Study on Genetic Diversity and Character Association of Yield and Its Components in Black Gram (*Vigna mungo* L. Hepper)

THESIS

Submitted to the

Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya

In partial fulfillment of the requirements for the Degree of

MASTER OF SCIENCE

In

AGRICULTURE

PLANT BREEDING AND GENETICS

by

NITESH KUMAR PANWAR

Department of Plant Breeding and Genetics
Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior
College of Agriculture, Indore (M.P.)

2017

CERTIFICATE – I

This is to certify that the thesis entitled **“Study on Genetic Diversity and Character Association of Yield and Its Components in Black Gram (*Vigna mungo* L. Hepper)”** submitted in partial fulfillment of the requirements for the Degree of **Master of Science in Agriculture** in the Department of **Plant Breeding and Genetics** of Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior (M.P.) is a record of the bona-side research work carried out by **Mr. Nitesh Kumar Panwar,** I.D. No. RH/MS/246/2011 under my guidance and supervision. The subject of the thesis has been approved by the Student’s Advisory Committee and the Director of Instruction.

No part of the thesis has been submitted for any other degree or diploma or has been published. All the assistance and help received during the course of this investigation have been acknowledged by the scholar.

Place - Indore

Date -

Signature

Dr. Indu Swarup

Chairman of the Advisory Committee

MEMBER OF STUDENT’S ADVISORY COMMITTEE

Chairman - (Dr. Indu Swarup) …………………….

Member - (Dr. Jagdish Singh) …………………….

Member - (Dr. S. Holkar) …………………….

Member - (Dr. R.K. Singh) …………………….

CERTIFICATE – II

This is to certify that the thesis entitled **“Study on Genetic Diversity and Character Association of Yield and Its Components in Black Gram (*Vigna mungo* L. Hepper)”** submitted by **Mr. Nitesh Kumar Panwar,** I.D. No. RH/MS/246/2011 to the Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior (M.P.) for the degree of **Master of Science in Agriculture** in the Department of **Plant Breeding and Genetics** has been accepted after evaluation by the External Examiner and approved by the Student’s Advisory Committee after an oral examination of the same.

Place- Indore

Date - Signature

(Dr. Indu Swarup)

Chairman Advisory Committee

MEMBERS OF THE ADVISORY COMMITTEE

Chairman (Dr. Indu Swarup) ……………………….

Member (Dr. Jagdish Singh) ……………………….

Member (Dr. S. Holkar) ……………………….

Member (Dr. R.K. Singh) ……………………….

Head of the Department (Dr. Jagdish Singh) ……………………….

Dean of the college (Dr. Ashok Krishna) ……………………….

Director of Instruction (Dr. B. S. Baghel) ……………………….

ACKNOWLEDGEMENT

I avail this opportunity to express my deep sense of gratitude to my respectable Advisor and Guide and Chairman of the Advisory Committee **Dr. Indu Swarup**, Senior Scientist, Department of Plant Breeding and Genetics, College of Agriculture, Indore for this illuminating guidance, and encouragement and generous help throughout the course of investigation.

I extend my sincere gratitude to other member of my advisory committee **Dr. Jagdish Singh** (HOD), Principal Scientist, Department of Plant Breeding and Genetics, **Dr. S. Holkar,** Associate Professor, Department of Plant Breeding and Genetics and **Dr. R.K. Singh**, Assistant Professor Department of Plant Pathology for their precious suggestions and helping attitude during the research work.

With profound respect, I wish to express my sincere gratitude to **Prof. A.K. Singh,** Hon'ble Vice Chancellor of RVSKVV Gwalior, **Dr. B.S. Baghel,** Director of Instructions of RVSKVV Gwalior, **Dr. H.S. Yadav** Director Research Service of RVSKVV Gwalior, **Dr. Mridula Billore,** Dean Faculty, RVSKVV Gwalior and **Dr. A. Krishna**, Dean, College of Agriculture, Indore (M.P.), for providing necessary facilities during the experiment.

I thank to all my friends Mayank Jain, Ajay Kadi, Gauri Shankar, Pooja Puri, Nitika Patidar, Lokendra Singh, Kishan Singh and others, those helped me directly or indirectly during course of investigation. My special thanks to Shri Ramchandra Ji, and Shri Ashok Ji for their thankful help at field.

I don't have world to express my deep sense of gratitude to my father Shri Lalit Kumar Panwar, mother Smt. Radha Devi and sister Ms. Vibha Panwar whose sacrifices, blessings, encouragement, love and devotion have made my education possible.

Place: Indore **(Mr. Nitesh Kumar Panwar)**

Date:

List of Contents

List of Tables/ Graphs

List of Abbreviation

S.N.	**Abbreviation/Symbol**	**Stands for**
1	ANOVA	Analysis of Variance
2	PCV	Phenotypic coefficient of varation
3	GCV	Genotypic coefficient of varation
4	σ_p	Phenotypic standard deviation
5	h^2_{bs}	Heritability in Broad sence
6	GAM	Genetic advance as percent of mean
7	r_{xy}	Correlation coefficient between character x and y.
8	V(x)	Variance of character x.
9	V(y)	Variance of character y.
10	r_{1y} to r_{ly}	Coefficient of correlation between causal factor 1 to I and dependent character y
11	r_{12} to $r\ l_{-1,}l$	Coefficient of correlation among causal factors themselves
12	P_{1y} to P_{ly}	Direct effects of characters 1 to I on character y.
13	*et al.*	And others / Co- workers
14	*Viz.*	Namely
15	*Via*	Indirectly through
16	C.D.	Critical Difference
17	C.V.	Coefficient of Variation
18	d.f.	Degree of Freedom
19	S.Em.±	Standard error of mean
20	*i.e.*	That is
21	R	Total Number of Replication
22	SMW	Standard Meteorological week

CHAPTER- I

INTRODUCTION

Black gram (*Vigna mungo* (L.) Hepper), popularly known as urd bean, urid or mash is an important self-pollinating diploid grain legume and belongs to the family Fabaceae. The somatic chromosome number of this crop is 2n=22. It is grown mainly in rainy and/or summer seasons. The total area under black gram was 2.50 million hectares with 1.02 million tonnes of production and 410 kg/ha productivity in India (Anonymous, 2014-15). Black gram occupied an area of 0.86 million hectares with 0.35 million tonnes production and 410 kg/ha productivity in the state Madhya Pradesh (Anonymous, 2014-15).

The productivity of urd bean in the state as well as in India is very low due to various constraints like; non-availability of quality seed of high yielding variety, seeds germinate in mature pod itself if there is rains at maturity time of crop and the crop is highly sensitive to high intensity rains etc., all such factors cause heavy losses in terms of yield. Thus, the crop requires due attention to increase its production and productivity.

The existence of genetic variability is the prerequisite for crop improvement programme. Yield is a complex quantitative trait which cannot be improved by selecting individuals on *per se* performance basis. Thus, it can be improved by practicing selection for other traits which are highly heritable and are interrelated with the yield as well.

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 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.

Heritability along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone. The estimates of heritability help the plant breeder in selection of elite genotypes from genetically diverse populations. Genetic advance refers to the improvement in the mean genotypic value of selected individuals over the parental population and it helps in understanding the type of gene action involved in the expression of various polygenic characters. It also helps in deciding a breeding procedure for the genetic improvement of various polygenic traits by determining the gene action.

The yield is a complex character and governed by a large number of genes with negligible individual gene effects and largely influenced by environmental factors. As such, yield can be improved indirectly by considering the different yield contributing traits. Thus, the selection based on yield components would be effective for yield improvement. The knowledge of direct and indirect influence of yield contributing characters is of prime importance to select high yielding genotypes.

The correlation coefficient and path-coefficient analysis provide the information on the relative importance of various yield-contributing characters and thus, increases the efficiency of selection for higher yields based on yield components. Correlation coefficient analysis measures the mutual relationship between various plant characters and determines the components characters on which selection can be based for genetic improvement of yield. Path analysis splits the correlation coefficient into the measures of direct and indirect effects and determines the direct and indirect contribution of various characters towards yield.

Hybridization programme gives an opportunity to create wide spectrum of genetic variability. Black gram is a self-pollinated crop and lacked in genetic variability. Therefore choice of diverse parents for hybridization was 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 most effective and therefore, widely used for the classification of parental lines. The D^2 statistics evaluates large number of germplasm lines for genetic diversity and helps in the identification of genetically divergent genotype for their exploitation in hybridization programmes.

Further, the genetically diverse strains were required for hybridization programme, so the development of high yielding urd bean genotypes to enhances genetic diversity/variability. Thus, the present investigation was carried out with following objectives:-

1. To study the extent and nature of genetic variability existing in the population for seed yield and its contributing traits.
2. To identify the yield components through character association and path analysis.
3. To study the genetic divergence for selection of genetically diverse genotypes to be used as parents in hybridization programme.

CHAPTER - II

REVIEW OF LITERATURE

The relevant literatures pertaining to various aspects of present study were reviewed under the following heads.

2.1 Genetic variability

2.2 Heritability and Genetic advance

2.3 Correlation coefficient and Path coefficients analysis

2.4 Genetic divergence analysis

2.1. Genetic variability:-

Veeramani *et al.* (2005) reported high estimates PCV and GCV for plant height, number of branches per plant, number of seeds per pod and seed yield per plant.

Konda *et al.* (2009) recorded high estimates of GCV for plant height and hundred seed weight. Moderate GCV estimates were observed for days to 50% flowering, length of reproductive period and grain yield per plant.

Neelavathi and Govindarasu (2010) reported high genotypic variability for branches per plant, clusters per plant, pods per plant, biological yield and seed yield.

Senapati and Mishra (2010) studied the nature and magnitude of induced variability among the selected mutant cultures derived from 15 different mutagenic treatments. The magnitude of PCV and GCV were reported high for different traits which would be effective in isolation of different mutant lines with improvement for 100-seed weight, days to 50% flowering and pods per plant.

Meshram *et al.* (2013) recorded the highest GCV and PCV for number of pods per plant and grain yield per plant.

Deepshikha *et al.* (2014) recorded that high PCV for number of pods per plant, plant height at maturity and grain yield per plant while high GCV for number of pods per plant and grain yield per plant.

Patel *et al.* (2014) recorded that the highest GCV and PCV for grain yield per plant followed by number of pods per plant and number of cluster per plant.

Punia *et al.* (2014) observed wide range of variability for quantitative traits and reported that plant height, primary branches per plant and pods per plant showed high genetic variability.

Ramya *et al.* (2014) recorded high estimates of PCV and GCV for primary branches per plant, number of clusters per plant, number of pods per plant and single plant yield.

Kumar *et al.* (2015) evaluated 57 genotypes including 42 F1 hybrids and their 17 parents (14 lines, 3 testers) for 14 quantitative character. The analysis of variance revealed highly significant differences for all the 14 characters indicating presence of genetic variability among lines, testers, and hybrids. The highest GCV and PCV were recorded for pod weight followed by pods per plant, seeds per plant, plant height and seed yield.

Gowsalya *et al*. (2016) recorded the highest GCV for number of branches per plant, seed yield per plant, number of clusters per plant, branch length, number of pods per plant and plant height.

Priyanka *et al.* (2016) observed the genetic variability of quantitative and qualitative traits in 24 lines of black gram. The genotypes were highly variable for cluster per plant, pods per plant, seeds per pod and seed yield per plant. In general PCV was greater than their corresponding GCV.

2.2. Heritability and Genetic advance–

Konda *et al.* (2009) observed very high heritability for days to 50% flowering, days to maturity, plant height, length of reproductive period, 100-seed weight, protein content and crude fiber content. High genetic advance as per cent of mean was observed for plant height, crude fiber content, 100-seed weight and days to 50% flowering indicating that these traits were under the control of additive gene effects.

Neelavathi and Govindarasu (2010) recorded that high genotypic variability for branches per plant, clusters per plant, pods per plant, biological yield and seed yield along with high heritability and genetic advance.

Meshram *et al.* (2013) recorded high estimate of heritability for number of pods per plant and grain yield per plant.

Reni *et al.* (2013) reported higher estimate of heritability and genetic advance as percent of mean for grain yield (97.0%, 79.93%), pods per plant (91.0%, 65.50%) and plant height (78.0%, 31.74%).

Deepshikha *et al.* (2014) recorded that high heritable value coupled with high genetic advance as percent of mean for number of pods per plant, number of clusters per plant, number of seeds per pod, seed index and grain yield per plant.

Mandal and Majumdar (2014) observed presence of moderate magnitude of heritability in broad sense, genetic advance as percentage of mean, PCV and GCV in respect of seeds per pod, plant height and yield.

Patel *et al.* (2014) recorded high genetic advance coupled with high heritability for grain yield per plant, number of pods per plant and number of clusters per plant.

Ramya *et al.* (2014) revealed high heritability % and high genetic advance as % of mean for number of primary branches per plant and seed yield per plant.

Kumar *et al.* (2015) recorded the high heritability and genetic advance for days to 50% flowering and clusters per plant. High genetic advance as per cent of mean coupled with moderate to high heritability was reported for number of clusters per plant, pods per plant, seeds per plant, pod weight, seed yield per plant and fodder biomass.

Gowsalya *et al*. (2016) recorded high heritability for branch length, number of branches, plant height, clusters per plant, seed yield per plant, number of pods per plant and pod length. The highest genetic advance as per cent of mean was recorded for number of branches, seed yield per plant, cluster per plant, branch length, pods per plant and plant height. High heritability coupled with high genetic advance was observed for branch length, number of branches, plant height, clusters per plant, seed yield per plant and number of pods per plant.

Priyanka *et al.* (2016) recorded high heritability coupled with high GAM for pods per cluster, pod length, test weight, seeds per pod and seed yield per plant.

2.3. Correlation coefficient and Path coefficient analysis–

Chauhan *et al.* (2007) reported that seed yield per plant showed very strong positive association with pods per plant, number of clusters per plant, biological yield per plant, seeds per pod, harvest index, plant height, pods per cluster and primary branches per plant. Path analysis suggested the pods per plant followed by the seeds per pod, 100-seed weight and biological yield per plant as the major direct contributors towards expression of seed yield per plant.

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.

Ali *et al.* (2008) observed that characters *viz.,* pods per plant, pod length, seeds per pod and 100-seed weight were significantly and positively correlated with seed yield per plant. Similarly, the characters namely number of pods per plant, and 100-seed weight and number of seeds per pod exhibited positive association coupled with positive direct effect on seed yield per plant at both phenotypic and genotypic level.

Konda *et al.* (2008) revealed that the branches per plant, clusters per plant, pods per plant, seeds per pod, pod length and 100-seed weight exhibited significant and positive correlation with yield per plant. These characters also reported positive direct effect on yield per plant.

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.

Neelavathi and Govindarasu (2009) reported that characters biological yield and harvest index recorded strong positive correlation as well as high positive direct effects on seed yield.

Babu *et al.* (2010) revealed that significant positive correlation of clusters per plant with pods per plant and pods per cluster with pods per plant.

Parveen *et al.* (2011) recorded significant positive association of pods per plant, harvest index and clusters per plant with seed yield in parental germination 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.

Shivade *et al.* (2011) observed 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 levels.

Bharti *et al.* (2013) recorded a very strong positive association of grain yield per plant with number of clusters per plant, number of pods per cluster, number of seeds per pod, biological yield per plant and harvest index.

Pushpa *et al.* (2013) showed that pods per plant and plant height had highly significant genotypic and phenotypic correlation with grain yield.

Reni *et al.* (2013) observed that pods per plant, 100-seed weight, days to maturity and days to 50% flowering had positive direct effect on grain yield. 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.

Panigrahi *et al.* (2014) reported genetic variation and degree of association among yield and yield contributing traits were essential for developing high yielding genotypes in black gram.

