a result of interaction between genotypic and environmental components. Hence an insight into the magnitude of variability for various morph metric traits of a crop species is of utmost importance to plant breeder.

4.2 Analysis of variance

The mean sum of squares due to genotypes were highly significant at 1% level of significance for total plant height (cm), plant height (cm), branches per plant, days to first flowering, pods per plant, pod length (cm), seeds per pod, days to maturity, hundred seed weight (g) and seed yield per plant (g) (Table 2). This indicated the existence of wide range of genetic variability for all studied

characters in the germplasm. Hence, it offers a better scope for further improvement of breeding material by the selection of promising genotypes in blackgram breeding programme, however the character days to 50% flowering was found insignificant. Ghafoor and Ahmad (2003) also observed high genetic variance for plant height, maturity, pods, seed weight and grain yield. Various other workers viz., Pradhan and Misra (2005), Pervin *et al.*, (2007), Arulbalachandran *et al.,* (2010) and Neelavathi and Govindarasu (2010) have also reported high amount of genetic variability for the morph metric traits under study.

4.3 Parameters of variability

The estimates of various parameters of variability viz., mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), environmental coefficient of variation (ECV), heritability in broad sense (h^2bs) and genetic advance (GA) expressed as percentage of mean for different traits studied (Table 3 and 4 & Figure 1 and 2) are described as below:

4.3.1 Genetic variability, heritability and genetic advance

The knowledge of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) is helpful in predicting the amount of variation present in the given genetic stock which in turn helps in formulating an efficient breeding programme. PCV values were found to be higher than their corresponding GCV values for all the traits under study suggesting that the apparent variation is not only due to genotypes but also due to the influence of environment. Therefore, caution has to be exercised in making selection for these characters on the basis of phenotype alone, as environmental variation is unpredictable in nature. Similar findings have also been reported by Siddique *et al.,* (2006), Malik *et al.,* (2008) and Konda *et al.,* (2009).

The coefficient of variation alone cannot be used to partition the heritable components of variation (Burton 1952). This suggested that genetic coefficient of variation together with heritability estimates would give the best picture of the amount of genetic advance to be expected from selection. The information on heritability estimates is helpful in studying the inheritance of quantitative characters as well as for planning breeding programme with desired degree of expected general progress. Heritability in broad sense is of tremendous significance to the breeders as its magnitude indicates the reliability with which a genotype can be recognized by its phenotypic expression (Lush 1940).

For an effective selection programme, knowledge of the estimates of heritability alone is not sufficient and genetic advance if studied along with heritability is more useful (Johnson *et al*. 1955). Thus the genetic advance has an added edge over heritability as a guiding factor to breeders in various selection programmes. Genetic advance may and may not be in proportion to genetic variability and heritability estimates, because both heritability and high genetic variability are important to obtain higher genetic gain.

The estimates of various parameters of variability viz., mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), environmental coefficient of variation (ECV), heritability in broad sense (h^2bs) and genetic advance (GA) expressed as percentage of mean for different traits studied (Table 3 and 4 & Figure 1 and 2) are described as below:

Table 2. Analysis of variance of different characters of 20 Blackgram genotypes

Characters/Variety	Mean sum of square		
	Replication (r-1) = 2	Genotype (g-1) = 19	Error (r-1)(g-1) = 38
Total plant height (cm)	16.78	30.94**	7.38
Plant height (cm)	21.81	24.35**	4.16
Branches per plant	2.05	1.07**	0.18
Days to first flowering	1.27	3.79**	1.41
Days to 50% flowering	1.82	1.49	1.03
Pods per plant	8.22	4.00**	1.23
Pod length (cm)	0.03	0.24**	0.09
Seeds per pod	0.77	1.38**	0.31
Days to maturity	0.05	5.05**	1.17
Hundred seed weight (g)	0.01	0.12**	0.02
Seed yield per plant (g)	0.16	0.20**	0.03

** Significant at 1% level of probability

TPH = Total plant height (cm), PH =Plant height (cm), BPP = Branches per plant, DFF = Days to first flowering, D50%F = Days to 50% flowering, PPP = Pods per plant, PL = Pod length (cm), SPP = Seeds per pod, DM = Days to maturity, HSW = Hundred seed weight (g) and SYP = Seed yield per plant (g).

Total plant height (cm)

The grand mean of total plant height counted was 28.20 cm. It was ranged from 21.45 cm to 35.69 cm (Table 3). Highly significant difference was observed among the genotypes through the analysis of variance for this trait. The genotype G7 performed the maximum total plant height (35.69 cm) and the genotype G10 performed the lowest total plant height (21.45 cm)**.** Moderate PCV (13.84) and low GCV (9.94) were found for total plant height but greater than ECV (9.63). The estimate of heritability was moderate at 51.56% was moderate and genetic advance in percent of mean (14.70%) (Table 4).

Plant height

It ranged from 16.11cmto 29.89cm with a mean value of 22.43 cm (Table 3). Highest plant height was rewarded for the genotype G7 (29.89 cm) and the lowest G20. Moderate PCV (14.71) and GCV (11.56) were observed for this trait indicated that, it might provide better scope for improvement through selection (Table 4). High broad sense heritability (61.83%) coupled with moderate genetic advance (18.73) over percentage of mean were noticed. These traits, suggesting hybridization coupled with selection to exploit both type of gene action. High heritability along with high genetic advance for this character was also reported by Pradhan and Misra (2005) ,Rahim *et al,.* (2010) and Reddy *et al.* (2011). Similarly, high heritability for plant height was observed by Rahim *et al.,* (2010). Heritability for plant height revealed lesser influence of the environment and greater role of genetic component of variation, indicating that the selection for these traits on the basis of phenotypic expression would be more effective and can be relied upon.

Table 3. Mean performance of different characters of twenty blackgram genotypes

	TPH	PH	BPP	DFF	D50%F	PPP	PL	SPP	DM	HSW	SYP
G1	25.98	19.71	2.29	63.00	73.00	8.00	3.79	6.58	91.00	2.57	1.31
G2	27.59	22.66	2.85	61.33	71.00	9.68	4.31	6.44	90.00	2.33	1.45
G3	29.21	23.52	2.92	63.67	72.00	8.53	3.59	4.60	93.00	2.45	0.95
G4	32.36	21.20	2.33	64.00	73.00	8.53	3.76	5.33	92.00	2.44	1.07
G5	30.73	21.04	2.86	64.00	71.00	7.41	3.77	5.56	91.00	2.76	1.52
G6	28.83	19.46	4.55	62.00	71.67	8.27	4.13	6.57	90.00	2.34	1.18
G7	35.69	29.89	4.28	64.33	73.33	7.84	3.88	5.57	93.00	2.24	0.91
G8	27.05	21.48	3.60	62.00	71.33	10.45	3.83	6.15	89.33	2.37	1.41
G9	28.24	23.53	2.63	62.00	72.00	8.87	3.59	5.39	91.00	2.64	1.45
G10	21.45	20.59	3.70	63.00	73.33	8.90	4.09	6.61	93.00	2.31	1.05
G11	27.59	23.31	3.29	64.00	73.00	7.47	3.61	5.69	94.00	2.18	0.88
G12	31.40	27.09	3.07	62.00	72.00	8.27	3.50	5.52	90.67	2.84	1.35
G13	29.79	23.66	2.64	65.00	72.00	9.33	3.80	6.47	92.00	2.55	1.56
G14	27.13	20.62	2.60	64.33	72.00	9.15	3.48	5.21	90.00	2.60	1.39
G15	27.85	22.37	3.13	64.67	72.00	8.40	4.19	6.48	90.67	2.78	1.49
G16	28.71	23.55	2.73	62.00	73.00	11.77	4.11	5.67	92.00	2.54	1.50
G17	26.35	22.65	2.84	62.00	72.00	10.04	4.46	6.00	92.00	2.14	1.33
G18	29.47	24.29	3.54	62.33	72.00	10.43	3.75	5.60	89.33	2.64	1.85
G19	26.66	21.95	3.47	62.00	72.00	10.48	4.10	4.36	91.00	2.73	1.67
G20	21.85	16.11	3.16	63.00	72.00	8.27	3.59	6.73	91.00	2.43	1.32
Min	21.45	16.11	2.29	61.33	71	7.41	3.48	4.36	89.33	2.14	0.88
Max	35.69	29.89	4.55	65	73.33	11.77	4.46	6.73	94	2.84	1.85
Mean	28.20	22.43	3.12	63.03	72.18	9	3.87	5.83	91.3	2.49	1.33
CV%	9.63	9.09	13.58	1.88	1.4	12.3	7.55	9.54	1.19	5.66	12.43

TPH = Total plant height (cm), PH = Plant height (cm), BPP = Branches per plant, DFF = Days to first flowering, D50%F = Days to 50% flowering, PPP = Pods per plant, PL = Pod length (cm), SPP = Seeds per pod, DM = Days to maturity, HSW = Hundred seed weight (g) and SYP = Seed yield per plant (g).

Table 4. Estimation of genetic parameters of eleven characters of twenty blackgram genotypes

Parameters	$\sigma^2 p$	$\sigma^2 g$	$\sigma^2 e$	PCV	GCV	ECV	Heritability	Genetic advance (5%)	Genetic advance (% mean)
Total plant height (cm)	15.23	7.85	7.38	13.84	9.94	9.63	51.56	4.15	14.70
Plant height (cm)	10.89	6.73	4.16	14.71	11.56	9.09	61.83	4.20	**18.73**
Branches per plant	0.48	0.30	0.18	22.07	17.39	13.58	62.12	0.88	**28.24**
Days to first flowering	2.20	0.79	1.41	2.35	1.41	1.88	36.04	1.10	1.75
Days to 50% flowering	1.18	0.15	1.03	1.51	0.54	1.40	13.07	0.29	0.41
Pods per plant	2.15	0.93	1.23	16.29	10.68	12.30	43.00	1.30	14.43
Pod length (cm)	0.14	0.05	0.09	9.54	5.83	7.55	37.41	0.28	7.35
Seeds per pod	0.66	0.36	0.31	13.99	10.23	9.54	53.50	0.90	15.42
Days to maturity	2.46	1.29	1.17	1.72	1.25	1.19	52.42	1.70	1.86
Hundred seed weight (g)	0.05	0.03	0.02	9.38	7.48	5.66	63.55	0.31	12.28
Seed yield per plant (g)	0.08	0.06	0.03	21.87	17.99	12.43	67.67	0.41	**30.48**

$\sigma^2 p$ = Phenotypic variance, $\sigma^2 g$ = Genotypic variance and $\sigma^2 e$ = Environmental variance, PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, ECV = Environmental coefficient of variation.

