

EVALUATION OF GENETIC VARIABILITY IN BLACK GRAM (*VIGNA MUNGO L. HEPPE*) GERMPLASM

Nashra Aftab*, G.M. Lal, Ashish Sheera, N. Chandra Bose and Avneesh M. Tripathi

*Department of Genetics and Plant Breeding Naini Agriculture Institute
Sam Higginbottom University of Agriculture, Technology and Sciences, Allahabad,
Uttar Pradesh, India-211007*

Received-23.07.2018, Revised-25.08.2018

Abstract: The present investigation was conducted during kharif-2017-18 in the Field Experimentation Centre, Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture, Technology and Sciences, Allahabad to examine 39 Black Gram genotypes along with 2 check (T9 and AZAD.1) to evaluate Genetic variability, correlation for yield in black gram. The experiment was laid out in an Randomize Block Design replicate thrice. Analysis of variance showed highly significant differences among 39 genotypes of black gram for 13 characters studied. Moderate genotypic coefficient of variation and phenotypic coefficient of variation was recorded for number of clusters per plant, primary branches per plant and seed yield per plant. All characters showed High broad-sense heritability and high genetic advance as percent of mean was recorded for seed yield per plant and plant height. Biological yield, harvest index, seed yield per plant, exhibited high GCV, PCV and genetic parameters revealed that heritability (broad sense) and genetic advance as % of mean values were high for seed yield per plant indicating that selection would be fruitful for improvement of these traits.

Keywords: Black gram, Correlation, Genetic variability, Genotype

INTRODUCTION

Among pulses, Black Gram (*Vigna mungo* L.) is an important short duration crop widely cultivated in India which gives us an excellent source of easily digestible good quality protein and ability to restore the fertility of soil through symbiotic nitrogen fixation. The major constraints in achieving higher yield of this crop are lack of genetic variability, poor harvest index, suitable varieties and genotypes with adaptation to local condition. Yield is considered as an end product of a set of plant processes which are related to each other. It is very complex trait which controlled by poly genes and interlinked with other yield components, hence it is very difficult often to improve yield directly. It can be achieved by improving closely related traits. The systematic collection of black gram has displayed inadequate variability for biotic and abiotic genes. It is possible that genes for high productivity could have been lost due to overriding role of natural selection (Roopalakshmi *et al.*, 2003) and the genetic base of the present day collection remains poor (Delannay *et al.*, 1983) due to lack of variability owing to its autogamous nature. The creation of variability is difficult through hybridization due to its high self-pollination and flower droop (Deepalakshmi and Anandakumar, 2004) Besides the major constraints in achieving higher yield of blackgram is absence of suitable ideotypes for different cropping system, poor harvest index and susceptibility to disease (Soufmanien and Gopalakrishnan, 2004) . In order to improve yield and other polygenic characters, mutation breeding can be effectively utilized (Deepalakshmi and Anandakumar, 2004). Therefore genetic variability is the basic requirement for

making progress in crop breeding (Appalaswamy and Reddy, 2004). In India black gram is grown both in winter and summer as monocrop and inter crop, respectively. That is why no single plant type is appropriate for all production system. So the variability among the existing germplasm or the accessions is the primary need to develop appropriate plant type for specific production system. Black gram originated in India where it has been in cultivation from ancient times and is one of the most highly prized pulses of India. A successful breeding programme in black gram would need information on the nature and degree of genetic divergence in the available stock for choosing the right parents for further improvement (Falconer, 1981). Grain yield is complex character, which depends on its main components viz; number of pod per plant, pod length, number of seed per pod and 100 seed weight. These components are further dependent for their expression on several morphological and developmental traits, which are interrelated with each other and therefore, the parent selected for the breeding programmes aimed at increased seed yield should possess wide range of genetic variation for the above said morphological and developmental characters. Besides, it could be of interest to know the magnitude of variation due to heritable component, which in turn would be a guide for selection for the improvement of a population. In other words, for the improvement in any crop species, the knowledge of genetic variability for characters of economic importance and their heritability and genetic advance is of utmost importance in planning future breeding programme (Singh *et al.*, 2007). Therefore, the present investigation was carried out on set of 39 genetically

*Corresponding Author

diverse Black gram (*Vignamungo* L. Hepper) genotypes with the aim of assessing the genetic advance, heritability (Broad sense) and mean and component characters.