Patel *et al.* (2014) recorded that grain yield per plant was positively and significantly correlated with days to 50% flowering, days to maturity, number of branches per plant, number of clusters per plant, number of pods per plant, number of seeds per pod, pod length and 100-seed weight.

Punia *et al.* (2014) revealed that seed yield per plant showed strong positive correlation with number of pods per plant, number of branches per plant and strong negative correlation with days to 50% flowering and days to maturity. Path coefficient analysis also revealed that number of pods per plant and number of branches per plant had major direct and indirect effects on yield contributing traits in urd bean.

Kumar *et al.* (2015) revealed that characters *viz.*, branches per plant, pods per plant, seeds per pod, seeds per plant, 100-seed weight, pod weight and harvest index were highly significant and positively correlated with seed yield at both phenotypic and genotypic levels. However, characters *viz.*, seed yield, branches per plant, pods per plant and seeds per plant were highly significantly and positively correlated among themselves revealing their significant influence on seed yield.

Mathivathana *et al.* (2015) reported that plant height, number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod, 100 seed weight, total dry matter production had significantly positive association with seed yield per plant, further, due weightage would be given to these nine traits while, contracting selection index for improving seed yield. Path analysis revealed that dry matter production was the principle component responsible for increasing seed yield in black gram and it showed high positive direct effects on seed yield.

Gowsalya *et al*. (2016) recorded that seed yield per plant was positively and significantly correlated with pods per plant, clusters per plant, number of seeds per pod, plant height, branch length, 100 seed weight, number of branches and pod length at both phenotypic and genotypic levels. The characters 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, plant height and branch length.

Jyothsna *et al.* (2016) reported that, number of pods per plant had significant positive correlation with seed yield per plot at genotypic and phenotypic levels; number of seeds per pod showed significant positive correlation with seed yield per plot at genotypic level and plant height, number of seeds per plant and length of pod showed positive association with seed yield at phenotypic level. Path analysis studies revealed that number of pods per plant showed true relationship by establishing positive association and direct effect on seed yield both at genotypic and phenotypic levels and plant height and length of pod at phenotypic level and number of seeds per pod at genotypic level.

Mehra *et al.* (2016) recorded that, plant height, pods per plant, seeds per plant and 100-seed weight exhibited significant and positive correlation with seed yield both at genotypic and phenotypic levels. Correlation studies indicated that seed yield per plant showed significant positive correlation with seeds per plant, pods per plant, biological yield per plant, plant height and 100 seed weight. Path coefficient analysis showed highest positive direct effect for seeds per plant followed by biological yield per plant on seed yield both at phenotypic and genotypic levels.

Mohammad *et al.* (2016) reported that yield per plant was positively and significantly associated with number of pods per plant, pod length, weight per pod, harvest index and 100-seed weight but negatively associated with plant height, fresh weight and dry weight. The result of the present experiment had indicated that number of pods per plant, pod length and 100-seed weight were most important characters which exhibited positive correlation with yield per plant. It was observed that biomass per plant (0.73) had maximum positive direct effects on yield per plant, followed by, pods per plant (0.37) and seeds per pod (0.19) by path coefficient analysis. Plant height had negative direct effect on seed yield, followed by, dry weight, 100-seed weight and branches per plant.

Sohela *et al.* (2016) reported that yield per plant was positively and significantly associated with pods per plant, pod length, weight per pod, harvest index and 100-seed weight but negatively associated with plant height, fresh weight and dry weight. The result of the present experiment indicated that number of pod per plant, pod length and 100-seed weight were the most important characters which exhibited positively to yield per plant. It was observed that biomass per plant (0.73 g) had maximum positive direct effects on yield per plant followed by pods per plant (0.37), seeds per pod (0.19) by path coefficient analysis.

2.4. Genetic divergence–

Umadevi and Ganesan (2007) estimated genetic diversity in sixty black gram genotypes for yield, yield components and quality traits and among all the characters, the contribution of number of pods per plant was maximum (31.02%), followed by, grain yield (23.45%) and leaf number per plant (09.04%). The maximum inter-cluster distance was reported in cluster IV followed by cluster I (D= 35.481). Cluster IV showed the highest cluster mean for six characters *viz*., number of clusters per plant, number of pods per plant, number of seeds per pods, 1000-seed weight, apparent grain volume and grain yield.

Ali *et al.* (2008) estimated genetic divergence with the help of D^2 statistics for 31 genotypes of black gram and reported that seed yield per plant was observed to have highest contribution towards total divergence.

Chauhan *et al.* (2008) studied genetic diversity in 210 true breeding lines of urd bean and were grouped into 9 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).

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.

Niranjan and Rama Chandra (2009) evaluated forty five micro-mutant lines of black-gram variety PU-30 for genetic divergence. Using Tocher's method the mutants were grouped into 11 diverse genetic clusters. D^2 analysis showed that 100-seed weight, plant height and pod length had high contribution to genetic divergence.

Venkateswarlu *et al*. (2011) evaluated 70 accessions of black gram through D^2 statistics and grouped them into six clusters. They reported non-significant relationship between geographical and genetic diversity.

Singh *et al.* (2012) reported that 75 genotypes of black gram were grouped into seven clusters based on D^2 values and the clustering pattern showed that plant height, seed yield per plant, number of seeds per plant, number of seeds per pod and 1000-seed weight were major traits causing genetic divergence among genotypes.

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.

Panigrahi *et al.* (2014) reported genetic variation and degree of association among yield and yield contributing traits are essential for developing high yielding genotypes in black-gram. The genotypes belonging to different clusters are having showed maximum divergence for different characters and may be successfully utilized in hybridization programmes to get desirable transgressive segregants.

Sarkar (2014) recorded significant positive correlation of grain yield per plant with height, clusters per plant, pods per plant and biological yield plant based on the inter cluster D^2 values, genotypes with high inter cluster distance could be used in hybridization programme to have broad genetic base.

Geethanjali *et al.* (2015) reported that 52 genotypes were grouped into ten clusters. Cluster I consisted maximum accessions (24) followed by cluster II and III (8) and cluster IV with (6) and cluster V,VI,VII,VIII,IX and X consisted only 1 accession. The inter-cluster distances were greater than intra cluster distances, revealing that considerable amount of genetic diversity existed among the accessions. Maximum intra cluster distance was observed in cluster IV (6.91), followed by cluster III (6.32), cluster II (6.28) and cluster I (5.42) indicating that some genetic divergence still existed among the genotypes. Highest mean values exhibited for plant height in cluster X (68.33) and number of branches per plant, number of clusters per plant in cluster V (17.00) and number of pods per plant (30.33), number of seeds per pod in cluster VI (8.00), 100-seed weight in cluster X (5.43) and days to full maturity (54.67) and seed yield per plant in cluster III (68.94). The characters contributing maximum towards diversity among the accessions are days to initial flowering (22.85%), followed by, % disease incidence (21.64%), days to full maturity (19.23%), plant height (17.27%), 100 seed weight (5.58%).

Hadimani *et al.* (2016) reported that 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 maximum in cluster-VII followed by cluster-VI and cluster-III. Whereas, inter cluster distance was 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 highest mean value for most of the characters studied. Plant height contributed maximum to divergence followed by days to 50 per cent flowering, days to maturity, clusters per plant, 100-seed weight, and these traits can be utilized for future crop improvement programme.

Kamannavar *et al.* (2016) revealed that considerable amount of diversity among the genotypes and led to their grouping into eight clusters. The cluster-I comprising 14 genotypes was the largest, followed by, cluster-II and III with 5 and 4 genotypes respectively. Pods per plant (32.5%), seed yield per plant (30%) and plant height (21.5%) were mainly responsible for genetic diversity. Based on inter-cluster distance and mean performance of clusters for different traits, the crosses among genotypes like, DBG-5, DU-1, Manikya, KU-7638, and DBG-3 are expected to produce desirable segregants for yield and other yield related traits.

CHAPTER - III

MATERIAL AND METHODS

The present investigation entitled "**Study on genetic diversity and character association of yield and its component in Black gram (*Vigna mungo* (L.) Hepper)**" was carried out during *kharif* of 2016-17. A detailed account of the material employed and methods followed during the course of investigation has been embodied in this chapter.

3.1. Site of the experiment

The experiment was carried out at Research Farm, College of Agriculture, Indore (M.P.). Indore is situated between latitude 22º43' N and longitude 76°54' E and at an altitude of 567 meters above the mean sea level.

3.2. Climate and weather conditions

Indore belongs to *Malwa* plateau in western part of Madhya Pradesh. It has sub-tropical and semi-arid climate having a temperature ranged from minimum 5.7ºC to maximum 43.5ºC in winter and summer respectively. In this area most of the rainfall is received during mid-June to September. The weekly maximum and minimum temperatures, rainfall and relative humidity during crop period have been presented in Table 3.1. As per the meteorological data, (1062 mm) annual rainfall was recorded in the rainy season of 2016-17.

3.3. Experimental material:

The experimental material used in the present study comprised of forty six genotypes including standard checks. The experiment was laid down in a Randomized Block Design with three replications with the plot size of 4 rows 4m row length and the plant geometry was maintained at 30 cm × 10 cm. The material was sown with the onset of monsoon on June 29, 2016. All recommended package of practices were followed to raise good black gram crop during the conduct of experiment. The experimental material used in the present study comprised of forty six genotypes.

Table 3.1: Mean standard weekly meteorological data during crop season

SMW	Date	Temperature (^{0}C)		RH (%)	Rainfall (mm)	No. of Rainy days
		Max.	Min.			
26	June 25-July 01, 2016	31.7	25.3	82.2	41.4	4
27	July 02– 08	31.0	25.6	83.0	34.1	1
28	July 09 – 15	25.6	23.1	91.1	310.5	5
29	July 16 – 22	28.2	24.0	84.5	32.9	2
30	July 23 – 29	28.6	23.7	87.4	82.0	4
31	July 30 – Aug.05	27.4	23.1	90.7	103.5	5
32	Aug. 06 – 12	26.4	22.9	90.4	66.2	6
33	Aug. 13 – 19	27.4	23.1	84.1	1.4	0
34	Aug. 20 – 26	24.9	22.6	88.5	107.4	4
35	Aug. 27 – Sept	28.9	24.3	84.9	69.9	3
36	Sept. 03 – 09	28.1	23.0	81.1	9.2	1
37	Sept 10 – 16.	30.7	24.5	79.2	0.0	0
38	Sept. 17 – 23	30.0	24.4	83.7	30.0	2
39	Sept 24-30, 2016	32.9	24.3	74.6	0.0	0

Source: Meteorological observatory, AICRPDA, College of Agriculture, Indore.

Mean weekly standard metrological data during crop season 2016-17

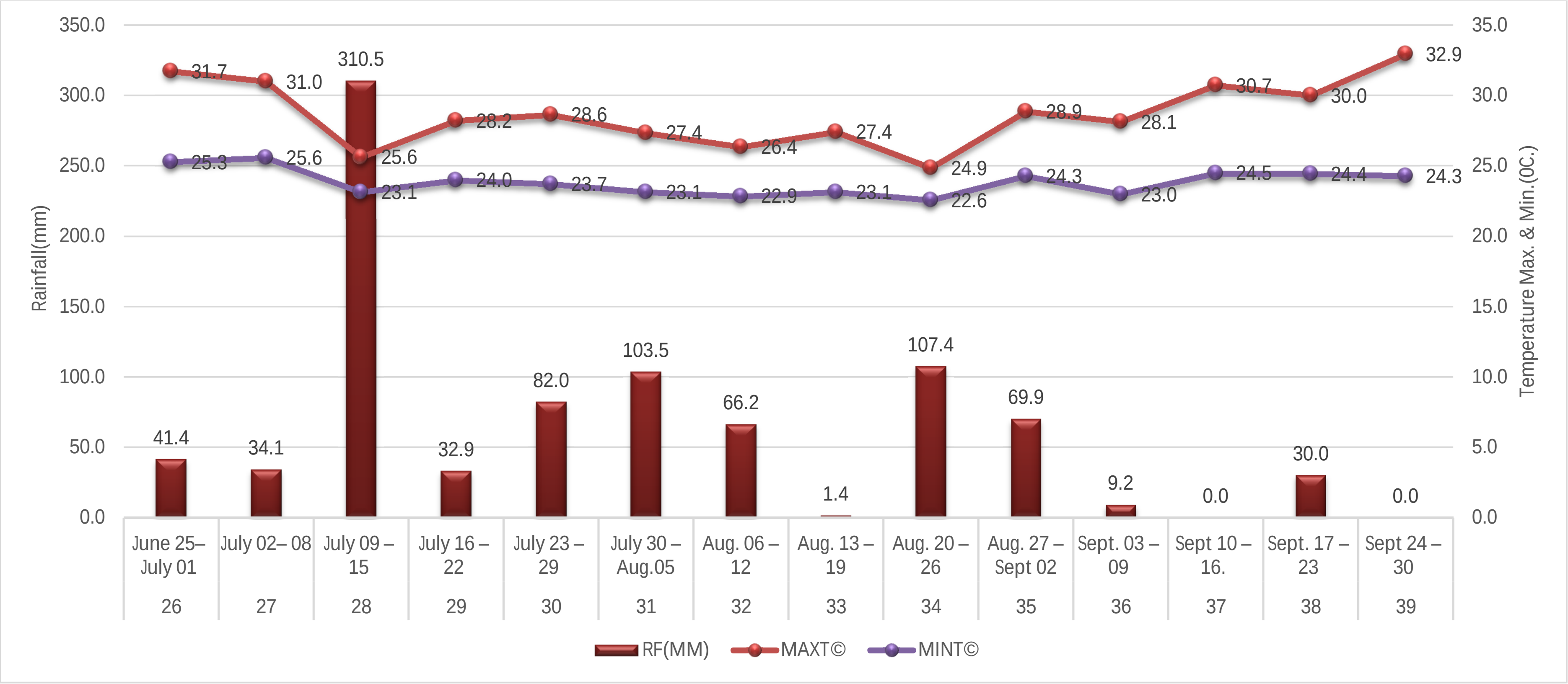

Table 3.2: List of black gram genotypes

S. No.	Name of Genotypes	S. No.	Name of Genotypes	S. No.	Name of Genotypes
1	KU7-522	**17**	KU8-278	**33**	IU-10
2	KU7-618	**18**	KU8-611	**34**	IU-466-9
3	KU7-619	**19**	KU8-638	**35**	JU-2
4	KU7-626	**20**	KU8-632	**36**	JU-840
5	KU7-635	**21**	RBU-466-D	**37**	JU-3
6	KU7-608	**22**	KU8-613	**38**	JU-86
7	IVU-466-9	**23**	KU8-621	**39**	TYPE-9
8	IVU-486	**24**	KU8-602	**40**	TPU-4
9	KU09-252	**25**	KU8-605	**41**	IU-466-9
10	KU7-629	**26**	KU8-612	**42**	IVU-486
11	KU7-354	**27**	KU8-636	**43**	IVU-466-D
12	KU7-632	**28**	KU8-532	**46**	LOCAL-D
13	KU7-369	**29**	KU8-534	**45**	IU-466-9
14	KU7-320	**30**	IU-421	**46**	IU-31-7
15	KU3-62	**31**	KU8-532		
16	KU8-606	**32**	KU8-476		

3.4. Observations recorded:

Observations were recorded on plot as well as single plant basis. Observations on plot basis were recorded for days to flower initiation, days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of pods per plant, number of seeds per plant, number of seeds per pod, 100 seed weight, biological yield per plant (g), harvest index, seed yield per plant. For recording single plant observations five competitive plants were randomly selected from each plot. Average of these five plants with respect to plant height (cm), number of primary branches per plant, number of pods per plant, number of seeds per plant, number of seeds per pod, 100 seed weight, biological yield per plant (g), harvest index and seed yield per plant (g) was used for statistical analysis. The following observations were recorded:

1. Days to flower initiation:

Number of days from the date of sowing to the date of first flower initiation was counted and recorded.