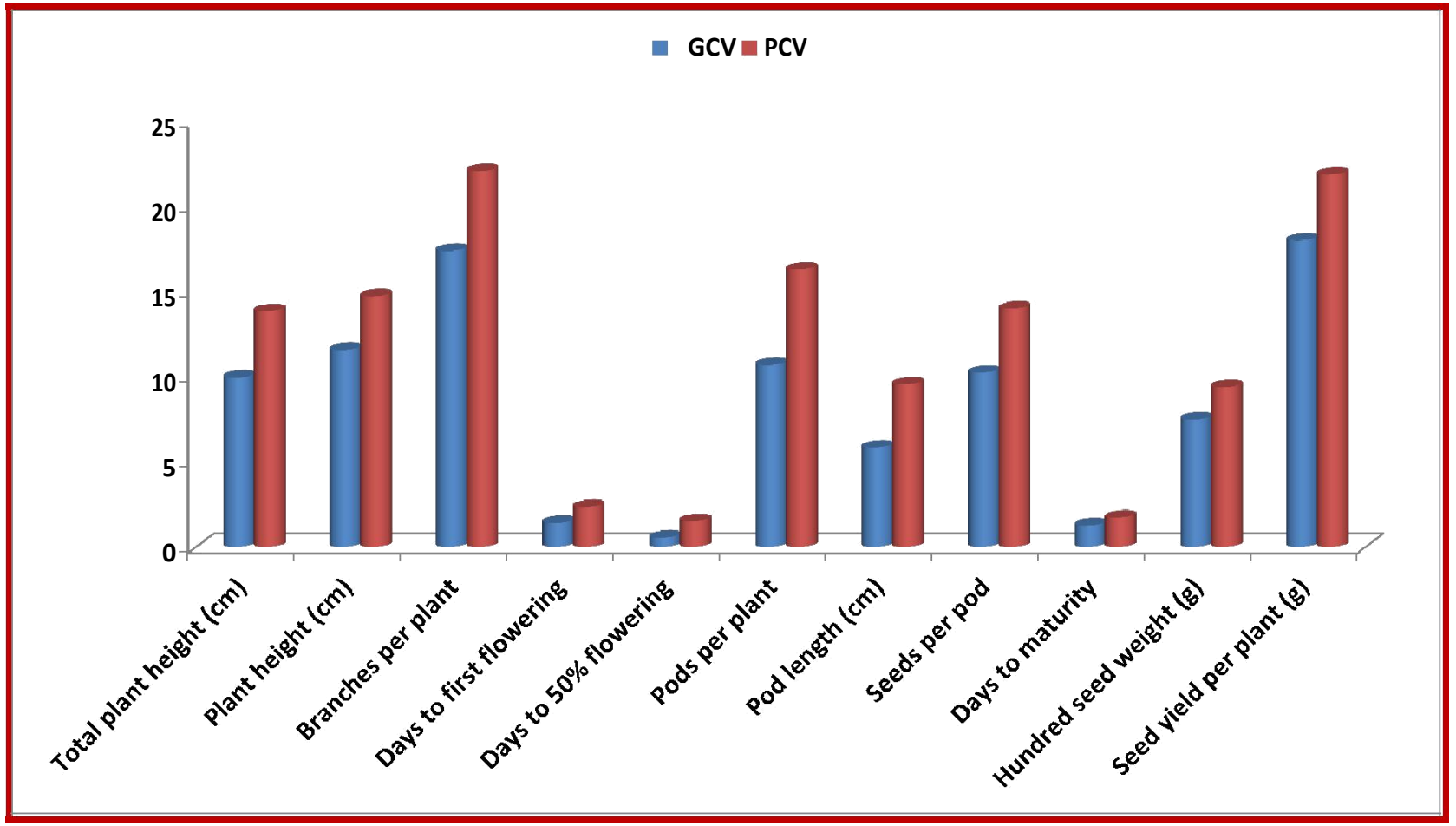


Figure 1. Genotypic and phenotypic variability of eleven characters for 20 blackgram genotypes

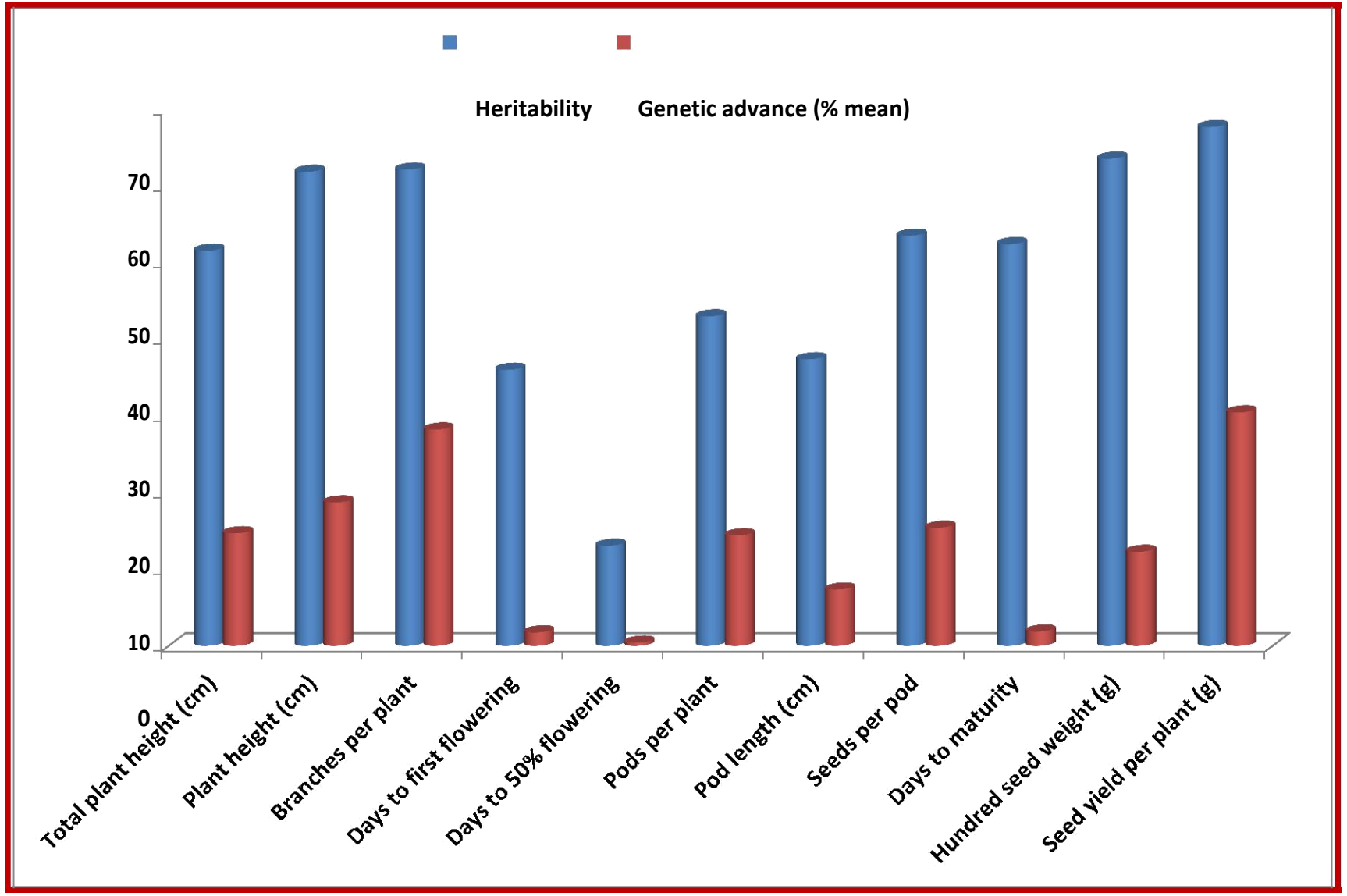


Figure 2. Heritability and genetic advance in percent of mean for eleven characters of 20 Blackgram genotypes

Branches per plant

The number of branches per plant ranged from 2.29 to 4.55 with a mean of 3.12 (Table 3). Maximum branches per plant were found by the genotype G6 (4.55) and minimum by genotype G1 (2.29). The genotypic, phenotypic and environmental variances observed were 0.30, 0.48 and 0.18, respectively. Branches per plant exhibited higher PCV (22.07%) than GCV (17.39%) (Table 4), indicated that, there is environmental influence for the expression of the selection and less scope for improvement through selection. The heritability observed by this trait was high (62.12%) with high expected genetic advance over mean (28.24%) were recorded which indicating that these characters control by additive gene action. This result indicates that these characters were highly heritable and hence were less affected by the environment. The plant breeder, therefore, may make his selection safely on the basis of phenotypic expression of these characters.. High value of additive gene action is indication of high breeding value.

Days to first flowering

Days to first flowering ranged from 61.33 to 65 with mean value 63.03. Maximum days for first flowering required for the genotype G13 (65) and minimum for genotype G2 (61.33). PCV and GCV value for this trait were low. Character showing low PCV and GCV reveal low genetic variability. Low heritability along with low genetic advance over percent of mean was observed for this trait.

Days to 50% flowering

Days to 50% flowering ranged from 71 to 73.33 with mean value 72.18. Genotype G10 (73.33) was expressed maximum days to first flowering and minimum by both genotypes G2 and G5 (71). Low PCV and GCV value were denoted by this trait indicates low genetic variability for this trait. Broad sense heritability along with genetic advance over percent of mean was low for this trait.

Pods per plant

The number of pods per plant ranged from 7.41to 11.77 with mean value 9.00. The maximum pods per plant was observed in genotype G16 (11.77) while minimum pods per plant was represent in the genotype G5 (7.41). The coefficient of variability at phenotypic and genotypic level was 16.29% and 10.68% respectively. The values for moderate heritability and moderate genetic gain over mean were 43.00% and 14.43%, respectively.

Pod length (cm)

Pod length ranged from 3.48to 4.46 cm with mean value 3.87 cm. The minimum pod length was represented by genotype G14 and G17 showed the maximum pod length. The PCV and GCV obtained were 9.54% and 5.83%respectively. The values of moderate heritability (37.41%) along with low genetic advance as per cent mean (7.35%) were observed for this trait.