MATERIALS AND METHODS

The experimental material for the present investigation consisted of 39 genotypes obtained from the Department of Genetic and Plant Breeding, SHUATS, Allahabad. The present experiment was conducted in randomized block design at Field Experimentation Centre, Department of Genetics and Plant Breeding, Allahabad during *kharif*, 2017. The Allahabad district is situated at 25.280 N and 81.540 E with an altitude of 98m above sea level. Allahabad is located in the south-eastern of Uttar Pradesh and has a sub-tropical climate with extremes of summer and winter. Recommended cultural practices were followed to raise healthy crop. Five competitive plants from each genotype were randomly selected for recording observations on thirteen characters, viz., Days to 50 per cent flowering, Days to 50 per cent pod setting, Plant height (cm), Number of primary branches per plant, number of clusters per plant, number of pods per plant, Pod length (cm), days to maturity, Number of seeds per pod, Biological yield per plant (g), Harvest index (%), Seed index (g) and Seed yield per plant (g). Analysis of variance was carried out as per standard procedure (Fisher, 1938). Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) (Burton, 1952), heritability (Burton and Devane, 1953), genetic advance (Johnson *et al.*, 1955), were estimated.

RESULTS AND DISCUSSION

Analysis of variance

Analysis of variance revealed significant differences for all the characters indicating sufficient variability among the genotypes. The perusal of data revealed that the mean sum of squares due to genotypes showed highly significant for all the 13 quantitative characters. Significant genetic variation in various component characters exhibited by the genotypes indicated these characters might be effective. The results from analysis of variance among 39 blackgram[*Vignamungo*(L.) Hepper] genotypes for 13 quantitative characters are presented in Table.1. The analysis of variance revealed the existence of significant differences among the genotypes for all the traits. Hence, the data on all the 13 traits which showed significant differences among the entries were subjected to further statistical analysis. The quantitative characters are governed by many genes and are more influenced by environment. The phenotype observed is not transmitted entirely to next generation. Therefore, it is necessary to know the proportion of observed variability that is

heritable. Heritability estimates provides the assessment of amount of transmissible genetic variability to total variability, happens to be the most important basic component that determines the genetic improvement or response to selection. However, the degree of improvement attained through selection is not only dependent on heritability but also on the amount of genetic variation present in the breeding population and the extent of selection pressure applied by the breeder (Panigrahi *et al.* 2014).

Mean and Range of genotypes

The mean value, range, parental mean, hybrid mean, check mean, grand mean, standard error of mean and critical difference (CD) of parents and hybrids for all 13 characters which revealed a wide range of variation for all traits.

Days to 50% Flowering

In case of parents, the mean recorded for days to 50% flowering was 40.61. The highest mean, 49.66 was exhibited by AZAD-1. The lowest mean, 38.33 was showed by KPU-63-189. In case of crosses, the mean recorded for days to 50% flowering was 38.48. The highest mean, 49.00 was exhibited by cross SHUATS URD 54 (PU-31×KU-13-01). The lowest mean, 34.66 was showed by cross SHUATS URD 68 (MASH-338×IU-02-1-3).

Days to 50% pod setting

In case of parents, the mean recorded for days to 50% pod setting was 51.76. The highest mean, 57.33 was exhibited by AZAD-1. The lowest mean, 47.00 was showed by KPU-63-189. In case of crosses, the mean recorded for days to 50% pod setting was 48.25. The highest mean, 56.33 was exhibited by cross SHUATS URD 64 (MASH-338×T4). The lowest mean, 40.00 was showed by cross SHUATS URD 68 (MASH-338×IU-02-1-3).

Plant height (cm)

The population means of parents for the character, plant height was recorded as 55.60 cm, which ranged from 47.6 to 69.2 for parents PU-38 and T4 respectively. The parent T4 was found to be statistically significant with respect to other twelve parents. The population mean of crosses for plant height was recorded as 62.19 cm, which ranged from 43.7 to 83.6 for SHUATS URD 68 (MASH-338×IU-02-1-3) and SHUATS URD 71 (PU-11-14×UTTARA) respectively.

No. of Primary branches per plant

Among the parents, the mean performance for number of primary branches per plant was 2.41. The highest mean, 2.93 was calculated for parent LBG-648 and lowest mean, 1.86 was calculated for the parent PU-31. In case of crosses, mean performance for number of primary branches per plant was 3.40. The highest mean, 4.26 was calculated for the cross SHUATS URD 70 (PU-31×MU-06) and the lowest mean 2.33 for the cross, SHUATS URD 60 (PU-38×LBG-648).

Number of clusters per plant

Among the parents, the mean performance for number of clusters per plant was 9.64. The number of clusters per plant ranged from 7.60 for the parent VALLABH URD to 12.73 for the parent T4. In case of crosses, the mean performance for number of clusters per plant was 8.24. The highest mean, 12.33 was calculated for the cross SHUATS URD 55 (PU-31×KPU-13-192) and lowest mean, 5.00 was exhibited by the cross SHUATS URD 61 (PU-38×KPU-13-192).