2. Days to 50% flowering:

Number of days taken from the date of sowing to the date when 50% plants flowered in a plot.

3. Days to maturity:

Sowing to till the 80 per cent pods matured was counted and recorded.

4. Plant height (cm):

The plant height was measured in cm from the base of the plant to the main stem apical bud over last foliage.

5. Number of primary branches per plant:

The branches emerging from the main stem were counted and recorded.

6. Number of pods per plant:

The pods emerging from primary and secondary branches were counted and recorded.

7. Number of seeds per plant:

The effective pods were picked up and threshed carefully by hand and the average number of seeds counted and recorded.

8. Number of seeds per pod:

Count the number of seeds from a single pod and record number of seeds per pod or Total number of seeds per pod = Total number of seeds per plant / Total number of pods per plant.

9. 100-seed weight (g):

Two samples of 100 seeds were drawn randomly from bulked seed of five selected plants and were weighed in gram with the help of an electronic balance and mean of samples recorded as 100- seed weight.

10. Biological yield per plant (g):

Biological yield per plant (total biomass) was recorded in grams.

11. Harvest index (%):

The harvest index was calculated by the following equation:

Harvest index (%) = (Economic yield/Biological yield per plant) x100

12. Seed yield per plant (g):

The pods of selected five plants from each plot were threshed and winnowed. The seeds obtained from each plant were weighed in grams.

3.5. Statistical procedures:

The data collected on the quantitative characters were subjected for statistical analysis and following different statistical parameters were worked out.

3.5.1. Analysis of variance (ANOVA):

The data on various characters were subjected to statistical analysis by using appropriate method of analysis of variance as described by Panse and Sukhatme (1954). The range and estimates of mean, phenotypic, genotypic and environmental variances, standard error, coefficient of variation and critical difference were obtained for all the 12 traits. The significant differences between genotypes for the characters under study were tested by F- test.

Analysis of variance was done separately for each character for all treatments. The model of analysis of variance was given below.

Source variation	Degree of freedom	Sum of square	Mean sum of square	F value calculated
Replications	r-1	SSr	MSSr	MSSr/MSSe
Treatments	t-1	SSt	MSSt	MSSt/MSSe
Error	(r-1)(t-1)	SSe	MSSe	
Total	(rt-1)	TSS		

Where,

t = Number of treatments (genotypes)

r = Number of replications

The standard error was calculated as,

$$\text{SEm} = \sqrt{\text{MSSe}/r}$$

The significance of treatments mean squares and replication mean squares were tested by comparing with error mean squares referring to ‘F’ table values at 5 and 1 per cent level of probabilities.

3.5.2. Estimation of genetic variability parameters:

3.5.2.1. Genotypic, phenotypic and environmental variance:

Variance due to genotype, phenotype and environment were computed as follows.

Genotypic variance (σg^2)= $\frac{\text{MS due to genotypes} - \text{Ms due to error}}{r\ (replication)}$

Environmental variance (σe^2) = Error mean sum of squares

Phenotypic variance (σp^2) = $\sigma g^2 + \sigma e^2$ (MS due to error)

Where, ‘r’ is number of replications.

3.5.2.2. Genotypic and phenotypic coefficient of variation:

Genotypic and phenotypic coefficients of variation were estimated according to Burton and Devane (1953) based on estimate of genotypic and phenotypic variance.

Genotypic co-efficient of variation (GCV):

$$GCV(\%) = \frac{\sigma g}{\bar{X}} \times 100$$

Phenotypic co-efficient of variation (PCV):

$$PCV(\%) = \frac{\sigma p}{\bar{X}} \times 100$$

Where,

$\bar{X}$ = General mean

σg = Genotypic standard deviation

σp = Phenotypic standard deviation

GCV and PCV were classified as suggested by Burton and Devane (1953)

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

3.5.2.3. Heritability (h^2):

The broad sense heritability (h^2bs) was estimated by following the procedure suggested by Weber and Moorthy (1952) as indicated here below.

$$h^2 = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Where,

h^2 (%) = Heritability (Broad sense)

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

Heritability values was categorized as (low, moderate and high) followed by Robinson *et al.* (1951).

Low	: (below 50 per cent),
Moderate	: (50-70 per cent)
High	: (above 70 per cent)

3.5.2.4. Expected genetic advance:

Genetic advance for each character was predicted by the formula given by Johnson *et al*. (1955).

$$GA = h^2 \text{ x } \sigma_p \text{ x } k$$

Where, k = Selection differential (2.06) at 5 per cent selection intensity

h^2 = Heritability in broad sense

σ_p = Phenotypic standard deviation

3.5.2.5. Genetic advance as per cent of mean (GAM):

Genetic advance as percentage over mean was worked out as suggested by Johnson *et al*. (1955).

Genetic advance over mean (GAM) = $\frac{GA}{\bar{X}} \times 100$

Where,

GA = Genetic advance

$\bar{X}$ = General mean

The genetic advance as per cent of mean was categorized as suggested by Johnson *et al.* (1955) and the same is given below.

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

3.5.3. Correlation coefficient analysis:

Phenotypic, genotypic and environmental correlation coefficient between characters were computed utilizing respective components of variance and co-variance, by following formula suggested by Miller *et al.* (1958).

$$r_{xy} = \frac{\text{Cov.}_{\text{x, y}}}{\sqrt{\text{V}_\text{x} \times \text{V}_\text{y}}}$$

Where,

r_{xy} = Correlation coefficient between character x and y,

$\text{Cov}_{x,y}$ = Co-variance of character x and y,

V_x = Variance of character x, and

V_y = Variance of character y.

To test the significance of phenotypic and environmental correlation coefficient, the estimated values were compared with the tabulated values of Fisher and Yates (1938) at t-2 d.f. at two levels of probability, *viz.*, 5% and 1%.

3.5.4. Path coefficient analysis:

The proportion of direct and indirect contributions of various characteristics to the total correlation coefficient with seed yield was estimated through path coefficient analysis as suggested by Wright (1921, 1934) and elaborated by Dewey and Lu (1959).

Path coefficient is a standardized partial regression, which measures the direct influence of one variable upon another and allows partition of correlation coefficient into components of direct and indirect effects.

To estimate various direct and indirect effects, the following set of simultaneous equations were formed and solved.

$r_{1y} = P_{1y} + r_{12}P_{2y} + r_{13}P_{3y} + \ldots + r_{1l}P_{ly}$

$r_{2y} = r_{2y}P_{1y} + P_{2y} + r_{23}P_{3y} + \ldots + r_{2l}P_{ly}$

.

.

$r_{ly} = r_{l1}P_{1y} + r_{l2}P_{2y} + r_{l3}P_{3y} + \ldots + P_{ly}$

Where,

r_{1y} to r_{Iy} = Coefficient of correlation between causal factor 1 to I and dependent character r y,

r_{12} to $r_{I-1,I}$ = Coefficient of correlation among causal factor themselves, and

P_{1y} to P_{Iy} = Direct effects of characters 1 to I on character r y,

Residual effect, which measures the contribution of the characters not considered in the causal scheme, was obtained as:

Residual effect (P_{RY}) = $\sqrt{1 - R^2}$

Where,

$$R^2 = \sum_{iy} P_i^2 Y + 2 \sum_{\substack{i \neq j \\ i > j}} P_{iy} \; P_{jy} \; R_{ij}$$

3.5.5. Multivariate analysis:

3.5.5.1. Estimation of Wilk's (Λ) criterion:

To test the significance of difference between lines, taking all the characters simultaneously, 'V' statistic was calculated which was based on Wilk's (Λ) criterion (Wilks, 1932). The sum of squares and sum of products of error and error + variety were utilized for estimation of "Λ".

To calculate the value of "Λ" following relationship was used:

$$"\Lambda" = \frac{|E|}{|E + V|}$$

Where,

$|E|$ was the determinant of error sum of squares and sum of products matrix and $|E + V|$ was the determinant of the "error + variety' sum of squares and sum of products matrix.

χ^2 was used to test the significance of "Λ" as

$$\chi^2_{pq} = V = - m \log_e \Lambda$$

Where,

$m = n - \frac{p+q+1}{2}$ with pq degree of freedom.

Where,

n = total number of observations –1,

p = number of characters,

q = k – 1, and

k = number of lines

3.5.5.2. Estimation of Genetic divergence (D^2 statistic):

Mahalanobis (1928) D^2 statistic was used for assessing the genetic divergence between different populations. The D^2 analysis was carried out using the data recorded on germplasms. Mahalanobis generalized distance (D^2) between any two populations is given by the formula

$$D^2 = \sum \lambda^{ij} \sigma^i \sigma^j$$

Where,

D^2 = Square of generalized distance

λ^{ij} = Reciprocal of the common dispersal index

σ^i= µi1 - µi2 (Difference between mean value of the two lines for the ith character)

σ^j= µj1 - µj2 ((Difference between mean value of the two lines for the jth charecter)

µ = General mean

Since the formula for computation requires inversion of higher order determinants, transformation of the original correlated unstandardized character mean (Xs) to standard uncorrelated variable (Ys) was done to simplify the computational procedure. The D^2 values were obtained as the corresponding uncorrelated (Ys) values of any two uncorrelated genotypes (Rao, 1952).

Clustering D^2 values:

All the n (n-1)/2D^2 values were clustered using Toucher's method (Rao, 1952).

Intra and inter-cluster distance:

The intra and inter-cluster distances were calculated by following the formula described by Singh and Choudhary (1977).

$$\textbf{Square of intra cluster distance} = \frac{\sum D_i^2}{N}$$

Where,

ΣD_i^2 = Sum of distances between all possible combinations (N) of the entries included in the cluster

N = Number of all possible combinations

$$\textbf{Square of inter-cluster distance} = \frac{\sum D_{ij}^2}{n_i n_j}$$

Where,

ΣD_{ij}^2 = Sum of distances between all possible combinations ($n_i n_j$) of the entries included in the cluster

n_i = Number of entries in the cluster i

n_j =Number of entries in the cluster j

3.5.5.3. Determination of population constellations:

Population constellations were determined by Tocher's method described by Rao (1952). A cluster or constellation may be explained as a group of populations or genotypes such that any two populations belonging to the same cluster showed, on the average, a smaller D^2 value than those belonging to different clusters.

Rao (1952) suggested that two closely related populations of low D^2 value be pooled together and then a third population of similar D^2 value be added to this group such that it did not increase the average D^2 value appreciably. This process is continued. Any population, which sharply increases the average D^2 value, should not be included in that group.

After formation of first cluster, the process is repeated to form second, third etc., clusters using remaining populations until all populations are included in one or the other cluster. After cluster formation average intra and inter-cluster distances were calculated. The square root of corresponding average D^2 values represents the distance within and between groups.

CHAPTER-IV

RESULTS

The experimental results of the present study have been reported in this chapter under the following headings:

4.1. Analysis of variance

4.2. Parameters of genetic variability

4.2.1. Mean performance and range

4.2.2. Phenotype and genotype coefficient of variation

4.2.3. Heritability estimates

4.2.4. Genetic advance

4.3. Study of relationship of seed yield and its contributing traits:

4.3.1. Correlation coefficient estimate

4.3.2. Path analysis

4.4. Study of genetic divergence

4.4.1. D^2 analysis

4.1. Study of genetic variability:

4.1. Analysis of variance:

Analysis of variance showed highly significant differences among all twelve traits under study that is, for days to flower initiation, days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of pods per plant, number of seeds per plant, number of seeds per pod, 100-seed weight, biological yield per plant, harvest index, and seed yield per plant (Table 4.1).

4.2. Parameters of genetic variability:

The genetic variability parameters namely, mean, range, phenotypic coefficients of variation (PCV), genotypic coefficients of variation (GCV), heritability in broad sense (%), genetic advance and expected genetic advance (as per cent of mean) for all the twelve characters were estimated and have been presented in Table 4.2. The results obtained have been described below:

Table 4.1: ANOVA showing values of mean sum of squares for different traits in Black gram

Source of variation	**Replication**	**Genotypes**	**Error**
d. f.	02	45	90
Characters	**Mean sum of square**		
Days to flower initiation	12.53	4.204**	2.40
Days to 50% flowering	0.24	26.95**	9.04
Days to maturity	9.37	24.12**	9.79
Plant height	1.28	19.31**	1.49
No. of primary branches/plant	0.51	0.57**	0.20
No. of pods/plant	3.72	43.81**	11.62
No. of seeds/plant	746.50	2844.88**	556.41
No. of seeds/pod	0.14	0.64**	0.21
100-seed weight	5.61	0.79**	0.13
Biological yield/plant	0.36	25.19**	4.25
Harvest index	73.56	172.47**	50.04
Seed yield/plant	1.17	4.74**	0.93

****** Significant at 1% level of significance

***** Significant at 5% level of significance

4.2. Parameters of genetic variability:

The genetic variability parameters namely, mean, range, phenotypic coefficients of variation (PCV), genotypic coefficients of variation (GCV), heritability in broad sense (%), genetic advance and expected genetic advance (as per cent of mean) for all the twelve characters were estimated and have been presented in Table 4.2. The results obtained have been described below:

4.2.1. Mean performance and range:

The present study revealed that among the characters studied, most of the characters showed uniform distribution of values at both side of mean and thus follow normal distribution for all the traits under study.

1. **Days to flower initiation:** This trait was ranged from 31.50 days (KU7-608) to 37.00 days (IU-466-9) with grand mean of 35.06 days. Further, 19 genotypes showed earliness in flower initiation.
2. **Days to 50% flowering:** This trait was ranged from 41.00 days (KU7-522 and KU7-619) to 52.50 days (KU8-636 and IU-421) with grand mean of 47.33 days. Further, 21 genotypes showed earliness in 50% flowering.
3. **Days to maturity:** This trait was ranged from 62.33 days (KU7-619) to 74.50 days (KU8-608) with grand mean of 69.33 days. Further, 19 genotypes exhibited earliness in maturity.
4. **Plant height (cm):** The plant height was ranged from 10.73 (KU7-635) to 19.43 (KU8-476) with mean plant height of 14.45 cm. Further, 22 genotypes showed tall plants.
5. **Number of primary branches per plant:** The number of primary branches ranged from 2.30 (KU7-608, KU8-613 and KU8-605) to 4.43 (KU8-632) with mean of 3.16 number of primary branches per plant. Further, 24 genotypes showed more branches per plant.
6. **Number of pods per plant:** This trait was ranged from 10.10 (KU7-635) to 30.63 (KU8-632) with mean of 16.16 pods per plant. Further, 17 genotypes exhibited more pods per plant.

7. **Number of seeds per plant:** This trait was ranged from 62.30 (KU7-635) to 230.03 (KU8-632) with mean of 106.61 seeds per plant. Further, 20 genotypes showed more number of seeds per plant.
8. **Number of seeds per pod:** This trait was ranged from 4.97 (KU09-252) to 7.50 (KU8-613) with mean of 6.39 seeds per pod. Further, 24 genotypes exhibited more seeds in plants.
9. **100-seed weight (g):** The trait was ranged from 3.03g (IU-421) to 5.03 g (KU8-638) with mean of 3.98 g. Further, 29 genotypes showed more 100-seed weight.
10. **Biological yield per plant (g):** This trait was ranged from 5.10 g (KU7-635) to 17.80 g (KU8-632) with mean of 10.75 g. Further, 23 genotypes exhibited more biological yield of plants.
11. **Harvest index (%):** This trait was ranged from 21.23 g (KU8-532) to 63.10 g (KU7-618) with mean of 39.76 g. Further, 25 genotypes showed more harvest index.
12. **Seed yield per plant (g):** This trait was ranged from 2.13 g (KU09-252) to 8.37 g (KU8-632) with mean of 4.12 g. Further, 17 genotypes more seed yield in plants.