Seeds per pod

Significant difference among genotypes for seeds per pod was noticed. It ranged from 4.36to 6.73 with average value 5.83. Genotype G20 presented highest numbers seeds per pod while genotype G19 showed the lowest number of seeds per pod. The moderate PCV and GCV for this character were 13.99% and 10.23%, respectively. It showed moderate heritability 53.50% along with moderate genetic advance over mean 15.42%. High heritability for seeds per pod was observed by Rahim *et al.,* (2010).

Days to maturity

The range of days to maturity from 89.33 to 94 was observed. Genotype G8 performed the minimum days to maturity while genotype G11 represented maximum days to maturity. Low genotypic and phenotypic coefficient of variation was observed by this trait. The difference between PCV and GCV was of lower magnitude for this traits. It indicates that there is little influence

of environment on the expression of these characters. Selection for improvement of such characters should be avoided. These finding are in agreement with the results obtained by Sarkar *et al.*, (2006), Pervin *et al,*. (2007). Moderate heritability (52.42) with low genetic advance were performed by this trait.

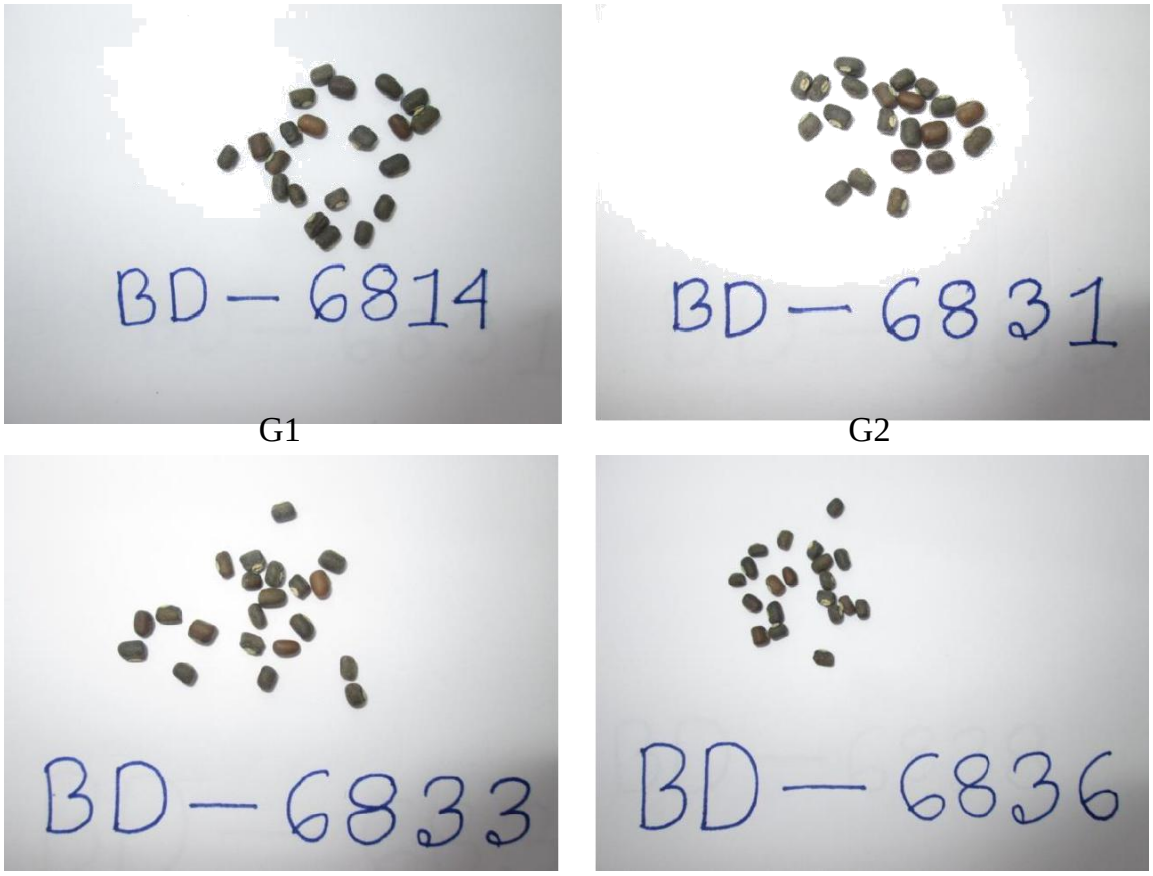
Hundred seed weight (g)

The mean hundred seed weight noticed was 2.49 g with a range from 2.14 g to 2.84 g. The genotype G12 showed the maximum hundred seed weight and the minimum hundred seed weight was recorded in the genotype G17. The values 9.38 and 7.48 were noticed for PCV and GCV, respectively. The difference between PCV and GCV was of lower magnitude for this trait and it was indicated that there is little influence of environment on the expression of these characters. Selection for improvement of such characters should be avoided. The high heritability estimate was 63.55% with moderate genetic advance over mean was12.28%. High heritability for 100-grain weight was observed by Rahim *et al.*, (2010).

Seed yield per plant (g)

The mean seed yield per plant was noticed 1.33 g with a range from 0.88 g to 1.85g in the genotype G11 and G18, respectively. Highest phenotypic coefficient of variability (21.87%) and genotype coefficient of variability (17.99%) was observed. Highest GCV and PCV for seed yield per plant which indicated that, it might provide better scope for improvement through selection. Highest heritability (67.67%) and genetic advance over mean (30.48%) were recorded which indicating that these characters were under the influence of additive gene action. This result indicates that these characters were highly heritable and hence were less affected by the environment. The plant breeder, therefore, may make his selection safely on the basis of phenotypic expression

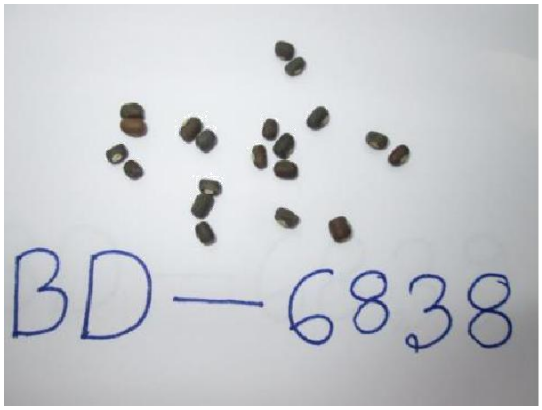
of this trait. Highest heritability along with highest genetic advance was observed in this character by Pradhan and Misra (2005) attributed to additive gene actions. Reddy *et al*. (2011) also reported high heritability coupled with high genetic advance for seed yield per plant. Rahim *et al*,. (2010) observed high heritability and genetic advance over mean was supported this results. Neelavathi and Govindarasu, (2010) also observed high heritability and genetic advance for seed yield per plant. High heritability coupled with high genetic advance for these traits indicate preponderance of additive gene action in the inheritance of these traits and selection would be effective. High value of additive gene action is indication of high breeding value.



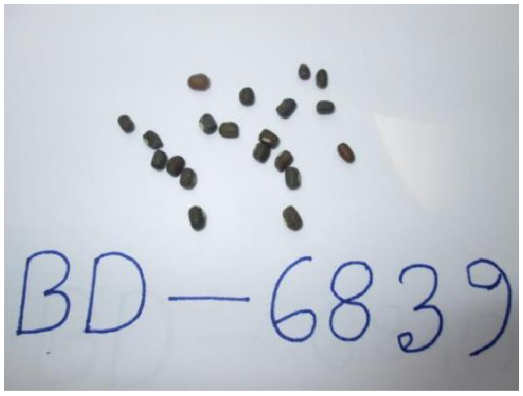
G1 G2

G3 G4

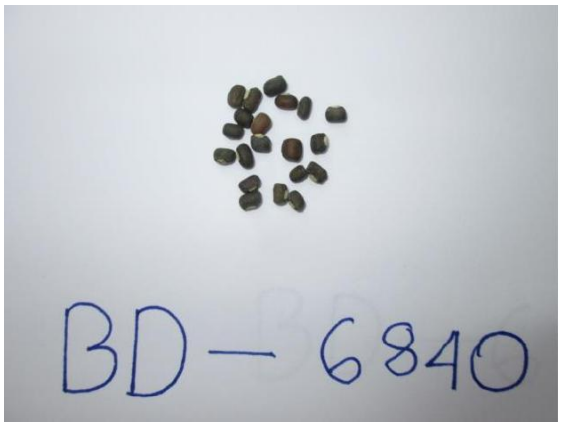
Plate 2. Photographs of seed of genotypes G1 to G4



