CHARACTER ASSOCIATION AND GENETIC DIVERSITY ANALYSIS IN BLACKGRAM (*Vigna mungo* L.)

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JUNE, 2021

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BY

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REGISTRATION NO.: 13-05696

A Thesis
submitted to Institute of Seed Technology
Sher-e-Bangla Agricultural University, Dhaka
in partial fulfillment of the requirements
for the degree of

MASTER OF SCIENCE (MS)

IN

INSTITUTE OF SEED TECHNOLOGY

SEMESTER: JAN-JUNE, 2021

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CERTIFICATE

This is to certify that the thesis entitled **"CHARACTER ASSOCIATION AND GENETIC DIVERSITY ANALYSIS IN BLACKGRAM (*Vigna mungo* L.)"** submitted to the **Institute of Seed Technology**, Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of **MASTERS OF SCIENCE (M.S.)** in **SEED TECHNOLOGY**, embodies the result of a piece of *bona fide* research work carried out by **MD. HAMIDUL ISLAM**, Registration No. **13-05696** under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.

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

June, 2021
Dhaka, Bangladesh

(Dr. Md. Sarowar Hossain)
Supervisor

Dedicated to

My

Beloved Parents

ACKNOWLEDGEMENTS

The author seems it a much privilege to express his enormous sense of gratitude to the almighty Allah for there ever ending blessings for the successful completion of the research work.

The author wishes to express his gratitude and best regards to his respected supervisor, Dr. Md. Sarowar Hossain, Professor, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka, for his continuous direction, constructive criticism, encouragement and valuable suggestions in carrying out the research work and preparation of this thesis.

The author wishes to express his earnest respect, sincere appreciation and enormous indebtedness to his reverend Co-supervisor, Dr. Md. Abdur Rahim, Professor, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka, for his scholastic supervision, helpful commentary and unvarying inspiration throughout the research work and preparation of the thesis.

The author feels to express his heartfelt thanks to the honorable Director, Dr. Md. Ismail Hossain, Professor, Department of Horticulture along with all other teachers and staff members of the Institute of Seed Technology, Sher-e-Bangla Agricultural University, Dhaka, for their co-operation during the period of the study.

The author feels proud to express his deepest and endless gratitude to all of his course mates and friends to cooperate and help him during taking data from the field and preparation of the thesis. The author wishes to extend his special thanks to his lab mates, class mates and friends for their keen help as well as heartiest co-operation and encouragement.

The author expresses his heartfelt thanks to his beloved parents, elder sister and brother and all other family members for their prayers, encouragement, constant inspiration and moral support for his higher study. May Almighty bless and protect them all.

The Author

CHARACTER ASSOCIATION AND GENETIC DIVERSITY ANALYSIS IN BLACKGRAM (*Vigna mungo* L.)

ABSTRACT

A field experiment was conducted with 29 genotypes of blackgram (*Vigna mungo* L.) at the experimental field of Sher-e-Bangla Agricultural University, Dhaka to study the character association and genetic diversity during August to November 2019. The genotypes were found significantly different among them for all the characters studied. Comparatively phenotypic variances were higher than the genotypic variances for all the characters examined. Plant height, number of branches per plant, days to first flowering, days to 50% flowering, days to 80% maturity, number of pods per plant, 100 seed weight and yield per plant showed high broad base heritability. The significant positive correlation with seed yield per plant was found in number of branches per plant (G = 0.519**, P = 0.342**), pod length (G = 0.732**, P = 0.367**), number of pods per plant (G = 0.758**, P = 0.709**), number of seeds per pod (G = 0.691**, P = 0.354**) and 100 seed weight (G = 0.240*, P = 0.223*). Path co-efficient analysis revealed that plant height, number of branches per plant, days to 50% flowering, days to 80% maturity, pod length, number of pods per plant, number of seeds per pod and 100 seed weight had the positive direct effect on yield per plant whereas, days to first flowering had the negative direct effected. The genotypes were grouped into five clusters. The highest inter-cluster distance was observed between clusters I and V (60.988) and the maximum intra-cluster distance was found in cluster IV (0.256). Considering group distance diversity pattern and other agronomic performance, the lines G16 (BD-6861), G27 (BARI-4) and G28 (BARI-1) could be considered as suitable genotypes for fruitful hybridization in future.

LIST OF CONTENTS

LIST OF CONTENTS (CONT'D)

LIST OF CONTENTS (CONT'D)

LIST OF TABLES

LIST OF FIGURES

LIST OF PLATES

LIST OF APPENDICES

COMMONLY USED SOME ABREVIATIONS

Full word	**Abbreviation**
At the rate	@
Agro Ecological Zone	AEZ
Analysis of variance	ANOVA
And others	*et al.*
Bangladesh Agricultural Research Institute	BARI
Bangladesh Bureau of Statistics	BBS
Bangladesh	BD
By way of	Via
Cultivars	cv.
Centimeter	Cm
Canonical Variate Analysis	CVA
Cluster Analysis	CA
Degrees of Freedom	Df
Days to 50% flowering	D50%F
Days After Sowing	DAS
Days to Maturity	DM
Duncan`s Multiple Range Test	DMRT
Etcetera	etc.
Environmental variance	σ^2e
Food and Agricultural Organization	FAO
Genotypic variance	σ^2g
Gram	g
Genotype	G
Genetic Advance	GA
Genotypic coefficient of variation	GCV
Genetic Advance	GA
Heritability in broad sense	h^2b
International Center for Agricultural Research in Dry Areas	ICARDA
Indian Agricultural Research Institute	IARI
Journal	J.
Kilogram	Kg
Meter	M
Mean sum of square	MS
Murate of Potash	MP

COMMONLY USED SOME ABREVIATIONS (CONT'D)

Full word	Abbreviation
Ministry of Agriculture	MOA
Number	No.
Namely	Viz.
Principal Component Analysis	PCA
Principal Coordinate Analysis	PCO
Phenotypic coefficient of variation	PCV
Percent	%
Phenotypic variance	σ^2p
Percentage of Coefficient of Variation	CV%
Plant height	PH
Primary branches per plant	PBP
Residual Effect	R
Randomized Complete Block Design	RCBD
Science	Sci.
Standard Error	SE
Siliqua length	LS
Seed yield per plant	SYP
Square meter	m^2
Sher-e-Bangla Agricultural University	SAU
Triple Super Phosphate	TSP
Thousand seed weight	TSW
University	Uni.
Variety	var.

CHAPTER I

INTRODUCTION

Pulses are a wonderful gift of nature, also known as grain legumes, are the major source of protein in Asia and constitute an important supplement to the predominantly cereal-based diet (Sahoo and Jaiwal, 2008). Black gram [*Vigna mungo* (L.) Hepper], popularly known as urdbean, urid or mash is an important self-pollinating diploid grain legume and belongs to the family Fabaceae. The somatic chromosome number is 2n = 22 (Dana, 1980 and Radhikaben *et al*., 2020). Blackgram locally known as maskalai grows well in north or north-west part of Bangladesh, especially in Rajshahi and Chapai Nowabganj districts.

It is mainly a day neutral warm season crop commonly grown in semi-arid to sub-humid low land tropics and sub-tropics. But it is grown in both winter and summer in India. It has been distributed mainly in tropical to sub-tropical countries where it is mainly grown in cropping systems as a mixed crop, catch crop and sequential crop besides growing as sole crop under residual moisture conditions after the harvest of rice and also before and after the harvest of other summer crops under semi irrigated and dry land conditions. The crop is resistant to adverse climatic conditions and improves the soil fertility by fixing atmospheric nitrogen in the soil. This pulse originated in south and southeast Asia (Indian sub-continent) but widely grown in India, Pakistan, Bangladesh, Myanmar, Thailand, Philippines, China and Indonesia (Poehlman, 1991).

Blackgram is a rich source of protein (20.8 to 30.5 percent) with total carbohydrates ranging from 56.5 to 63.7 percent. It is also a good source of phosphoric acid and calcium. It contains a wide variety of nutrients and is popular for its fermenting action and thus it is largely used in making fermented foods (Hadimani *et al*., 2016). Blackgram, cultivated as a sole crop and intercrop. Pulses are “nutritional powerhouse”, rich in protein, high in fibre content and provide ample quantity of vitamins and minerals. Proximate composition of black gram seed (per 100g) is energy (346 Kcal), protein (24g), fat (1.60g), carbohydrate (63.40g) and total dietary fibre (16.20g). It is extensively used in various culinary preparations and recommended for diabetes. Like other pulses, it also enriches the soil fertility, improves the soil structure and used as green fodder for cattle.

Global production of pulses is about 77.6 million tons from an area of 85 million hectares (FAO Stat 2016). While annual global production of urad is about 2.7 million metric tons. Bangladesh is a large producer as well as consumer of black gram. It produces 43287 metric tons of black gram annually from about 47191 ha area, with an average productivity of 917 kg ha^{-1} (BBS, 2019).

It is well known that 50 g pulses/person/day should be consumed in addition to other sources of protein such as cereals, milk, meat and egg which is a very difficult task to achieve as the production and productivity of pulse crop including black gram is very low. The low productivity of black gram attributed to excessive vegetative growth, high rate of flower and fruit drop, non-synchronous maturity, pod shattering, susceptibility to diseases and pests etc. Lack of good quality seeds and crop management, extremely limited use of rhizobial sources, phosphatic fertilizers, fungicides and pesticides also contribute to lower productivity.

The knowledge of nature and magnitude of genetic variability for characters of economic importance and cause and effects of relationship of yield and yield components for the available genotypes are of utmost essential which helps in planning the future breeding programme for genetic improvement for yield potential of any crop species. The estimates of heritability alone will not be of much value for selection on phenotypic performance. Genotypic coefficient of variation (GCV) along with heritability estimates would provide a better picture of the genetic gain to be expected by phenotypic selection. Hence, it is suggested that genetic gain should be considered in conjunction with heritability. The study of inheritance of various developmental and productive traits through the estimation of different genetic parameters like components of variances, genotypic and phenotypic coefficients of variability, heritability and genetic advance is helpful for framing the effective breeding programme (Pushpa *et al*., 2013).

Knowledge on heritability and genetic advance of the character indicate the scope for the improvement of a trait through selection. Seed yield being a complex character is very difficult to improve by selecting the genotypes for yield, therefore identifying the characters which are closely related and have contributed to yield becomes highly essential. The correlation coefficient gives a measure of the relationship between traits and provides the degree to which various characters of crop are associated with productivity. The estimates of correlation coefficients mostly indicate the inter-relationships of the characters whereas path analysis permits the understanding of the cause and effect of related characters (Wright, 1921).

Hybridization programme gives an opportunity to create wide spectrum of genetic variability. Black gram is a self-pollinated crop and is lacking in variability. Therefore, choice of diverse parents for hybridization is one of the important considerations for creating new genetic variability. Several biometrical approaches have been shown to be useful in selecting parents for successful hybridization programme. D^2 analysis has been found the most effective and therefore, widely used for the classification of parental lines. The multivariate analysis based on Mahalanobis D^2 cluster analysis is used for divergence analysis. The D^2 analysis classifies the genotypes in to relatively homogeneous groups in such a way that within cluster diversity is minimized and between cluster diversity is maximized. The respective genotypes from diverse clusters can be utilized in breeding programme depending upon breeding objectives. However, reports on study of genetic diversity in urdbean are limited in literature (Parmeswaappa and Patil, 1994 and Verma and Katna 1997). The results of earlier studies are relevant only for the material and environment involved in a particular study and can not be generalized. Therefore, study on genetic divergence on the available germplasm under the environment where it is to be exploited is essential for successful utilization of germplasm resources for the development of superior urdbean varieties (Chauhan *et al*. 2008).

Genetic diversity is an important factor and also a prerequisite in any hybridization programme. Therefore, the present study is conducted in blackgram to study the genetic diversity and genetic parameters like variability, heritability and genetic advance, correlation and path coefficient effects of different yield components on seed yield with following objectives.

1. To study the interrelationships of yield contributing characters among themselves and with seed yield; and their direct and indirect effects
2. To study the genetic diversity among the genotypes of blackgram
3. To find out suitable parental groups future breeding program.

CHAPTER II

REVIEW OF LITERATURE

The present investigation had undertaken to assess variability, correlation, path analysis and genetic diversity of thirteen characters in 64 genotypes of black gram. The relevant literatures related to various aspects of present study entitled "Character association and genetic diversity analysis in blackgram (*Vigna mungo* L.)" are reviewed under the following heads.

2.1. Genetic variability, heritability and genetic advance
2.2. Correlation coefficient analysis
2.3. Path coefficient analysis
2.4. Genetic divergence

2.1 Genetic variability, heritability and genetic advance

The extent of improvement of a character would depend mainly on the amount of variability in the population where selection has to be made. Hence the study of legacy of various developmental and productive traits through the estimation of different genetic parameters like components of variances, genotypic and phenotypic coefficients of variability, heritability and genetic advance is helpful for framing the effective breeding programme. The most important objective in any crop improvement programme is to increase the seed yield. The extent of improvement of a character would depend mainly on the amount of variability in the population where selection has to be made. Therefore, it is necessary to know the proportion of observed variability that is heritable (Heritability). Heritability estimates along with genetic gain is more helpful than the heritability value alone in predicting the result for selection of the best individuals (Johnson *et al,* 1955).

Radhikaben *et al*. (2020) conducted a study with 13 genotypes of blackgram. The analysis of variance revealed significant differences between genotypes indicating presence of sufficient amount of variability in all the thirteen studied characters. The studied materials revealed wide range of variation by virtue of exhibiting highly significant genotypic differences for all the thirteen traits *viz*., days to 50% flowering, plant height, branches per plant, clusters per plant, pods per plant, seeds per pod, pod length, 100-seed weight, seed yield per plant, days to maturity, straw yield, harvest index, and protein (%). In their investigation, high heritability with high genetic advance as percent of mean was recorded for branches per plant, clusters per plant, plant height, seed yield per plant, harvest index and straw yield which indicated the predominance of additive gene action along with lesser influence of environment, thus infers high scope of further improvement through selection for these traits.

Chaithanya *et al*. (2019) carried out an investigation on 28 blackgram genotypes during Kharif-2018 to study about genetic variability, heritability and genetic advance. ANOVA showed highly significant genetic variability for all 28 blackgram genotypes for 12 characters studied indicating that significant amount of genetic variability present in the material. High GCV and PCV was observed in harvest index (%) (10.1, 12.68) followed by seed yield per plant (9.79, 12.17). High heritability coupled moderate genetic advance as percent of mean were observed in number of pods per plant, pod length, number of primary branches per plant, harvest index, biological yield and seed yield per plant. Mean performance for seed yield per plant and other characters taken into consideration genotype VALLAB URD may be considered as best genotype followed by Shuats Urd (ABL)-95 and KU-96-7.

Kumar and Devi (2018) conducted experiment to examine the 48 blackgram genotypes to study the genetic diversity. Analysis of variance showed highly significant differences among 48 genotypes for 13 quantitative characters studied. Maximum GCV and PCV variances was reported for seed yield per plant, pod per plant, harvest index and cluster per plant. High heritability coupled with high genetic advance as percent of mean was reported for seed yield per plant.

Mahesha *et al.* (2017) investigated 32 genotypes of black gram to obtain estimates of variability, heritability, genetic advance and divergence. High estimates of GCV and PCV were observed for seed index (18.96; 19.46) followed by number of clusters per plant (16.72; 17.64), number of branches per plant (15.26; 15.76), plant height (11.05; 13.19) and seed yield per plant (10.47; 11.19). High heritability coupled with minimum genetic advance was recorded for seed index.

The genetic variability parameters were studied in a RIL (Recombinant Inbred Line) population consisting of 193 lines and their parents by Sowmini and Jayamani (2013). The higher estimates of PCV were observed for all the traits when compared with GCV. However, GCV was found to be high for the traits single plant yield, number of clusters per plant and number of pods per plant. High heritability per cent was observed with days to maturity, number of seeds per pod and hundred seed weight. High genetic advance as per cent of mean was observed for plant height, number of clusters per plant, number of pods per plant, single plant yield and hundred seed weight. High heritability coupled with high genetic advance as per cent of mean was observed for hundred seed weight. Transgressive segregants were observed for all the traits and finally these could be used further for yield testing apart from utilizing it as pre breeding material.

Hemalatha *et al*. (2017) evaluated 25 black gram genotypes along with one check to study the genetic variability and correlation. Maximum genotypic and phenotypic variance was recorded for harvest index, plant height and number of pods per plant. Maximum GCV and PCV were recorded for harvest index (32.48 and 33.24) followed by number pods per plant (31.28 and 31.33) and seed yield per plant (29.76 and 30.49). High heritability was recorded for number of pods plant (99.71%), days to maturity (96.68%), days to 50 percent flowering (95.75%), harvest index (95.44%) and seed yield per plant (95.29%). High heritability coupled with high genetic advance as percent of mean was recorded for number of pods per plant.

Gaibriyal *et al***.** (2017) conducted experiment involving 36 genotypes of black gram to estimate the extent of genetic variability and heritability. High PCV was recorded for number of clusters per plant, while medium values were found in plant height and number of primary branches per plant. Medium GCV was reported in plant height and number of clusters per plant. High heritability was showed by traits like seed index (90%), seed yield per plant (89%), number of pods per plant (67%) and harvest index (61%). The expected genetic advance and genetic advance as per cent of mean of black gram genotypes was higher for seed yield per plant (17.10) followed by plant height (11.24), days to maturity (2.02) and seeds per pod (0.12).

Chubatemsu *et al*. (2017) observed considerable variation among five urdbean lines for six traits. A relatively higher estimate of PCV and GCV were observed for number of pods per plant. The highest estimates of heritability were observed for days to maturity (99%) followed by days to 50 percent flowering (94.17%), 100 seed weight (85%) and number of pods per plant, while number of seeds per pod recorded the lowest heritability. The number of pods per plant (24.47%) showed high genetic advance as percent of mean.

Gowsalya *et al.* (2016) evaluated eleven quantitative characters in 80 genotypes of blackgram during *rabi* 2014-15 seasons to assess the genetic variability and character association. The genotypes differed significantly for all the characters studied. The highest GCV recorded for number of branches per plant (29.18), seed yield per plant (25.04), number of clusters per plant (21.44), number of pods per plant (19.03) and plant height (16.90). High heritability coupled with high genetic advance was observed for number of branches per plant, plant height, number of clusters per plant, seed yield per plant and number of pods per plant.

Sohel *et al*. (2016) conducted an investigation aimed to study the correlation coefficients and path coefficients between the genotypes to establish the selection criteria. Ten germplasms of blackgram were evaluated through 11 morphological traits. Among the morphological traits pod weight (g) 8.81%, harvest index (7.72%), number of branches plant^{-1} (6.18%) and 100-seed weight (g) 5.24% had shown the highest level of coefficient of variation. Grain yield plant^{-1} had the highest heritability (99.43) and seeds pod^{-1} had the lowest heritability (53.10).