4.2.2. Phenotypic and genotypic coefficient of variation:

The phenotypic and genotypic coefficients of variation were estimated from the corresponding variances and were used for the assessment of genetic variability among the characters studied. Phenotypic coefficient of variation (PCV) and genotypic coefficients of variation (GCV) were worked out for all the characters under study and have been presented in (Table 4.2).

The GCV and PCV are categorized as low (10%>), moderate (10-20%) and high (20%<) as suggested by Burton and Devana (1953). The estimated GCV and PCV helped in getting a clear understanding of the variability present among various genotypes.

The GCV values were lower than PCV values for all the characters under study. The high GCV of (27.33%) was recorded for seed yield per plant, followed by, number of seeds per plant (25.91%), biological yield per plant (24.57%) and number of pods per plant (20.26%). The moderate GCV was

Table 4.2. Parameters of Genetic variability for various traits in Black gram

S. No.	Characters	Mean	Range		PCV (%)	GCV (%)	Heritability (Broad Sense) (%)	Genetic advance	Genetic advance as % of mean
			Min	Max					
1	**Days to flower initiation**	35.06	31.50	37.00	04.94	02.21	19.90	00.71	02.02
2	**Days to 50% flowering**	47.33	41.00	52.50	08.19	05.16	39.80	03.17	06.69
3	**Days to maturity**	69.33	62.33	74.50	05.51	03.15	32.80	02.58	03.72
4	**Plant height (cm)**	14.45	10.73	19.43	18.87	16.86	79.80	04.48	31.00
5	**No. of primary branches/plant**	03.16	02.30	04.43	18.09	11.01	37.00	00.44	13.92
6	**No. of pods/plant**	16.16	10.10	30.63	29.24	20.26	48.00	04.68	28.96
7	**No. of seeds/plant**	106.61	62.30	230.03	34.07	25.91	57.80	43.26	40.57
8	**No. of seeds/pod**	06.39	04.97	07.50	09.31	05.94	40.70	00.50	07.82
9	**100-seed weight (g)**	03.98	03.03	05.03	14.96	11.73	61.50	00.76	19.09
10	**Biological yield/plant (g)**	10.75	05.10	17.80	31.17	24.57	62.10	04.29	39.90
11	**Harvest index (%)**	39.76	21.23	63.10	23.97	16.06	44.90	08.82	22.18
12	**Seed yield/plant (g)**	04.12	02.13	08.37	36.04	27.33	57.50	01.76	42.71

observed for plant height (16.86%), harvest index (16.06%), 100-seed weight (11.73%) and number of primary branches per plant (11.01%). The low GCV was showed for number of seeds per pod (5.94%), days to 50% flowering (5.16%), days to maturity (3.15%) and days to flower initiation (2.21%).

The high PCV value was observed for seed yield per plant (36.04%), followed by, number of seeds per plant (34.07%), biological yield per plant (31.17%), number of pods per plant (29.24%) and harvest index (23.97%). The moderate PCV for plant height (18.87%), number of primary branches per plant (18.09%) and 100-seed weight (14.96%). The low PCV for number of seeds per pod (9.31%),days to 50% flowering (8.19%) and days to maturity (5.51%) and days to flower initiation (4.94%).

The difference between PCV and GCV was moderate to high for all the traits under study. Maximum difference between PCV and GCV values was recorded for number of pods per plant (8.98%), followed by, seed yield per plant (8.71%),number of seeds per plant (8.16%),harvest index (7.91%), number of primary branches par plant (7.08%) and biological yield per plant (6.60%), while for number of seeds per pod (3.37%), 100 seed weight (3.23%), days to 50% flowering (3.03%),days to flower initiation (2.73%), days to maturity (2.36%) and plant height (2.01%) showed low gap between PCV and GCV.

4.2.3. Heritability estimates:

The estimates of heritability in broad sense for yield and attributing characters have been presented in Table 4.2. The prediction regarding heritability in broad sense was made as suggested by Robinson (1951) as low (<50%), moderate (50-70%) and high (>70%).

In present investigation high heritability was reported for the character *viz*., plant height (79.8%).The moderate heritability was observed for the characters *viz*., biological yield per plant (62.1), 100-seed weight (61.5), number of seeds per plant (57.8) and seed yield per plant (57.5).

The characters namely, number of pods per plant (48.0), harvest index (44.9), number of seeds per pod(40.7), days to 50% flowering (39.8), number of primary branches per plant (37.0) and days to maturity (32.8) and days to flower initiation (19.9)were recorded with low heritability.

4.2.4. Genetic advance:

Genetic advance was estimated for all the characters under study and are presented in (Table 4.2).The genetic advance as percentage of mean was categorized as suggested by Johanson *et al.* (1955) and classified into three major classes i.e., High (> 20%), Medium (10-20%), Low (<10%).

High genetic advance as percentage of mean was recorded for seed yield per plant (42.71%), followed by, number of seeds per plant (40.57%), biological yield per plant (39.90%), plant height (31.00%), number of pods per plant (28.96%) and harvest index (22.18%).

Genetic advance as percentage of mean was recorded moderate for 100-seed weight (19.09%) and number of primary branches per plant (13.92%). While, low genetic advance as percentage of mean were recorded for the characters *viz*., number of seeds per pod (7.82%), days to 50% flowering (6.69%) and days to maturity (3.72%) and days to flower initiation(2.02%).

4.3 Study of relationship of seed yield and its contributing traits:

4.3.1. Correlation coefficient estimate:

Estimates of phenotypic and genotypic correlation coefficient between seed yield and its contributing characters and among themselves were calculated and have been presented in Table 4.3. In general, the genotypic correlation coefficients were slightly higher in magnitude than the corresponding phenotypic correlation coefficients.

Correlation coefficient with seed yield:

1. **Seed yield per plant (g):**

At phenotypic level, seed yield per plant showed highly significant positive correlation coefficient with number of seeds per plant (0.893), number of pods per plant (0.835), biological yield per plant (0.725), harvest index (0.413) and significant positive correlation coefficient was observed for number of seeds per pod (0.359) and 100-seed weight (0.328).

Table 4.3: Estimates of Phenotypic and Genotypic correlation coefficient of various characters of black gram

Characters		Days to 50% flowering	Days to maturity	Plant height	No of primary branch/plant	No of pods per plant	No of seeds per plant	No of seeds per pod	100 seed weight	Biological yield per plant	Harvest index	Seed yield per plant
Days to flower initiation	**P**	0.325*	0.350*	0.105	0.174	-0.033	0.002	0.024	0.181	0.050	0.103	0.082
	G	0.420	0.617	0.437	0.444	-0.130	0.021	0.377	0.257	0.051	0.148	0.110
Days to 50% flowering	**P**		0.861**	-0.078	0.071	0.119	-0.136	0.150	-0.038	0.140	-0.057	0.104
	G		0.842	-0.004	0.108	0.343	0.338	0.357	-0.203	0.303	-0.207	0.224
Days to maturity	**P**			-0.082	0.044	-0.010	-0.008	0.083	-0.049	-0.030	-0.019	-0.031
	G			0.071	0.209	0.347	0.297	0.279	-0.118	0.204	-0.053	0.210
Plant height	**P**				0.106	-0.042	-0.014	0.050	0.266	0.273	-0.189	0.122
	G				0.152	-0.070	-0.036	-0.001	0.355	0.322	-0.221	0.170
No of primary branch/plant	**P**					0.290*	0.292*	-0.048	0.039	0.348*	-0.079	0.250
	G					0.583	0.509	-0.372	0.057	0.558	-0.080	0.478
No of pods per plant	**P**						0.938**	0.215	-0.072	0.717**	0.191	0.835**
	G						0.971	0.253	-0.089	0.759	0.044	0.854
No of seeds per plant	**P**							0.385**	-0.054	0.753**	0.231	0.893**
	G							0.440	-0.082	0.751	0.093	0.881
No of seeds per pod	**P**								0.016	0.165	0.234	0.359*
	G								0.084	0.181	0.292	0.487
100 seed weight	**P**									0.023	0.441**	0.328*
	G									0.075	0.533	0.412
Biological yield / plant	**P**										-0.250	0.725**
	G										-0.384	0.734
Harvest index	**P**											0.413**
	G											0.322

At genotypic level, seed yield per plant showed high positive correlation coefficient with number of seeds per plant (0.881), number of pods per plant (0.854) and biological yield per plant (0.734), while moderate correlation coefficient was observed with number of seeds per pod (0.487), number of primary branches per plant (0.478), 100-seed weight (0.412) and harvest index (0.322). The traits namely, days to 50% flowering (0.224), days to maturity (0.210), plant height (0.170), and days to flower initiation (0.110), showed positive and low value of correlation coefficient with seed yield per plant.

Correlation coefficient amongst different characters:

Phenotypic and genotypic correlation coefficient amongst different characters have been presented in Table 4.3.

2. Days to flower initiation:

At phenotypic level, days to flower initiation exhibited moderate, positive and significant correlation coefficient with days to 50% flowering (0.325) and days to maturity (0.350).

At genotypic level, days to flower initiation showed moderate and positive association with days to maturity (0.617), number of primary branches per plant (0.444) plant height (0.437) and days to 50% flowering (0.420).

3. Days to 50% flowering:

At phenotypic level, days to 50% flowering exhibited positive and highly significant correlation coefficient with days to maturity (0.861).

At genotypic level, days to 50% flowering showed strong and positive correlation coefficient with days to maturity (0.842).

4. Days to maturity:

At phenotypic level, none of the characters showed significant correlation with days to maturity.

At genotypic level, days to maturity showed moderate positive correlation coefficient with number of pods per plant (0.347), number of seeds per plant (0.297) and number of seeds per pod (0.279).

5. Plant height:

At phenotypic level, none of the characters showed significant correlation with plant height.

At genotypic level, plant height showed moderate positive correlation coefficient with 100-seed weight (0.355) and biological yield per plant (0.322).

6. Number of primary branches per plant:

At phenotypic level, number of primary branches per plant had positive and significant correlation coefficient with biological yield per plant (0.348), number of seeds per plant (0.292) and number of pods per plant (0.290).

At genotypic level, number of primary branches per plant showed moderate positive correlation coefficient with number of pods per plant (0.583), biological yield per plant (0.558) and number of seeds per plant (0.509).

7. Number of pods per plant:

At phenotypic level, number of pods per plant exhibited high positive and highly significant correlation coefficient with number of seeds per plant (0.938) and biological yield per plant (0.717).

At genotypic level, number of pods per plant showed strong and positive correlation coefficient with number of seeds per plant (0.971) and biological yield per plant (0.759).

8. Number of seeds per plant:

At phenotypic level, number of seeds per plant showed positive and highly significant correlation coefficient with biological yield per plant (0.753) and number of seeds per pod (0.385).

At genotypic level, number of seeds per plant showed positive correlation coefficient with biological yield per plant (0.751) and number of seeds per pod (0.440).

9. Number of seeds per pod:

At phenotypic level, number of seeds per pod showed positive and non-significant correlation coefficient with harvest index (0.234) and biological yield per plant (0.165).

At genotypic level, number of seeds per pod showed positive correlation coefficient with harvest index (0.292).

10. 100-seed weight:

At phenotypic level, harvest index (0.441) showed highly significant correlation coefficient with 100-seed weight.

At genotypic level, 100-seed weight showed moderate positive correlation coefficient with harvest index (0.533).

11. Biological yield per plant:

At phenotypic level, biological yield per plant showed negative and non-significant correlation coefficient with harvest index (-0.250).

At genotypic level, biological yield per plant showed negative correlation coefficient with harvest index (-0.384).

4.3.2. Path analysis:

The estimate of path coefficient has been furnished in the Table 4.4 (phenotypic path) and Table 4.5 (genotypic path). In general the genotypic direct effects as well as indirect effect were slightly higher in magnitude as compared to corresponding phenotypic direct and indirect effects. The measurement of the direct and indirect effects were characterize as negligible (0.00 to 0.09), low (0.10 to 0.19), moderate (0.20 to 0.29), high (0.30 to 0.99) and very high (> 1.00) as suggested by Lenka and Mishra (1973).

(a) Direct effects:

Phenotypic path analysis (Table 4.4) showed that number of seeds per plant (0.531) and biological yield per plant (0.327) registered high and positive direct effects on yield. Harvest index (0.252) and 100-seed weight (0.237) registered the moderate direct effect and the rest of characters *viz.*, plant height, days to maturity, number of pods per plant number of seeds per pod,

Table 4.4: Phenotypic path coefficient analysis for yield and its contributing traits of black gram genotypes

Characters	Days to flower initiation	Days to 50% flowering	Days to maturity	Plant height	No of primary branch/plant	No of pods per plant	No of seeds per plant	No of seed per pod	100 seed weight	Biological yield per yield	Harvest index	Phenotypic correlation with seed yield/plant
Days to flower initiation	**-0.001**	0.000	0.002	0.003	-0.006	-0.003	0.001	0.000	0.043	0.016	0.026	0.082
Days to 50% flowering	0.000	**-0.001**	0.004	-0.002	-0.002	0.009	-0.072	0.003	-0.009	0.046	-0.014	0.104
Days to maturity	0.000	-0.001	**0.004**	-0.003	-0.001	-0.001	-0.005	0.001	-0.012	-0.010	-0.005	-0.031
Plant height	0.000	0.000	0.000	**0. 031**	-0.004	-0.003	-0.007	0.001	0.063	0.089	-0.048	0.122
No of primary branch/plant	0.000	0.000	0.000	0.003	**-0.033**	0.023	0.155	-0.001	0.009	0.114	-0.020	0.250
No of pods per plant	0.000	0.000	0.000	-0.001	-0.010	**0.078**	0.498	0.004	-0.017	0.234	0.048	0.835
No of seeds/plant	0.000	0.000	0.000	0.000	-0.010	0.073	**0.531**	0.007	-0.013	0.246	0.058	0.893
No of seeds/pod	0.000	0.000	0.000	0.002	0.002	0.017	0.204	**0.018**	0.004	0.054	0.059	0.359
100 seed weight	0.000	0.000	0.000	0.008	-0.001	-0.006	-0.028	0.000	**0.237**	0.007	0.111	0.328
Biological yield/plant	0.000	0.000	0.000	0.008	-0.012	0.056	0.400	0.003	0.005	**0.327**	-0.063	0.725
Harvest index	0.000	0.000	0.000	-0.006	0.003	0.015	0.122	0.004	0.104	-0.082	**0.252**	0.413

Residual effect = 0.0401

Note: Underlined and bold values denote direct effect

Table 4.5: Genotypic path coefficient analysis for yield and its contributing traits of black gram genotypes

Characters	**Days to flower initiation**	**Days to 50% flowering**	**Days to maturity**	**Plant height**	**No of primary branch/ plant**	**No of pods per plant**	**No of seeds per plant**	**No of seeds per pod**	**100-seed weight**	**Biological yield per plant**	**Harvest index**	**Genotypic correlation with Seed yield/ plant**
Days to flower initiation	**0.041**	-0.047	0.151	-0.034	-0.166	0.174	0.074	-0.215	0.306	-0.049	-0.124	0.110
Days to 50% flowering	0.017	**-0.112**	0.206	0.000	-0.040	-0.462	1.175	-0.204	-0.241	-0.288	0.174	0.224
Days to maturity	0.025	-0.095	**0.244**	-0.006	-0.078	-0.466	1.035	-0.159	-0.140	-0.194	0.044	0.210
Plant height	0.018	0.000	0.017	**-0.078**	-0.057	0.093	-0.127	0.001	0.423	-0.306	0.186	0.170
No of primary branch/plant	0.018	-0.012	0.051	-0.012	**-0.374**	-0.784	1.774	0.213	0.068	-0.531	0.067	0.478
No of pods/ plant	-0.005	-0.039	0.085	0.005	-0.218	**-1.344**	3.381	-0.144	-0.106	-0.724	-0.037	0.854
No of seeds/plant	0.001	-0.038	0.073	0.003	-0.190	-1.306	**3.482**	-0.252	-0.097	-0.716	-0.078	0.881
No of seeds/pod	0.015	-0.040	0.068	0.000	0.139	-0.340	1.533	**-0.572**	0.100	-0.173	-0.245	0.487
100-seed weight	0.010	0.023	-0.029	-0.028	-0.021	0.120	-0.285	-0.048	**1.190**	-0.072	-0.447	0.412
Biological yield	0.002	-0.034	0.050	-0.025	-0.208	-1.021	2.615	-0.104	0.090	**-0.953**	0.322	0.734
Harvest index	0.006	0.023	-0.013	0.017	0.030	-0.059	0.323	-0.167	0.635	0.366	**-0.839**	0.322

Residual effect = -0.0011

Note: Underlined and bold values denote direct effect number of primary branches per plant, days to flower initiation and days to 50% flowering showed negligible direct effects on seed yield per plant.