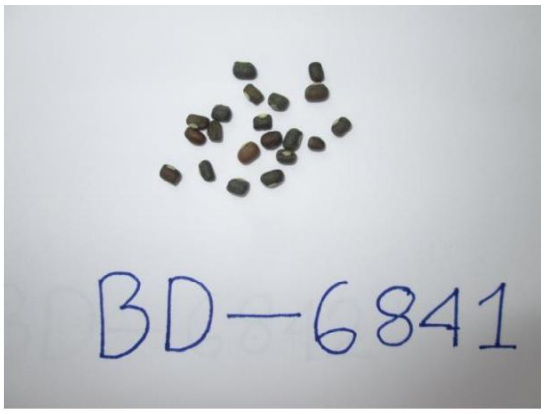
G5



G6

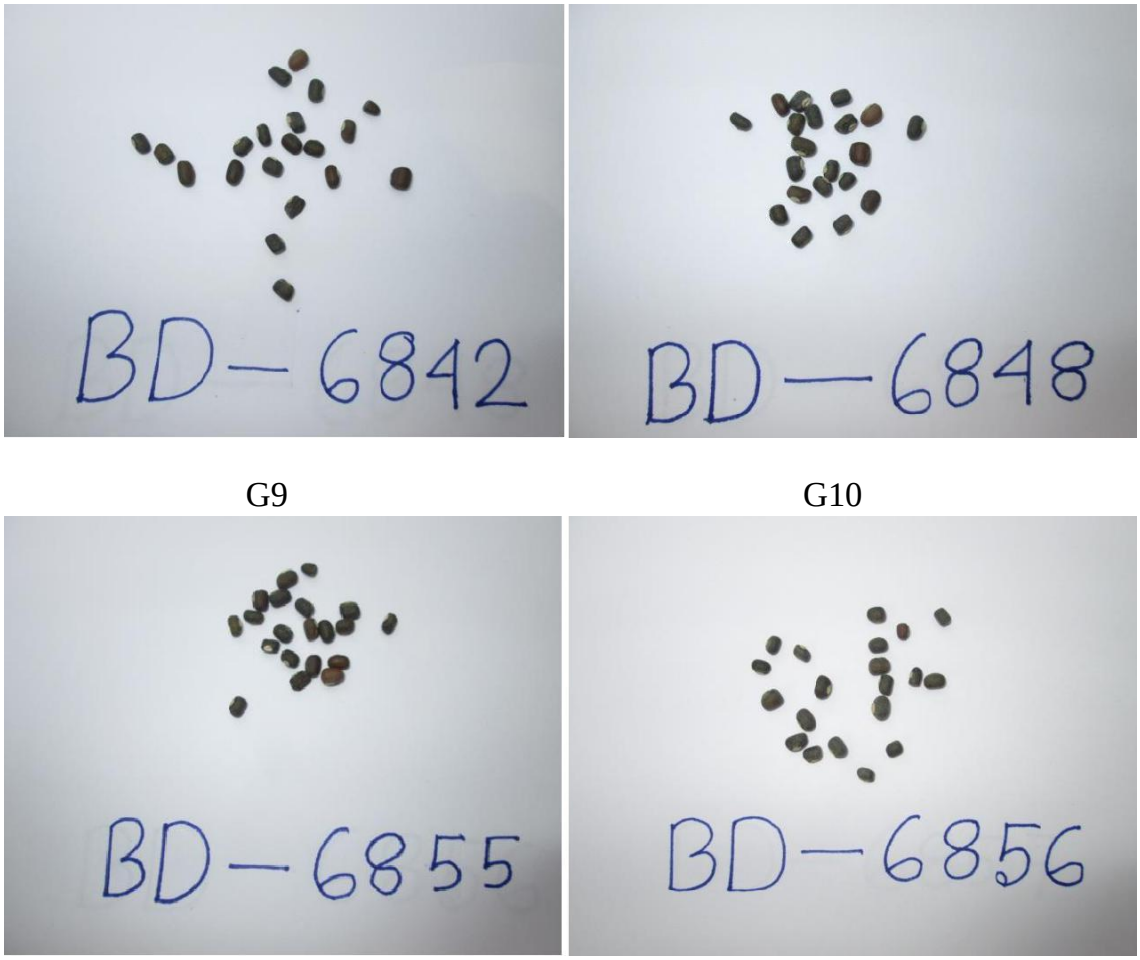


G7



G8

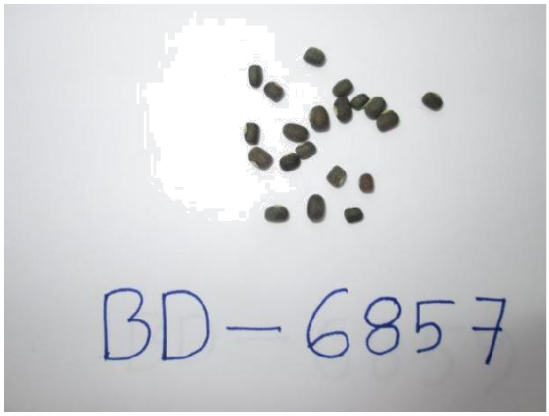
Plate 3. Photographs of seed of genotypes G5 to G8



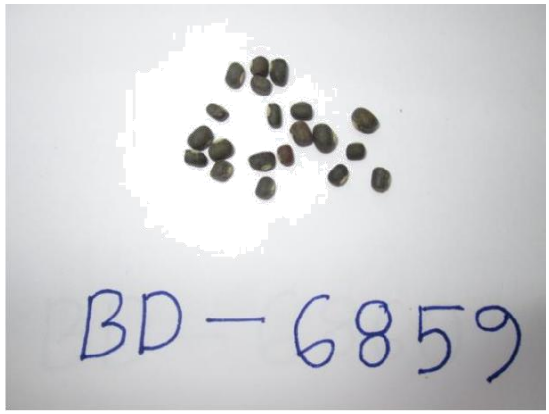
G9 G10

G11 G12

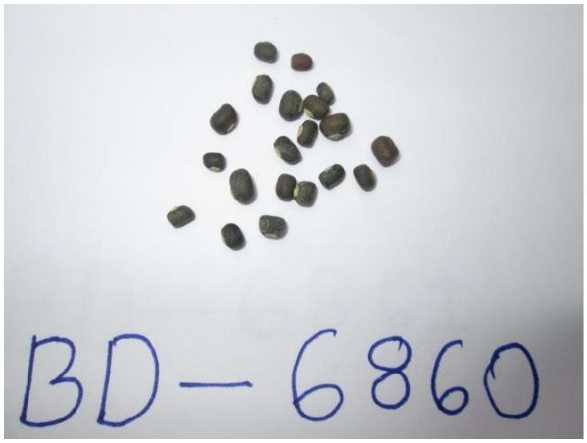
Plate 4. Photographs of seed of genotypes G9 to G12



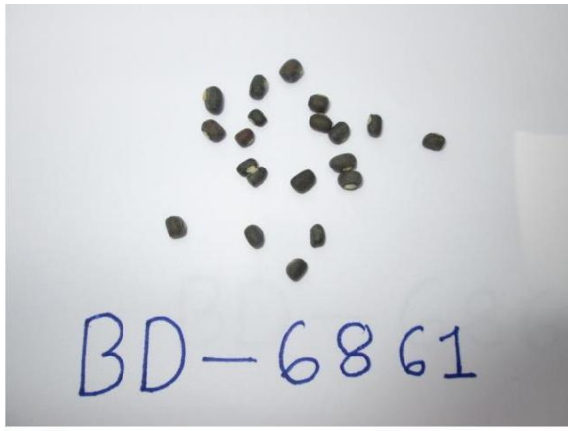
G13



G14

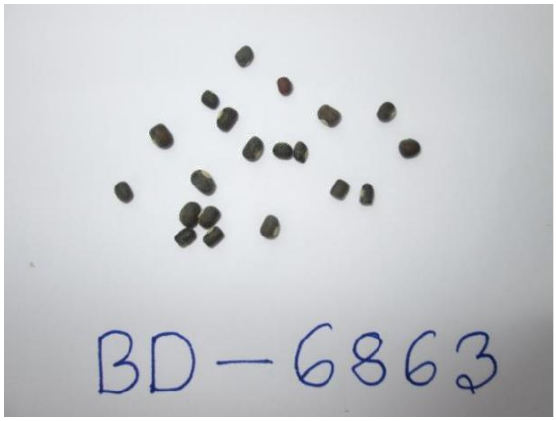


G15

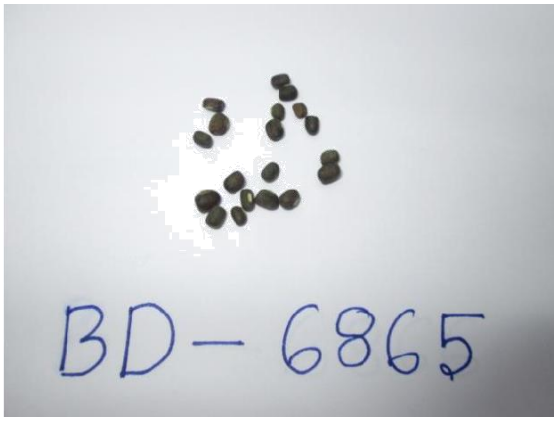


G16

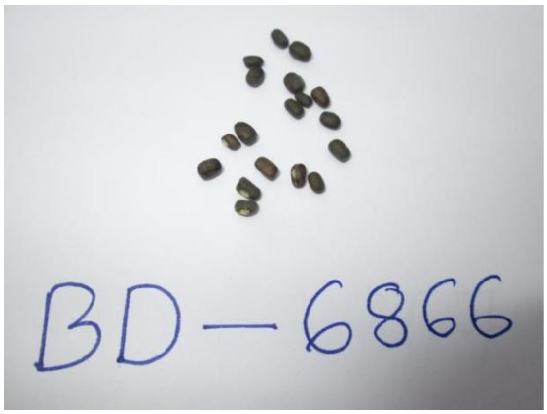
Plate 5. Photographs showing of seed of genotypes G13 to G16



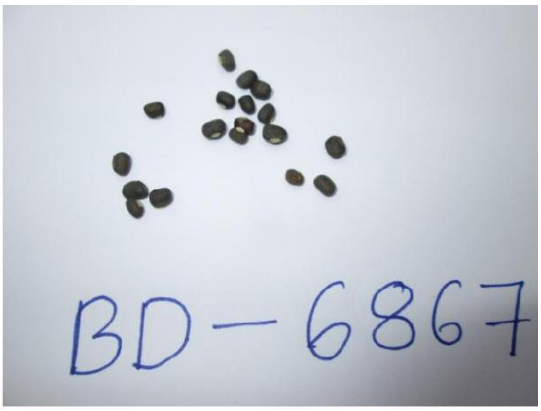
G17



G18



G19



G20

Plate 6. Photographs showing of genotypes G17 to G20

4.4 Correlation coefficients

Yield is a complex character and is a function of several component characters and their interaction with environment. Direct selection based on yield alone will not be very effective in crop improvement programmes. Grafius (1956) had also opined that the improvement of complex characters such as seed yield might be accomplished better through component breeding. Therefore, it is also important to gather information on association of yield with other characters and among themselves, and their basis to identify characters for increasing the efficiency of both direct and indirect selection and thereby defining an ideal plant type.

In order to understand the nature and magnitude of correlations among seed yield per plant and other traits along with their casual factors, estimate of correlation coefficients at phenotypic and genotypic levels and their direct and indirect effects through path coefficient analysis were performed and the results obtained are discussed as under:

Correlation coefficients at phenotypic and genotypic levels

The results on the correlations computed at phenotypic and genotypic levels for all possible paired combinations are presented in Tables 5 and 6 respectively.

Genotypic correlations are generally of lower magnitude than phenotypic correlation because of masking effect of environment (Table 5). If genotypic and phenotypic correlations are of same magnitude, it indicates the lack of environmental influence and high heritability of the association.