Jyothsna *et al.* (2016) carried out an experiment to estimate the genetic parameters like variability, heritability and genetic advance for six quantitative characters. High PCV and GCV were recorded for seed yield per plant showing sufficient variation among the genotypes studied. Heritability estimates were high for number of pods per plant (70.90%) and seed yield (81.80%). High heritability coupled with high genetic advance was also observed for the above characters indicating the importance of additive gene action in governing the inheritance of these traits.

Pervin *et al*. (2007) observed a wide range of variability in black gram for five quantitative traits. They reported that heritability in the broad sense with genetic advance expressed as percentage of mean was comparatively low.

Sateesh *et al.* (2016) evaluated 25 genotypes of the black gram for the estimation of genetic variability parameters. High GCV and PCV was observed for number of pods per plant (34.54%; 35.23%) followed by seed yield per plant (32. 52%; 34.95%), number of branches per plant (26.10%, 29.69%) and plant height (16.88%, 21.62%). High heritability coupled with high expected genetic advance was observed in number of pods per plant (96%, 89.42%).

Priyanka *et al.* (2016) conducted experiment to estimate the genetic variability of quantitative and qualitative traits in 24 lines of black gram. Except for days to maturity a significant variation was noted for all the traits. The genotypes were highly variable for number of clusters per plant, number of pods per plant, number of seeds per pod and seed yield per plant. Broad- sense heritability was higher for all the traits except for days to 50 percent flowering (42.50%) and number of branches per plant (51.38%). High heritability coupled with high GAM was observed for the characters number of pods per cluster (68.32%; 28.04), pod length (82.60%; 34.15) and seed yield per plant (94.10%; 27.51).

Reena *et al.* (2016) studied 75 morphologically diverse genotypes of black gram and reported that the mean sum of squares due to genotypes were highly significant at 1% level of significance for days to 50% flowering, days to maturity, plant height, number of pods per plant, number of seeds per pod and seed yield per plant. The highest heritability was found in days to maturity (86.0%) followed by seed yield per plant (76.8%) while the lowest heritability was recorded in 100-seed weight (28.8%). The highest genetic advance as percent of mean was recorded in seed yield per plant (58.29%).

Srivastava and Singh (2012) reported that the estimates of genotypic coefficient of variability, heritability and genetic advance were high for seed yield per plant, 100-seed weight, number of seeds per pod, number of pods per plant and number of nodes on main stem in mugbean.

Mandal *et al***.** (2014) noted the presence of moderate magnitude of heritability in broad sense, genetic advance as percentage of mean, phenotypic and genetic coefficient of variability in respect of number of seeds per pod (44.8%; 0.6%; 11.2; 7.5) and plant height (53.3%; 8.2%; 27.4; 20.0) and yield among 135 genotypes of blackgram.

Yashoda *et al.* (2016) studied 46 genotypes of black gram for genetic variability, correlations, and direct and indirect effects for twelve quantitative characters. Plant height had shown the highest heritability coupled with genetic advance, followed by seed yield per plant and pod length. The genotypes exhibited higher PCV and GCV values for seed yield per plant, number of pods per plant and number of clusters per plant. Low values of GCV and PCV recorded for plant height, days to 50 percent flowering, pod length, number of seeds per pod and days to maturity.

Dharmendra *et al***.** (2014) examined 36 black gram genotypes along with one check to study genetic variability, correlation and path analysis. The maximum genotypic variation (Vg) and phenotypic variation (Vp) were obtained for plant height (64.11 and 92.55) and the lowest values were recorded in pod length followed by number of seeds per pod. The estimates of GCV and PCV were the maximum for number of clusters per plant (14.25; 19.79) followed by plant height (11.51; 13.83), number of primary branches per plant (9.88; 14.26) and seed yield per plant (8.70; 8.74).

Punia *et al***.** (2014) observed wide range of variability for quantitative traits among 133 accessions of urdbean. Among the eight quantitative characters, number of pods per plant (21.3 to 66.2) had the maximum variation followed by plant height (47.3 to 113.3cm) and seed yield per plant (4.45 to 22.10g). Plant height, number of primary branches per plant and number of pods per plant showed high genetic advance and moderate heritability.

Panigrahi *et al*. (2014) reported high genetic variability among 19 black gram accessions. High GCV was shown by seed yield per plant (31.96) followed by number of pods per plant (27.58), number of clusters per plant (25.56) and number of primary branches per plant (22.89). High heritability along with high genetic advance as per cent of mean (GAM) was recorded by seed yield per plant (84.88%; 60.66%), number of clusters per plant (83.77%; 48.20%) and number of pods per plant (84.14%; 52.11%) which revealed that selection could be effective for these characters.

Sanjeev *et al***.** (2014) examined heritability among 109 genetically diverse strains of black gram. Heritability (broad sense) estimates were high (> 80%) for all the characters except number of pods per cluster (70.60 %). High genetic advance was recorded for plant height followed by days to maturity, harvest index, days to 50 percent flowering and ranged from 0.319 to 49.025%. However, genetic advance as per cent of mean was high for seed yield per plant, number of clusters per plant and harvest index.

Pushpa *et al*. (2013) carried out experiments to determine the genetic parameters and character association in 16 elite lines of urdbean during *kharif* season. Significant variation was noted for all the traits. The character plant height showed moderate PCV and GCV indicating that there is scope for improvement of this trait. High heritability coupled with high genetic advance for seed yield per plant (97.0%; 79.93%), number of pods per plant (91.0%; 65.50%) and plant height (78.0%; 31.74%) showed that all these traits are controlled by additive type of gene action.

Arulbalachandran *et al.* (2010) observed high Genetic variability, heritability and genetic advance for all quantitative traits in black gram mutants.

Suresh *et al.* (2013) studied yield and its contributing characters in M_4 populations of mungbean genotypes and evaluated the genotypic and phenotypic coefficient of variations, heritability, genetic advance and concluded that high heritability (broad) along with high genetic advance as per cent of mean was observed for the trait plant height, number of pods per plant, number of seeds per pod, 100 seed weight and single plant yield indicating that these characters would be amenable for phenotypic selection.

Meshram *et al.* (2013) studied pure line seeds of black gram variety viz. T-9, TPU-4 and one promising genotype AKU-18 treated with gamma irradiation (15kR, 25kR and 35kR) with the objective to assess the variability in M_3 generation. The highest GCV and PCV and high estimates of heritability were recorded for the characters sprouting percentage, number of pods plant^{-1} and grain yield plant^{-1} (g). High heritability accompanied with high genetic advance was recorded for number of pods plant^{-1} governed by additive gene effects and therefore selection based on phenotypic performance will be useful to improve character in future.

Neelavathi and Govindarasu (2010) studied seventy-four diverse genotypes of blackgram under rice fallow condition for yield and its component traits. High genotypic variability was observed for branches per plant, clusters per plant, pods per plant, biological yield and seed yield along with high heritability and genetic advance, suggesting effective improvement of these characters through a simple selection programme.

Suresh *et al.* (2010) conducted a study in mungbean *Vigna radiata* (L.) Wilczek) with eight 'lines' and four 'testers' crossed in a Line x Tester design for 13 traits. High heritability coupled with high genetic advance as percent of mean were observed for plant height, number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, 100 seed weight, harvest index and single plant yield confirming the additive gene action.

Rahim *et al.* (2010) studied genotypic and phenotypic variance, coefficient of variance, heritability, genetic advance, was evaluated for yield and its contributing characters in 26 mung bean genotypes. High heritability (broad) along with high genetic advance in percent of mean was observed for plant height, number of pods per plant, number of seeds per pod, 1000-grain weight and grain yield per plant.

Byregouda *et al.* (1997) evaluated eighteen black gram 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.

2.2 Correlation coefficient analysis

Correlation studies indicate the magnitude of association between pairs of characters and are useful for selecting genotypes with desirable combinations of characters thereby assist the plant breeder in crop improvement. Since, yield of plant is a complex, polygenically inherited trait, direct selection is not effective. But it could be improved through a number of component characters, which are simple in inheritance and less subjected to environmental influences. Hence, the knowledge of association of yield components with yield and among themselves would be of help to the breeder in obtaining improved yields.

Arya *et al.* (2017) evaluated 30 black gram genotypes for correlation studies and observed that seed yield per plant at genotypic and phenotypic level was significantly and positively correlated with (0.685), pods per plant (0.614) and harvest index (0.914). Negative significant correlation exhibited by number of seeds per pod (-0.406).

Sohel *et al*. (2016) conducted an investigation on genetic variability and correlation study between yield components of the genotypes of this crop aimed to study the correlation coefficients and path coefficients between the genotypes to establish the selection criteria which might help to develop genotypes of high yielding potential. Ten germplasms of blackgram were evaluated through 11 morphological traits. Among the morphological traits pod weight (g) 8.81%, harvest index (7.72%), number of branches plant^{-1} (6.18%) and 100-seed weight (g) 5.24% had shown the highest level of coefficient of variation. Relationship between physiological characters and yield contributing attributes was studied through analysis of correlation. In the present study, out of 55 associations, 22 associations were positively significant and the rest 16 were negatively significant. Yield plant^{-1} was positively and significantly associated with pods plant^{-1}, pod length, weight pod^{-1}, harvest index and 100-seed weight but negatively associated with plant height, fresh weight and dry weight. Sohel *et al.* (2016) also found that yield per plant was positively and significantly associated with number of pods per plant (0.944), pod length (0.645 cm), harvest index (0.958) and 100-seed weight (0.800) but negatively associated with plant height (0.922 cm), indicated that number of pods per plant, pod length and 100-seed weight were the most important characters contributing to yield plant.

Gowsalya *et al.* (2016) found a positive association of seed yield per plant with number of pods per plant, number of clusters per plant, number of seeds per pod, plant height, 100 seed weight, number of branches per plant and pod length both phenotypic and genotypic level.

Jyothsna *et al***.** (2016) evaluated 12 genotypes of black gram and revealed the significant positive association of number of pods per plant (0.581**, 0.484**) and number of seeds per pod (0.275**, 0.039*) with seed yield at both genotypic and phenotypic levels and negative association of plant height (-0.079) and pod length (-0.057) with seed yield at phenotypic level.

Reena *et al***.** (2016) reported that seed yield per plant was positively and significantly associated with number of pods per plant (0.832**), plant height (0.578**) and 100-seed weight (0465**). Where as association of days to 50% flowering, days to maturity, primary branches per plant, seeds per pod and harvest index were not significant.

Yashoda *et al***.** (2016) investigated 46 genotypes of black gram for correlation studies and revealed that seed yield per plant had a high positive and significant association with number of pods per plant (0.712) followed by number of clusters per plant (0.551).

Kanimoli *et al***.** (2015) studied correlation coefficient in 65 genotypes of black gram and reported that seed yield per plant had significant positive association with plant height (0.525**), number of primary branches per plant (0.573**), number of clusters per plant (0.685**), number of pods per cluster (0.478**), number of pods per plant (0.726**), number of seeds per pod (0.441**) and 100 seed weight (0.667**).

Vijay *et al***.** (2015) studied fourteen characters in 14 lines of black gram. The correlation analysis indicated that number of branches per plant, number of pods per plant, number of seeds per pod, 100 seed weight and harvest index were highly significant and positively correlated with seed yield per plant.

Panigrahi *et al***.** (2014) recorded significant positive association of majority of the yield contributing traits with seed yield per plant except for plant height and days to 50 percent flowering both at genotypic and phenotypic levels.

Punia *et al.* (2014) found a very strong positive correlation of seed yield per plant with number of pods per plant (0.54**) and number of branches per plant (0.26**) and strong negative correlation with days to 50 per cent flowering (-0.19*) and days to maturity (-0.21*).

Pushpa *et al.* (2013) evaluated 16 elite genotypes of black gram for correlation studies and reported that seed yield per plant had positive and highly significant phenotypic and genotypic correlation with number of pods per plant (rp=0.8665 rg=0.9301) and plant height (rp=0.2251 rg=0.2371); hence these traits could be used for the improvement of grain yield resulting in the evolution of high yielding varieties of black gram.

Suresh *et al.* (2013) evaluated yield and its contributing ch0aracters in M_4 populations of blackgram genotypes to the correlation studies and concluded that the number of pods per plant were high positive and highly significant with single plant yield.

Pushpa *et al.* (2013) conducted studies on elite lines of urdbean and showed that pods per plant and plant height had highly significant genotypic and phenotypic correlation with grain yield. Hence these traits could be used for the improvement of grain yield resulting in the evolution of high yielding varieties of blackgram.

Shivade *et al.* (2011) studied thirty-six genotypes of black gram with three replications for correlations and concluded that the yield contributing characters *viz*. plant height, number of branches per plant, number of clusters per plant, number of pods per plant, number of pods per cluster, length of pod, number of seeds per pod and dry matter per plant had strong positive association with seed yield per plant at both the phenotypic and genotypic level.

The study conducted by Konda *et al.* (2008) revealed that the branches per plant, clusters per plant, pods per plant, seeds per pod, pod length and hundred seed weight exhibited significant and positive correlation with yield per plant.

Shivade *et al*. (2011) recorded significant strong positive association of plant height, number of branches per plant, number of clusters per plant, number of pods per plant, number of pods per cluster, length of pod and number of seeds per pod with seed yield per plant at both the phenotypic and genotypic level.

Parveen *et al.* (2011) conducted studies on eight parents and their 28F_1 crosses for twelve component characters including seed yield and revealed significant positive association of pods per plant, harvest index and clusters per plant with seed yield in parental generation whereas in F_1 generation, significant positive association of clusters per plant, pods per plant, days to maturity, days to 50% flowering, pods per cluster and 100-seed weight with seed yield was observed.

Makeen *et al.* (2009) revealed that the phenotypic correlation estimates showed that pods per plant and clusters per plant had highly significant positive correlation with seed yield per plant. In addition, the trait like 100-seed weight and plant height showed moderate positive association with seed yield, suggesting that these traits may be given second priority in the selection programme in black gram.

Singh *et **al.*** (2007) evaluated 34 diverse genotypes of black gram for correlation studies and observed that seed yield had positive and significant association with number of pods per plant, plant height, pod length, number of seeds per pod, days to flowering and days to maturity, while negative correlation with primary branches per plant. The number of pods per plant with plant height and pod length; pod length with number of seeds per pod and plant height had positive and significant correlations.

Mallikarjuna *et al.* (2006) studied 180 germplasm lines of mung bean comprising both indigenous and exotic collections along with checks and revealed that the traits plant height and number of clusters per plant recorded highly significant and positive association with grain yield, while number of seeds per pod showed negative association with seed yield.

Srividhya *et al.* (2005) carried out correlation analysis in the 15 F_2 crosses derived from 6 x 6 diallel cross in urdbean and revealed that seed yield/plant was positively and significantly associated with pods/plant, c1usters/ plant, seeds/pod, 100-seed weight and biomass and concluded that the selection criteria based on these characters along with days to maturity and plant height will give fruitful results for yield improvement in urdbean.

Kumar *et al.* (2003) studied the correlation studies among 10 traits of 25 genetically diverse black gram. Seed yield was positively and significantly correlated with all the characters. The 100-seed weight showed the highest positive direct effect on seed yield, followed by the number of pods per plant.

Ghafoor *et al.* (2000) observed a high correlation of grain yield with branches, pods per plant, seeds per pod, seed weight and biological yield and indicated the importance of these characters in determining yield potential for black gram.

Mahto and Mahto (1997) while working on 11 cultivars of black gram found that seed yield was highly and positively correlated with 100-seed weight, days to 50 percent flowering, plant height, number of primary branches per plant, number of seeds per pod and days to maturity.

2.3 Path coefficient analysis

Yield is a complex dependent character and is contributed by several component characters. Path analysis identifies the yield components which directly and indirectly influence the yield. Hence help to find out guidelines for better selection of quantitative traits for building up the ultimate yield.

Jyothsna ***et al.*** (2016) found that number of pods per plant (0.743, 0.694) showed positive direct effect on seed yield at both genotypic and phenotypic levels and plant height (0.099), pod length (0.027) at phenotypic level and number of seeds per pod (0.149) at genotypic level.

Arya *et al.* (2017) identified that positive direct effect on seed yield per plant was exhibited by 100 seed weight (0.119), days to maturity (0.100), pods per plant (0.042) and seeds per pod (0.007). The characters harvest index (1.020) recorded the maximum and positive magnitude of direct effect on seed yield per plant and their association with seed yield was also highly significant and positive.

Sohel *et al*. (2016) conducted an investigation aimed to study the correlation coefficients and path coefficients between the genotypes to establish the selection criteria which might help to develop genotypes of high yielding potential. Ten germplasms of blackgram were evaluated through 11 morphological traits. Among the morphological traits pod weight (g) 8.81%, harvest index (7.72%), number of branches plant^{-1} (6.18%) and 100-seed weight (g) 5.24% had shown the highest level of coefficient of variation. The result of the present experiment indicated that number of pod plant^{-1}, pod length and 100-seed weight were the most important characters which exhibited positively to yield plant^{-1}. It was observed that biomass plant^{-1} (0.73 g) had maximum positive direct effects on yield plant^{-1} followed by pods plant^{-1} (0.37), seeds pod^{-1} (0.19) by path coefficient analysis.

Gowsalya *et al.* (2016) evaluated in 80 genotypes of black gram and recorded that number of pods per plant, number of seeds per pod and 100 seed weight exerted high positive direct association with seed yield. Number of pods per plant showed highly positive indirect effect on seed yield via number of clusters per plant, number of branches per plant and plant height.

Reena *et al.* (2016) identified the highest positive direct effect of seeds per plant (0.442) and 100 seed weight (0.237) and negative direct effect of plant height (-0.003) on the seed yield both at phenotypic and genotypic levels.

Sateesh *et al.* (2016) evaluated 25 genotypes of blackgram and reported the maximum positive direct effect of number of branches per plant and negative direct effect of plant height on seed yield per plant.

Yashoda *et al.* (2016) reported that days to 50 percent flowering (0.080), days to maturity (0.110), plant height (0.115), number of pods per plant (0.604), number of seeds per pod (0.022) and 100 seed weight (0.134) had positive direct effects on seed yield per plant. While the characters, number of primary branches per plant (-0.156), number of clusters per plant (-0.063) and pod length (-0.088) had negative direct effects on seed yield per plant.

Kanimoli *et al.* (2015) carried out path coefficient analysis by using 10 genotypes of black gram and observed that 100 seed weight (0.015) had high direct effect on seed yield. Remaining traits noticed negligible effect on seed yield per plant.

Panigrahi *et al.* (2014) found that positive direct effect was exhibited by days to 50 percent flowering (0.3189), number of primary branches per plant (0.4917), number of pods per plant (0.8488) and 100 seed weight (0.6511) while days maturity (-0.0791), plant height (-0.0841), number of clusters per plant (-0.7227), number of seeds per pod (-0.1956) and pod length (-0.1068) expressed negative direct effect on yield per plant.

Punia *et al.* (2014) observed that number of pods per plant (0.44) followed by number of primary branches per plant (0.20) and number of seeds per pod (0.17) had high positive direct effect on seed yield per plant.

Suresh *et al.* (2013) evaluated yield and its contributing characters in M_4 populations of blackgram genotypes to conduct path coefficient analysis and concluded that number of pods per plant followed by number of seeds per pod were the important characters for increasing yield in blackgram.