Study of genotypic path analysis (Table 4.5) revealed that number of seeds per plant (3.482) and 100-seed weight (1.190) registered very high positive direct effects on seed yield. However, number of pods per plant (-1.344) registered very high negative direct effect on seed yield. Whereas, biological yield per plant (-0.953), harvest index (-0.839), number of seeds per plant (-0.572) and number of primary branches per plant (-0.374) showed high negative direct effects on seed yield. Whereas, Days to maturity (0.244) registered moderate positive direct effect on seed yield per plant.

(b) Indirect effect:

(1) Days to flower initiation:

At phenotypic level, days to flower initiation recorded the negligible indirect effects for characters namely, days to 50% flowering, days to maturity, plant height, number of seeds per plant, number of seeds per pod, 100-seed weight, number of primary branches per plant, number of pods per plant, biological yield per plant and harvest index exhibited on seed yield per plant.

At genotypic level, days to flower initiation recorded the high positive indirect effect of 0.306 *via* 100-seed weight on seed yield. However, moderate negative indirect effect of -0.215 *via* number of seeds per pod. Whereas, low positive indirect effect of 0.174 *via* number of pods per plant and *via* days to maturity (0.151) on seed yield per plant.

(2) Days to 50% flowering:

At phenotypic level, days to 50% flowering recorded negligible indirect effects *via* characters namely, days to flower initiation, days to maturity, plant height, number of seeds per plant, number of seeds per pod, 100-seed weight, number of primary branches per plant, number of pods per plant, biological yield per plant and harvest index exhibited on seed yield per plant.

At genotypic level, days to 50% flowering recorded very high positive indirect effect of 1.175 *via* number of seeds per plant on seed yield, whereas, high negative indirect effect of -0.462 *via* number of pods per plant on seed yield. However, moderate positive indirect effect of 0.216 *via* days to maturity on seed yield, whereas, moderate negative indirect effect of -0.204 *via* number of seeds per pod, *via* 100-seed weight (-0.241) and *via* biological yield per plant (-0.288) on seed yield, whereas, low positive indirect effect of 0.174 *via* harvest index on seed yield per plant.

(3) Days to maturity:

At phenotypic level, days to maturity recorded negligible indirect effects through characters namely, days to flower initiation, days to 50% flowering, plant height, number of seeds per plant, number of seeds per pod, 100-seed weight, number of primary branches per plant, number of pods per plant, biological yield per plant and harvest index exhibited on seed yield per plant.

At genotypic level, days of maturity recorded very high positive indirect effect of 1.035 *via* number of seeds per plant on seed yield per plant. However, high negative indirect effect of -0.466 *via* number of pods per plant on seed yield per plant.

(4) Plant height (cm):

At phenotypic level, plant height recorded negligible indirect effects *via* characters namely, days to flower initiation, days to 50% flowering, days to maturity, number of seeds per plant, number of seeds per pod, 100-seed weight, number of primary branches per plant, number of pods per plant, biological yield per plant and harvest index exhibited on seed yield per plant.

At genotypic level, plant height recorded high positive indirect effect of 0.423 *via* 100-seed weight on seed yield, whereas, high negative indirect effect of *via* biological yield per plant and low positive indirect effect of 0.186 *via* harvest index on seed yield per plant.

(5) Number of primary branches per plant:

At phenotypic level, low indirect effect was exerted through number of seeds per plant (0.155) and biological yield per plant (0.114) on seed yield per plant. Whereas, negligible indirect effect through harvest index, 100-seed weight, number of seeds per pod, number of pods per plant, plant height, days to maturity, days to 50% flowering and days to flower initiation on seed yield per plant.

At genotypic level, this trait recorded very high positive indirect effect through number of seeds per plant (1.774) on seed yield. Whereas, high negative indirect effect of -0.531 *via* biological yield per plant and *via* number of pods per plant (-0.784) on seed yield. However, moderate indirect effect *via* number of seeds per pod (0.213) on seed yield per plant.

(6) Number of pods per plant:

At phenotypic level, this trait recorded low indirect effect for number of seeds per plant (0.498) and biological yield per plant (0.234) on seed yield per plant. Whereas, the negligible indirect effect exerted through number of primary branches per plant, 100-seed weight, number of seeds per pod, plant height, days to maturity, days to 50% flowering, days to flower initiation and harvest index on seed yield per plant.

At genotypic level, very high indirect effect of 3.381 was exerted *via* number of seeds per plant on seed yield. However, high negative indirect effect of -0.724 *via* biological yield per plant on seed yield. Whereas, moderate negative indirect effect of -0.218 *via* number of primary branches per plant on seed yield per plant.

(7) Number of seeds per plant:

At phenotypic level, this trait recorded moderate indirect effect for biological yield per plant (0.246) on seed yield per plant, whereas the negligible indirect effect exerted through 100-seed weight, harvest index, number of seeds per pod, number of pods per plant, plant height, days to maturity, days to 50% flowering, days to flower initiation and number of primary branches per plant on seed yield per plant.

At genotypic level, this trait recorded very high negative indirect effect through number of pods per plant (-1.306) on seed yield. Whereas, high negative indirect effect was recorded through biological yield per plant (-0.716) on seed yield. However, moderate negative indirect effect through number of seeds per pod (-0.252) on seed yield per plant.

(8) Number of seeds per pod:

At phenotypic level, moderate indirect effect was exerted through number of seeds per plant (0.204) on seed yield per plant, whereas negligible indirect effect was exerted through 100-seed weight, biological yield per plant, harvest index, number of pods per plant, plant height, days to maturity, days to 50% flowering, days to flower initiation and number of primary branches per plant on seed yield per plant.

At genotypic level, number of seeds per pod recorded very high positive indirect effect *via* number of seeds per plant (1.533) on seed yield. However, high negative indirect effect was recorded through number of pods per plant (-0.340) on seed yield, whereas, moderate negative indirect effect was recorded through harvest index (-0.245) on seed yield. However, low positive indirect effect was recorded through number of primary branches per plant (0.139) and 100-seed weight (0.100) on seed yield per plant.

(9) 100-seed weight:

At phenotypic level, this trait recorded moderate indirect effect for harvest index (0.111) on seed yield per plant, whereas negligible indirect effect was exerted through number of seeds per plant, number of seeds per pod, number of pods per plant, biological yield per plant, plant height, days to maturity, days to 50% flowering, number of primary branches per plant and days to flower initiation, on seed yield per plant.

At genotypic level, high negative indirect effect of -0.447 *via* harvest index on seed yield was recorded, whereas, moderate negative indirect effect of -0.285 *via* number of seeds per plant and low indirect effect of 0.120 was exerted *via* number of pods per plant on seed yield per plant.

(10) Biological yield per plant:

At phenotypic level, high indirect effect of 0.400 was exerted *via* number of seeds per plant on seed yield per plant, while negligible indirect effect through days to flower initiation, days to 50% flowering, days to maturity, plant height, number of pods per plant, number of seeds per pod, 100-seed weight, harvest index and number of primary branches per plant on seed yield per plant.

At genotypic level, biological yield per plant recorded very high positive indirect effect of 2.615 through number of seeds per plant on seed yield. However, very high negative indirect effect of -1.021 was recorded through number of pods per plant on seed yield, whereas, high positive indirect effect of 0.322 through harvest index on seed yield. However, moderate negative indirect effect of -0.208 *via* number of primary branches per plant on seed yield per plant.

(11) Harvest index:

At phenotypic level, this trait recorded low indirect effect for number of seeds per plant (0.122) and 100-seed weight (0.104) on seed yield per plant, whereas negligible indirect effect exerted through biological yield per plant, days to flower initiation, days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of pods per plant and number of seeds per pod on seed yield per plant.

At genotypic level, this trait recorded high positive indirect effect for 100-seed weight (0.635), biological yield per plant (0.366) and number of seeds per plant (0.323) on seed yield per plant.

The residual effect for phenotypic and genotypic path coefficient analysis recorded negligible (0.0401) and (-0.0011) respectively.

4.4. Study of genetic divergence:

The analysis of variance (Table 4.1) revealed highly significant differences among genotypes for all the twelve characters under investigation. From the estimates of variances and co–variances, D^2 – statistic, which utilizes Wilk's criterion, a simultaneous test for all the twelve characters was done, which also showed highly significant differences among genotypes of black gram. These differences suggest the existence of considerable divergence among the experimental material under study.

4.4.1. D^2 analysis:

Based on the estimates of genetic divergence, all the forty six genotypes of black gram were grouped into 12 different clusters (Table 4.6). Generalized distance was estimated through Mahalanobis' D^2 – statistic.

Among the twelve clusters, cluster VIII was the largest including 9 genotypes followed by cluster IX, VI and I had 5 genotypes each. Clusters VII and III had 4 genotypes each. Clusters XI, X and V had 3 genotypes each. Cluster XII and IV had 2 genotypes each and cluster II including 1 genotype.

(i) The intra and inter-Cluster average distance:

The average distance within and between clusters and average inter and intra cluster D^2 values have been presented in Table 4.7. In this table, the diagonal values are mean intra cluster and off the diagonal values are inter cluster distances.

The highest (D= 9.900) inter cluster distance was observed between cluster II and V followed by cluster I and II (9.781), cluster II and XI (9.701), cluster II and VII (9.375), cluster II and IX (9.267), cluster II and III (7.459), cluster II and VIII (7.445) and cluster II and VI (7.323) indicating wide diversity between genotypes in these clusters and the lower cluster distance of D = 2.333 was observed between cluster VIII and IX followed by cluster III and XII (2.577), cluster III and VIII (2.558), cluster VIII and XII (2.719), cluster IV and XII (2.815) and cluster VI and IX (2.883) indicating close relationship between genotypes in these clusters. The highest (D = 2.148) intra-cluster distance was found for cluster I followed by cluster XI (1.900). The cluster II registered the lowest intra-cluster distance of 0.000, followed by, cluster IV recording 0.724.

(ii) Cluster mean:

Clusters means of all 12 characters have been presented in Table 4.8.

1. Days to flower initiation:

The cluster mean was the highest for days to flower initiation observed in cluster VIII (36.00) and lowest by cluster I (33.67).

2. Days to 50% flowering:

The cluster mean was the highest for days to 50% flowering exhibited by cluster XII (51.25) and lowest by cluster I (41.63).

3. Days to maturity:

The cluster mean was the highest for days to maturity in cluster VII (72.50) and lowest by cluster I (64.40).

4. Plant height (cm):

The cluster mean was the highest for plant height in cluster X (17.28) and lowest by cluster III (11.75).

5. Number of primary branches per plant:

The cluster mean was the highest for number of primary branches per plant in cluster II (4.43) and lowest by cluster VII (2.67).

6. Number of pods per plant:

The cluster mean was the highest for number of pods per plant in cluster II (30.63) and lowest by cluster V (11.99).

7. Number of seeds per plant:

The cluster mean was the highest for number of seeds per plant in cluster II (230.03) and lowest by cluster V (69.61).

8. Number of seeds per pod:

The cluster mean was the highest for number of seeds per pod in cluster VII (7.18) and lowest by cluster XI (5.40).

9. 100-seed weight:

The cluster mean was the highest for 100-seed weight in cluster VI (4.49) and lowest by cluster I (3.53).

10. Biological yield per plant (g):

Cluster mean was the highest for biological yield per plant in cluster II (17.80) and lowest by cluster V (6.12).

11. Harvest index (%):

Cluster mean was the highest for harvest index in cluster V (51.40) and lowest by cluster XI (24.92).

12. Seed yield per plant (g):

Cluster mean was the highest for seed yield per plant in cluster II (8.37) and lowest by cluster XI (2.69).

(iii) Cluster characteristics:

The cluster I was characterized for earliness in flower initiation (33.73 days), days to 50% flowering (41.63 days), days to maturity (64.40 days) and small seeded that is low 100 seed weight (3.53 g).

The cluster II was characterized for more number of primary branches per plat (4.43), number of pods per plant (30.63), number of seeds per plant (230.03), seed yield per plant (8.37) and high biological yield per plant (17.80 g).

The cluster III was characterized for dwarf plant type that is low plant height (11.75 cm).

The cluster IV was characterized for less number of pods per plant (11.99), number of seeds per plant (69.61), low biological yield per plant (6.12 g) and high harvest index (51.40 %).

The cluster VI was characterized for bold seeded that is 100 seed weight (4.49 g).

The cluster VII was characterized for late maturity (72.50 days), less number of primary branches per plant (2.67) and more number of seeds per pod (7.18).

The cluster VIII was characterized for delayed flower initiation (36.00 days).

The cluster X was characterized for tall plant type that is plant height (17.28 cm).

The cluster XI was characterized for less number of seeds per pod (5.40), low harvest index (24.92 %) and low seed yield per plant (2.69 g).

The cluster XII was characterized for delayed 50% flowering (51.25 days).