Seed yield per plant exhibited significant and positive correlation with pods per plant (0.622^{**} and 0.519^{**}) and hundred seed weight (0.686^{**} and 0.543^{**}) and insignificant positive correlation with branches per plant (0.238 and 0.176), pod length (0.201 and 0.105) and seeds per pod (0.089 and 0.086) at both genotypic and phenotypic levels indicating these traits could be utilize in improvement of

seed yield per plant (Table 5 & 6). Whereas it was significant negatively correlated with days to first flowering (-0.431** and -0.181), days to 50% flowering (-0.949** and -0.281*) and days to maturity (-0.799** and -0.594**), hence these traits could be utilized in improving the early variety. Shivade *et al.,* (2011) also observed positive association of branches per plant, pods per plant, length of pod and seeds per pod with seed yield per plant at the phenotypic level. Similarly, Reddy *et al.* (2011) reported a significant positive correlation of pods per plant, seeds per pod and pod length with seed yield. Bhareti *et al.* (2011) reported that days to 50% flowering had negative genotypic and phenotypic correlation with seed yield per plant in black gram.

Plant height exhibited significantly positive correlation with days to 50% flowering (0.558**), total plant height (0.801**) and days to maturity (0.378**) at genotypic level (Table 5). Significantly positive correlation was also observed for branches per plant with pod length (0.378**). Pods per plant showed significantly positive correlation with pod length (0.599**), whereas a negative significant correlation with days to first flowering (-0.924**) and days to maturity (-0.412**). Pods per plant and 100 seed weight are usually associated negatively with each other (Nagarjuna and Reddy 2001) but positive correlation between these two traits was also confirmed by Konda *et al.* (2008).

Pod length also exhibited significantly positive correlation with seeds per pod (0.430**) and negative correlation with hundred seed weight (-0.406**) in both levels (Table 5 & 6). Similarly seeds per pod showed significant negatively correlation with 100-seed weight (-0.324*). Days to maturity showed significant negative correlation with hundred seed weight (-0.530**).

The estimates of genotypic correlations, in general, were of higher magnitude than their respective phenotypic correlations for most of the traits, revealing that there is a strong inherent association between various characters and the

genotypes were not super-imposed by the environmental conditions. This supports the results of Bhareti *et al.* (2011) and Reddy *et al.* (2011) where they reported higher magnitude of genotypic correlation coefficients to their corresponding phenotypic correlation coefficients. This indicates that phenotypic estimates of correlation coefficient represent the genotypic correlation coefficient and yield improvement through these traits, which were significant and positively correlated, would be effective.

Correlation coefficients are quite helpful in determining the components of a complex trait like seed yield, an exact picture of the relative importance of direct and indirect influence of each component trait is not provided by such studies as these estimates provide nature and magnitude but not its cause. Path coefficient analysis (Wright, 1921; Dewey and Lu, 1959) under such circumstances plays an important role in partitioning the correlations into direct and indirect effects of a specific causal factor.

Table 5. Genotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of Blackgram

	TPH	PH	BPP	DFF	D50%F	PPP	PL	SPP	DM	HSW
PH	0.801**									
BPP	0.084	0.197								
DFF	0.381**	0.124	-0.346**							
D50%F	0.074	0.558**	-0.043	0.594**						
PPP	-0.235	0.044	-0.063	-0.924**	-0.360**					
PL	-0.190	0.094	0.378**	-0.551**	-0.199	0.599**				
SPP	-0.447**	-0.426**	0.195	0.050	0.125	-0.136	0.430**			
DM	0.123	0.378**	-0.044	0.427**	1.250**	-0.412**	-0.107	-0.159		
HSW	0.135	-0.003	-0.398**	0.102	-0.543**	-0.000	-0.406**	-0.324*	-0.530**	
SYP	-0.143	-0.130	0.238	-0.431**	-0.949**	0.622**	0.201	0.089	-0.799**	0.686**

** = Significant at 1%. * = Significant at 5%.

TPH = Total plant height (cm), PH = Plant height (cm), BPP = Branches per plant, DFF = Days to first flowering, D50%F = Days to 50% flowering, PPP = Pods per plant, PL = Pod length (cm), SPP = Seeds per pod, DM = Days to maturity, HSW = Hundred seed weight (g) and SYP = Seed yield per plant (g).

Table 6. Phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of Blackgram

	TPH	PH	BPP	DFF	D50%F	PPP	PL	SPP	DM	HSW
PH	0.661**									
BPP	0.056	0.157								
DFF	0.169	0.030	0.025							
D50%F	0.017	0.049	0.071	0.165						
PPP	-0.108	0.041	-0.080	-0.202	-0.001					
PL	-0.144	-0.169	0.073	-0.185	-0.030	0.257*				
SPP	-0.363**	-0.327*	0.045	-0.077	-0.092	-0.155	0.225			
DM	0.028	0.144	-0.020	0.421**	0.426**	-0.216	0.030	-0.163		
HSW	0.152	0.060	-0.204	0.039	-0.180	0.048	-0.244	-0.243	-0.346**	
SYP	-0.055	-0.071	0.176	-0.181	-0.281*	0.519**	0.105	0.086	-0.594**	0.543**

** = Significant at 1%. * = Significant at 5%.

TPH = Total plant height (cm), PH = Plant height (cm), BPP = Branches per plant, DFF = Days to first flowering, D50%F = Days to 50% flowering, PPP = Pods per plant, PL = Pod length (cm), SPP = Seeds per pod, DM = Days to maturity, HSW = Hundred seed weight (g) and SYP = Seed yield per plant (g).

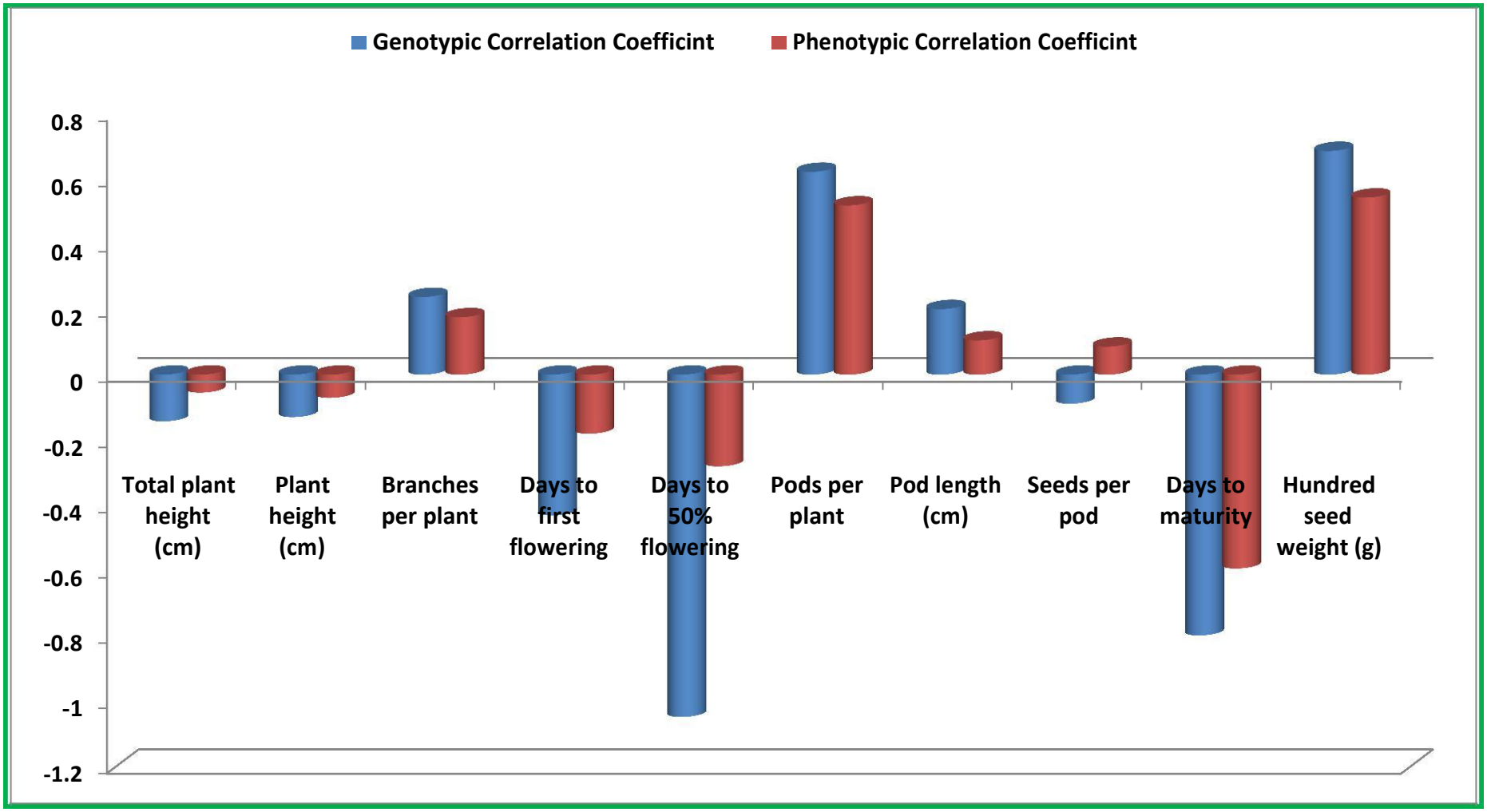


Figure 3. Genotypic and Phenotypic Correlation Coefficient with yield for ten characters of Blackgram

4.5 Path coefficient analysis

In order to find out the direct and indirect contribution of different characters towards seed yield per plant, the path coefficient analysis was done and is presented in Table 7. TPH had negative direct effect on yield because TPH showed positive indirect effect via PH but DFF negative indirect effect via PL and negative effect suppressed the positive effect. PH had positive direct effect on yield because TPH showed negative indirect effect via TPH but positive indirect effect via DFF. BPP had negative direct effect on yield because it showed positive indirect effect via PH and negative indirect effect via DFF. DFF had positive direct effect on yield because it showed indirect effect via TPH but positive indirect effect via PH. D50%F had positive direct effect on yield because it showed negative indirect effect via TPH but positive indirect effect via DFF. PPP had positive direct effect on yield because it showed negative indirect effect via DFF but positive indirect effect via DM. PL had positive direct effect on yield because it showed negative indirect effect via DFF but positive indirect effect via TPH.