Pushpa *et al.* (2013) observed positive direct effect of number pods per plant (rp=0.9420 rg=1.1396), 100 seed weight (rp=0.1088 rg=0.1345), days to maturity (rp=0.0915 rg=0.1143) and days to 50 percent flowering on grain yield per plant.

Pervin *et al.* (2007) conducted path analysis studies on eight parents and their 28F1 crosses for twelve component characters including seed yield and found that number of seeds per pod, harvest index, pods per plant and number of primary branches per plant showed high positive direct effects on seed yield in parents whereas in crosses, seeds per pod, pods per plant, harvest index and days to maturity showed high positive direct effect on seed yield. Hence selection based on these traits would be effective in increasing the seed yield.

Reddy *et al.* (2011) reported that days to 50% flowering, days to maturity, number of pods per plant, seed protein content, shoot dry matter per plant and 100-seed weight were exhibited positive direct effect on seed yield in blackgram.

Shivade *et al.* (2011) studied thirty-six genotypes of black gram and reported direct and indirect effects for fifteen yield contributing characters. The selection based on number of clusters per plant, number of pods per plant, dry matter per plant, plant height, number of branches per plant, number of seeds per pod, length of pod and number of pods per cluster could help in genetic improvement of seed yield per plant.

Makeen *et al*. (2009) reported that twenty-two mutants of Urdbean variety T9 were evaluated for path analysis and revealed that pod length, pod cluster/plant and 100-seed weight had positive direct effects on seed yield/plant.

Priya and Reddy (2008) conducted path analysis in green gram and stated that the characters pods per plant, pods per cluster and seeds per pod had high positive direct effects on grain yield in F_3 progenies. High and positive indirect effects for most of the characters were observed through pods per plant, pods per cluster and seeds per pod.

Singh *et al.* (2007) evaluated 34 diverse genotypes of black gram and observed positive direct effect of pods per plant, plant height and pod length on seed yield per plant.

Kaveri *et al.* (2007) reported that number of clusters per plant exerted maximum direct effect on seed yield. Number of clusters per plant had been reported to be the most prominent yield component in blackgram.

Patel *et al.* (2007) conducted path analysis and indicated that positive and high direct effects of days to maturity, number of pods per cluster, number of pods per plant, number of seeds per pod, leaf area, protein content and number of leaves per plant have high and positive direct contribution towards seed yield per plant.

Mishra and Pradan (2006) evaluated 27 genotypes of mung bean and reported that the maximum positive direct effect on seed yield per plant was exhibited by pod length, clusters per plant and 100-seed weight.

Veeramani *et al.* (2005) reported that direct effect on seed yield was exerted by the characters namely, number of clusters per plant, number of pods per plant and pod length. Among the indirect effects, the character plant height influences the number of pods per plant and number of clusters per plant.

In green gram Parameswarappa (2005) studied path analysis and indicated that clusters per plant exerted maximum direct effect on seed yield per plant followed by pods per plant in all three environments. Pods per plant had the highest positive direct effect on yield followed by test seed weight and number of branches.

Induced variability, character association and path-coefficient analysis studies in greengram by Momin and Mishra (2004) reported that the characters pods per plant, 100-Seed weight, and seeds per pod showed high positive direct and indirect effects on yield.

Thirteen genotypes of green gram were evaluated by Venkateswarlu (2001) and stated that pods per plant and seeds per plant had maximum positive direct effect on seed yield. Days to maturity, clusters per plant, plant height, 100-seed weight and seeds per pod exhibited high indirect effect on seed yield via pods per plant.

Path coefficient analysis by Gopikrishnan *et al.* (2002) in urdbean revealed that pods per plant had the highest direct effect on seed yield followed by seed weight, plant height and days to 50% flowering. The characters clusters per plant and pods per cluster had negative direct effect on seed yield. Pods per plant exhibited maximum positive direct effect as well as high indirect effect through other components on yield.

Haritha and Reddysekhar (2002) evaluated 50 genotypes of mung bean and reported that phenotypic positive indirect effect of plant height and branches per plant through clusters per plant and pods per plant. Genotypically, it showed negative indirect effect of clusters per plant and days to maturity through plant height and seeds per pod, and pods per cluster through days to 50% flowering.

NagarjunaSagar and Reddy sekhar (2001) reported that biological yield per plant, harvest index and pods per plant showed high direct effects on grain yield. High indirect effects were recorded for the other traits through biological yield per plant, harvest index and pods per plant in black gram.

2.4 Genetic divergence

Many breeding efforts have been carried out to improve the yield of this crop and to break the yield plateau. Genetic diversity is an important factor and also a prerequisite in any hybridization programme. Crosses involving genetically diverse parents are likely to produce not only high heterotic effects but also desirable transgressive segregants in the later segregating generations. Multivariate analysis by Mahalanobis (1936), D^2 statistic is a powerful tool in quantifying the degree of divergence among all possible pairs of population at genotypic level. The availability of genetically diverse germplasm is the basic need for the progress in plant breeding. Choice of parents for hybridization is one of the important considerations for creating new variability. Several biometrical approaches have been shown to be useful in selecting parents for successful hybridization programmes. D^2 analysis has been found most effective and, therefore, widely used for the classification of parental lines.

Kumar and Devi (2018) conducted the present investigation to examine the 48 blackgram genotypes to study the genetic diversity. Divergence analysis among forty-eight genotypes for 13 Characters was carried out using Mahalanobi's D^2 statistics. The genotypes were grouped into 7 clusters. The contribution of number of pods per plant was maximum (54.43%) followed by harvest index (14.98). The maximum intercluster distance was reported in cluster V and VI (229.034). The maximum intra cluster distance was reported in cluster V (39.199).

Gowsalya *et al.* (2017) estimated genetic diversity in 80 genotypes of urdbean and were grouped into twelve different clusters. Cluster I had the maximum of 41 genotypes followed by cluster V and VI with 11 genotypes in each and clusters VIII, XI and XII had one genotype each. The maximum intra cluster distance was found in cluster I. Maximum inter-cluster distance was found between cluster III and XI followed by cluster XI and VII, XI and X, XI and III. Cluster VI had the highest mean value for number of seeds per pod, number of clusters per plant and number of pods per plant. Cluster IV recorded highest mean value for seed yield per plant and number of primary branches per plant. Number of primary branches per plant (37.09%), plant height (20.16%) and 100 seed weight (12.34%) had the maximum contribution to divergence.

Mahesha *et al.* (2017) estimated genetic diversity among 32 genotypes of black gram and grouped them into 6 heterogeneous clusters. Among these clusters, cluster II (11) had the maximum number of genotypes. Per cent contribution towards the total divergence was the maximum through seed index (29.44 %) followed by number of branches per plant (16.33%) and number of clusters per plant (16.13%). Also, cluster III and V went the most diversed to each other.

Vinod Kumar Reddy *et al.* (2017) investigated 40 genotypes of blackgram for genetic divergence and grouped them into seven clusters with the help of D^2 statistics. The maximum intra-cluster (D^2) was registered for, cluster I (215.881), followed cluster III (182.631), cluster 7 (161.748), cluster V (128.352), cluster IV (127.216) and cluster II (82.517). Inter-cluster distance (D^2) was found the maximum between cluster V (1009.307) followed by cluster III (950.981). Minimum inter-cluster distance was found between cluster I (341.205). Among all the characters, seed yield per plant and number of seeds per pod contributes the maximum to divergence. Cluster 4 showed the maximum cluster mean value for seed yield per plant.

Hadimani *et al*. (2016) carried out genetic Mahalanobis's D analysis and 64 genotypes were grouped into 12 clusters where, cluster-I was the largest with 19 genotypes followed by cluster-II and cluster-III with 13 genotypes each, cluster-VII with 7 genotypes, cluster-VI with 6 genotypes. Whereas cluster-IV, cluster-V and clusters-VIII to XII had one genotype in each cluster. The intra cluster distance was the maximum in cluster-VII followed by cluster-VI and cluster1III. Whereas inter cluster distance was the maximum between cluster-IV and cluster-XII. The cluster means estimated for 14 characters revealed that the cluster-IV showed lowest mean values and cluster-V showed the highest mean value for most of the characters studied. Plant height contributed the maximum to divergence followed by days to 50 per cent flowering, days to maturity, clusters per plant, 100 seed weight, these traits can be utilized for future crop improvement programme.

Jayamani and Sathya (2013) studied divergence analysis among fifty genotypes for pod characteristics and grouped into 10 clusters. Based on cluster mean and divergence, it was concluded that the hybridization between genotypes in cluster I and X could produce desirable recombinants for grain yield.

Singh *et al*. (2012) evaluated 75 genotypes of blackgram were grouped into seven clusters by D^2 analysis. The clustering pattern showed that plant height, seed yield per plant, number of seeds per plant and number of seeds per pod were major traits causing genetic divergence among genotypes.

Srimathy *et al.* (2012) conducted divergence analysis of 46 genotypes including 20 genotypes of blackgram and 26 accessions of *V. mungo var. silvestris.* The genotypes were grouped into twelve clusters. This study showed clear grouping of *V. mungo var. silvestris* accessions from the cultivated blackgram (*V. mungo*) genotypes. Based on cluster mean and divergence, it was concluded that the hybridization between accessions of *V. mungo var. silvestris* in clusters I and XII and cultivated genotypes in the other clusters could produce desirable recombinants for plant type, important economic traits and grain yield.

Venkateswarlu *et al.* (2011) investigated 70 accessions of black gram through D^2 statistics and grouped them into six clusters. They reported no significant relationship between geographical and genetic diversity.

Singh *et al.* (2009) carried out studies on genetic divergence consisting of 80 germplasm collections of mungbean for 12 quantitative characters by using Mahalanobis's D^2 statistics and grouped them into 11 non distinct overlapping clusters. The study revealed that no parallelism was observed between genetic and geographic diversity.

Niranjan and Rama Chandra (2009) evaluated forty-five micromutant lines of blackgram variety PU-30 for genetic divergence. Using Tocher's method the mutants were grouped into 11 diverse genetic clusters. D2 analysis showed that 100-seed weight, plant height and pod length had high contribution to genetic divergence.

Genetic divergence of twelve genotypes was estimated over four environments in a study conducted by Gantait and Das (2009). Maximum divergence was between WBU-105 and LBG-708 (D=18.38) during first year rabi season while first year *Prekharif* the maximum divergence was between LBG-708 and T-9 (D=15.91). The cluster numbers and their compositions varied considerably in different seasons over two years.

Elangaimannan *et al.* (2008) studied 55 genotypes of black gram were grouped into seven clusters by D^2 analysis. Cluster I was the largest (34 genotypes) followed by clusters IV (8), II (6), V (4) and 3 mono genotypic clusters (III, VI and VII). The maximum intra-cluster distance was observed in cluster I suggesting that genotypes are having diverse genetic architecture. The inter-cluster distance was high between cluster II and VI (D^2 = 767.84) and clusters II and V (D^2=513.48), there by indicated wide range of variation among the clusters formed. The per cent contribution towards genetic diversity was high in number of pods per plant (26.12%).

Chauhan *et al.* (2008) analyzed genetic diversity in 210 true breeding lines of urdbean and were grouped into nine different clusters. The highest number of genotypes appeared in cluster IX which contained 38 entries. The highest intra cluster distance was recorded for cluster II (3.00), while the lowest was observed in cluster IX (1.964). The maximum inter cluster distance was observed between cluster II and III (6.904). The different clusters showed considerable differences in intra cluster group means of 12 characters and genotypes having distinctly different mean performance for various characters.

Elangaimannan *et al.* (2008) studied genetic divergence in thirty-four genotypes of black gram, grouped them into seven clusters by using Mahalanobi's D^2 statistics. Inter cluster distance was maximum between cluster II and cluster VI which serve as potential parents for hybridization.

Genetic divergence in fifty-five genotypes of black gram was studied by Elangaimannan *et al.* (2008) and clustering was done using Mahalanobis D^2 statistics. The genotypes were grouped into seven clusters. The maximum intracluster distance was observed in clusters suggesting that genotypes are having diverse genetic architecture. The inter cluster distance was high between clusters II and VI there by indicating wide range of variation in number of pods per plant.

Umadevi *et al***.** (2007) evaluated 60 genotypes of black gram *(Vigna mungo* L.*)* Hepper) and found that the genotypes were grouped into four clusters. Among all the characters, the contribution of number of pods per plant (31.02%) was maximum followed by seed yield (23.45%). The maximum inter cluster distance was reported in cluster IV. Cluster IV showed the highest cluster mean for six characters namely, number of clusters per plant (16.83), number of pods per plant (40.77), number of seeds per pod (8.37) and 100 seed weight (6.20). Cluster II and III showed high cluster mean for protein content (16.80).

Konda *et al.* (2007) conducted cluster analysis in forty genotypes of black gram and were grouped into seven clusters. The cluster means estimated for 12 characters revealed that the cluster II with eight genotypes had the lowest mean value for days to 50% flowering and maturity. Genotypes in cluster IV showed the highest mean value for seeds per pod, 100 seed weight, grain yield per plant and protein content.

Sixty black gram genotypes of black gram were studied by Umadevi and Meenakshi Ganesan (2007) and were grouped into four clusters. Among all the characters, the contribution of number of pods per plant was maximum followed by grain yield and leaf number per plant. Cluster IV showed the highest cluster mean for six characters namely, number of clusters per plant, number of pods per plant, number of seeds per pod, 100 seed weight, apparent grain volume and grain yield.

The sixty urdbean genotypes were grouped into 17 clusters in a study by Shanthi *et al.* (2006). Among all the characters, the contribution of number of pods per plant was the maximum followed by number of branches per plant and single plant yield. The maximum inter cluster distance was between cluster II and XVII. The maximum intra cluster distance was reported in cluster XVI followed by cluster III.

Rangarao *et al.* (2006) assessed the genetic diversity in sixty genotypes of mung bean for thirteen characters. The genotypes were grouped into eight clusters. Days to maturity, 100 seed weight, number of pods per plant and total dry matter contributed the maximum towards diversity.

Selvi *et al.* (2003) studied genetic variation among 52 accessions of *Vigna* species that include 15 accessions of *V. unguiculata,* 15 accessions of *V. mungo,* 19 accessions of *V. radiata,* and one accession each of the wild species *V. aconitifolia, V. trilobata,* and *V. radiate* var *sublobata* belonging to the subgenera *Ceratotropis* and *Vigna* using morphological traits. The clustering based on morphological traits grouped the various subgenera of *Vigna* into one cluster but failed to reflect the real genetic relationship among different species.

Haritha and Reddy Sekhar, (2003) evaluated fifty genotypes of mung bean for 13 traits through D^2 and metroglyph methods and grouped them into 10 and eight clusters and reported that the characters *viz.,* 100 seed weight and seed yield contributed more towards the total divergence and indicated that D^2 analysis was more potent compared to metroglyph analysis.

Fifty mung bean genotypes were grouped into seven clusters by Haritha and Reddy Sekhar (2002) based on similarity correlation values. The genotypes of cluster seven showed the maximum values for most of the characters.

Singh (2001) studied multivariate analysis of divergence among fifty genotypes of black gram for eight characters. It revealed considerable genetic diversity among genotypes and their grouping into seven clusters. Pods per plant contributed the maximum towards divergence followed by days to 50 per cent flowering and yield per plant.

Two hundred germplasm lines, along with six commercial varieties of mung bean were evaluated over four diverse environments for seed yield and its components by Raje and Rao (2000). The genotypes were grouped into seven clusters and found that genetic diversity was found to be unrelated to geographical diversity.

Patil (2000) reported that thirty-six genotypes of greengram were grouped into five clusters based on the D^2 values. Pods per plant and plant the height had highest contribution to the genetics divergence.

Thirty mung bean genotypes were evaluated by Manivannan *et al.* (1998) for eight yield components. Genotypes were grouped into eight clusters based on their genetic diversity. Plant height contributed the most towards divergence followed by pod length, number of pods, seeds per pod and clusters per plant.

Genetic diversity in seventy genotypes of black gram was estimated using Mahalanobis's D^2 value and results indicated considerable diversity in the material studied by Pariya *et al.* (1997). The genotypes were grouped into eight clusters using multivariate analysis. The characters viz., plant height, pods per plant and clusters per plant contributed the maximum to the genetic diversity.

CHAPTER III

MATERIALS AND METHODS

To carry out the experiment 29 selected cultivars were used as lines and these were done among parents in 2019-2020, the lines were grown in the experimental farm.

3.1 Experimental site

The experiment was carried out at the experimental field of Sher-e-Bangla Agricultural University, Dhaka-1207 during August to November 2019. The location of the experimental site was situated at 23°74′N latitude and 90°35′E longitudes with an elevation of 8.6 meter from the sea level. Photograph showing experimental sites (Appendix 1).

3.2 Soil and Climate

The soil of the experimental site was in the subtropical zone which belongs to Agro-ecological zone of “Madhupur Tract” (AEZ No. 28). The soil was clay loam in texture and olive gray with common fine to medium distinct dark yellowish brown mottles. The pH was 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 29 blackgram genotypes collected from BARI and the Dept. of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, which were used as experimental materials. The materials used in that experiment is shown in Table 1.

Table 1. **Genotypes of black gram used for the experiment with sources of collection**

Genotypes	Accession number	Source
G1	BD-6814	BARI
G2	BD-6831	BARI
G3	BD-6833	BARI
G4	BD-6836	BARI
G5	BD-6838	BARI
G6	BD-6839	BARI
G7	BD-6840	BARI
G8	BD-6841	BARI
G9	BD-6847	BARI
G10	BD-6848	BARI
G11	BD-6853	BARI
G12	BD-6855	BARI
G13	BD-6857	BARI
G14	BD-6859	BARI
G15	BD-6860	BARI
G16	BD-6861	BARI
G17	BD-6863	BARI
G18	BD-6865	BARI
G19	BD-6866	BARI
G20	BD-6867	BARI
G21	BD-6871	BARI
G22	BD-6872	BARI
G23	BD-6873	BARI
G24	BD-10036	BARI
G25	BD-10038	BARI
G26	BARI Mash-3	BARI
G27	BARI Mash-4	BARI
G28	BARI Mash-1	BARI
G29	BARI Mash -2	BARI

Source: Bangladesh Agricultural Research Institute (BARI)

3.4 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 tilt. Weeds and other stubbles were removed carefully from the experimental plot and leveled properly.

3.5 Application of manure and fertilizer

The crop was fertilized as the rate of 10 tons of cow dung, 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 cow dung, 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.

3.6 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 144 m^2. Each replication size was 16 m × 2 m, and the distance between replications was 1 m. The spacing between row was 50 cm. Seeds were sown in line in the experimental plots on 30 August 2019. 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.

3.7 Sowing of seeds

Seeds of blackgram genotypes were grown in separate line in the experimental field on 30 August 2019. The row spacing was 25 cm having plant spacing 10 cm within the row. The seedlings emerged with in four days.

3.8 Irrigation and drainage

One post sowing irrigation was given by sprinkler after sowing of seeds to bring proper moisture condition of 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.