Table 4.6: Clustering pattern of forty six genotypes of black gram on the basis of genetic divergence

Cluster Number	Constituent genotypes	Number of genotypes
I	KU7-522, KU7-619, KU7-626, KU7-608, IVU-486	5
II	KU8-632	1
III	KU7-632, KU8-611, KU8-612, KU8-532	4
IV	KU7-320, KU8-278	2
V	KU7-618, KU7-635, IU-466-9	3
VI	RBU-466-D, KU8-476, JU-86, TYPE-9, IVU-466-D	5
VII	KU8-613, KU8-605, KU8-532, IU-421	4
VIII	IVU-486, KU7-354, KU7-369, KU8-602, IU-466-9, JU-2, IU-466-9, IVU-486, IU-31-7	9
IX	KU7-629, KU8-606, KU8-638, IU-10, JU-3	5
X	KU3-62, JU-840,TPU-4	3
XI	KU09-252,KU8-532, LOCAL-D	3
XII	KU8-621, KU8-636	2

Table 4.7: Average intra and inter cluster D^2 values between the clusters in black gram

Clusters	**I**	**II**	**III**	**IV**	**V**	**VI**	**VII**	**VIII**	**IX**	**X**	**XI**	**XII**
I	**2.148**											
II	9.781	**0.000**										
III	3.797	7.459	**1.290**									
IV	6.512	4.176	3.746	**0.724**								
V	4.025	9.900	4.026	6.418	**1.568**							
VI	4.286	7.323	3.591	3.986	4.859	**1.620**						
VII	4.941	9.375	3.182	5.693	4.416	4.704	**1.801**					
VIII	4.834	7.445	2.558	4.053	3.634	3.013	3.303	**1.578**				
IX	3.853	9.267	3.518	5.756	3.147	2.883	3.757	2.333	**1.768**			
X	5.278	6.944	3.454	4.565	5.932	3.768	4.966	3.028	3.917	**1.758**		
XI	4.085	9.701	3.565	6.585	4.887	5.125	5.323	4.298	3.794	3.792	**1.900**	
XII	6.025	5.997	2.577	2.815	5.466	4.237	4.276	2.719	4.620	3.161	4.902	**1.427**

Table 4.8. Clusters means for 12 characters under study in black gram

Characters	Cluster mean											
	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
Days to flower initiation	33.73	35.67	34.50	34.50	35.78	34.13	35.38	36.00	35.43	35.67	34.17	35.75
Days to 50% flowering	41.63	47.50	49.12	49.00	45.67	45.40	50.88	48.94	46.63	47.17	47.39	51.25
Days to maturity	64.40	69.50	69.88	70.50	70.22	66.70	72.50	71.31	68.70	69.22	68.56	72.25
Plant height	12.01	13.63	11.75	12.58	12.18	16.88	12.42	15.92	17.11	17.28	14.52	12.12
No of primary branches/plant	2.99	4.43	3.15	3.47	3.22	2.93	2.67	3.29	2.87	3.59	3.34	3.47
No of pods/plant	14.06	30.63	18.67	24.27	11.99	17.01	13.38	16.27	12.95	17.72	14.08	19.22
No of seeds/plant	88.56	230.03	115.30	166.38	69.61	116.99	96.31	106.64	82.16	124.91	79.57	137.30
No of seeds/pod	6.24	6.80	6.24	6.63	5.88	6.76	7.18	6.44	6.29	6.46	5.40	6.40
100-seed weight	3.53	4.03	3.63	4.20	4.41	4.49	3.54	4.15	4.42	3.59	3.58	4.00
Biological yield/plant	7.74	17.80	10.47	13.95	6.12	12.25	8.29	10.80	9.39	15.38	12.09	14.53
Harvest index	39.34	48.33	38.42	46.90	51.40	43.16	40.37	42.11	38.70	28.24	24.92	36.62
Seed yield/plant (g)	2.89	8.37	4.09	6.58	3.03	5.25	3.28	4.41	3.54	4.28	2.69	5.27

CHAPTER – V

DISCUSSION

The discussion is confined to the following heads,

5.1 Genetic variability

5.2 Heritability and Genetic advance

5.3 Correlation coefficient and path analysis

5.4 Genetic divergence

5.1. Genetic Variability:

A broad-spectrum of genetic variability is fundamental requisite for success of a plant breeding programme since it provides opportunity to breeders to make selection for desirable superior individuals from genetically diverse base population. Since, many characters of economic importance are highly influenced by environmental conditions, the improvement of a crop mainly depends upon the amount, nature and magnitude of genotypic variability present in the population. Wide range of variability existing among the genotypes to be tested for all the characters is also necessary to isolate significantly superior genotypes.

Analysis of variance revealed highly significant differences among the genotypes for all the traits *viz.,* days to flower initiation, days to 50 % flowering, days to maturity, plant height, number of primary branches per plant, number of pods per plant, number of seeds per plant, number of seeds per pod, biological yield per plant, harvest index, 100-seed weight and seed yield per plant indicating the presence of considerable genetic variability in the experimental material. These results were in agreement with the findings of Arulbalachandran *et al.* (2010) for plant height, number of branches per plant, number of pods per plant, number of seeds per pod, yield per plant and 100-seed weight; Neelavathi and Govindarasu (2010) for branches per plant, pods per plant, biological yield and seed yield; Meshram *et al.* (2013) for number of pods per plant and grain yield per plant; Punia *et al.* (2014) for plant height, primary branches per plant and pods per plant and Kumar *et al.* (2015) for pods per plant, seeds per plant, plant height and seed yield;

A perusal of the genetic parameters revealed that seed yield per plant followed by biological yield per plant, number of seeds per plant and number of pods per plant exhibited high phenotypic and genotypic coefficient of variation suggesting that the existence of sufficient genetic variability for these traits in the population. Thus, it provides the basis for selection of desirable genotypes from the diverse population for enhancement of black gram production. These results were in consonance with the findings of Veeramani *et al.* (2005); Senapati and Mishra (2010); Meshram *et al*. (2013); Deepshikha et al. (2014); Patel *et al.* (2014); Ramya *et al.* (2014); Kumar *et al.* (2015) and Gowsalya *et al.* (2016).

The PCV and GCV were low for days to flower initiation, days to 50% flowering, days to maturity and number of seeds per pod. A comparison of difference between phenotypic coefficient of variation and genotypic coefficient of variation estimates showed wide differences in respect of number of pods per plant, seed yield per plant, number of seeds per plant, harvest index, number of primary branches per plant, biological yield per plant, number of seeds per pod, 100-seed weight and days to 50% flowering. This might have been due to larger influence of environment on the expression of these traits. Days to flower initiation, days to maturity and plant height showed least differences between PCV and GCV, indicating the greater role of genetic factors influencing the expression of these characters. This indicated the utility of these characters in the selection programme.

5.2. Heritability and genetic advance:

Selection based on the particular character will be effective when its heritability estimates is high. Burton (1952) suggested that genotypic coefficient of variation together with heritability estimates would give the best picture of the extent of advance to be expected by selection. The total variability present in the population was not transmitted as such, only its heritable portion was transmitted to the next generation. The knowledge of heritable proportion of genetic variability present in the population can be obtained by another genetic parameter that is heritability estimates.

Heritability estimate in broad sense is the ratio of genotypic variance to the phenotypic variance and is expressed in percentage. It is an index of transmission of a character from parents to their off-springs. It helps the plant breeders in the selection of superior genotypes from the genetically variable population.

Estimates of heritability value was high for plant height and this character may be used to construct selection indices so that the progress made through them would be high. These result were in consonance with the finding of Konda (2009) and Reni et al. (2013) for plant height.

The estimates of heritability are influenced by various factors such as sample size, sampling methods, effects of linkage, method of estimation and population density etc. and other biotic and a-biotic factors hence their utility will be restricted. Thus, heritability values coupled with genetic advance would be more reliable and useful in formulating selection criteria. Genetic advance is the product of selection intensity, heritability and phenotypic standard deviation.

Plant height showed high value of heritability coupled with high genetic advance as per cent of mean indicating lesser influence environmental factors on the expression of this character and prevalence of additive gene action in their inheritance, hence, are amenable for simple selection. These results were in accordance with the findings of Konda (2009) for plant height.

Moderate heritability with high genetic advance was recorded for seed yield per plant, biological yield per plant and number of seeds per plant indicating lesser influence of environment but prevalence of additive gene action, hence, amenable for selection.

The character like number of seeds per pod, days to maturity, days to 50% flowering and days to flower initiation had low values for heritability and genetic advance, may not respond favorably to selection.

5.3. Correlation coefficient and path analysis:

Correlation coefficient studies:

The knowledge of association of yield and other traits is basic need to identify the major yield component characters in the experimental material. Correlation could be phenotypic, genotypic or environmental. Correlation coefficient is a statistical measure which is used to find out the degree and direction of relationships between two or more variables. Thus, it measures the mutual relationship between two or more variables. It provides better understanding of yield components which helps the plant breeder during selection (Robinson *et al.* 1951; Johnson *et al.* 1955). For the selection purpose, phenotypic correlation coefficient is of little practical value unless genetic correlation coefficients between pair of characters were in the same directions when estimated separately. Genotypic correlation coefficients provide a measure of genetic association between characters and were generally used in selection of one character as a means of improving another. Genetic correlation coefficient may be accounted by linkage and pleiotropy. Environmental correlation coefficient indicated non-genetic values and arises due to the fact that several observations are affected by the same amount of environmental factors. Therefore, the knowledge of correlation coefficient is of great significance.

Correlation coefficient studies showed that for most of characters pairs, genotypic and phenotypic associations were in the same direction and the genotypic estimates were higher than the phenotypic ones, indicating an inherited association between the characters.

Seed yield per plant, the most important economic trait, exhibited positive association with days to 50% flowering, plant height, biological yield per plant, number of pods per plant, number of seeds per plant, number of seeds per pod, number of primary branches per plant, 100 seed weight and harvest index both at phenotypic and genotypic level. Positive association of plant height, number of primary branches per plant, number of pods per plant, number of seeds per plant, and number of seeds per pod with seed yield per plant have also been reported by Konda *et al.* (2008); Parveen *et al.* (2011) Bharti *et al.* (2013); Patel *et al.* (2014); Kumar *et al.* (2015); Gowsalya *et al.* (2016) and Mehra *et al.* (2016).

These results suggested that the characters days to 50% flowering, plant height, biological yield per plant, number of pods per plant, number of seeds per plant, number of seeds per pod, number of primary branches per plant, 100 seed weight and harvest index were positively correlated with seed yield. These results indicated that simultaneous improvement in seed yield through these traits could be achieved within a short period by simple selection procedures.

Hence, on the basis of correlation coefficient studies, it is obvious, that the characters *viz*., days to flower initiation, days to 50% flowering, plant height, biological yield per plant, number of pods per plant, number of seeds per plant, number of seeds per pod, number of primary branches per plant, 100 seed weight and harvest index were positively correlated with seed yield and also among themselves indicating their utility in selection programme for improving yield potential of population.

Path coefficient analysis:

Correlation coefficient provides information regarding the direction and magnitude of relationship between two or more variables. Path coefficient analysis, on the other hand, is an efficient statistical technique specially designed to quantify the inter-relationships of different components and their direct and indirect effects on the seed yield. Through this technique, yield-contributing components can be ranked and specific traits producing a given correlation coefficient can be revealed. These will in turn impair the true association existing between a component and seed yield and a change in any one component was likely to disturb the whole network of cause and effect. Thus, each component has two paths of action *viz*., (1) The direct influence on seed yield (2) Indirect effects through components which are not revealed from the correlation coefficient studies. The path analysis that was first suggested by Wright (1921) provides an effective measure of direct and indirect causes of association and depicts the relative importance of each factor involved in contributing to the final product that is, seed yield. In order to obtain the such relations, the cause and effect of relationship between yield *per se*, eleven yield components was studied in black gram through path coefficient analysis and the results have been discussed below.

As the result of this study, it revealed that number of seeds per plant registered the maximum positive direct effect followed by 100-seed weight, days to maturity and days to flower initiation, while the correlation coefficient of these four traits with seed yield per plant was also positive. Therefore, a true relationship exists between seed yield per plant with number of seeds per plant, 100-seed weight, days to maturity and days to flower initiation. These results were in agreement with the findings of Bharti *et al.* (2013) and Mehra *et al.* (2016) for seeds per plant.

Number of pods per plant showed positive correlation coefficient with seed yield per plant; exhibited considerable negative direct contribution. This negative direct contribution was converted into positive correlation coefficient mainly due to its positive indirect effects *via.* Number of seeds per plant, days to maturity and plant height.

Biological yield per plant had positive correlation coefficient with seed yield per plant; exhibited negative direct contribution. This negative direct contribution was converted into positive correlation coefficient mainly due to its positive indirect effects *via* number of seeds per plant, harvest index, 100-seed weight, days to maturity and days to flower initiation.

Harvest index had positive correlation coefficient with seed yield per plant; exhibited negative direct contribution. This negative direct contribution was converted into positive correlation coefficient mainly due to its positive indirect effects *via* 100-seed weight, biological yield per plant, number of seeds per plant, number of primary branches per plant, days to 50% flowering, plant height and days to flower initiation.

The result obtained from genotypic correlation coefficient and path analysis indicated that the characters namely; number of seeds per plant and 100-seed weight exhibited strong positive correlation coefficient and high magnitude of positive direct effects on seed yield. Hence, it is suggested that while exercising selection index more weightage should be given to number of seeds per plant and 100-seed weight as an important components influencing seed yield of black gram.

Correlation coefficient analysis at phenotypic and genotypic levels indicated that apart from number of seeds per plant and 100-seed weight other traits like number of pods per plant, number of primary branches per plant, number of seeds per pod, biological yield per plant, harvest index, days to 50% flowering, plant height and days to flower initiation were positive correlated with seed yield per plant. It is therefore suggested that preference should also be given to these traits in selection programme to isolate superior strains with genetic potentiality for higher seed yield.

The residual effects were reported to be negligible at both phenotypic and genotypic levels. This indicated that most of the components, which contribute for seed yield have already been included in the present investigation.

5.4. Genetic divergence:

Genetic divergence study is a vital tool for the evaluation of entries and selection of parents for the breeding programme. So, present study was aimed at analysis of genetic divergence among the 46 genotypes and to identify the superior and divergent lines for formulating the crossing programme.

Wilk’s lambda criterion was used for simultaneous test of significance of differences in the mean values of the twelve characters and the pooled effect was found significant indicating a wide spectrum of diversity among the genotypes.

D^2 analysis:

The multivariate analysis giving the D^2 value, the 46 genotypes were grouped into twelve clusters.

The inter-cluster distances were greater than intra-cluster distances, revealing that considerable amount of genetic diversity existed among the genotypes of different clusters. Average intra-cluster distance revealed that cluster II, which contained one genotype, had lowest intra-cluster distance. It indicated that these genotypes were closely related in their evolutionary process and passed through similar evolutionary factors. Highest intra-cluster distance of 2.148 was observed for cluster I which comprises of five genotypes. This suggests that these five genotypes possess all most same genetic makeup with minute difference due to evolutionary channel.

Inter-cluster distance is the main criterion for selection of genotypes for hybridization programme using D^2 analysis. Genotypes belonging to the clusters with maximum inter-cluster distance are genetically more divergent and hybridization between genotypes of divergent clusters is likely to produce wide spectrum of genetic variability with desirable segregates. The maximum inter-cluster distance of 9.900 was recorded between cluster V and cluster II followed by cluster II and I (9.781), cluster XI and II (9.701), cluster VII and II (9.375), cluster IX and II (9.267), cluster III and II (7.459) and cluster VI and II (7.323).It suggested that if the diverse genotypes from these diverse groups were used in breeding programme, it was expected to produce a wide range of genetic variability in the population. The lowest inter-cluster distance of 2.333 was recorded between cluster IX and VIII which indicates that the genotypes of these clusters were genetically less diverse and were almost with same genetic makeup or follows more or less same evolutionary phases during development.

Sometimes a breeder is asked to improve a particular trait of a variety which was otherwise suitable. For this a donor parent is required. Information about a range of suitable donors thus becomes inevitable. Estimates of cluster mean make information readily available. Cluster means for the twelve traits of all the twelve clusters were worked out. It was found that Cluster I had lowest mean value for days to flower initiation, days to 50% flowering and days to maturity which indicates the selection of the genotypes from cluster I for the development of short duration/early maturing genotypes. Cluster VI had the highest mean value for 100-seed weight. This suggested that genotypes from cluster VI may be selected for development bold seeded genotypes. Cluster II had the highest mean value for number of primary branches per plant, number of pods per plant number of seeds per plant, biological yield per plant and seed yield per plant. Cluster III had lowest mean value for plant height and the genotypes of this cluster will be useful for development of short stature plant in black gram. To improve any particular trait donor may be selected from these clusters for hybridization program to evolve high yielding strains.