SPP had negative direct effect on yield because it showed positive indirect effect via TPH but negative indirect effect via PH. DM had negative direct effect on yield because it showed negative indirect effect via TPH but positive indirect effect via DFF. HSW had negative direct effect on yield because it showed negative indirect effect via TPH but positive indirect effect via DM because there are the environmental influence. These results are in conformity to the study of Rao and Suryawanshi (1988), Patil and Deshmukh (1989), Natarajan and Rathinasamy (1999), Pariya *et al.,* (1999), Nagarjuna and Reddy (2001), Gupta *et al,.* (2003), Umadevi and Meenakshi Ganesan (2005), Chauhan *et al.* (2007), Konda *et al.* (2008), Reddy *et al.,* (2011) and Parveen *et al.,* (2011), where they reported that pods per plant is the major direct contributor towards seed yield per plant.

Low residual effects to the tune of 0.312 indicated that most of the variation in dependent trait was well explained by the contributing traits studied. R^2 values was found to be 68.8% indicating that 68.8% of the variability has been covered by the traits studied under present investigation. Although associations and their direct and indirect effects were vary in nature and magnitude. Therefore, the results from the present study indicated that plant height , days to first flowering, pod length and pods per plant would be the best selection indices for increasing seed yield per plant in blackgram. Swaminathan (1973) also quoted that an increase in the yield of pulses could be achieved by enhancing pod number.

Table 7. Partitioning of genotypic correlations into direct and indirect effects of ten important characters by path analysis of blackgram

Characters	Direct effect	Indirect effect via										Genotypic correlation with yield
		TPH	PH	BPP	DFF	D50%F	PPP	PL	SPP	DM	HSW	
TPH	-2.432	-	1.544	-0.005	0.753	0.005	-0.068	-0.089	0.57	-0.32	-0.10	-0.143
PH	1.928	-1.948	-	-0.011	0.245	0.034	0.013	0.044	0.54	-0.98	0.00	-0.13
BPP	-0.055	-0.204	0.380	-	-0.684	-0.003	-0.018	0.178	-0.25	0.11	0.30	0.238
DFF	1.977	-0.927	0.239	0.019	-	0.036	-0.266	-0.259	-0.06	-1.11	-0.08	-0.431
D50%F	0.061	-0.180	1.076	0.002	1.174	-	-0.104	-0.094	-0.16	-3.24	0.42	-0.949
PPP	0.288	0.572	0.085	0.003	-1.827	-0.022	-	0.282	0.17	1.07	0.00	0.622**
PL	0.470	0.462	0.181	-0.021	-1.089	-0.012	0.173	-	-0.55	0.28	0.31	0.201
SPP	-1.27	1.09	-0.82	-0.01	0.10	0.01	-0.04	0.20	-	0.41	0.25	0.089
DM	-2.59	-0.30	0.73	0.00	0.84	0.08	-0.12	-0.05	0.20	-	0.41	-0.799
HSW	-0.77	-0.33	-0.01	0.02	0.20	-0.03	0.00	-0.19	0.41	1.37	-	0.686**

Residual effect: 0.312** = Significant at 1%. * = Significant at 5%.

TPH = Total plant height (cm), PH = Plant height (cm), BPP = Branches per plant, DFF = Days to first flowering, D50%F = Days to 50% flowering, PPP = Pods per plant, PL = Pod length (cm), SPP = Seeds per pod, DM = Days to maturity, HSW = Hundred seed weight (g) and SYP = Seed yield per plant (g).

4.6 Genetic diversity

D^2 statistics is a powerful tool for estimating genetic diversity among different genotypes and to identify the parents for hybridization to obtain desirable recombinants. The assessment of genetic diversity helps in reducing the number of breeding lines from the large germplasm and the progenies derived from diverse parents are expected to show a broad spectrum of genetic variability and provide better scope to isolate superior recombinants.

4.6.1 Grouping of genotypes into clusters

The assessment of genetic divergence of germplasm is essential to know the spectrum of diversity. In the present investigation, 20 genotypes of blackgram genotypes were considered for the assessments of genetic diversity by multivariate analysis as per Mahalanobis' (1936) concept of generalize distance (D^2) considering eleven important quantitative characters. Based on D^2-value, the genotypes were grouped into five clusters (Table 8 & Figure 5). Cluster V was the largest followed by cluster IV. Cluster V, IV, II, III consisted of 7, 6, 4, 2 genotypes, respectively and remaining cluster I consisted of one genotype. Seven genotypes viz., G1, G2, G6, G8, G14, G17 and G19 were included in cluster V and six genotypes viz., G3, G4, G5, G11, G13 and G15 were included in cluster IV.

4.6.2 Nonhierarchical clustering

With the application of covariance matrix for nonhierarchical clustering, 20 blackgram genotypes were grouped into five different clusters. Highest 35% genotypes were included in cluster V and it was followed by 30% in clusters IV, 20% in cluster II, 10% in cluster III and 5% in cluster I (Table 8). These results confirmed the clustering pattern of the genotypes according to the D^2 statistics.

4.6.3 Principal component analysis

Eigen values of principal component axis, percent of total variation and cumulative variation accounted for them obtained from principal component analysis are presented in Table 9. The first principal axis, total plant height largely accounted for the variation among the genotypes which alone contributed 28.96% of the total variation among the genotypes. The first four characters of the principal component axes with eigen values above unity accounted for 75.94% of the total variation among the eleven traits. The rest eight traits contributed remaining 24.06% of total variation. Based on principal component scores I and II obtained from the principal component analysis, a two-dimensional scatter diagram (Z_1-Z_2) using component score 1 as X axis and component score 2 as Y axis was constructed, which has been presented in Figure 4.

Table 8. Distribution of twenty genotypes in different clusters

Cluster no.	Genotypes	No. of populations	Percent
I	G7	1	5
II	G9, G12, G16, G18	4	20
III	G10, G20	2	10
IV	G3, G4, G5, G11, G13, G15	6	30
V	G1, G2, G6, G8, G14, G17, G19	7	35
Total		20	100

Table 9. Eigen values and yield percent contribution of eleven characters of twenty genotypes

Principal component axes	Eigen values	Percent variation	Cumulative % of Percent variation
I	3.185	28.96	28.96
II	2.264	20.58	49.54
III	1.732	15.75	65.29
IV	1.171	10.65	75.94
V	0.796	7.24	83.18
VI	0.593	5.39	88.57
VII	0.470	4.28	92.85
VIII	0.361	3.29	96.14
TX	0.253	2.30	98.44
X	0.094	0.85	99.29
XI	0.080	0.71	100.00

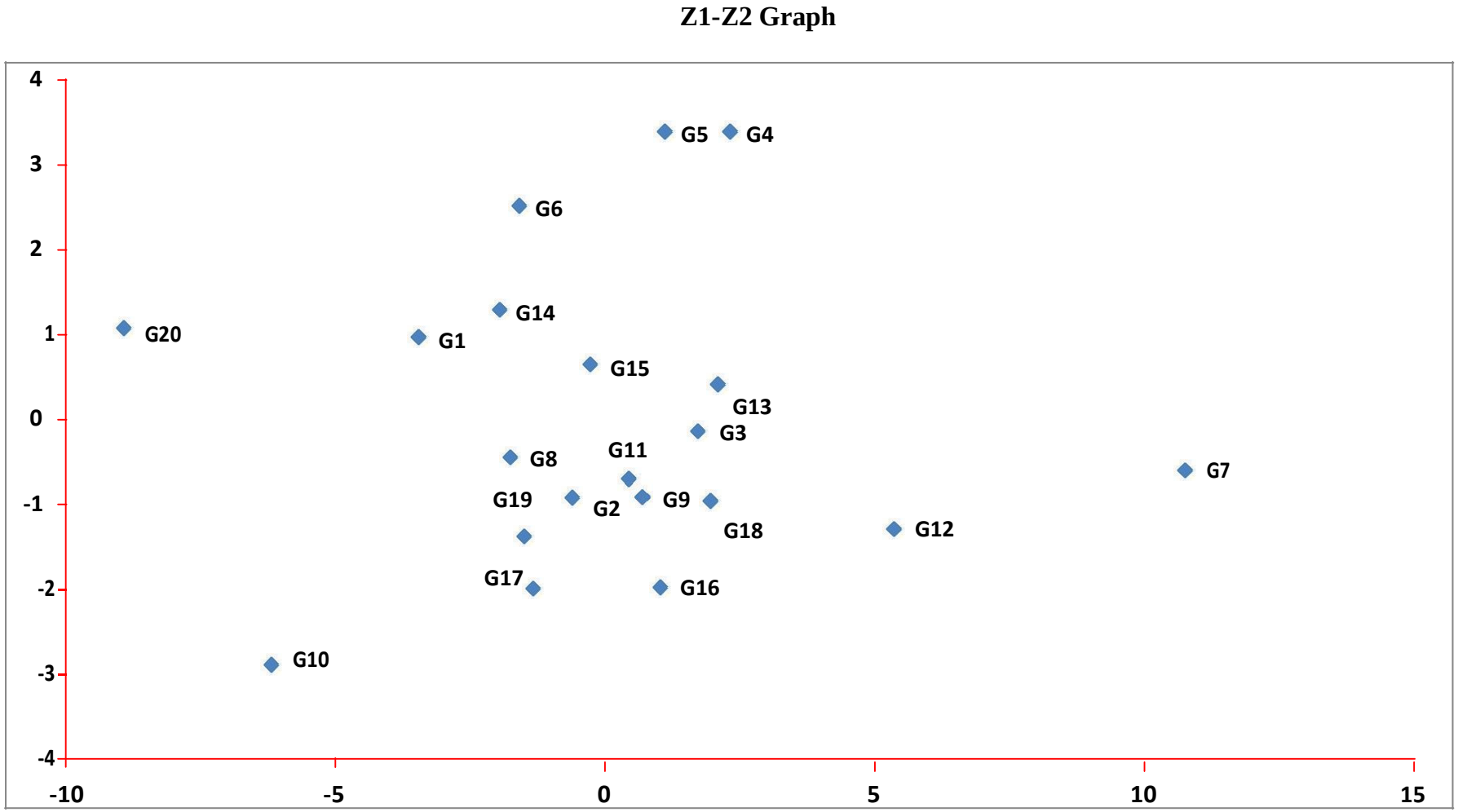


Figure 4. Scatter diagram of 20 Blackgram genotypes based on their principal component scores.