3.9 Intercultural operation

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.

3.10 Harvesting of sample plants

The crop was harvested in different dates according to maturity. Harvesting was started on 18th November 2019. When 80% of the plants showed maturity symptoms the crop was assessed to attain maturity. The harvesting was done by visual observation. Eighty-seven (87) 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.

3.11 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.

Plate 1. Seedling stage of blackgram

Plate 2. Vegetative growth stage of blackgram

Plate 3. Experimental field

Plate 4. Flowering stage

Plate 5. Intercultural operation (Application of pesticide)

Plate 6. Data collection

Plate 7. Fruiting stage

Plate 8. Maturity and Harvesting

1) **Plant height (cm):** It was measured in centimeter (cm) from the base of the plant to the tip of the longest shoot. Data were taken at the time of maturity from randomly 87 selected plants from each replication and average plant height in cm was recorded.
2) **Number of branches per plant:** The total number of branches arisen from the main stem of a plant was counted as the number of branches per plant. At the time of maturity, data were from randomly 87 selected plants and average was recorded.
3) **Days to 1st flowering:** Days to 1st flowering were recorded from sowing date to the date of 1st flower appear to plants.
4) **Days to 50% flowering:** Days to 50% flowering were recorded from sowing date to the date of 50% flowering of every entry.
5) **Days to 80% maturity:** Total number of days taken from the date of sowing to the eighty percent maturity of plants in each plot.
6) **Pod length (cm):** This measurement was taken in centimeter (cm) from the base to the tip of a pod of the ten representative pods from each replication and mean value was recorded.
7) **Number of pods per plant:** Total number of pods from randomly selected 87 plants was counted and mean was considered as the number of pods per plant.
8) **Number of seeds per pod:** All pods from the sample plants was collected and 10 pods was randomly selected. Seeds obtained from them, were counted and average numbers was recorded which was considered as the number of seeds per pod.
9) **100-seed weight (g):** From each genotype of 10 randomly selected plants, weight of 100 seeds was recorded and mean value was measured in gram.
10) **Seed yield per plant (g):** All the seeds produced by representative 10 plants were weighed in gram and mean weight was considered as the seed yield per plant.

3.12 Statistical analysis

Genetic diversity was estimated following Mahalanobis's (1936) generalized distance (D^2). Selection of parents 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 (1977) reported that the quantification of genetic diversity through biometrical procedures had made it possible to choose genetically diverse parents for a successful hybridization program. Statistical analysis such as Mahalanobis D^2 and Canonical Variate Analysis (CVA), which quantify the differences among several quantitative traits are efficient method of evaluating genetic diversity. Mean data of each quantitative character were subjected to both univariate and multivariate analysis. For univariate analysis of variance, analysis was done individually and least of significance was done by F-Test. Mean, range, co-efficient of variation (CV) and correlation was estimated using MSTAT computer program. Multivariate analysis *viz*., Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CLU) and Canonical Variate Analysis (CVA) were done by using GENSTAT and Excel program.

3.12.1 Estimation of genetic parameters

Estimation of phenotypic (σ^2p), genotypic (σ^2g) and environmental (σ^2e) variance were calculated by the following formula (Johnson *et al.*, 1955).

$$\text{Genotypic variance } (\delta^2 g) = \frac{MSG - MSE}{r}$$

Where,

MSG = Mean Square due to Genotypes.

MSE = Mean Square Error

r = Number of replication

Phenotypic variance ($\sigma^2 p$) = $\sigma^2 g + \sigma^2 e$

Where,

$\sigma^2 g$ = Genotypic variance

$\sigma^2 e$ = Environmental variance = MSE

3.12.2 Estimation of genotypic coefficient of variation and phenotypic coefficient of variation

Genotypic and phenotypic coefficients of variation were estimated according to the formula given by Burton (1953) and Singh and Chaudhary (1985).

$$\text{Genotypic Co-efficient of Variation (GCV\%)} = \frac{\sqrt{\sigma^2 g}}{\bar{X}} \times 100$$

Where,

$\sigma^2 g$ = Genotypic variance

$\bar{X}$ = Population means

$$\text{Phenotypic Co-efficient of Variation (PCV\%)} = \frac{\sqrt{\sigma^2 p}}{\bar{X}} \times 100$$

Where,

$\sigma^2 p$ = Phenotypic variance

$\bar{x}$ = Population means

3.12.3 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,

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$=Phenotypic variance

3.12.4 Estimation of genetic advance

Expected genetic advance under selection was estimated using the formula suggested by Johnson *et al*. (1955).

$$\text{Genetic advanced (GA)} = \frac{\sigma^2 g}{\sigma^2 p} \times K \times \sigma p$$

Where,

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$=Phenotypic variance

σp = Phenotypic standard deviation

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

3.12.5 Estimation of genetic advance in percent of mean GA (%)

Estimate by the following formula suggested by Johnson *et al*. (1955).

$$\text{Genetic advance in percent of mean GA (\%)} = \frac{\text{GA}}{\overline{\text{X}}} \times 100$$

Where,

GA = Expected Genetic Advance

$\overline{\text{X}}$ = Population means

3.12.6 Estimation of correlation

The genotypic and phenotypic correlation estimated by the formula suggested by Johnson *et al*. (1955).

$$\text{Genotypic correlation } r_{gxy} = \frac{Cov_{gxy}}{\sqrt{(\sigma^2 g_x \times \sigma^2 g_y)}}$$

Where,

Cov_{gxy} = Genotypic covariance between the trait x and trait y

$\sigma^2 g_x$ = Genotypic variance of the trait x

$\sigma^2 g_y$ = Genotypic variance of the trait y

Similarly,

$$\text{Phenotypic correlation } r_{pxy} = \frac{Cov_{pxy}}{\sqrt{(\sigma^2_{px} \times \sigma^2_{py})}}$$

Where,

$Cov_{px\,y}$ = 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

3.12.7 Path co-efficient analysis

Path co-efficient analysis was done according to the procedure employed by Dewey and Lu (1959) also quoted in Singh and Chaudhary (1985),using simple correlation values. In path analysis, correlation co-efficient is partitioned into direct and indirect independent variables on the dependent variable. In order to estimate direct and indirect effect of the correlated characters, say x1, x2 and x3 yield y, a set of simultaneous equations (three equations in this example) is required to be formulated as shown below:

$$r_{yx1} = P_{yx1} + P_{yx2}r_{x1x2} + P_{yx3}r_{x1x3}$$

$$r_{yx2} = P_{yx1}r_{x1x2} + P_{yx2} + P_{yx3}r_{x2x3}$$

$$r_{yx3} = P_{yx1}r_{x1x3} + P_{yx2}r_{x2x3} + P_{yx3}$$

Where, r’s denotes simple correlation co-efficient and P’s denote path co-efficient (Unknown). P’s in the above equations may be conveniently solved by arranging them in matrix from.

Total correlation, say between x1 and y is thus partitioned as follows:

P_{yx1} = The direct effect of x1 on y.

$P_{yx2}r_{x1x2}$ = The indirect effect of x1 via x2 on y.

$P_{yx3}r_{x1x3}$ = The indirect effect of x1 via x3 on y.

After calculating the direct and indirect effect of the characters, residual effect (R) was calculated by using the formula given below (Singh and Chaudhary, 1985):

$P^2_{RY} = 1 - \sum P_{iy} \cdot riy$

Where,

$P^2_{RY} = (R^2)$; and hence residual effect, $R = (P^2_{RY})^{½}$

P_{iy} = Direct effect of the character on yield

riy = Correlation of the character with yield.

3.12.8 Estimation of Genetic Diversity

3.12.8.1 Principal component analysis (PCA)

Principal component analysis, one of the multivariate techniques, is used to examine the interrelationship among several characters and can be done from the sum of squares and product matrix for the characters. Therefore, principal component was computed from the correlation matrix and genotype scores obtained from the first components (which has the property of accounting for maximum variance) and succeeding components with latent roots greater than the unity (Gopikrishnan *et al.* 2002). Contribution of the different morphological characters towards divergence is discussed from the latent vectors of the first two principal components.

3.12.8.2 Principal coordinate analysis (PCO)

Principal coordinate analysis is equivalent to principal component analysis but it is used to calculate inter-unit distances. Through the use of all dimensions of P it gives the maximum distances between each pair of the n point using similarity matrix (Gopikrishnan *et al.* 2002).

3.12.8.3 Canonical vector analysis (CVA)

The canonical vector analysis computed a linear combination of original variability that maximize the ratio in between group to within group variation to be finding out and thereby giving functions of the original variability that can be used to discriminate between groups. Finally, a series of orthogonal transformations sequentially maximizing the ratio among groups within the group variations.

3.12.8.4 Average intra-cluster distances

The average intra-cluster distances for each cluster were calculated by taking possible D^2 values within the member of a cluster obtained from the Principal Coordinate Analysis (PCO). The formula used was D^2/n, where D^2 is the sum of distances between all possible combinations (n) of the genotype included in the cluster. The square root of the average D^2 values represents the distances (D) within cluster.

3.12.8.5 Clustering

To divide the genotypes of the study into some number of mutually exclusive groups clustering were done using non-hierarchical classification. Starting from some initial classification of the genotypes into required groups, the algorithm repeatedly transfers genotypes from one group to another so long as such transfers improve the criterion, the algorithm switches to a second stage which examine the effect of swapping two genotypes of different classes and so on.

CHAPTER IV

RESULTS AND DISCUSSION

The results of the present investigation of character association and genetic diversity analysis in blackgram (*Vigna mungo* L.) presented and discussed here under the following headings:

4.1 Mean, range, analysis of variance and genetic parameters

The results are showed to analysis of variance (ANOVA), range, grand mean, CV%, mean performance, genotypic and phenotypic variance, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense (h^2b) and expected genetic advance in percent of mean (GA) for all the 10 traits of 29 genotypes are furnished in Table 2 to Table 5. Genotypic and phenotypic coefficient of variation is shown in Table 5; heritability and genetic advance as percent of mean is also represented in Table 5. Out of the 10 traits studied, plant height and number of branches per plant are considered as growth attributing characters. Days to first flowering and days to 50% flowering were regarded as earliness attributes. Days to 80% maturity, pod length, number of pods per plant, number of seeds per pod and 100 seed weight were considered as reproductive traits. Yield per plant was the economic trait. The character wise details of these variability are discussed below of the genotypes evaluated for 10 characters are presented below:

4.1.1 Plant height

The variation for plant height was substantial from 67.44 cm to 135.67 cm with general mean of 101.74 cm (Table 3). The coefficient of variation of this trait was 4.89%. The maximum plant height was observed by the genotype G28 (135.67

cm) followed by G5 (129.56 cm), G25 (129.12 cm), G4 (128.70 cm) and the minimum was in G17 (67.44 cm) (Table 2).

From the result of the experiment, it was observed that plant height was varied significantly among the 29 blackgram genotypes. These results were found in agreement with the findings of Pushpa *et al*. (2013), Savithramma *et al*. (1999), Singh *et al*. (2000) and Sharma *et al*. (2006) for plant height in blackgram.

The plant height exhibited high genotypic co-efficient of variation (GCV) (23.67%) and phenotypic co-efficient of variation (PCV) (24.16%) (Table 5 and Figure 1). The phenotypic coefficient of variation was higher than the genotypic coefficient of variation which suggested that environment had a significant role on the expression of this trait. Mahesha and Gabriel (2017) also found moderate GCV and PCV for plant height (11.05; 13.19) by investigating 32 genotypes of blackgram. Gaibriyal *et al.* (2017) found high PCV with medium GCV for plant height among 36 genotypes of blackgram. The magnitude of heritability estimates for plant height was high (95.91%) with high genetic advance (48.57%) along with high genetic advance over percent mean (47.74%) (Table 5 and Figure 2) indicating apparent variation was due to genotypes. So, selection based on this trait would be effective. Radhikaben *et al*. (2020) also recorded high heritability with high genetic advance as percent of mean of plant height of blackgram which indicates the predominance of additive gene action along with lesser influence of environment, thus infers high scope of further improvement through selection for these traits. Similar result was also observed by Kumar and Devi (2018) in blackgram.

Table 2. Mean performance for 10 different characters in 29 lines of blackgram (*Vigna mungo* L.) genotypes

Genotype	PH	NBP	DFF	D50%F	D80%M	PL	NPP	NSP	100 SW	YPP
G1	103.09	6.68	37.00	42.00	74.00	4.72	81.67	6.93	3.30	18.05
G2	107.49	5.00	42.67	46.33	79.67	4.67	82.55	7.33	3.32	19.19
G3	126.22	4.89	41.33	44.67	79.33	4.45	89.78	6.93	3.13	18.97
G4	128.70	5.89	41.33	46.00	79.33	4.34	76.11	6.87	3.26	16.39
G5	129.56	5.78	38.67	41.33	79.00	4.68	101.22	7.40	3.05	23.69
G6	118.33	7.56	39.00	44.33	78.00	4.47	93.89	6.93	3.14	21.40
G7	115.67	5.89	36.67	43.33	80.67	4.32	76.11	7.13	3.18	17.77
G8	127.00	6.33	41.33	44.00	80.00	4.62	85.67	7.47	3.51	25.59
G9	120.78	5.11	38.67	43.67	77.33	4.47	54.00	6.60	3.61	12.93
G10	127.00	7.44	41.33	45.00	76.33	4.41	84.55	6.93	3.08	15.90
G11	88.72	7.33	32.00	36.33	77.33	4.55	89.78	6.80	4.00	24.53
G12	105.56	6.78	40.33	44.00	79.33	4.42	87.55	6.67	3.32	20.00
G13	69.45	6.33	31.33	38.33	75.00	4.57	69.89	6.60	3.83	17.93
G14	89.78	5.56	32.00	37.00	74.00	4.34	72.33	6.80	3.33	16.21
G15	109.65	6.56	38.67	42.33	78.33	4.33	94.55	7.00	2.96	19.83
G16	120.70	7.66	40.33	45.33	77.67	4.97	117.00	7.73	3.44	31.92
G17	67.44	4.67	31.33	37.33	75.67	4.56	85.11	6.20	4.26	23.12
G18	75.79	5.44	31.33	37.33	78.33	4.45	84.67	6.73	3.76	22.32
G19	72.00	5.33	34.33	40.00	75.00	4.51	80.78	6.53	3.59	15.73
G20	126.16	7.44	39.00	43.67	73.33	4.59	113.11	7.00	2.82	21.65
G21	71.53	5.67	33.00	37.00	73.33	4.49	93.78	6.27	3.90	22.53
G22	68.52	6.89	30.33	36.00	75.67	4.59	95.44	6.87	4.05	26.62
G23	70.11	4.78	29.00	36.00	70.00	4.68	75.11	6.87	4.20	21.38
G24	117.00	4.55	37.67	43.00	73.00	4.27	53.00	6.07	2.80	10.84
G25	129.12	5.22	41.67	45.33	73.00	4.67	84.22	6.33	3.39	19.24
G26	74.00	5.22	29.67	35.67	70.33	4.44	66.11	6.47	4.25	19.44
G27	80.67	6.11	27.33	35.00	67.00	4.99	58.33	6.73	5.19	20.11
G28	135.67	5.11	40.67	45.67	76.00	4.31	87.33	6.40	3.69	20.24
G29	74.67	5.67	32.67	39.67	73.33	4.79	65.00	7.00	3.70	17.60
SE(±)	4.503	0.176	0.866	0.703	0.621	0.034	2.824	0.071	0.097	0.783
CV(%)	4.89	11.73	3.38	2.52	2.00	5.00	4.25	7.10	1.00	9.51

PH = Plant height (cm), NPB = Number of branches per plant, DFF = Days to first flowering, D50%F = Days to 50% flowering, D80%M = Days to 80% maturity, PL = Pod length (cm), NPP = Number of pods per plant, NSP = Number of seeds per pod, 100 SW = 100 seed weight (g), YPP = Yield per plant

Table 3. Range, mean, CV (%) and standard deviation of 29 blackgram (*Vigna mungo* L.) genotypes

Parameters	**Range**		**Mean**	**SD**
	Maximum	**Minimum**		
PH	135.67	67.44	101.74	24.247
NBP	7.66	4.55	5.96	0.947
DFF	42.67	27.33	36.23	4.661
D50%F	46.33	35.00	41.23	3.786
D80%M	80.67	67.00	75.84	3.343
PL	4.99	4.27	4.54	0.183
NPP	117.00	53.00	82.71	15.205
NSP	7.73	6.07	6.81	0.383
100 SW	5.19	2.80	3.55	0.521
YPP	31.92	10.84	20.04	4.214

PH = Plant height (cm), NPB = Number of branches per plant, DFF = Days to first flowering, D50%F = Days to 50% flowering, D80%M = Days to 80% maturity, PL = Pod length (cm), NPP = Number of pods per plant, NSP = Number of seeds per pod, 100 SW = 100 seed weight (g), YPP = Yield per plant

4.1.2 Number of branches plant^{-1}

Number of branches plant^{-1} among the genotypes was ranged from 4.55 to 7.66 with mean value of 5.96 (Table 3). Number of branches per plant were varied significantly among the genotypes (Table 4). The maximum number of branches plant^{-1} was observed by the genotype G16 (7.66) followed by G6 (7.56), G10 (7.44), G20 (7.44) whereas the minimum was in G24 (4.55) (Table 2). These results were found in agreement with the findings of Gowsalya *et al*. (2016), Parameswarappa and Lamani (2005) and Sharma *et al*. (2006) for number of branches per plant in blackgram.

The coefficient of variation (CV) of this trait (number of branches plant^{-1}) was 11.73% (Table 5). The number of branches plant^{-1} exhibited moderate GCV (14.37%) and PCV (18.55%) (Table 5 and Figure 1). The phenotypic coefficient of variation was higher than the genotypic coefficient of variation which suggested that environment had a significant role on the expression of this trait. Supported result was also observed by Mahesha *et al.* (2017) and they recorded moderate GCV and PCV for number of branches per plant (15.26 and 15.76, respectively). Sateesh *et al.* (2016) found high GCV and PCV for number of branches per plant in blackgram. Medium heritability estimates for number of branches plant^{-1} (60.01%) were found with low genetic advance (1.37%) along with high genetic advance over percent mean (22.94%) (Table 5 and Figure 2). Radhikaben *et al*. (2020) found similar result with the present study and recorded high heritability with high genetic advance as percent of mean for branches per plant. Chaithanya *et al*. (2019) recorded high heritability coupled moderate genetic advance as percent of mean for number of branches per plant.