To improve seed yield, genotypes from cluster II (KU8-632) and cluster IV (KU7-320 and KU8-278) would be right choice; cluster I (KU7-522, KU7-619, KU7626, KU7-608 and IVU-486) for earliness in flower initiation, 50% flowering and maturity could be used to develop short duration black gram varieties. To develop dwarf variety, genotypes from Cluster III and for tall variety genotypes from Cluster X (KU3-62, JU-840 and TPU-4) would be an ideal choice.

Practical utility:

Based on the study of genetic divergence the following entries were identified which can be used in breeding programme.

Table: 5.1 Study of genetic divergence showing the following entries identified in breeding programme

Cluster number	**Number of genotypes**	**Name of genotypes**	**Desirable characteristics**
I	5	KU7-522, KU7-619, KU7-626, KU7-608, IVU-486	Early to flower initiation, 50% flowering and maturity
II	1	KU8-632	Highest biological yield per plant, more primary branches per plant, number of pods per plant, number of seeds per plant and seed yield per plant.
III	4	KU7-632, KU8-611, KU8-612, KU8-532	For dwarfness
VI	5	RBU-466-D, KU8-476, JU-86, TYPE-9, IVU-466-D	Highest 100-seed weight with bolder seeds
VII	4	KU8-613, KU8-605, KU8-532, IU-421	More number of seeds per pod
X	3	KU3-62, JU-840,TPU-4	For tallness

It may be inferred from the present study that the genotypes with high genetic divergence are likely to produce potential crosses for exploitation of hybrid vigour for commercial production.

CHAPTER – VI

SUMMARY, CONCLUSION AND SUGGESTIONS FOR FURTHER WORK

A field experiment was conducted with forty six black gram genotypes, raised in Randomized Block Design with three replications during *kharif* season of 2016-17 at field of Regional Research Centre on Pulses, College of Agriculture, Indore (M.P.).

The observations were recorded on days to flower initiation, days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of pods per plant, number of seeds per plant, number of seeds per pod, 100-seed weight, biological yield per plant, harvest index and seed yield per plant from five competitive plants selected randomly from in each plot for collecting the information on existing genetic variability, heritability, expected genetic advance, genetic divergence, inter relationship among traits and direct and indirect contribution of traits. The salient findings of the present investigation entitled **"Study on genetic diversity and character association of yield and its component in Black gram (*Vigna mungo* (L.) Hepper.)"** have been listed below:

Summary:

1. The analysis of variance revealed highly significant differences among genotypes for all the characters studied indicating the existence of sufficient genetic variability in the experimental population.

2. Seed yield per plant, followed by, number of pods per plant, biological yield per plant and number of seeds per plant exhibited high phenotypic and genotypic coefficient of variation values suggested that high amount of genetic variability was present in the population for these traits.

3. A comparison of difference between phenotypic coefficient of variation and genotypic coefficient of variation estimates showed wide differences in respect of number of pods per plant, seed yield per plant, number of seeds per plant, harvest index, number of primary branches per plant, biological yield per plant, number of seeds per pod, 100-seed weight and days to 50% flowering. This might have been due to larger influence of environment on the expression of these traits. Days to flower initiation, days to maturity and plant height showed least differences between PCV and GCV, indicating the greater role of genetic factors influencing the expression of these characters. Thus, it indicated the utility of these characters in the selection programme.

4. The estimates of heritability in broad sense for most of the traits were low to moderate. High estimates were observed for number of plant height (79.80%). Moderate for biological yield per plant, 100 seed weight, seed yield per plant and number of seeds per plant, while days to flower initiation, days to 50% flowering, days to maturity, number of primary branches per plant number of pods per plant, harvest index, number of seeds per pod registered the low heritability. Plant height has high value of heritability coupled with high genetic advance as per cent of mean indicating lesser influence of environment on the expression of these characters and prevalence of more additive gene action in their inheritance, hence, are amenable for simple selection.

5. The characters *viz*., biological yield per plant, number of pods per plant, number of seeds per plant, number of primary branches per plant, 100-seed weight, plant height, harvest index, number of seeds per pod, days to 50% flowering and days to flower initiation recorded positive correlation coefficient with seed yield both at genotypic and phenotypic level.

6. Path coefficient analysis revealed a higher and positive direct effect for number of seeds per plant and 100-seed weight on yield.

7. The forty six genotypes of black gram were grouped into twelve clusters based on D^2 values. Among the twelve clusters, cluster VIII was largest including 9 genotypes, followed by, cluster IX, VI and I had 5 genotypes each. Clusters VII

and III had 4 genotypes each. Clusters XI, X and V had 3 genotypes each. Cluster XII and IV had 2 genotypes each and cluster II including 1 genotype.

8. The highest (D= 9.900) inter cluster distance was observed between cluster II and V, followed by, cluster I and II (9.781), cluster II and XI (9.701), cluster II and VII (9.375), cluster II and IX (9.267), cluster II and III (7.459), cluster II and VIII (7.445) and cluster II and VI (7.323) indicating wide diversity between genotypes in these clusters and the lower cluster distance of D = 2.333 was observed between cluster VIII and IX followed by cluster III and XII (2.577), cluster III and VIII (2.558), cluster VIII and XII (2.719), cluster IV and XII (2.815) and cluster VI and IX (2.883) indicating close relationship between genotypes in these clusters. The highest (D = 2.148) intra-cluster distance was found for cluster I followed by cluster XI (1.900). The cluster II registered the lowest intra-cluster distance of 0.000, followed by, cluster IV recording 0.724.

9. The cluster I (KU7-522, KU7-619, KU7-626, KU7-608 and IVU-486) for earliness in flower initiation, 50% flowering and maturity; cluster III (KU7-632, KU8-611, KU8-612 and KU8-532) for dwarf plant type; cluster X (KU3-62, JU-840 and TPU-4) for tall plant type; cluster II (KU8-632) for more number of primary branches per plant, number of seeds per plant, number of pods per plant, biological yield per plant and seed yield per plant; cluster VI (RBU-466-D, KU8-476, JU-86, TYPE-9 and IVU-466-D) for high 100-seed weight that is bolder seeds may be used as suitable parents for hybridization programme in black gram.

Conclusion:

1. The analysis of variance revealed highly significant differences among genotypes for all the characters studied indicating the existence of sufficient genetic variability in the experimental population. Seed yield per plant, followed by, number of pods per plant, biological yield per plant and number of seeds per plant had high phenotypic and genotypic coefficient of variation values further suggested that the high existence of genetic variability was present in population for these traits. Plant height has high value of heritability coupled with high

genetic advance as per cent of mean indicating lesser influence of environment on the expression of these characters and prevalence of more additive gene action in their inheritance.

2. Magnitude of phenotypic coefficients of variation in selected black gram germplasm was higher than genotypic coefficients of variation, indicating that environmental factors were influencing characters expression. High genetic advance and moderate heritability was recorded for seed yield per plant, biological yield per plant and number of seeds per plant hence selections based on the traits could improve productivity in black gram directly.

3. The characters *viz*., biological yield per plant, number of pods per plant, number of seeds per plant, number of primary branches per plant, 100-seed weight, plant height, harvest index, number of seeds per pod, days to 50% flowering and days to flower initiation recorded positive correlation coefficient with seed yield both at genotypic and phenotypic level. The magnitude of genotypic correlation coefficient was higher than phenotypic correlation coefficient indicating that the association of the traits with seed yield controlled the genetic factors like linkage and/or pleotropism. Path coefficient analysis revealed a higher and positive direct effect for number of seeds per plant and 100-seed weight on yield should be given due weight-age in selection of parents for hybridization for yield improvement.

4. The highest inter cluster distance was observed between cluster V and II (9.900) indicating wide diversity between genotypes in these clusters. A cross between these two cluster’s genotypes is expected to give a heterotic hybrid and wide spectrum of variability. Therefore, these genotypes may be used as parents for hybridization.

5. The cluster I (KU7-522, KU7-619, KU7-626, KU7-608 and IVU-486) for earliness flower initiation, 50% flowering and maturity; cluster III (KU7-632, KU8-611, KU8-612 and KU8-532) for dwarf plant type; cluster X (KU3-62, JU-840 and TPU-4) for tall plant type; cluster II (KU8-632) for more number of primary branches per plant, number of seeds per plant, number of pods per plant,

biological yield per plant and seed yield per plant; cluster VI (RBU-466-D, KU8-476, JU-86, TYPE-9 and IVU-466-D for 100) for seed weight that is bolder seeds may be used as suitable parents for hybridization programme.

Suggestions for further work:

The following suggestions have been made for further study:-

- The genetic variability reported for different characters in relation to yield should be exploited for future genetic improvement of black gram.
- Characters showing high heritability with high genetic advance should be utilized in direct selection.
- A better crop ideotype should be developed using findings from association analysis.
- The promising diverse genotypes identified can be tested for combining ability and inheritance of yield and its contributing traits for further use in breeding programme.

BIBLIOGRAPHY

Ali, M. N.; Gupta, S.; Bhattacharyya, S. and Sarkar, H. K. (2008). Character study in urd bean (*Vigna mungo* (L.) Hepper). *Environ. Eco*. **26** (2A): 952-954.

Anonymous. (2014-15). Area and production of black gram statistical database. www.ipga.co.in *and* www.mpkrishi.org.

Babu, A.; Kamala, V.; Sivaraj, N.; Sunil, N.; Pandravada, S. R.; Vanaja, M. and Varaprasad, K.S. (2010). DIVA-GIS approaches for diversity assessment of pod characteristics in black gram (*Vigna mungo* (L.) Hepper). *Current. Sci.,* **98** (5): 616-619.

Bharti, B.; Kumar, R.; Bind, H. N.; Kumar, A. and Sharma, V. (2013). Correlation and path analysis for yield and its components in blackgram (*Vigna mungo* L.). *Progressive Res*. 8 (special issue): 617620.

Burton, G. W. (1952). Quantitative inheritance in grasses. *Proc.6th Int. Grassland Cong.* 1:224-83.

Burton, G.W. and Devane, R.W. (1953). Estimating heritability in tall foscue (*Festuca arubdinaces*) from replicated clonal material. *Agron. J.,* 45:478-481.

Chauhan, M. P.; Mishra, A. C. and Singh, A. K. (2007). Correlation and path analysis in urd bean. *Legume Res*., **30** (3): 205-208.

Chauhan, M. P.; Mishra, A. C.; Singh, A. K. (2008). Genetic divergence studies in urd bean (*Vigna mungo* L.) *Legume Res*.; **31** (1): 63-67.

Deepshikha; Lavanya, R. G. and Kumar, S. (2014). Assessment of Genetic Variability for Yield and Its Contributing Traits in Blackgram. *Trends in Biosci,* **7** (18): 2835-2838, 2014.

Dewey, O. R. and Lu, K.H. (1959). A correlation and path coefficient analysis of component of crested wheat grass seed production. *J. Agron.* 57:515-18.

Elangaimannan, R.; Anbuselvam, Y. and Karthikeyan, P. (2008). Genetic diversity in blackgram (*Vigna mungo* (L.) Hepper). *Legume Res*., **31** (1): 57-59.

Fisher, R. A. and Yates, F. (1938). Statistical tables for biological, agricultural and medicinal research. 5 Aufl. Oliver and Boyd. Edinburgh.

Geethanjali; Anuradha, C.; and Suman (2015). Genetic Diversity for Yield and its Components in Black gram (*Vigna mungo* L.). vol. 4, Issue: 8:2277 – 8179.

Gowsalya, P.; Kumaresan, D.; Packiaraj, D. and KannanBapu, R. J. (2016). Genetic variability and character association for biometrical traits in Blackgram (*Vigna mungo* (L.) Hepper). *Electron. J. Plant Breed., vol.*: 7 no. 2, 0975-928.

Hadimani, A.; Konda, C. R.; Nidagundi, J. M. and Patil, R. (2016). Genetic diversity analysis in Black gram [*vigna mungo* (L.) Hepper] based on quantitative traits. *Green Farming Vol.* (3): 598-601.

Jayamani, P. and sathya, M. (2013). Genetic diversity in pod characters of blackgram (*Vigna mungo* L. Hepper). *Legume Res.,* **36** (3):220-223.

Johnson, H. W.; Robinson, H. F. and Comstock, R. E. (1955). Genotypic phenotypic correlation in soybean and their implication in selection. *Agron. J.,* 47: 477-485.

Jyothsna, S.; Patro, T.S.S.K.; Ashok, S.; Sandhya Rani, Y. and Neeraja, B. (2016). Character association and path analysis of seed yield and its yield components in black gram (*Vigna mungo* (L.) Hepper). *Int. J. Theo. Appli. Sci.* **8** (1): 12-16.

Kamannavar, P. Y.; Revanappa, S.B.; Vijaykumar, A. G.; Basamma, K. and Ganajaxi (2016). Nature of genetic diversity for seed yield and its component traits in urdbean [*Vigna mungo* (L.) Hepper]. *Indian J. Agric. Res.,* **50** (1) 2016: 96-98.

Konda, C. R.; Salimath, P. M. and Mishra, M. N. (2008). Correlation and Path coefficient analysis in black gram. [*Vigna mungo* (L.) Hepper]. *Legume Res*., **31** (3): 202-205.

Konda, C.R.; Salimath, P.M. and Mishra, M.N. (2009). Genetic variability studies for productivity and its components in black gram [*Vigna mungo* (L.) Hepper]. *Legume Res.,* **32** (1): 59-61.

Kumar, G. V.; Vanaja, M.; Lakshmi, N. J. and Maheshwari, M. (2015). Studies of variability, heritability and genetic advance for quantitative traits in black gram (*Vigna mungo* (L.) Hepper). *Agric. Res. J.* **52**(4):28-31.

Kumar, G. V.; Vanaja, M.; Sathish, P.; Vagheera, P. and Lakhsmi, N. J. (2015). Correlation analysis for quantitative traits in blackgram (*Vigna mungo* (L.) Hepper) in different seasons. *Int. J. of Scientific and Res. Publications*. **5** (4): 1-10.

Lenka, D. and Mishra, B. (1973). Path coefficient analysis of yield in rice varieties. *Indian J. Agric. Sic.*, 43: 376-379.

Mahalanobis, P.C. (1928). On the generalised distance in statistics. *Proc. Nat. Acad. Sci.*, 19: 201-208.

Makeen, K.; BabuSuresh, G.; Lavany, G.R. and Kumari, A. (2009). Genetic divergence and character association in micromutants of urdbean (*Vigna mungo* L.) variety T9. *Academic J. Plant Sci.* **2** (3): 205-208.

Mandal, A. B. and Majumdar, N. D. (2014). Genetic divergence, heritability and genetic advance in Black gram (*Vigna mungo* (L.) hepper). *J. of the Andaman Sci. Association*. **19** (1): 9-13.

Mathivathana, M. K.; Shunmugavalli, N.; Muthuswamy A. and Harris, C. V. (2015). correlation and path analysis in black gram. *Agric. Sci. Digest*., **35** (2): 158-160.

Mehra, R.; Tikle, A.N.; Saxena, A.; Munjal, A.; Rekhakhandia, and Singh, M. (2016). Correlation, path-coefficient and genetic diversity in black gram [*Vigina mungo* (L) Hepper] *Int. Res. J. Plant Sci.,* **7** (1): 001-011.

Meshram, M. P.; Ali, R. I.; Patil, A. N. and Meena Sunita (2013). Variability studies in M3 generation in black gram (*Vigna mungo* (L.) Hepper*). Int. Quarterly J. Life Sci.* **8** (4): 1357-1361.

Miller, P.A.; Williams, C.V.; Robinson, H.F. and Comstock, R.E. (1958). Estimates of genotypic and environmental variance and covariance in upland cotton and their implication in selection. *Agron. J.*, **50** (3): 126-131.

Mohammad, R. M.; Mohammad M. R.; Habiba, U.; Das, K.R. and Mohammad S.I. (2016). Correlation and Path coefficient analysis of black gram. *European Academic Res.* **3** (10): 10906-10917.