4.6.4 Inter cluster distance

The intra and inter cluster D^2 values are presented in Table 10and the nearest and farthest cluster from each cluster based on D^2 value is manifested in Table 11. It was demonstrated that inter cluster distance was higher than the intra cluster distance. Highest inter-cluster distance was observed between cluster I and III (16.058) followed by cluster I and V (12.360) (Table 10 & 11) and cluster II and I (11.414). Kumar *et al.* (2002) reported minimum inter-cluster distance as 27.14 between cluster I and cluster II and maximum (77.30) between cluster II and cluster III. The minimum inter cluster distance was observed between clusters II and V (5.088) indicated close relationship among the genotypes included (Table 10 & 11, Figure 5).

4.6.5 Intra cluster distance

In the present study highest intra-cluster distance was observed in cluster V (1.54) followed by cluster IV and II with average intra-cluster distance of 0.87 and 0.54, respectively (Table 10). Chauhan *et al.* (2008) recorded highest intra-cluster distance of 3.00 while lowest was found up to 1.96. High values of intra-cluster distances revealed that genotypes within the same cluster were quite diverse, hence selection of parents within cluster would also be effective and a good chance is there to develop good segregates by hybridizing among parents within clusters.

Results pertaining to inter and intra-cluster distances clearly indicates that there is a wide genetic diversity in the population under study. Crosses involving most divergent clusters would be expected to manifest maximum heterosis and release of desirable recombinants in segregating generations (Singh and Gautam, 1987).

Table 10. Intra (Bold) and inter cluster distances (D^2) for twenty genotypes

Cluster	I	II	III	IV	V
I	**0.00**	11.414	16.058	8.798	12.360
II		**0.54**	8.842	7.640	5.088
III			**0.00**	8.698	5.541
IV				**0.87**	5.999
V					**1.54**

Table 11. The nearest and farthest clusters from each cluster based on D^2 values in Blackgram

Sl No.	Cluster	Nearest Cluster with D^2 values	Farthest Cluster with D^2 values
1	**I**	**IV (**8.798)	**III (**16.058)
2	**II**	**V (**5.088)	**I (**11.414)
3	**III**	**V (**5.541)	**I (**16.058)
4	**IV**	**V (**5.999)	**I (**8.798)
5	**V**	**II (**5.088)	**I (**12.360)

4.6.6. Cluster diagram

The genotypes were distributed according to the grapevine in the scatter diagram into five groups, which indicated that considerable diversity existed among the genotypes (Figure 5). Cluster diagram showing the average intra and inter cluster distances of 20 genotypes. The values along the lines are inter cluster distances and the values within the circle are intra cluster distances.

4.6.7 Cluster Mean

Cluster V exhibited highest cluster mean for pod length (Table 12). Cluster IV for days to first flowering and cluster III for seeds per pod showed highest cluster mean. Lowest cluster mean for days to 50% flowering and days to maturity was found in cluster V. Highest cluster means for hundred seed weight and seed yield per plant was found in cluster II (Table 12). Cluster I exhibited highest cluster means for total plant height, plant height, Branches per plant, Days to first flowering, Days to 50% flowering and Days to maturity. Cluster V was found best for pod length. Cluster IV was found best for late flowering plant. Cluster III was best for seeds per pod. Characters hundred seed weight and seed yield per plant were performed best in cluster II. Cluster I better for six traits viz., total plant height, plant height, Branches per plant, Days to first flowering, Days to 50% flowering and Days to maturity.

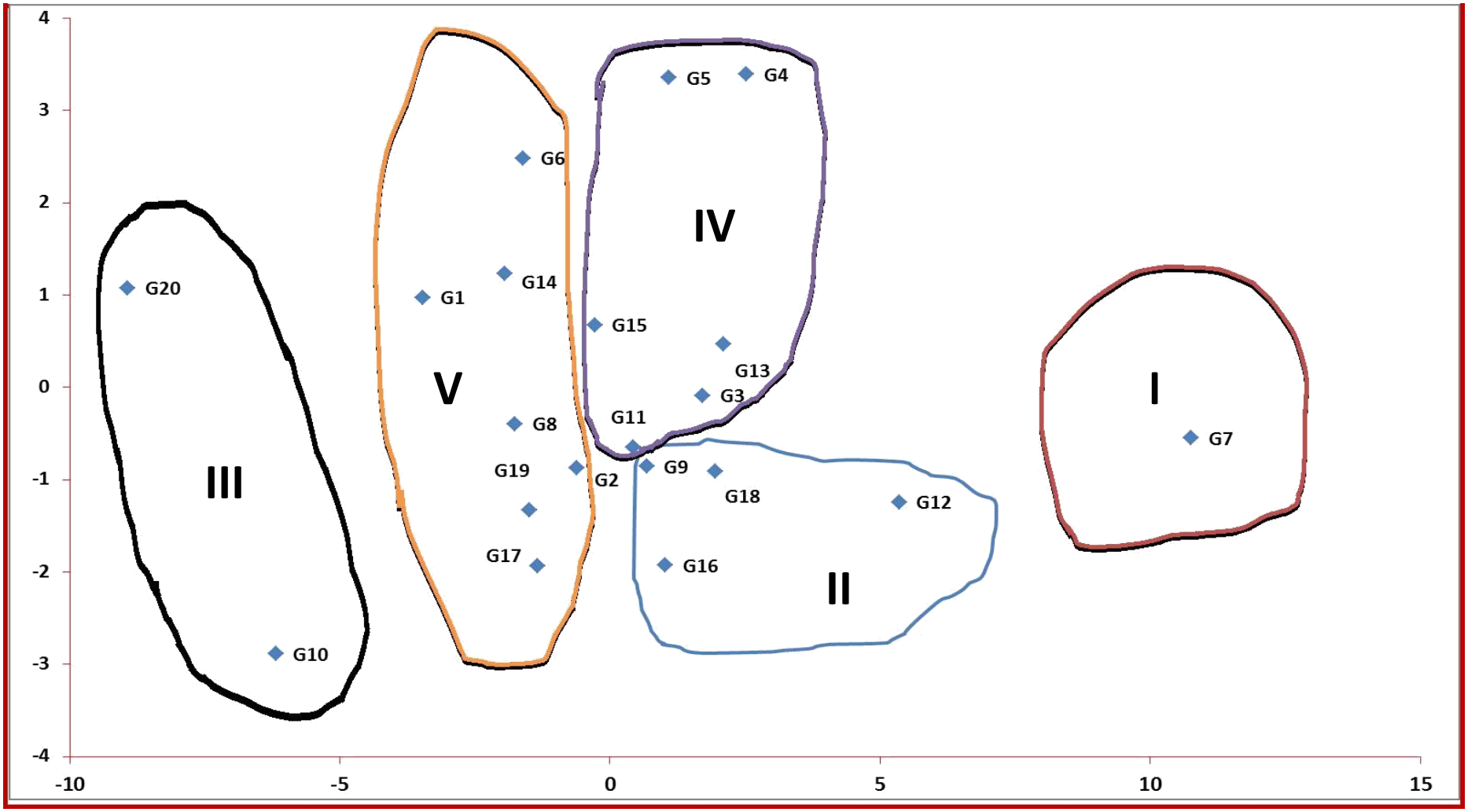


Figure 5. Cluster diagram showing average intra and inter cluster distances of 20 genotypes in blackgram

Table 12. Cluster mean of eleven yield and yield related characters of twenty blackgram genotypes

Characters	I	II	III	IV	V
Total plant height (cm)	35.69**	29.45	21.65*	29.59	27.08
Plant height (cm)	29.89**	24.61	18.35*	22.52	21.22
Branches per plant	4.28**	2.99	3.43	2.86*	3.17
Days to first flowering	64.33**	62.08*	63.00	64.22**	62.38
Days to 50% flowering	73.33**	72.25	72.67	72.17	71.86*
Pods per plant	7.84*	9.84**	8.59	8.28	9.44
Pod length (cm)	3.88	3.74*	3.84	3.79	4.01**
Seeds per pod	5.57	5.55*	6.67**	5.69	5.90
Days to maturity	93.00**	90.75	92.00	92.11	90.48*
Hundred seed weight (g)	2.24*	2.67**	2.37	2.53	2.44
Seed yield per plant (g)	0.91*	1.54**	1.19	1.25	1.39

* = minimum
** = maximum

4.6.8 Canonical variants analysis

Characters Contribution towards the divergence obtained from canonical variants analysis is presented in Table 13. The character, which gave high magnitude was considered for primary differentiation (vector 1) while the characters, which gave higher value was considered for secondary differentiation (vector 2). The characters represent equal magnitude in both the vectors then the character was considered for primary and secondary differentiation.

In vector-1 the important characters for genetic divergence were days to 50% flowering (0.5127), pods per plant (0.3421), seeds per pod (0.2466), hundred seed weight (1.6384) (Table 13).In vector-2, branches per plant (0.1875), days to first flowering (1.5580), pod length (2.6364), days to maturity (0.6164) and hundred seed weight (0.3329) were important because all traits had positive signs. In both the vectors, only hundred seed weight had positive signs, which indicated it is the important character and higher contribution to the genetic divergence among the materials studied.

Neelavathi and Govindarasu (2010) and Senapati and Misha (2010) also reported that pods per plant and 100-seed weight were the major contributor towards genetic divergence, while Elangaimannan *et al*. (2008) and Sarkar *et al.,* (2006) found pods per plant to be the major contributor. Vaithiyalingan (2004) found 100-seed weight as major contributor towards genetic divergence.