Table 4. Analysis of variance for different characters in blackgram (*Vigna mungo* L.) genotypes

Parameters	Mean sum of square		
	Replication (r-1) = 2	Genotype (G-1) = 28	Error (r-1)(G-1) = 56
PH	14.411	1763.68*	24.719
NBP	4.578	2.692**	0.489
DFF	0.287	65.169*	1.502
D50%F	2.391	43.002*	1.081
D80%M	0.356	33.515*	2.297
PL	0.190	0.099**	0.052
NPP	17.947	693.562*	12.332
NSP	0.183	0.441**	0.234
100 SW	0.022	0.814**	0.001
YPP	0.675	53.277*	3.631

PH = Plant height (cm), NPB = Number of branches per plant, DFF = Days to first flowering, D50%F = Days to 50% flowering, D80%M = Days to 80% maturity, PL = Pod length (cm), NPP = Number of pods per plant, NSP = Number of seeds per pod, 100 SW = 100 seed weight (g), YPP = Yield per plant

Table 5. Estimation of genetic parameters in ten characters of 29 blackgram (*Vigna mungo* L.) genotypes

Parameters	σ^2p	σ^2g	σ^2e	PCV	GCV	ECV	Heritability	GA (5%)	GA in % mean
PH	604.37	579.66	24.72	24.16	23.67	4.89	95.91	48.57	47.74
NBP	1.22	0.73	0.49	18.55	14.37	11.73	60.01	1.37	22.94
DFF	22.72	21.22	1.50	13.16	12.72	3.38	93.39	9.17	25.31
D50%F	15.05	13.97	1.08	9.41	9.07	2.52	92.82	7.42	17.99
D80%M	12.70	10.41	2.30	4.70	4.25	2.00	81.92	6.02	7.93
PL	0.07	0.02	0.05	5.72	2.78	5.02	23.52	0.13	2.77
NPP	239.41	227.08	12.33	18.71	18.22	4.25	94.85	30.23	36.55
NSP	0.30	0.07	0.23	8.08	3.86	7.10	22.81	0.26	3.80
100 SW	0.27	0.26	0.01	14.68	14.65	0.89	99.54	1.07	30.11
YPP	20.18	16.55	3.63	22.42	20.30	9.51	82.01	7.59	37.87

PH = Plant height (cm), NPB = Number of branches per plant, DFF = Days to first flowering, D50%F = Days to 50% flowering, D80%M = Days to 80% maturity, PL = Pod length (cm), NPP = Number of pods per plant, NSP = Number of seeds per pod, 100 SW = 100 seed weight (g), YPP = Yield per plant, σ^2g = Genotypic variance, σ^2p = Phenotypic variance, σ^2e = Environmental variance, GCV = Genotypic Co-efficient of Variation, PCV = Phenotypic Co-efficient of Variation, GA = Genetic advanced

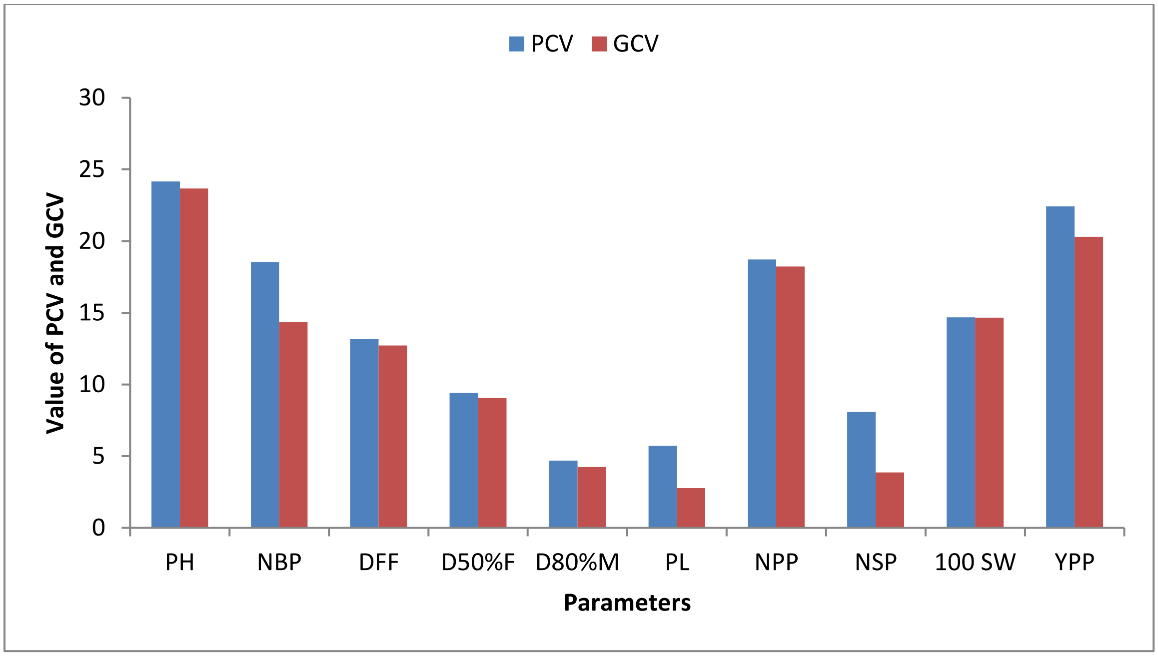

Figure 1. Genotypic and phenotypic coefficient of variation in blackgram (*Vigna mungo* L.) genotypes

PH = Plant height (cm), NPB = Number of branches per plant, DFF = Days to first flowering, D50%F = Days to 50% flowering, D80%M = Days to 80% maturity, PL = Pod length (cm), NPP = Number of pods per plant, NSP = Number of seeds per pod, 100 SW = 100 seed weight (g), YPP = Yield per plant

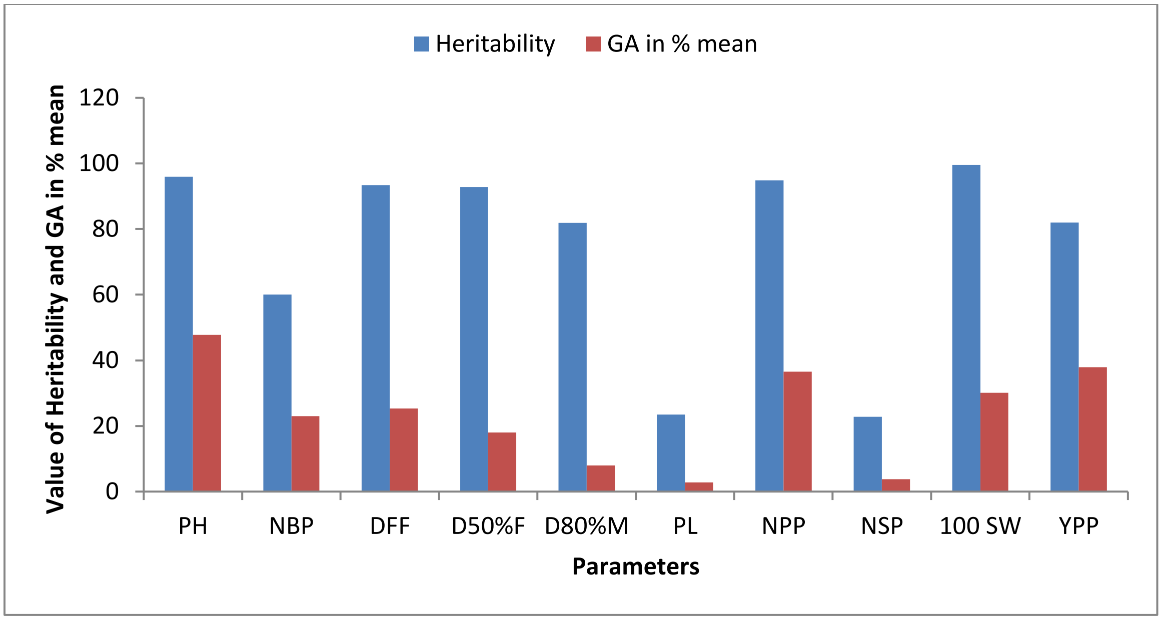

Figure 2. Heritability and genetic advance over mean in blackgram (*Vigna mungo* L.) genotypes

PH = Plant height (cm), NPB = Number of branches per plant, DFF = Days to first flowering, D50%F = Days to 50% flowering, D80%M = Days to 80% maturity, PL = Pod length (cm), NPP = Number of pods per plant, NSP = Number of seeds per pod, 100 SW = 100 seed weight (g), YPP = Yield per plant

4.1.3 Days to 1st flowering

The genotypes varied significantly for the days to 1st flowering and it ranged from 27.33 days to 42.67 with the general mean 36.23 days (Table 3). The CV value of days to 1st flowering was observed 3.38%. The maximum days to 1st flowering was observed in genotype G2 (42.67) followed by G3, G4 and G10 (41.33) and the lowest was found in the genotype G27 (27.33) (Table 2). Similar result was also observed by Singh *et al*. (2000) and Pushpa *et al*. (2013) for days to flowering in blackgram.

The genotypic variance (21.22) is lower than phenotypic variance (22.72) (Table 5). Thus, genes controlling this trait possessed considerable influence of environment on the expression of the character. The genotypic co-efficient of variation (GCV) and phenotypic co-efficient of variation (PCV) were moderate with value of 12.72% and 13.16%, respectively (Table 5 and Figure 1). High heritability (93.39%) was found with low genetic advance (9.17%) along with high genetic advance over percent mean (25.31%) (Table 5 and Figure 2).

4.1.4 Days to 50% flowering

Days to 50% flowering varied from 35.00 to 46.33 days with mean value of 41.23 days (Table 3). Days to 50% flowering were varied significantly among the 29 genotypes of blackgram (*Vigna mungo* L.) (Table 4). The CV value of days to 50% flowering was 2.52%. The maximum days to 50% flowering was found in G2 (46.33 days) followed by G4 (46.00 days) whereas the minimum (35.00 days) was from G27 (Table 2). High days to 50% flowering shown late maturity and lowest days to 50% flowering showed early maturity of a variety and it was essential for release early maturing variety. These results were found in agreement with the findings of Priyanka *et al*. (2016), Parameswarappa and Lamani (1994) and Savithramma *et al*. (1999) for days to 50% flowering in blackgram.

The genotypic variance (13.97) is lower than phenotypic variance (15.05) (Table 1 and Figure 5). For the expression of the character considerable influence of environment on days to 50% flowering was possessed regarding genes controlling this trait. The GCV and PCV were low with value of 9.07% and 9.41% respectively, along with high heritability (92.82%) with low genetic advance (7.42%) and moderate genetic advance as percent of mean (17.99%) (Table 2 and Figure 5). Low GCV and PCV were also recorded by Yashoda *et al.* (2016) for days to 50 percent flowering in blackgram. Hemalatha *et al*. (2017) also recorded high heritability for days to 50 percent flowering in blackgram. Similar result was also observed by Chubatemsu *et al*. (2017).

4.1.5 Days to 80% maturity

Days to 80% maturity were varied significantly due to genotypic variation of blackgram (Table 4). Days to 80% maturity varied from 67.00 days to 80.67 days with mean value of 75.84 days (Table 3). The CV value of days to 80% maturity was 2.00%. The maximum days to 80% maturity (80.67 days) was found in G7 followed by G8 (80.00 days) whereas the minimum (67.00 days) was from G27 (Table 2). Similar result was also observed by Gowsalya *et al*. (2016), Singh *et al*. (2000) and Savithramma *et al*. (1999) for days to maturity in blackgram.

The genotypic variance (10.41) is lower than phenotypic variance (12.70) (Table 5) which suggested that environment had a significant role on the expression of this trait (days to 80% maturity). The GCV and PCV were low (4.25% and 4.70%, respectively) (Table 5 and Figure 1). Yashoda *et al.* (2016) also found lower values of GCV and PCV for days to maturity by investigating 46 genotypes of blackgram. High heritability (81.92%) was found with low genetic advance (6.02%) along with low genetic advance over percent mean

(7.93%) (Table 5 and Figure 2). Reena *et al.* (2016) recorded the highest heritability (86.0%) for days to maturity in 75 genotypes of blackgram. High heritability was also recorded by Hemalatha *et al*. (2017) for days to maturity (96.68%) in blackgram.

4.1.6 Pod length

Pod length varied significantly among the blackgram genotypes which was ranged from 4.27 cm to 4.99 cm with the mean value of 4.54 cm and CV value of 5.00 (Table 3). The maximum pod length was observed in the genotype G27 (4.99 cm) followed by G16 (4.97 cm) while the minimum was observed in the genotype G24 (4.27 cm) (Table 2). The mean sum of square was significant (2.53) which indicated considerable amount of variation for this trait in the varieties (Table 4). These results were found in agreement with the findings of Priyanka *et al*. (2016), Singh *et al*. (2000) and Savithramma *et al*. (1999) for pod length in blackgram.

The genotypic and phenotypic variance for pod length was seen as value of 0.02 and 0.07, respectively. Pod length exhibited low GCV (2.78%) and PCV (5.72%) values (Table 5 and Figure 1). As PCV is higher than GCV thus it can be concluded that the trait is controlled by its genotype as well as influence of environment. This result was in accordance with the findings of Yashoda *et al.* (2016) and recorded Low values of GCV and PCV for pod length in blackgram. A low heritability estimate of 23.52%, low genetic advance (0.13%) with low genetic advance in percent of mean (2.77%) was observed (Table 5 and Figure 2). Low heritability with combination of low genetic advance in percent of mean suggested that this character was less affected by environment with simple gene interaction.

4.1.7 Number of pods per plant

Number of pods per plant ranged from 53.00 to 117.00 with the mean of 82.71 which was significant among the genotypes while the CV value was 4.25% (Table 3). The maximum pods per plant (117.00) was found in the genotype G16 followed by G20 (113.00) while the minimum (53.00) was observed in G24 (Table 2). Similar result was also observed by Priyanka *et al*. (2016), Gowsalya *et al*. (2016), Meshram *et al*. (2013), Parameswarappa and Lamani (2005) and Sharma *et al*. (2006) for number of pods per plant in blackgram.

The phenotypic variance (239.41) was higher than genotypic variance (227.08) (Table 5) that indicates high influence of environment on this character. The moderate phenotypic coefficient of variation (PCV) (18.71%) and genotypic coefficient of variation (GCV) (18.22%) (Table 5 and Figure 1) indicated presence of considerable variability among the genotypes. Chubatemsu *et al*. (2017) registered relatively higher estimate of PCV and GCV for number of pods per plant while Hemalatha *et al*. (2017) recorded high GCV and PCV for number pods per plant (31.28 and 31.33, respectively). Gowsalya *et al.* (2016) recorded moderate GCV (19.03) for number of pods per plant. The heritability (94.85%) estimate for this trait was high with high genetic advance (30.23%) and high genetic advance in percent of mean (36.55%) were found (Table 5 and Figure 2). So, these traits could be exploited for further improvement through selection procedures. Hemalatha *et al*. (2017) also found similar result with the present study and recorded high heritability coupled with high genetic advance as percent of mean for number of pods per plant among 25 black gram genotypes along with one check. Chaithanya *et al*. (2019) and Anu *et al.* (2017) also found similar result with the present study.

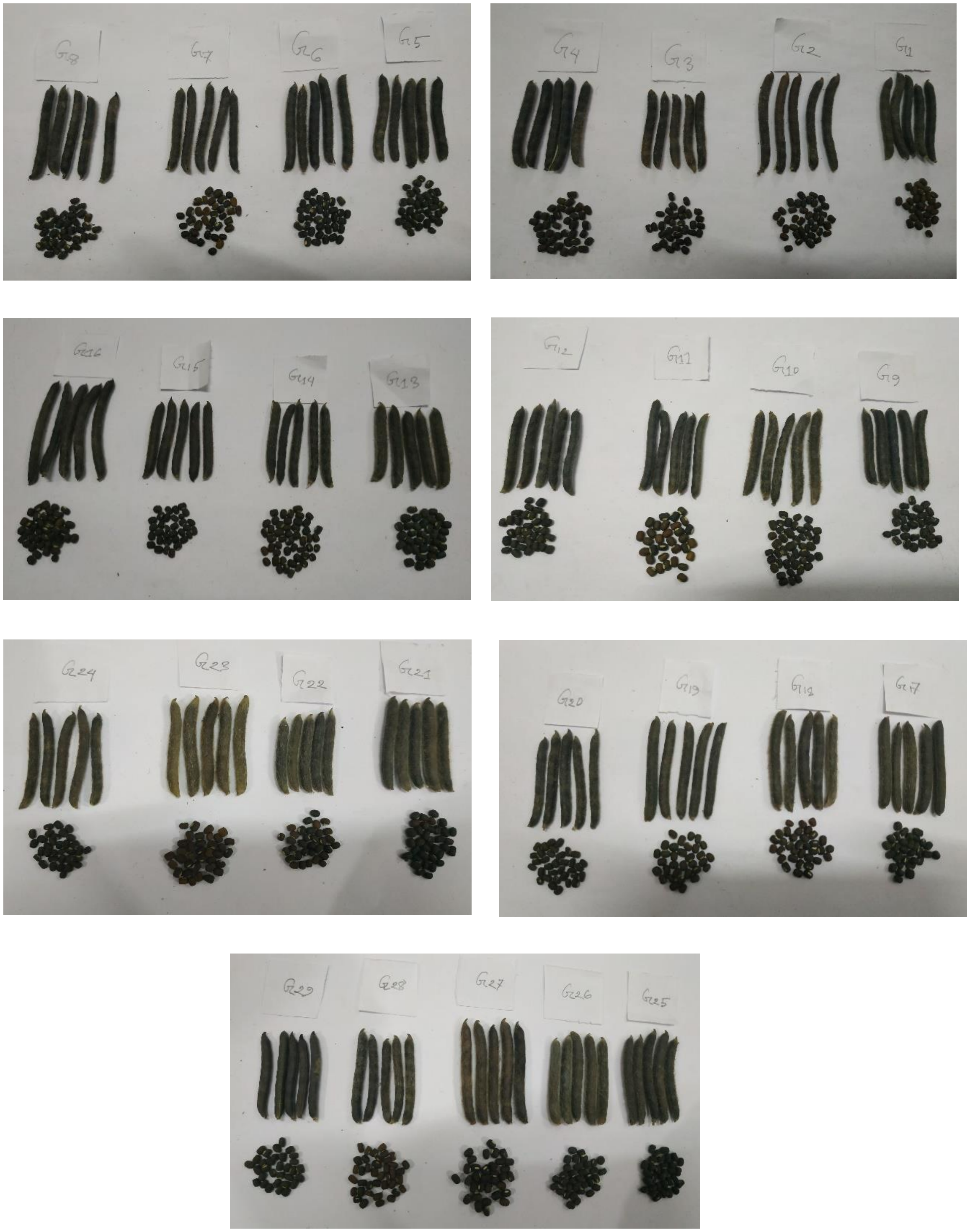

Plate 9. Pictures showing morphological variation of pod and seed of 29 genotypes of blackgram

4.1.8 Number of seeds per pod

Number of seeds per pod varied significantly among the 29 genotypes of blackgram (Table 4). Seeds per pod ranged from 6.07 to 7.73 with the average of 6.81 and CV value of 7.10 (Table 3). The maximum seeds per pod was given by the genotype G16 (7.73) followed by G8 (7.47), G5 (7.40), G2 (7.33) and the minimum was observed from the genotype G24 (6.07) (Table 2). Similar result was also observed by Gowsalya *et al*. (2016), Singh *et al*. (2000) and Savithramma *et al*. (1999) for number of seeds per pod in blackgram.