Neelavathi, S. and Govindarasu, R. (2009). Character association and component analysis in rice fallow black gram. *Res. on Crops*. **10** (2): 308-310.

Neelavathi, S. and Govindarasu, R. (2010). Analysis of variability and diversity in rice fallow black gram [*Vigna mungo* (L.) Hepper]. *Legume Res*. **33** (3): 206 – 210.

Niranjan, S. and Rama Chandra, M. (2009). Genetic divergence and selection indices among the micro mutant lines in blackgram [*Vigna mungo* (L.) Hepper]. *J. Crop Sci. Biotech*. **12** (2): 69-72.

Panigrahi, k. k.; Mohanty, A. and Baisakh, B. (2014). Genetic divergence, variability and character association in landraces of blackgram (*Vigna Mungo* L. Hepper). *J. Crop and Weed*, **10** (2):155-165.

Parveen, S. I.; Sekhar, M. R.; Reddy, D. M. and Sudhakar P. (2011). Correlation and path coefficient analysis for yield and yield components in blackgram (*Vigna mungo* (L.) Hepper). *Int. J. Applied Biology and Pharmaceutical Technology*, **2** (3): 619-625.

Patel, R.V.; Patil, S.S.; Patel, S.R. and Jadhav, B.D. (2014). Genetic variability and Character association in blackgram [*Vigna mungo* (L.) Hepper]. *Trends in Biosci.* **7** (23): 3795-3798.

Panse, V. G. and Sukhatme, P. V. (1954). Statistical Methods for Agricultural workers. ICAR, New Delhi, 97-151.

Priyanka, S.; Rangaiah, S.; and Showkath Babu, B. M. (2016). Genetic variability estimates of quantitative and qualitative traits in black gram. *Int. J. Agric. Sci. ISSN*: 0975-3710 & *E-ISSN*: 0975-9107, **8** (40):1821-1824.

Punia, S. S.; Gautam, N. K.; Baldev, R.; Verma, P.; Dheer, M.; Jain, N. K.; Koli, N.R.; Mahavar, R. and ` Jat, V. S. (2014). Genetic variability and correlation studies in urdbean (*Vigna mungo* L. Hepper) *Legume Res.,* **37**(6): 580 584.

Pushpa, R.Y.; Koteswara Rao, Y.; Satish, Y. and Sateesh Babu, J. (2013). Estimates of genetic parameters and path analysis in blackgram (*Vigna mungo* (L.) Hepper). *Int. J. of Plant, Animal and Environ. Sci.* 3: 4.

Ramya, B.; Nallathambi. G. and Ram, S. G. (2014). Genetic variability, heritability and Genetic advance in induced mutagenesis black gram (*Vigna mungo* (L.) Hepper). *Plant Archives*, **14** (1):139-141.

Rao, C.R. (1952). Advanced statistical methods in biometrical research. John Wiley and Sons Inc., New York.

Reni, Y. P.; Koteswara R. Y.; Satish, Y. and Sateesh, J. B. (2013). Estimates of genetic parameters and path analysis in blackgram (*Vigna mungo* (L.) Hepper). *Int. J. of Plant, Animal and Environ. Sci.* **3** (4):231 234.

Robinson, H. F.; Comstock, R. E. and Harvey. P. M. (1951). Genotypic and phenotypic correlations in corn and their implications in selection. *Agron. J*, 43: 262-67.

Sarkar, B. (2014). Genetic diversity study for grain yield and its components in urd bean (*Vigna mungo* (L.) Hepper) using different clustering methods. *J. Food Legumes* **27** (2):99-103.

Senapati, N. and Mishra, R. C. (2010). Genetic divergence and variability studies among micro mutants in black gram [*Vigna mungo* (L.) Hepper]. *Legume Res*., **33** (2): 108-113.

Shivade, A. H.; Rewale, P. A. and Patil, B. S. (2011). Correlation and Path analysis for yield and yield components in black gram [*Vigna mungo* (L.) Hepper]. *Legume Res.*, **34** (3): 178 - 183, 2011.

Singh M.; Swarup I.; Billore M. and Chaudhari P.R. (2012). Genetic diversity for yield and its components in blackgram (*Vigna mungo* L.). *Res. J. of Recent Sci.* **2** (ISC-2012): 4-6.

Singh, I. P.; Kumar, S.; Singh, J. D. and Singh, K. P. (2007). Genetic variation, character association and path analysis between grain yield and its component in black gram [*Vigna mungo* (L.) Hepper]. *Prog. Agric*., **7** (1/2): 113-115.

Singh, R. K. and Choudhary, B. D. (1977) Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi. 318.

Sohela, H. M.; Miaha, R.; Mohiuddinb, J. S.; Islamc, S.; Rahmand, M. and Haquee, A. (2016). *J. Biosci. Agric. Res*. **7** (02): 621-629.

Umadevi, M. and Ganesan, N. M. (2007). D^2 analysis for yield and quality characters in blackgra (*Vigna mungo* (L.) Hepper). *Legume Res*., **30** (3):197-200.

Venkateswarlu, O.; Reddy, D. K. R.; Jyothi, G. L. S and Obaiah, M. C. (2011). Genetic parameters and Inter-relationship analysis in blackgram [*Vigna mungo.* (L.) Hepper]. Agricultural Research Communication Centre, Karnal, India. *Legume Res*., **34** (2): 149-152.

Veeramani; Venkatesan, N. M.; Thangavel, P. and Ganesan, J. (2005). Genetic variability, heritability and genetic advance analysis in segregating generation of black gram (*Vigna mungo* (L.) Hepper). *Legume Res*. **28** (1):49-51.

Weber, C.R. and Moorthy, H.R. (1952). Heritable and non-heritable relationship and variability of oil content and agronomic characters in the F2 generation of soybean crosses. *Agron. J*., 44: 202-209.

Wilk's, S. S. (1932). Certain generalizations in the analysis of variance. *Biometrics*. 24:471.

Wright, S. (1921). Correlation and causation. *J. Agric. Res*., 20: 257-87.

Wright, S. (1934). The analysis of variance and correlation between relatives with respect to deviation from an optimum. *J. Genet*., 30: 243-256.

Appendix Mean performance of yield and its components of 46 genotypes of Blackgram

S.N.	Genotypes	Days to flower initiation	Days to 50% flowering	Days to maturity	Plant height	No. of primary branches/plant	No. of pods/ plant	No. of seed/plant	No. of seed/ pod	100 seed weight	Biological yield/ plant	Harvest index	Seed yield/ plant
1	KU7-522	34.50	41.00	64.00	12.27	3.63	12.73	77.70	6.30	3.50	6.20	44.60	2.67
2	KU7-618	35.33	45.00	68.67	12.20	3.07	13.77	78.00	5.77	4.50	5.97	63.10	3.70
3	KU7-619	35.67	41.00	62.33	13.63	3.30	14.20	92.27	6.30	3.50	10.27	31.20	3.23
4	KU7-626	35.00	41.67	65.33	12.07	2.87	13.30	83.17	6.43	3.30	6.30	39.10	2.30
5	KU7-635	36.50	47.00	72.00	10.73	3.30	10.10	62.30	6.07	4.23	5.10	48.90	2.37
6	KU7-608	31.50	42.50	65.67	11.10	2.30	16.20	106.77	6.20	3.27	8.87	35.70	3.10
7	IVU-466-9	32.00	42.00	64.67	10.97	2.87	13.87	82.90	5.97	4.10	7.07	46.10	3.17
8	IVU-486	36.50	48.00	70.67	17.87	4.10	15.77	106.97	6.63	4.50	11.10	43.03	4.77
9	KU09-252	34.00	47.67	69.67	18.20	3.30	12.97	64.10	4.97	3.50	10.07	23.70	2.13
10	KU7-629	35.67	47.67	70.00	16.20	2.77	14.77	92.17	6.30	4.03	10.77	34.07	3.73
11	KU7-354	35.33	49.00	71.67	14.30	3.30	15.87	94.87	6.30	4.03	9.77	38.80	3.83
12	KU7-632	34.83	50.50	69.50	12.43	2.80	17.30	103.80	6.53	3.50	10.80	34.43	3.70
13	KU7-369	36.67	46.00	71.50	17.00	3.20	19.20	122.30	6.20	3.80	11.10	45.80	4.90

S.N.	Genotypes	Days to flower initiation	Days to 50% flowering	Days to maturity	Plant height	No. of primary branches/plant	No. of pods/plant	No. of seed/plant	No. of seed/pod	100 seed weight	Biological yield/plant	Harvest index	Seed yield/plant
14	KU7-320	35.00	48.50	70.00	12.73	3.30	25.73	179.13	6.63	4.23	15.10	46.77	7.07
15	KU3-62	36.50	47.00	67.67	17.73	3.63	14.77	124.97	6.30	3.50	14.20	30.67	4.30
16	KU8-606	35.67	46.00	70.50	19.10	2.63	13.80	88.70	6.43	4.03	10.30	36.63	3.50
17	KU8-278	34.00	49.50	71.00	12.43	3.63	22.80	153.63	6.63	4.17	12.80	47.03	6.10
18	KU8-611	35.50	47.00	68.00	11.80	3.23	18.30	109.50	5.93	4.03	10.13	42.83	4.33
19	KU8-638	36.50	45.50	67.50	16.63	2.80	11.60	74.60	6.13	5.03	8.13	46.00	3.63
20	KU8-632	35.67	47.50	69.50	13.63	4.43	30.63	230.03	6.80	4.03	17.80	48.33	8.37
21	RBU-466-D	34.00	45.00	64.00	15.10	2.80	19.00	136.13	7.13	4.50	11.80	52.10	6.13
22	KU8-613	35.50	48.00	69.50	11.63	2.30	11.13	85.03	7.50	4.00	8.00	41.43	3.33
23	KU8-621	35.83	50.00	71.00	11.30	3.30	19.63	156.20	6.63	3.50	14.43	38.10	5.40
24	KU8-602	35.83	50.00	72.00	17.30	3.30	15.80	109.50	6.80	5.00	12.10	44.53	5.43
25	KU8-605	36.00	51.50	74.50	11.30	2.30	13.30	95.80	7.30	4.00	8.93	42.50	3.80
26	KU8-612	33.33	49.50	71.50	11.27	3.63	19.10	122.90	6.50	3.50	11.13	35.03	4.23
27	KU8-636	35.67	52.50	73.50	12.93	3.63	18.80	118.40	6.17	4.50	14.63	35.13	5.13
28	KU8-532	34.00	51.50	72.50	13.93	2.97	14.80	103.30	6.93	3.13	8.80	37.23	3.03
29	KU8-534	34.33	49.50	70.50	11.50	2.93	20.00	125.00	6.00	3.50	9.80	41.40	4.10
30	IU-421	36.00	52.50	73.50	12.80	3.10	14.30	101.10	7.00	3.03	7.43	40.30	2.93

S.N.	Genotypes	Days to flower initiation	Days to 50% flowering	Days to maturity	Plant height	No. of primary branches/plant	No. of pods/ plant	No. of seed/plant	No. of seed/ pod	100 seed weight	Biological yield/ plant	Harvest index	Seed yield/ plant
31	KU8-532	34.50	49.50	69.50	12.93	3.10	15.93	92.10	5.80	3.23	13.00	21.23	2.70
32	KU8-476	33.50	46.00	66.50	19.43	2.93	16.43	115.13	6.63	3.97	11.43	40.10	4.60
33	IU-10	33.33	48.00	68.50	15.30	2.63	12.80	79.10	6.13	4.00	8.30	37.50	3.13
34	IU-466-9	36.00	49.00	70.00	14.80	2.93	14.80	101.07	6.80	4.00	10.60	40.83	4.00
35	IU-2	36.00	49.50	69.00	15.50	2.93	18.63	130.53	6.60	4.00	13.00	47.43	5.13
36	JU-840	34.50	44.00	67.00	16.80	3.50	18.60	119.13	6.43	4.03	17.63	26.73	4.70
37	JU-3	36.00	46.00	67.00	18.30	3.50	11.80	76.23	6.43	5.00	9.43	39.30	3.70
38	JU-86	34.67	46.50	66.00	15.13	2.83	14.50	96.73	6.43	5.00	11.30	43.23	4.80
39	TVPE-9	34.50	46.00	68.50	17.43	3.30	16.00	107.80	6.80	4.50	12.93	37.43	4.80
40	TPU-4	36.00	50.50	73.00	17.30	3.63	19.80	130.63	6.63	3.23	14.30	27.33	3.83
41	IU-466-9	37.00	52.00	73.50	14.80	3.30	15.13	90.90	6.07	4.00	10.00	36.33	3.60
42	IVU-486	35.17	49.00	71.00	15.30	3.43	15.43	101.90	6.27	3.97	9.93	40.83	4.00
43	IVU-466-D	34.00	43.50	68.50	17.30	2.80	19.13	129.13	6.80	4.50	13.80	42.93	5.93
44	DLOCAL-D	35.50	45.00	66.50	12.43	3.63	13.33	82.50	5.43	4.00	13.20	29.83	3.23
45	IU-466-9	35.50	45.00	70.00	13.60	3.30	12.10	68.53	5.80	4.50	7.30	42.20	3.03
46	IU-31-7	35.50	48.00	72.50	16.43	3.13	15.80	101.73	6.30	4.03	9.60	41.43	4.03

S.N.	Genotypes	Days to flower initiation	Days to 50% flowering	Days to maturity	Plant height	No. of primary branches/plant	No. of pods/ plant	No. of seed/plant	No. of seed/ pod	100 seed weight	Biological yield/ plant	Harvest index	Seed yield/ plant
	General mean	35.06	47.33	69.33	14.45	3.16	16.16	106.61	6.39	3.98	10.75	39.76	4.12
	SE (d) ±	1.26	2.45	2.55	0.99	0.37	2.78	19.25	0.37	0.30	1.68	5.77	0.79
	SE(m) ±	0.79	3.00	3.25	0.49	0.06	3.86	185.28	0.06	0.04	1.41	16.64	0.31
	CD (5%)	0.89	1.73	1.80	0.70	0.25	1.96	13.61	0.26	0.20	1.19	4.08	0.55
	CV (%)	4.42	6.35	4.51	8.47	14.36	21.08	22.12	7.16	9.28	19.18	17.79	23.48

VITA

The author of the thesis Mr. Nitesh Kumar Panwar s/o Shri Lalit Kumar Panwar was born on February 14, 1993 at Chittaurgarh (Raj.).

He passed his High School in the year 2008 from Aacharya Shri Nanesh Sr. Sec. School, Danta, Chittaurgarh (Raj.) with 66.67 per cent marks. After that he passed Higher Secondary in the year 2010 acquiring 66.92 per cent marks from B.R. Shikshan Sansthan Sr. Sec. School, Chailasi, Sikar (Raj).

He completed his B.Sc. (Hort.) from RVSKVV Gwalior, Mandsaur Campus – K.N.K. College of Horticulture, Mandsaur (M.P.) in the year 2015 achieving 78.10 per cent marks.

After completing graduation he was selected for M.Sc. (Ag.) degree program in Plant Breeding and Genetics and was admitted to College of Agriculture, Indore under Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior (M.P.) in the year 2015. He has passed all the required courses in M.Sc.

He was allotted interesting problem as **“Study on Genetic Diversity and Character Association of Yield and its Components in Black Gram (*Vigna mungo* L. Hepper*)”*** for thesis work which has been duly completed and presented in this thesis. He is now submitting the thesis after completing the course with 7.8 OGPA out of 10.00 point scale.

During the entire period of his education from schooling to post graduation he was very sincere and honest towards his studies.

Nitesh Kumar Panwar