Table 13. Relative contributions of the eleven characters of twenty blackgram genotypes varieties to the total divergence

Characters	Principal Component	
	Vector-1	Vector-2
Total plant height (cm)	-0.6933	-0.2164
Plant height (cm)	-0.1842	-0.4812
Branches per plant	-0.3047	0.1875
Days to first flowering	-1.4132	1.5580
Days to 50% flowering	0.5127	-1.7328
Pods per plant	0.3421	-0.0110
Pod length (cm)	-1.3829	2.6364
Seeds per pod	0.2466	-0.1557
Days to maturity	-0.6876	0.6164
Hundred seed weight (g)	1.6384	0.3329
Seed yield per plant (g)	-1.3121	-3.6645

4.6.9 Selection genotypes

The genotypes under the cluster I exposed highest value of total plant height, plant height, branches per plant, days to first and 50% flowering and days to maturity (Table 13). So, genotypes from cluster I could be use as variety for tall plant. The genotypes of cluster II produced highest hundred seed weight and seed yield per plant. So, selection could be maintained for this cluster for high yield. The genotype of cluster III possessed highest seeds per pod. The genotypes of cluster V produced lowest days to 50% flowering and days to maturity. Considering diversity pattern and other agronomic performance genotypes G16 and G18 from cluster II, Genotypes G10 and G20 from cluster III, genotype G7 from cluster I and genotypes G8 and G14 from cluster V could be considered suitable genotypes for developing open pollinated varieties and further use for efficient hybridization in future. Involving of such diverse lines in inter cluster genotypes crossing program could produce desirable segregates. So, more divergent genotypes are recommended to use as parents in future hybridization program.

The present study revealed that the cluster I with high mean values maximum desirable traits are desired to be crossed with cluster III which possessed low mean values of three characters for getting high heterosis. Same cross between clusters I and V for three characters and cluster I and II for three traits. This finding was strongly supported with identification of similar cluster combinations from interpretation of inter cluster distance made in the present study and thereby the expected progenies inculcate traits in a positive direction and further selection would be more effective.

Table 14. Selection of genotypes for further use

Cluster	Genotypes	Special feature
Cluster V	G8 and G14	Early maturing
Cluster I	G7	Tall plant and late maturing
Cluster III	G10 and G20	Highest number of seeds producer
Cluster II	G16 and G18	High yielding and broad seeder

CHAPTER V
SUMMARY AND CONCLUSION

The present investigation was undertaken to study nature of variation and association among seed yield and related traits in blackgram to identify the superior genotypes based on yield and other desirable attributes.

The experimental material consisting of 20 varieties of blackgram were raised in RCBD design with three replications at experimental farm of department of genetics and plant breeding, Sher-e-Bangla Agricultural University, Dhaka during Rabi season 2015-16. The data was recorded on seed yield per plant and various other morphological traits viz., total plant height (cm), plant height (cm), branches per plant, days to first flowering, days to 50% flowering, pods per plant, pod length (cm), seeds per pod, days to maturity and hundred seed weight (g).

Analysis of variance indicated significant differences among all the traits studied suggesting prevalence of wide range of genetic variability and scope of selection for these traits, except days to 50% flowering.

Highest plant height was rewarded for the genotype G7 and the genotype G20 showed the minimum plant height. Maximum branches per plant were found by the genotype G6 and minimum for genotype G1. Genotype G10 needed maximum days to first flowering and minimum by both genotypes G2 and G5. The maximum pods per plant were observed in genotype G16 while minimum in the genotype G5. Genotype G8 required minimum days to maturity while genotype G11 required maximum. The genotype G12 showed the maximum hundred seed weight and the minimum was recorded in the genotype G17. The highest and lowest yield per plant was observed in the genotype G18 and G11, respectively.

High PCV and GCV were observed for branches per plant, seed yield per plant, pods per plant and plant height. high heritability coupled with high genetic advance was observed in seed yield per plant, branches per plant and plant height indicating preponderance of additive gene action in the inheritance of these traits and selection would be effective.

Seed yield per plant exhibited significant and positive correlation with pods per plant and hundred seed weight and insignificant positive correlation with branches per plant, pod length and seeds per pod at both genotypic and phenotypic levels indicating these traits could be utilize in improvement of seed yield per plant. Whereas it was significant and negatively correlated with days to first flowering, days to 50% flowering and days to maturity, hence these traits could be utilized in improving the early variety.

Through path analysis the direct effects were found to be positive and high for plant height, days to first flowering, pod length and pods per plant. Based on D^2-value, twenty genotypes were grouped into five clusters. Cluster V was the largest followed by cluster IV, II, III which consisted of 7, 6, 4, 2 genotypes, respectively and remaining cluster I consisted of one genotype. Highest inter-cluster distance was observed between cluster I and III followed by cluster I and V. Highest intra-cluster distance was observed in cluster V followed by cluster IV and II. Genotypes of cluster I could be use as variety for tall plant. The genotypes of cluster II produced high yield. The genotype of cluster III possessed highest seeds per pod. The genotypes of cluster V were early maturing varieties.

CONCLUSION

There was sufficient genetic variability among the genotypes for all the traits under study. Hence selection of these characters simultaneously would bring improvement in yield. Among the genotypes studied, G16 and G18 from cluster II, genotypes G10 and G20 from cluster III, genotype G7 from cluster I and genotypes G8 and G14 from cluster V had potential for higher yield based on the genetic merit of yield factors. These genotypes can be further tested over years across locations to select for direct release as varieties. Besides, these genotypes can be used in cross-breeding programs to generate transgressive segregates for each traits further selection.

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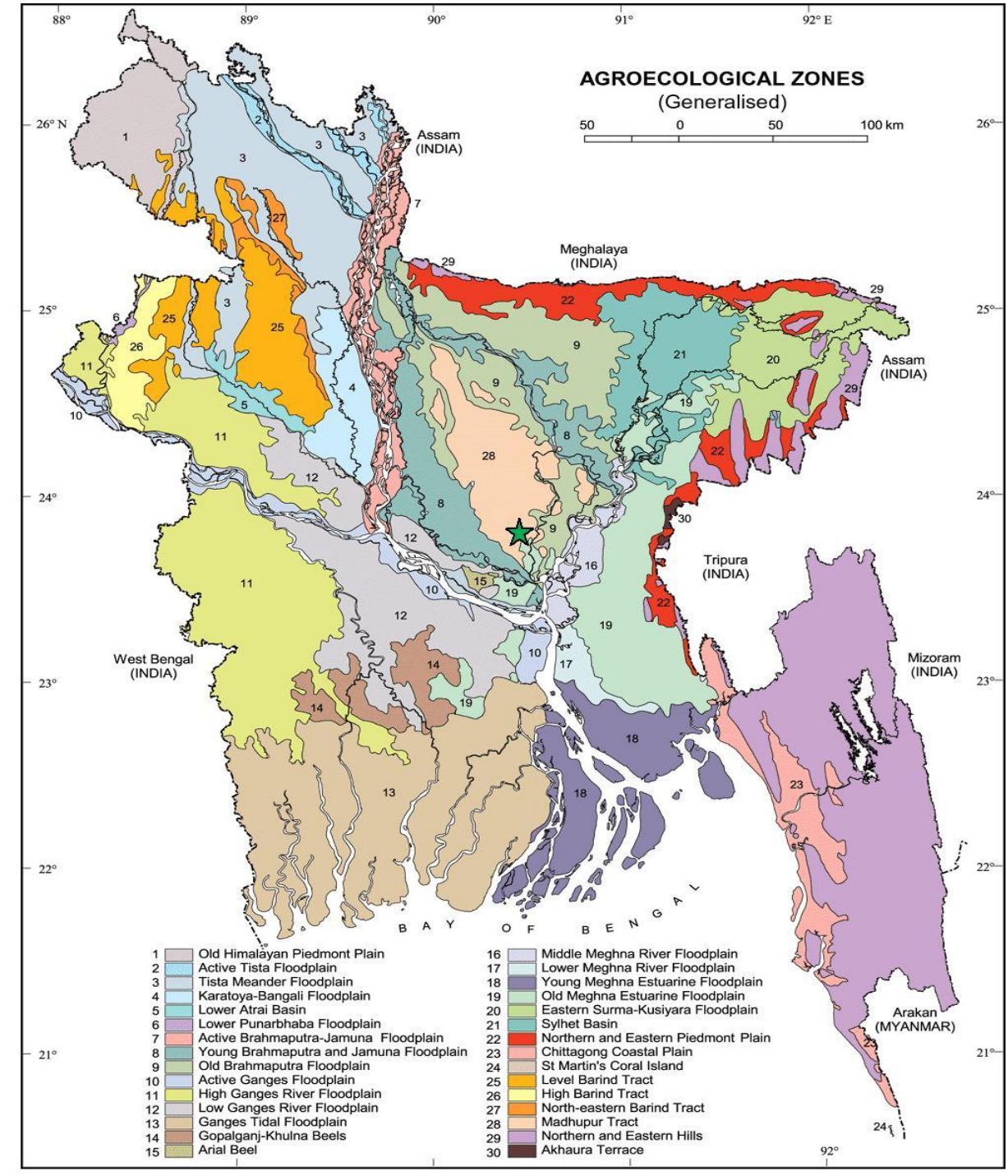
APPENDICES

Appendix I. Map showing the experimental site under the study



The experimental site under the study

Appendix II. Physical and chemical characteristics of initial soil (0-15 cm depth) of the experimental site

A. Physical composition of the soil

Soil separates	%	Method employed
Sand	36.90	Hydrometer method (Day, 1915)
Silt	26.90	Do
Clay	36.66	Do
Texture class	Clay loam	DO

B. Chemical composition of the soil

Sl No.	Soil characteristics	Analytical data	Method employed
1	Organic carbon (%)	0.82	Walkley and black, 1947
2	Total N (Kg/ha)	1790.00	Bremner and Mulvaney, 1965
3	Total S (ppm)	225.00	Bardsley and Lanester, 1965
4	Total P (ppm)	840.00	Olsen and Sommers, 1982
5	Available N (Kg/ha)	54.00	Bremner, 1965
6	Available P (Kg/ha)	69.00	Olsen and Dean, 1965
7	Exchangeable K (Kg/ha)	89.50	Pratt, 1965
8	Available S (ppm)	16.00	Hunter, 1984
9	p^H (1:2.5 soil to water)	5.55	Jackson, 1958
10	CEC	11.23	Chapman, 1965

Source: Central library, Sher-E-Bangla Agricultural University, Dhaka.

Appendix III. Monthly average temperature, relative humidity and total rainfall and sunshine of the experimental site during the period from November, 2015 to February, 2016.

Month	Air temperature (°c)		Relative humidity (%)	Rainfall (mm) (total)	Sunshine (hr)
	Maximum	Minimum			
November, 2015	34.7	18.0	77	227	**5.8**
December, 2015	32.4	16.3	69	0	**7.9**
January, 2016	29.1	13.0	79	0	**3.9**
February, 2016	**28.1**	**11.1**	**72**	**1**	**5.7**

Source: Bangladesh Meteorological Department (Climate & Weather Division), Agargoan, Dhaka – 1212.