The genotypic variance (0.07) was lower than the phenotypic variance (0.30). Low GCV and PCV were observed as 3.86 and 8.08, respectively (Table 5 and Figure 1). This indicates little influence of environment upon the character. Yashoda *et al.* (2016) also showed similar result with the present study and found low values of GCV and PCV for number of seeds per pod. It showed low heritability (22.81%) with low genetic advance (0.26%) and low genetic gain in percent of mean (3.80%) for this trait (Table 5 and Figure 2). Low heritability with low genetic advance and low genetic advance in percent of mean indicates that this trait was under additive and non-additive gene control and selection for genetic improvement for this trait would be effective. This result was in accordance with the findings of Chubatemsu *et al*. (2017) and they recorded lowest heritability for number of seeds per pod in blackgram. Sohel *et al*. (2016) also found low heritability in blackgram for number of seeds per pod.

4.1.9 Weight of 100 seeds

Significantly variation was found for 100 seed weight of blackgram among the 29 genotypes (Table 2) which ranged from 2.80 g to 5.19 g with the mean value of 3.55 g and CV value of 1.00% (Table 3). The maximum 100 seed weight was observed in the genotype G27 (5.19 g) and the minimum was observed in the genotype G24 (2.80 g) (Table 2). The mean sum of square was significant in blackgram (*Vigna mungo* L.) which allows showing the presence of considerable variation for this trait. Similar result was also observed by Priyanka *et al*. (2016), Singh *et al*. (2000) and Savithramma *et al*. (1999) for 1000-seed weight in blackgram.

100 seed weight was registered moderate PCV (14.68%) and GCV (14.65%). As PCV is near about same with GCV, there is no considerable influence of environment on this trait (Table 5 and Figure 1). It showed high heritability (99.54%), very low genetic advance (1.07%) and high genetic gain in percent of means (30.11%) was found for this trait (Table 5 and Figure 2). High heritability with high genetic advance as percent mean suggests that the character is governed by the additive and non-additive gene action. Thus, selection may be effective in this trait for the improvement of the crop. High estimates of heritability were also observed for 100 seed weight (85%) by Chubatemsu *et al*. (2017). Similar result was also observed by Srivastava and Singh (2012). High heritability coupled with high genetic advance as percent of mean were also observed by 100 seed weight of blackgram.

4.1.10 Yield per plant

Yield per plant varied significantly among the 29 lines of blackgram (*Vigna mungo* L.) (Table 4). Among the genotypes, yield per plant was ranged from 10.84 g to 31.92 g with average of 20.04 g and CV value of 9.51 (Table 3). The maximum yield per plant was observed in G16 (31.92 g) followed by G22 (26.62 g), G8 (25.59 g), G11 (24.53 g) while the minimum yield per plant was observed in G24 (10.84 g) (Table 2). These results were found in agreement with the findings of Priyanka *et al*. (2016), Gowsalya *et al*. (2016), Pushpa *et al*. (2013), Meshram *et al*. (2013) and Parameswarappa and Lamani (2005) grain yield per plant in blackgram.

Seed yield per plant exhibited high estimates of PCV (22.42%) and GCV (20.30%) (Table 5 and Figure 1) where genotypic variance (16.55) was lower than phenotypic variance (20.18). Chaithanya *et al*. (2019) also found similar result with the present study and observed high GCV and PCV for seed yield per plant. Kumar and Devi (2018), Hemalatha *et al*. (2017) and Mahesha *et al.* (2017) also obtained the maximum GCV and PCV for seed yield per plant. It also recorded the high heritability (82.01%), low genetic advance (7.59%) with high genetic advance in percent of mean (37.87%) for this trait (Table 5 and Figure 2) which suggested that selection would be effective for this trait as there were additive gene effects on gene in controlling this trait. High heritability with high genetic advance as percent of mean was also recorded by Radhikaben *et al*. (2020) for seed yield per plant which indicates the predominance of additive gene action along with lesser influence of environment, thus infers high scope of further improvement through selection for these traits. Hemalatha *et al*. (2017) also recorded high heritability coupled with high genetic advance as percent of mean for seed yield per plant of blackgram.

4.2 Correlation analysis

The seed yield is a complex character and depends on different independent characters therefore it is essential to know the relationship between the yield and its component characters. In order to get knowledge of interrelationship between yield contributing characters, correlation coefficients were computed in all possible combinations among the characters under study at phenotypic and genotypic level and presented in Table 6 and 7 respectively.

It is necessary to have the estimates of correlation of yield with other characters for which the genotype could be assessed visually. The phenotypic and genotypic correlation reveals the extent of association between different characters, thus, it helps to base selection procedure to a required balance, when two opposite desirable characters affecting the principal characters are being selected. A positive correlation occurs due to coupling phase of linkage and negative correlation arises due to repulsion phase of linkage of genes controlling different traits. No correlation indicates that genes concerned are located far apart on the same chromosome or they are located on different chromosomes.

4.2.1 Plant height (cm)

Plant height showed non-significant and negative interaction with seed yield per plant ($G = -0.101^{NS}$, $P = -0.080^{NS}$) both at genotypic and phenotypic levels (Table 6 and 7). Significant positive associations between plant height and other characters indicate that the traits were governed by same gene and simultaneous improvement would be effective. It had significant and positive interaction with days to first flowering (G = 0.908**, P = 0.868**), days to 50% flowering (G = 0.893**, P = 0.852**), days to 80% maturity (G = 0.520**, P = 0.465**), number of pods per plant (G = 0.263*, P = 0.268*) and number of seeds per pod (G = 0.461**, P = 0.266*). It also exhibited insignificant and positive interaction with number of branches per plant ($G = 0.192^{NS}$, $P = 0.167^{NS}$). Similarly, it had significant and negative interaction with 100 seed weight (G = -0.699**, P = -0.687**) (Table 6 and 7). Again, pod length at genotypic level, it was significant and negatively correlated with plant height but at phenotypic level, it showed insignificant and negative correlation with plant height (G = -0.335**, P = -0.097^{NS}). Insignificant association of these traits indicated that the association between these traits is largely influenced by environmental factors. Jyothsna *et al.* (2016) found similar result with the present study and found non-significant and negative association between plant height and seed yield per plant at phenotypic level. Panigrahi *et al.* (2014) recorded significant positive association of majority of the yield contributing traits with seed yield per plant except for plant height both at genotypic and phenotypic levels. Sohel *et al*. (2016) also found negative association between plant height and seed yield per plant both at genotypic and phenotypic levels.

Table 6. Genotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of blackgram (*Vigna mungo* L.)

Characters	NBP	DFF	D50%F	D80%M	PL	NPP	NSP	100 SW	YPP
PH	0.192^{NS}	0.908**	0.893**	0.520**	-0.335**	0.263*	0.461**	-0.699**	-0.101^{NS}
NBP		0.144^{NS}	0.148^{NS}	0.264*	0.266*	0.619**	0.740**	-0.266*	0.519**
DFF			0.987**	0.582**	-0.311**	0.351**	0.491**	-0.787**	-0.083^{NS}
D50%F				0.516**	-0.283**	0.255*	0.466**	-0.753**	-0.167^{NS}
D80%M					-0.440**	0.373**	0.635**	-0.411**	0.198^{NS}
PL						0.226*	0.217*	0.633**	0.732**
NPP							0.662**	-0.364**	0.758**
NSP								-0.453**	0.691**
100 SW									0.240*

PH = Plant height (cm), NPB = Number of branches per plant, DFF = Days to first flowering, D50%F = Days to 50% flowering, D80%M = Days to 80% maturity, PL = Pod length (cm), NPP = Number of pods per plant, NSP = Number of seeds per pod, 100 SW = 100 seed weight (g), YPP = Yield per plant

Table 7. Phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of blackgram (*Vigna mungo* L.)

Characters	**NBP**	**DFF**	**D50%F**	**D80%M**	**PL**	**NPP**	**NSP**	**100 SW**	**YPP**
PH	0.167^{NS}	0.868^{**}	0.852^{**}	0.465^{**}	-0.097^{NS}	0.268^{*}	0.266^{*}	-0.687^{**}	-0.080^{NS}
NBP		0.165^{NS}	0.108^{NS}	0.171^{NS}	0.204^{NS}	0.470^{**}	0.326^{**}	-0.208^{NS}	0.342^{**}
DFF			0.941^{**}	0.504^{**}	-0.141^{NS}	0.328^{**}	0.231^{*}	-0.762^{**}	-0.099^{NS}
D50%F				0.463^{**}	-0.120^{NS}	0.243^{*}	0.216^{*}	-0.725^{**}	-0.148^{NS}
D80%M					-0.155^{NS}	0.330^{**}	0.266^{*}	-0.372^{**}	0.192^{NS}
PL						0.148^{NS}	0.515^{**}	0.291^{**}	0.367^{**}
NPP							0.356^{**}	-0.356^{**}	0.709^{**}
NSP								-0.224^{*}	0.354^{**}
100 SW									0.223*

PH = Plant height (cm), NPB = Number of branches per plant, DFF = Days to first flowering, D50%F = Days to 50% flowering, D80%M = Days to 80% maturity, PL = Pod length (cm), NPP = Number of pods per plant, NSP = Number of seeds per pod, 100 SW = 100 seed weight (g), YPP = Yield per plant

4.2.2 Number of branches per plant

Both at genotypic and phenotypic levels, number of branches per plant showed positive and significant interaction with seed yield per plant (G = 0.519**, P = 0.342**) (Table 6 and 7). These suggesting if number of primary branches increases then yield per plant also increases. It also showed positive and significant interaction with number of pods per plant (G = 0.619**, P = 0.470**) and number of seeds per pod (G = 0.740**, P = 0.326**) both at genotypic and phenotypic levels. Similarly, number of branches per plant had insignificant and positive correlation with days to first flowering (G = 0.144^{NS}, P = 0.165^{NS}) and days to 50% flowering (G = 0.148^{NS}, P = 0.108^{NS}) both at genotypic and phenotypic levels. Again, at genotypic level, it had significant and positive correlation with days to 80% maturity (G = 0.264*) and pod length (G = 0.266*) but at phenotypic level, it had insignificant and positive correlation with days to 80% maturity (P = 0.171^{NS}) and pod length (P = 0.204^{NS}). Likewise, number of branches per plant had significant and negative correlation at genotypic level and insignificant negative correlation at phenotypic level with 100 seed weight (G = -0.266*, P = -0.208^{NS}). Similar result was also observed by Kanimoli *et al.* (2015) and Vijay *et al.* (2015) and they reported that seed yield per plant had significant positive association with number of primary branches per plant.

4.2.3 Days to first flowering

Days to first flowering at genotypic and phenotypic levels showed negative and insignificant interaction with seed yield per plant (G = -0.083^{NS}, P = -0.099^{NS}) (Table 6 and 7). These suggest that days to first flowering had no significant effect to increase seed yield per plant. Insignificant association of these traits indicated that the association between these traits was largely influenced by environmental factors. But it showed positive and significant interaction with days to 50% flowering (G = 0.987**, P = 0.941**), days to 80% maturity (G = 0.582**, P = 0.504**), number of pods per plant (G = 0.351**, P = 0.328**) and number of seeds per pod (G = 0.491**, P = 0.231**) both at genotypic and phenotypic levels (Table 6 and 7). Similarly, days to 50% flowering had significant and negative correlation with 100 seed weight (G = -0.787**, P = -0.762**) both at genotypic and phenotypic levels. Again, at genotypic level, it had significant and negative correlation with pod length (G = -0.311**) but at phenotypic level, it had insignificant and negative correlation with pod length (P = -0.141^{NS}).

4.2.4 Days to 50% flowering

Days to 50% flowering showed non-significant and negative correlation with seed yield per plant (G = -0.167^{NS}, P = -0.148^{NS}) both at genotypic and phenotypic levels (Table 6 and 7) which indicates that days to 50% flowering had no significant contribution to increase seed yield per plant and the association between these traits was largely influenced by environmental factors. However, days to 50% flowering had significant positive correlation with days to 80% maturity (G = 0.516**, P = 0.463**), number of pods per plant (G = 0.255*, P = 0.243*) and number of seeds per pod (G = 0.466**, P = 0.216*) both at genotypic and phenotypic levels (Table 6 and 7). Similarly, it had significant and negative correlation at genotypic and phenotypic levels with 100 seed weight (G = -0.753**, P = -0.725**). But it had significant negative correlation at genotypic level (G = -0.283**) and insignificant negation correlation at phenotypic level (P = -0.120^{NS}) with pod length (Table 6 and 7). Reena *et al.* (2016) also reported non-significant correlation between seed yield per plant and days to 50% flowering. Panigrahi *et al.* (2014) also found non-significant correlation between seed yield per plant and days to 50% flowering both at genotypic and phenotypic levels.

4.2.5 Days to 80% maturity

At genotypic and phenotypic levels, days to 80% maturity showed positive and insignificant interaction with seed yield per plant (G = 0.198^{NS}, P = 0.192^{NS}) (Table 6 and 7). Insignificant association of these traits indicated that the association between these traits was largely influenced by environmental factors. Days to 80% maturity showed positive and significant interaction with number of pods per plant (G = 0.373**, P = 0.330**) and number of seeds per pod (G = 0.635**, P = 0.266*) both at genotypic and phenotypic levels (Table 6 and 7). Similarly, it had significant and negative correlation with 100 seed weight (G = -0.411**, P = -0.372**) both at genotypic and phenotypic levels. Again, at genotypic level, days to 80% maturity had significant and negative correlation with pod length (G = -0.440**) but at phenotypic level, it had insignificant and negative correlation with pod length (P = -0.155^{NS}). Similar result was also observed by Reena *et al.* (2016) and reported insignificant interaction between days to maturity to seed yield per plant.

4.2.6 Pod length

Pod length at genotypic and phenotypic levels showed significant and positive correlation with seed yield per plant (G = 0.732**, P = 0.367**) (Table 6 and 7) which indicated that the traits were governed by same gene and simultaneous improvement would be effective. However, pod length had also significant positive correlation with number of seeds per plant (G = 0.217*, P = 0.515**) and 100 seed weight (G = 0.633**, P = 0.291**) both at genotypic and phenotypic levels (Table 6 and 7). But it had significant positive correlation at genotypic level (G = 0.226*) and insignificant positive correlation at phenotypic level (P = 0.148^{NS}) with number of pods per plant (Table 6 and 7). Sohel *et al.* (2016) also found that yield per plant was positively and significantly associated with pod length. Gowsalya *et al.* (2016) also found a positive association of seed yield per plant with pod length both phenotypic and genotypic level.

4.2.7 Number of pods per plant

Number of pods per plant showed highly significant and positive correlation with seed yield per plant (G = 0.758**, P = 0.709**) whereas the significant and negative interaction was found in 100 seed weight (G = -0.364**, P = -0.356**) both at genotypic and phenotypic levels (Table 6 and 7). It had insignificant and positive correlation with number of seeds per pod (G = 0.662**, P = 0.356**) (Table 6 and 7). Significant association of these traits indicated that the traits were governed by same gene and simultaneous improvement would be effective. Yashoda *et al.* (2016) also revealed that seed yield per plant had a high positive and significant association with number of pods per plant (0.712). Similarly, Sohel *et al.* (2016) and Gowsalya *et al.* (2016) found a positive and significant association of seed yield per plant with number of pods per plant.

4.2.8 Number of seeds per pod

Number of seeds per pod showed highly significant and positive interaction with seed yield per plant (G = 0.691**, P = 0.354**) whereas it had significant and negative interaction with 100 seed weight (G = -0.453**, P = -0.224*) both at genotypic and phenotypic levels (Table 6 and 7). Significant association of these traits indicated that the traits were governed by same gene and simultaneous improvement would be effective. Gowsalya *et al.* (2016) also found similar result with the present investigation and observed a positive and significant association of seed yield per plant with number of seeds per pod both phenotypic and genotypic level.

4.2.9 Weight of 100 seeds

Both at genotypic and phenotypic levels, 100 seed weight showed significant and positive interaction with yield per plant (G=0.240*, P=0.223*) (Table 6 and 7). Significant association of these traits suggested that the association between these traits is largely influenced by same gene and simultaneous improvement would be effective. Gowsalya *et al.* (2016), Sohel *et al.* (2016) and Parveen *et al.* (2011) also found that yield per plant was positively and significantly associated with 100-seed weight.

4.3 Path Co-efficient analysis

In order to finding out a clear picture of the inter-relationship between seed yield per plant and other yield attributes, direct and indirect effects were worked out using path analysis at phenotypic level which also measured the relative importance of each component. Seed yield per plant was considered as a resultant (dependent) variable and plant height, number of branches per plant, days to 50% flowering, days to 80% maturity, pod length, number of pods per plant, number of seeds per pod and 100 seed weight were causal (independent) variables. The phenotypic correlation coefficients were partitioned into direct and indirect effects are presented in Table 8.

4.3.1 Plant height (cm)

Path analysis revealed that plant height had positive direct effect (0.080) on yield per plant. It had positive indirect effect on number of branches per plant (0.0009), days to 50% flowering (0.0216), days to 80% maturity (0.0449), number of pods per plant (0.2234) and number of seeds per pod (0.0419) (Table 8). Plant height had negative indirect effect on days to first flowering (-0.0912), pod length (-0.0003) and 100 seed weight (-0.4013) (Table 8). Plant height finally made significant positive correlation with seed yield (0.080). These results indicated that if plant height increases than seed yield also increases mostly through the positive indirect effect of plant height with other characters. Yashoda *et al.* (2016) reported that plant height (0.115) had positive direct effects on seed yield per plant which supported the presenting. Singh *et al.* (2007) also found similar result with present study and found positive direct effect of plant height on seed yield per plant.

Table 8. Path coefficient analysis showing Direct (Diagonal) and indirect effects of different characters on yield of blackgram (*Vigna mungo* L.)

Characters	**PH**	**NBP**	**DFF**	**D50%F**	**D80%M**	**PL**	**NPP**	**NSP**	**100 SW**	**Genotypic correlation with yield**
PH	**0.080**	0.0009	-0.0912	0.0216	0.0449	-0.0003	0.2234	0.0419	-0.4013	-0.101^{NS}
NBP	0.0134	**0.005**	-0.0173	0.0027	0.0165	0.0006	0.3911	0.0513	-0.1214	0.519**
DFF	0.0696	0.0009	**-0.105**	0.0238	0.0487	-0.0004	0.2729	0.0364	-0.4455	-0.083^{NS}
D50%F	0.0684	0.0006	-0.0989	**0.025**	0.0447	-0.0004	0.2025	0.0340	-0.4240	-0.167^{NS}
D80%M	0.0373	0.0009	-0.0530	0.0117	**0.097**	-0.0005	0.2745	0.0418	-0.2176	0.198^{NS}
PL	-0.0078	0.0011	0.0148	-0.0031	-0.0150	**0.003**	0.1232	0.0812	0.1698	0.732**
NPP	0.0215	0.0025	-0.0344	0.0062	0.0318	0.0005	**0.833**	0.0560	-0.2078	0.758**
NSP	0.0214	0.0017	-0.0243	0.0055	0.0256	0.0016	0.2962	**0.157**	-0.1308	0.691**
100 SW	-0.0551	-0.0011	0.0801	-0.0184	-0.0360	0.0009	-0.2962	-0.0353	**0.584**	0.240*

Residual Effect (R) = 0.20141

Bold number indicate direct effect on yield per plant

**,* Correlation is significant at the 0.01 and 0.05 level, respectively

PH = Plant height (cm), NPB = Number of branches per plant, DFF = Days to first flowering, D50%F = Days to 50% flowering, D80%M = Days to 80% maturity, PL = Pod length (cm), NPP = Number of pods per plant, NSP = Number of seeds per pod, 100 SW = 100 seed weight (g), YPP = Yield per plant

4.3.2 Number of branches plant^{-1}

Number of branches per plant had the positive direct effect on yield per plant (0.005). This trait had positive indirect effect on plant height (0.0134), days to 50% flowering (0.0027), days to 80% maturity (0.0165), pod length (0.0006), number of pods per plant (0.3911) and number of seeds per pod (0.0513). Conversely, negative indirect effect was found on days to first flowering (-0.0173) and 100 seed weight (-0.1214) (Table 8). Number of primary branches per plant finally makes significant positive correlation with seed yield (0.005) which indicated that if number of branches per plant increases than seed yield also increases mostly through the positive indirect effect of number of branches per plant with other characters. This trait had also significant positive genotypic correlation (0.519**) with yield per plant. Sateesh *et al.* (2016) evaluated 25 genotypes of black gram and reported the maximum positive direct effect of number of branches per plant on seed yield per plant. Similar result was also observed by Panigrahi *et al.* (2014).

4.3.3 Days to first flowering

Path co-efficient analysis revealed that, days to first flowering had negative direct effect (-0.105) on yield per plant. This trait had positive indirect effect through plant height (0.0696), number of branches per plant (0.0009), days to 50% flowering (0.0238), days to 80% maturity (0.0487), number of pods per plant (0.2729) and number of seeds per pod (0.0364) on seed yield. Likewise, days to first flowering had negative indirect effect via pod length (-0.0004) and 100 seed weight (-0.4455) on yield per plant (Table 8).

4.3.4 Days to 50% flowering

Path co-efficient analysis indicated that, days to 50% flowering had positive direct effect (0.025) on yield per plant. It had positive indirect effect on plant height (0.0684), number of branches per plant (0.0006), days to 80% maturity (0.0447), number of pods per plant (0.2025) and number of seeds per pod (0.0340). Again, this trait had negative indirect effect on days to first flowering (-0.0989), pod length (-0.0004) and 100 seed weight (-0.4240) (Table 8). Similar result was also observed by Yashoda *et al.* (2016) and Panigrahi *et al.* (2014). Yashoda *et al.* (2016) reported that days to 50 percent flowering (0.080) had positive direct effects on seed yield per plant and Panigrahi *et al.* (2014) also found positive direct effects of days to 50 percent flowering on seed yield per plant.

4.3.5 Days to 80% maturity

Days to 80% maturity had positive direct effect (0.097) on yield per plant. It had positive indirect effect on plant height (0.0373), number of branches per plant (0.0009), days to 50% flowering (0.0117), number of pods per plant (0.2745) and number of seeds per pod (0.0418). Similarly, this trait had negative indirect effect on days to first flowering (-0.0530), pod length (-0.0005) and 100 seed weight (-0.2176) (Table 8). This trait had non-significant positive genotypic correlation (0.198^{NS}) with yield per plant. Yashoda *et al.* (2016) and Pushpa *et al.* (2013) also observed positive direct effect of days to maturity on yield per plant.

4.3.6 Pod length

It was recorded from path analysis that pod length had direct positive effect (0.003) on yield per plant. This trait had also indirect positive effect on number of branches per plant (0.0011), days to first flowering (0.0148), number of pods per plant (0.1232) and number of seeds per pod (0.0812) (Table 8). On the other hand, it showed indirect negative effect on plant height (-0.0078), days to 50% flowering (-0.0031) and days to 80% maturity (-0.0150) (Table 8). This trait had significant positive genotypic correlation (0.732**) with yield per plant. Sohel *et al*. (2016) found similar result with the present study. Makeen *et al*. (2009) also reported positive direct effect of pod length on yield per plant.

4.3.7 Number of pods per plant

Path co-efficient analysis recorded that number of pods per plant had the highest positive direct effect (0.833) on seed yield per plant followed by positive indirect effect on plant height (0.0215), number of branches per plant (0.0025), days to 50% flowering (0.0062), days to 80% maturity (0.0318), pod length (0.0005) and number of seeds per pod (0.0560) (Table 8). This trait had negative indirect effect on yield via days to first flowering (-0.0344) and 100 seed weight (-0.2078) (Table 8). This trait had significant positive genotypic correlation (0.758**) with yield per plant. Similar finding was also observed by Yashoda *et al.* (2016), Panigrahi *et al.* (2014) and Punia *et al.* (2014), they reported positive direct effect of number of pods per plant on seed yield per plant.

4.3.8 Number of seeds per pod

Path analysis indicated that number of seeds per pod had direct positive effect (0.157) on yield per plant. This trait had also indirect positive effect on plant height (0.0214), number of branches per plant (0.0017), days to 50% flowering (0.0055), days to 80% maturity (0.0256), pod length (0.0016) and number of pods per plant (0.2962). On the other hand, this trait showed indirect negative effect on days to first flowering (-0.0243) and 100 seed weight (-0.1308) (Table 8). The negative direct effect was mainly counter balanced by indirect positive effect of different characters. This trait had significant positive genotypic correlation (0.691**) with yield per plant. Similar result was also observed by Yashoda *et al.* (2016) who found positive direct effect of number of seeds per pod (0.022) on yield per plant. Pervin *et al.* (2007) also found positive direct effect of number of seeds per pod on yield per plant.

4.3.9 Weight of 100 seeds

Weight of 100 seeds had positive direct effect on yield per plant (0.584) and positive indirect effect on days to first flowering (0.0801) and pod length (0.0009) (Table 8). On the other hand, this trait showed negative indirect effect on plant height (-0.0551), number of branches per plant (-0.0011), days to 50% flowering (-0.0184), days to 80% maturity (-0.0360), number of pods per plant (-0.2962) and number of seeds per pod (-0.0353) (Table 8). This trait had significant positive genotypic correlation (0.240*) with yield per plant. Reddy *et al*. (2011) found similar result with the present study and reported that 100-seed weight were exhibited positive direct effect on seed yield in greengram. Similar result was also observed by Kanimoli ***et al.*** (2015) and Yashoda ***et al.*** (2016).

4.4 Genetic diversity analysis

Twenty-nine blackgram (*Vigna mungo* L.) genotypes were evaluated for ten characters to study the divergence and the data obtained was subjected to D^2 analysis. The genetic diversity of blackgram (*Vigna mungo* L.) advanced lines is presented in Table 9 to 12 and Figure 3 and 4.

4.4.1 Principal component analysis (PCA)

The PCA gives Eigen values of principal component axes of coordination of genotypes with the first axes totally accounted for the variation among the genotypes, whereas three of these Eigen values above unity accounted for 80.07% (Table 9). The first two principal axes accounted for 70.84% of the total variation among the characters describing 29 advanced lines of blackgram (*Vigna mungo* L.) genotypes. According to the principal axes I (Z_1) and II (Z_2), a two-dimensional chart ($Z_1 - Z_2$) of the genotypes. The scatter diagram revealed that there were five apparent clusters. The genotypes were distantly located from each other (Figure 3 and 4).

Table 9. Eigen values and percentage of variation in respect of 10 characters in blackgram (*Vigna mungo* L.) genotypes

Principal component axis	Eigen values	% of total variation accounted for	Cumulative percent
I	4.374	43.74	43.74
II	2.710	27.10	70.84
III	0.923	9.23	80.07
IV	0.708	7.08	87.15
V	0.574	5.74	92.89
VI	0.384	3.84	96.73
VII	0.175	1.75	98.48
VIII	0.095	0.95	99.43
IX	0.038	0.38	99.81
X	0.019	0.19	100.00

4.4.2 Non-hierarchical clustering

Twenty-nine blackgram (*Vigna mungo* L.*)* genotypes were grouped into five different clusters nonhierarchical clustering (Table 10). These results confirmed the clustering pattern of the genotypes obtained through principal component analysis. Based on the divergence Umadevi *et al*. (2007) grouped sixty genotypes of black gram into four clusters, Chauhan *et al*. (2008) studied 210 true breeding lines of urdbean and were grouped into nine different clusters, Elangaimannan *et al*. (2008) studied 55 genotypes of black gram were grouped into seven clusters, Venkateswarlu *et al*. (2011) investigated 70 accessions of black gram through D^2 statistics and grouped them into six clusters and Singh *et al*. (2012) studied 75 genotypes of black gram and grouped them in to six clusters. Similarly, Vinod *et al*. (2017) investigated 40 genotypes of black gram and distributed them in to seven clusters. Under the present study, cluster I had the highest number of genotypes (12) followed by II and III which had 6 genotypes each. On the other hand, cluster IV and V had 2 and 3 genotypes respectively (Table 10).

Table 10. Distribution of 29 blackgram (*Vigna mungo* L.) genotypes in five different clusters

Cluster	Total number of lines	Genotype Number	Genotype designation
I	12	G11, G13, G14, G17, G18, G19, G21, G22, G23, G26, G27, G29	BD-6853, BD-6857, BD-6859, BD-6863, BD-6865, BD-6866, BD-6871, BD-6872, BD-6873, BARI-3, BARI-4, BARI-2
II	6	G1, G2, G6, G7, G12, G15	BD-6814, BD-6831, BD-6839, BD-6840, BD-6855, BD-6860
III	6	G3, G4, G8, G10, G25, G28	BD-6833, BD-6836, BD-6841, BD-6848, BD-10038, BARI-1
IV	2	G9, G24	BD-6847, BD-10036
V	3	G5, G16, G20	BD-6838, BD-6861, BD-6867

Table 11. Cluster means for 10 characters of 29 blackgram (*Vigna mungo* L.) genotypes

Characters	Cluster				
	I	**II**	**III**	**IV**	**V**
PH	75.22	109.96	128.95	118.89	125.47
NBP	5.75	6.41	5.81	4.83	6.96
DFF	31.19	39.06	41.28	38.17	39.33
D50%F	37.14	43.72	45.11	43.33	43.44
D80%M	73.75	78.33	77.33	75.17	76.67
PL	4.58	4.49	4.47	4.37	4.75
NPP	78.03	86.05	84.61	53.50	110.44
NSP	6.66	7.00	6.82	6.33	7.38
100 SW	4.00	3.20	3.30	3.35	3.10
YPP	20.63	19.38	19.39	11.89	25.75

PH = Plant height (cm), NPB = Number of branches per plant, DFF = Days to first flowering, D50%F = Days to 50% flowering, D80%M = Days to 80% maturity, PL = Pod length (cm), NPP = Number of pods per plant, NSP = Number of seeds per pod, 100 SW = 100 seed weight (g), YPP = Yield per plant

According to the cluster means (Table 11), cluster III had higher cluster mean of plant height (128.95 cm) and cluster I had lower cluster mean of plant height (75.22 cm) which indicates that genotype of these cluster could be used for parent in future hybridization program for higher or lower plant height.

Again, cluster V showed better performance on number of branches per plant (6.96), pod length (4.75 cm), number of pods per plant (110.44), number of seeds per pod (7.38) and yield per plant (25.75 g). It indicated the genotype of this cluster could be used for future hybridization program for higher yield per plant through increased number of branches per plant, pod length, number of pods per plant and number of seeds per pod.

Similarly, Cluster I had higher cluster mean of 100 seed weight (4.00 g) which indicates that genotype of this cluster could be used for parent in future hybridization program for increasing 100 seed weight of blackgram.

Likewise, cluster I showed better performance in case of lower days to first flowering (31.19 days), days to 50% flowering (37.14 days) and days to 80% maturity (73.75 days). Thus, indicates that genotype of this cluster could be used as parent in future hybridization program for early flowering and maturity.

The genotypes included in cluster IV which had lower number of branches per plant (4.83), lower pod length (4.37 cm), number of pods per plant (53.50), number of seeds per pod (6.33) and yield per plant (11.89 g) while cluster IV had lower 100 seed weight (3.10 g). It indicated the genotype of these clusters could be considered as to be improved in future hybridization program for higher yield on selected aspects.

Moreover, cluster III had higher cluster mean for days to first flowering (41.28 days), days to 50% flowering (45.11 days) and days to 80% maturity (77.33 days) suggested that this cluster composed of late flowering genotypes.

4.4.3 Canonical variate analysis (CVA)

Canonical Variate Analysis (CVA) was done to compute the inter-cluster distances. The intra and inter-cluster distance (D^2) values were shown in Table 12. In this experiment, the inter-cluster distances were higher than the intra-cluster distances thus indicating broader genetic diversity among the genotypes of different groups. Sohel et al. (2016) reported that the inter-cluster distances were larger than the intra-cluster distances.

The highest inter-cluster distance was observed between clusters I and V (60.988), followed by between cluster IV and V (59.056), I and III (55.769), I and IV (51.723) and I and II (37.421). In contrast, the lowest inter-cluster distance was observed between cluster II and III (19.257) (Table 12 and Figure 3 and 4). However, the maximum inter-cluster distance was observed between the clusters I and V (60.988) indicating genotypes from these two clusters, if involved in hybridization may produce a wide spectrum of segregating population.

Table 12. Average intra and inter-cluster distances (D^2) for 29 blackgram (*Vigna mungo* L.) genotypes

Cluster	**I**	**II**	**III**	**IV**	**V**
I	**0.118**	37.421	55.769	51.723	60.988
II		**0.204**	19.257	34.776	29.657
III			**0.112**	33.824	26.995
IV				**0.256**	59.056
V					**0.127**

*Bold figures denote intra-cluster distance

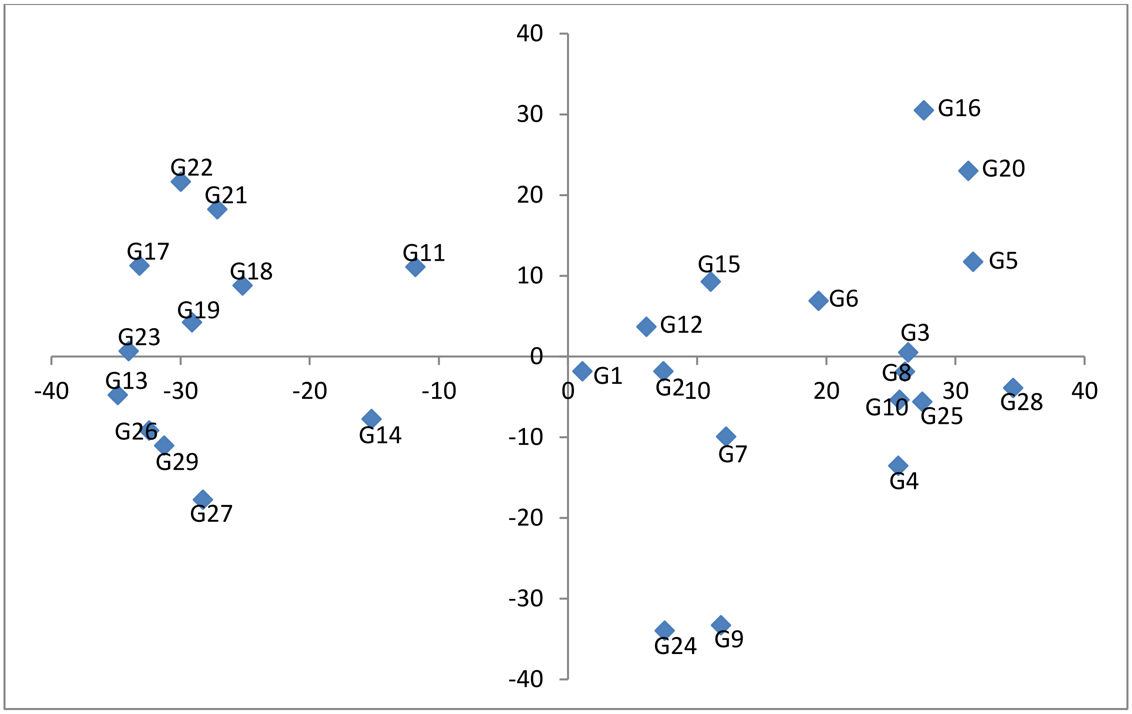

Figure 3. Scattered distribution of 29 blackgram (*Vigna mungo* L.) genotypes on principal component score

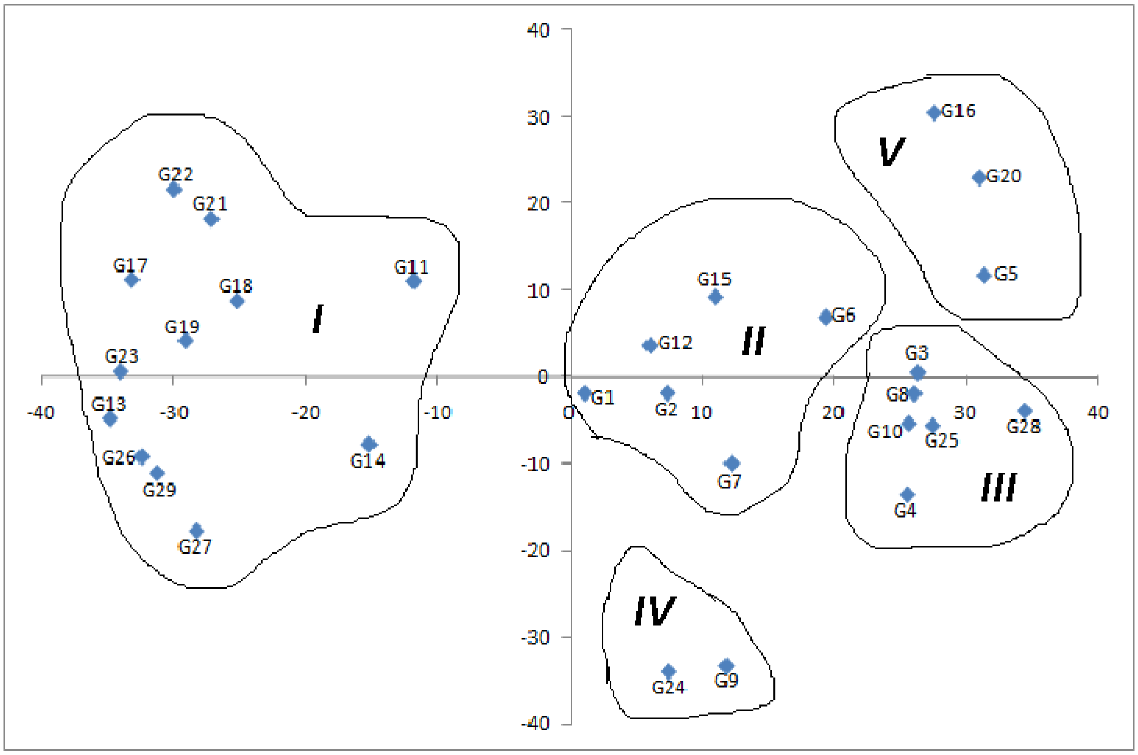

Figure 4. Scattered distribution of 29 blackgram (*Vigna mungo* L.) genotypes on principal component score superimposed with clustering

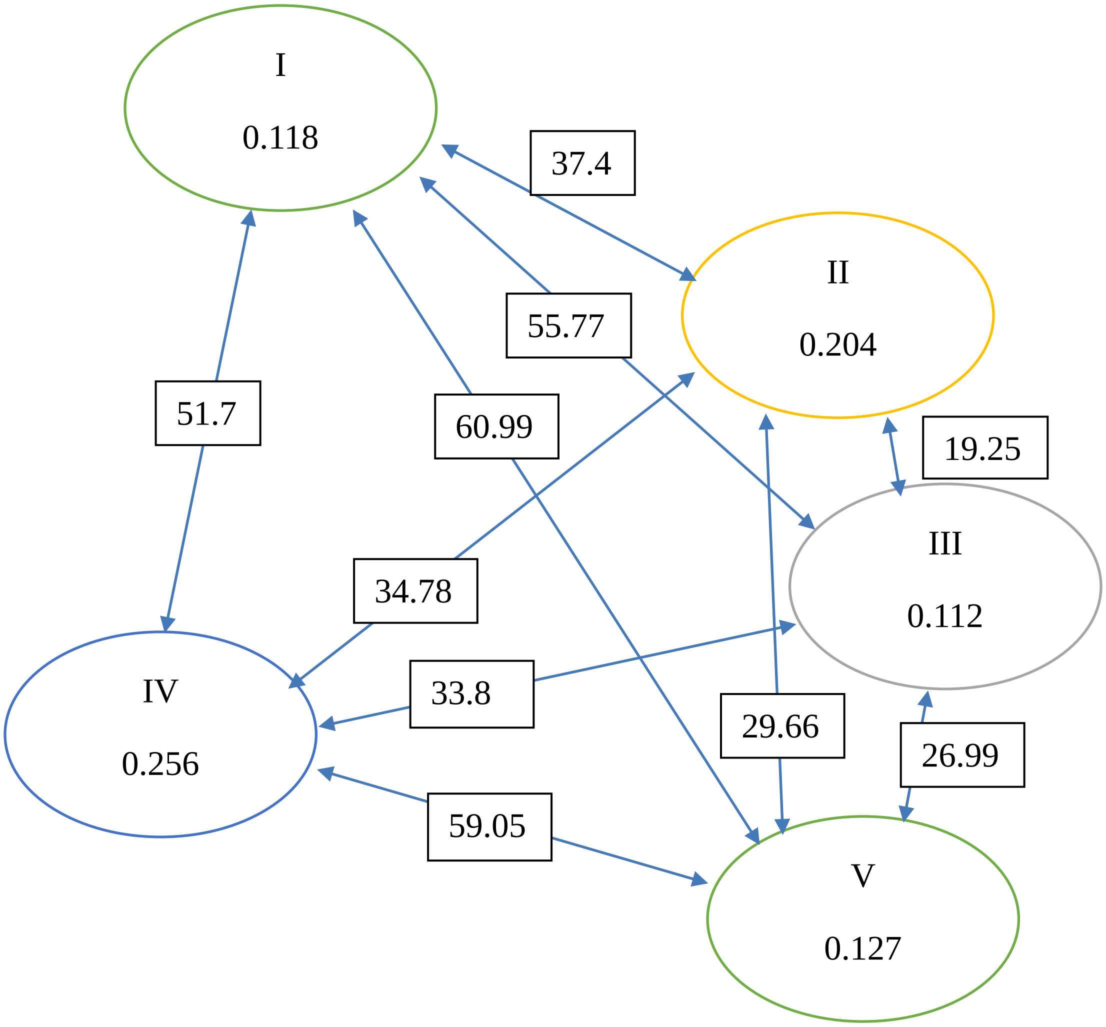

Figure 5. Intra and inter cluster distances of 29 genotypes in Blackgram

On the other hand, the maximum intra-cluster distance was found in cluster IV (0.256), which contained of 2 genotypes, while the minimum distance was found in cluster III (0.112) that comprises 6 genotypes. The different multivariate analysis was superimposed in Figure 3 and 4 from which it could be concluded that different multivariate techniques supplemented and confirmed one another.

A two-dimensional scatter diagram was constructed using component I as X-axis and component II as Y-axis, showing in the relative position (Figure 3). According to scatter diagram all the genotypes were apparently distributed into five clusters. It is assumed that the maximum amount of heterosis will be manifested in cross combination involving the genotypes belonging to most divergent clusters. Furthermore, for a practical plant breeder, the objective is to achieve high-level production in addition to high heterosis. Savithramma et al. (1999) reported that the parents separated by D^2 values of moderate magnitude generally showed higher heterosis.

Keeping this in view, it appeared that the crosses between the genotypes belonging cluster I with cluster V, cluster IV with cluster V, cluster I with cluster III and cluster I with cluster IV might produce high heterosis in respect of yield, earliness, tallness, higher number of pods per plant and seeds per pod which resulted higher yield per plant.

Also, the crosses between genotypes from cluster I with cluster V might produce high level of segregating population. So, the genotypes belonging to cluster V, cluster IV, cluster I, cluster III and cluster II have been selected for future hybridization program.

4.4.4 Contribution of traits towards divergence of the genotypes

The latent vectors (Z_1 and Z_2) obtained from principal component analysis (PCA). The important characters responsible for genetic divergence in the axis of differentiation in vector I (Z_1) were number of branches per plant (2.71), pod length (0.384), number of pods per plant (0.175), number of seeds per pod (0.095), days to first flowering (0.923) and seed yield per plant (0.019).

In the role of seed yield per plant in both vectors was important components for genetic divergence in these materials. On the other hand, the role of days to first flowering had a minor role in the genetic divergence. Gowsalya *et al*. (2017) and Mahesha *et al*. (2017) reported that the trait hundred seed weight had highest contribution to genetic divergence. Choudhury and Joshi (2001) concluded that plant height, secondary branches per plant, days to 1st flowering and 1000-seed weight contributed the maximum towards genetic divergence.

4.4.5 Selection of parents for future hybridization

Selection of genetically diverse parents is the principal task for any plant breeding activities. Therefore, considering the magnitude of genetic distance, contribution of character towards divergence, magnitude of cluster mean and agronomic performance the genotypes G16 (BD-6861) for higher seed yield per plant, number of seeds per pod, number of pods per plant and number of branches per plant, G27 (BARI-4) for higher 100 seed weight, pod length, early days to 1st flowering, 50% flowering and days to 80% maturity and G28 (BARI-1) for tallness were considered. Therefore, considering diversity pattern and other agronomic performance, the lines G16 (BD-6861), G27 (BARI-4) and G28 (BARI-1) could be considered as suitable genotypes for efficient hybridization in future. Involving of such diverse lines in crossing program could produce desirable segregants. So, more or less divergent genotypes might be suggested for future hybridization program.

CHAPTER V

SUMMARY AND CONCLUSION

A field experiment was conducted with 29 blackgram (*Vigna mungo* L.) genotypes, raised in randomized block design with three replications during August to November 2019 at the experimental farm of department of genetics and plant breeding, Sher-e-Bangla Agricultural University, Dhaka to assess character association and genetic diversity analysis. Data on various yield attributing characters such as, plant height (cm), number of branches per plant, days to first flowering, days to 50% flowering, days to 80% maturity, pod length (cm), number of pods per plant, number of seeds per pod, 100 seed weight (g) and yield per plant were recorded.

From variability analysis of blackgram genotypes, it was observed that significant variation exists among all the genotypes used for most of the characters studied. Plant height exhibited the highest in G28 (BARI-1) and the lowest in G17 (BD-6863). The highest number of branches per plant was recorded in G16 (BD-6861) and lowest number was recorded in G24 (BD-10036). The minimum days to days to first flowering, the minimum days to 50% flowering and minimum days to 80% maturity was found in G27 (BARI-4) whereas the maximum days to days to first flowering and the maximum days to 50% flowering was found in G2 (BD-6831) and the maximum days to 80% maturity was found in G7 (BD-6840). The maximum pod length and 100 seed weight was recorded from G27 (BARI-4) but the highest number of pods per plant, number of seeds per pod and seed yield per plant were recorded from G16 (BD-6861) whereas the lowest pod length, number of pods per plant, number of seeds per pod, 100 seed weight and seed yield per plant were found in G24 (BD-10036).

However, the phenotypic variance and phenotype coefficient of variation were higher than the corresponding genotypic variance and genotypic coefficient of variation for all the characters under the present study.

In case of plant height and number of pods per plant, this showed higher influence of environment for the expression of these characters. On the other hand, number of branches per plant, days to first flowering, days to 50% flowering, days to 80% maturity, pod length, number of seeds per pod, 100 seed weight and seed yield per plant showed least difference between phenotypic and genotypic variance suggesting additive gene action for the expression of the characters.

100 seed weight exhibits the highest value of heritability (99.54) while number of seeds per pod exhibits the lowest value of heritability (22.81). High heritability with high genetic advance in percent of mean was observed for plant height, number of branches per plant, days to first flowering, number of pods per plant, 100 seed weight and yield per plant indicating that these traits were under additive gene control and selection for genetic improvement for these traits would be effective. High heritability with moderate genetic advance in percent of mean was observed for days to 50% flowering, indicating medium possibility of selecting genotypes. High heritability with low genetic advance in percent of mean was observed for days to 80% maturity indicating that non-additive gene effects were involved for the expression of these characters and selection for such traits might not be rewarding.

Correlation coefficients among the characters were studied to determine the association between yield and yield components. In general, most of the characters showed the genotypic correlation co-efficient were higher than the corresponding phenotypic correlation co-efficient suggesting a strong inherent association between the characters under study and suppressive effect of the environment modified the phenotypic expression of these characters by reducing phenotypic correlation values. In few cases, phenotypic correlation co-efficient were 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. The significant positive correlation with seed yield per plant were found in number of branches per plant (G=0.519, P=0.342), pod length (G=0.732, P=0.367), number of pods per plant (G=0.758, P=0.709), number of seeds per pod (G=0.691, P=0.354) and 100 seed weight (G=0.240, P=0.223). In addition, there were non-significant positive correlation with seed yield per plant was also found in days to 80% maturity (G=0.198, P=0.192) whereas non-significant negative correlation with seed yield per plant was found in plant height (G=-0.101, P=-0.080), days to first flowering (G=-0.083, P=-0.099) and days to 50% flowering (G=-0.167, P=-0.148).

Path co-efficient analysis revealed that plant height, number of branches per plant, days to 50% flowering, days to 80% maturity, pod length, number of pods per plant, number of seeds per pod and 100 seed weight had the positive direct effect on yield per plant whereas days to first flowering had the negative direct effect on yield per plant. The genotypic correlation of number of branches per plant, pod length, number of pods per plant, number of seeds per pod and 100 seed weight with seed yield per plant was positive and considerably higher in magnitude. It is mainly due to high positive direct effect and positive indirect effects of other characters and selection would be effective for this trait. The path coefficient studies indicated that plant height, number of branches per plant, days to 50% flowering, days to 80% maturity, pod length, number of pods per plant. number of seeds per pod and 100 seed weight were the most important contributors to seed yield per plant which could be taken in consideration for future hybridization program.

Genetic diversity among black gram (*Vigna mungo* L.) genotypes was performed through Principal Component Analysis (PCA), Cluster Analysis, Canonical Variate Analysis (CVA) using GENSTAT computer program. The first three principal component axes accounted for 80.07% variation towards the divergence. Among five clusters, cluster I individually contained maximum number of genotypes (12) while cluster IV had only two genotypes.

According to PCA, D^2 and cluster analysis, the genotypes grouped into five divergent clusters using Z_1 and Z_2 values obtained from principal component scores. The highest inter-cluster distance was observed between clusters I and V (60.99) indicating genotypes from these two clusters, if involved in hybridization may produce a wide spectrum of segregating population while the lowest inter-cluster distance was observed between cluster II and III (19.26). On the other hand, the maximum intra-cluster distance was found in cluster IV (0.256), which contained of 2 genotypes, whereas the minimum distance was found in cluster III (0.112) that comprises 6 genotypes. Therefore, crossing between the genotypes cluster I with cluster V, cluster IV with cluster V, cluster I with cluster III and cluster I with cluster IV might produce high heterosis in respect of yield, earliness, tallness, higher number of pods per plant. Also, the crosses between genotypes from cluster I with cluster V might produce high level of segregating population. So, the genotypes belonging to cluster V, cluster IV, cluster I, cluster III and cluster II have been selected for future hybridization program.

Considering the magnitude of genetic distance, contribution of character towards divergence, magnitude of cluster means and agronomic performance, the genotypes G16 (BD-6861) for higher seed yield per plant, number of seeds per pod, number of pods per plant and number of branches per plant, G27 (BARI-4) for higher 100 seed weight, pod length, early days to 1st flowering, 50% flowering and days to 80% maturity and G28 (BARI-1) for tallness were considered.

CONCLUSION

Therefore, considering diversity pattern and other agronomic performance, the lines G16 (BD-6861), G27 (BARI-4) and G28 (BARI-1) could be considered as suitable genotypes for efficient hybridization in future.

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APPENDICES

Appendix I. Argo-Ecological Zone (AEZ) of Bangladesh showing the experimental location

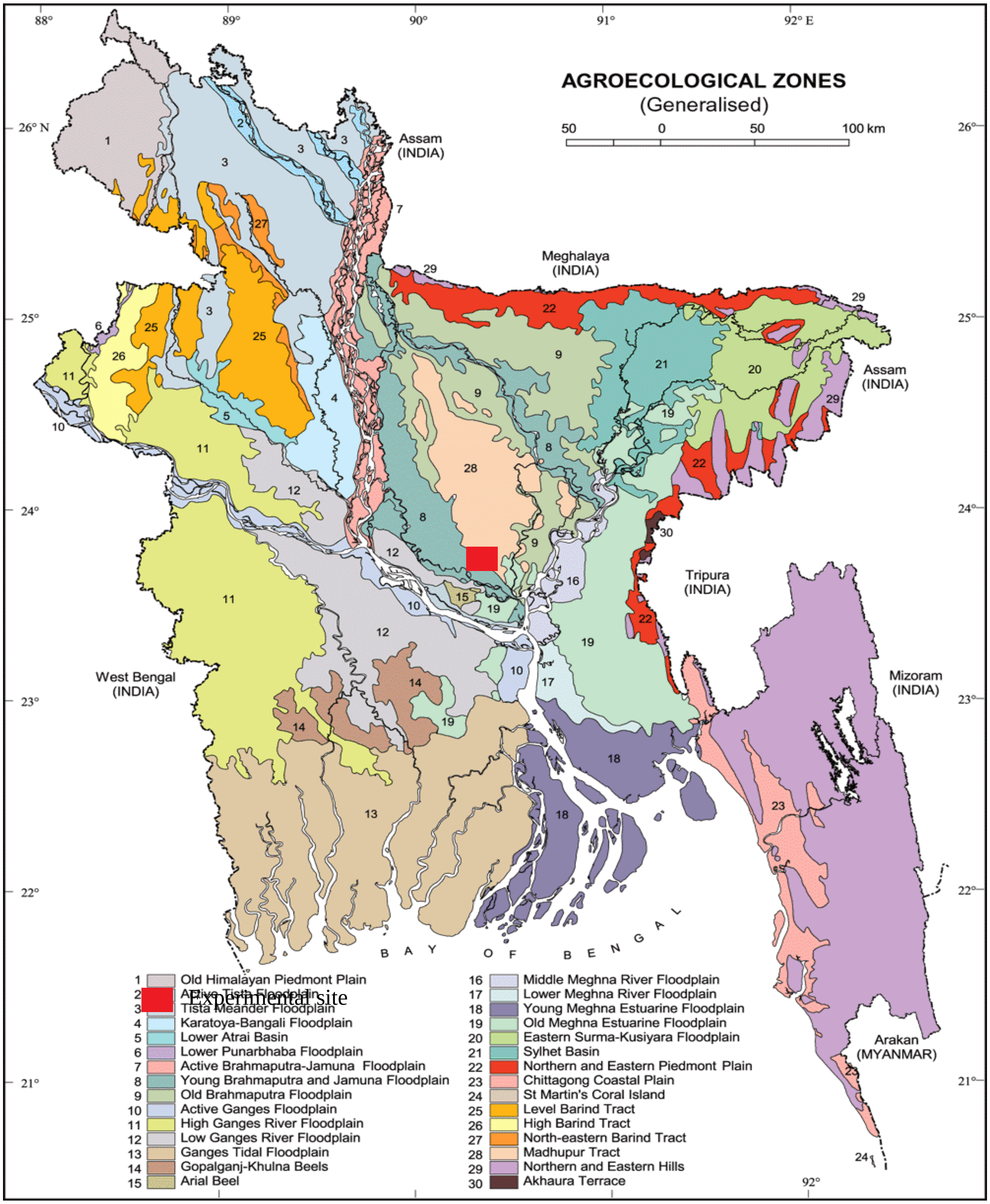

Figure 6. Experimental site

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

A. Physical composition of the soil

Soil separates	%	Methods employed
Sand	36.90	Hydrometer method (Day, 1965)
Silt	26.40	Do
Clay	36.66	Do
Texture class	Clay loam	Do

B. Chemical composition of the soil

Sl. No.	Soil characteristics	Analytical data	Methods employed
1	Organic carbon (%)	0.82	Walkley, 1947
2	Total N (kg/ha)	1790.00	Bremner and Mulvaney, 1982
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	pH (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 August to November 2019.

Year	Month	Air temperature (°C)			Relative humidity (%)	Rainfall (mm)
		Max	*Min*	*Mean*		
2019	August	31.00	25.60	28.30	80.00	348
2019	September	30.8	21.80	26.30	71.50	78.52
2019	October	30.42	16.24	23.33	68.48	52.60
2019	November	28.60	8.52	18.56	56.75	14.40

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

Appendix IV. Principal component score for 29 blackgram (*Vigna mungo* L.) genotypes

Genotype no.	Z1	Z2
G1	1.131	-1.843
G2	7.406	-1.813
G3	26.363	0.519
G4	25.588	-13.544
G5	31.39	11.738
G6	19.407	6.90
G7	12.258	-9.943
G8	26.101	-1.883
G9	11.87	-33.276
G10	25.691	-5.347
G11	-11.814	11.085
G12	6.081	3.668
G13	-34.839	-4.76
G14	-15.194	-7.734
G15	11.065	9.263
G16	27.572	30.499
G17	-33.165	11.25
G18	-25.184	8.791
G19	-29.102	4.251
G20	31.014	23.015
G21	-27.133	18.232
G22	-29.962	21.657
G23	-34.017	0.657
G24	7.492	-33.964
G25	27.454	-5.594
G26	-32.424	-9.164
G27	-28.268	-17.727
G28	34.476	-3.886
G29	-31.257	-11.05