Number of pods per plant

In case of parents, the mean performance for number of pods per plant was 24.80. The highest mean, 36.40 was showed by the parent AZAD-1 and lowest mean, 19.93 was exhibited by parent KU-96-7. In case of crosses, the mean performance for number of pods per plant was 26.79. The highest mean, 75.66 was calculated for the cross SHUATS URD 58 (PU-31×MU-06) and lowest mean, 14.40 was exhibited by the cross SHUATS URD 61 (PU-38×KPU-13-192).

Number of seeds per pod:

In case of parents, the mean recorded for number of seeds per pod was 6.55. The highest mean, 7.00 recorded for the parent PU-38 and lowest mean, 5.80 was exhibited by parent LBG-648. In case of crosses, the mean recorded for number of seeds per pod was 6.38. The highest mean, 7.00 was calculated for cross SHUATS URD 56 (PU-38×KPU-63-189) and SHUATS URD 63 (MASH 338×PU-38) and lowest mean, 5.33 was exhibited by cross SHUATS URD 57 (PU-31×KU-96-7).

Pod length (cm):

In case of parents, the mean performance for pod length was 3.98. The highest mean, 4.36 was showed by the parent KPU-13-192 and lowest mean, 3.53 was exhibited by parent T4. In case of crosses, the mean recorded for pod length was 4.21. The highest mean, 4.80 was calculated for the cross SHUATS URD 65 (MASH 338 × VBG-11-14) and lowest mean, 3.73 was exhibited by the cross SHUATS URD 68 (MASH 338 × IU-02-1-3).

Days to maturity:

In case of parents, the mean recorded for days to maturity was 62.54. The highest mean, 75.66 was recorded for the parent LBG-648 and lowest mean, 62.33 was showed by KU-13-01. In case of crosses, the mean recorded for days to maturity was 68.60. The highest mean, 75.33 was showed by the cross SHUATS URD 64 (MASH 338×T4) and lowest mean, 61.00 was recorded for the cross SHUATS URD 70 (PU-11-14×MU-06).

100 seed weight (g)

In case of parents, the mean recorded for seed index (100 seedweight) was 3.98. The highest mean, 5.71 was exhibited by the parent LBG-648 and lowest mean, 3.35 was showed by the T9. In case of crosses, the mean recorded for seed index was 3.79. The highest mean, 4.25 was showed by cross SHUATS URD 54 (PU-31×KU-13-01) and lowest mean, 2.86

was showed by the cross SHUATS URD 111- (PU-38×KPU-13-192).

Biological yield per plant (g)

In case of parents, the mean recorded for Biological yield per plant was 15.76. The highest mean, 19.53 was exhibited by the parent VBG-11-14 and lowest mean, 12.17 was showed by the LBG-648. In case of crosses, the mean recorded for Biological yield per plant was 19.94. The highest mean, 32.66 was showed by cross SHUATS URD 71 (PU-11-14×UTTARA) and lowest mean, 10.41 was showed by the cross SHUATS URD 70 (PU-11-14×MU-06).

Harvest index (%)

In case of parents, the mean recorded for harvest index was 33.34. The highest mean, 46.61 was exhibited by the parent IU-02-1-3 and lowest mean, 24.70 was showed by the KPU-13-192. In case of crosses, the mean recorded for harvest index was 38.26. The highest mean, 78.25 was showed by cross SHUATS URD 69 (PU-11-14×KU-13-01) and lowest mean, 14.31 was showed by the cross SHUATS URD 71 (PU-11-14×UTTARA).

Seed yield per plant (g)

In case of parents, the mean recorded for seed yield per plant was 5.17g. The highest mean, 8.78g was exhibited by the parent PU-11-14 and lowest mean, 3.06g was showed by the parent LBG-648. In case of crosses, the mean recorded for seed yield per plant was 7.05. The highest mean, 10.04 was showed by the cross SHUATS URD 59 (PU-38×T4) and lowest mean, 4.03 was showed by SHUATS URD 69 (PU-11-14×KU-13-01). From the foregoing discussion, it is interesting to note that the best five parents mean performance for seed yield per plant recorded highest for PU-11-14 followed by T4, MASH 338, KPU-63-189 and VBG-11-14. Whereas the best five crosses mean performance for seed yield per plant recorded highest for SHUATS URD 59 (PU-38×T4) followed by SHUATS URD 72 (PU-11-14×PU-38), SHUATS URD 64 (MASH 338×T4), SHUATS URD 58 (PU-31×MU-06) and SHUATS URD 55 (PU-31×KPU-13-192).

Estimation of genetic parameters

One of the important considerations in any crop improvement is the detailed study of genetic variability. Variability is a measure by estimation of mean Genotypic and Phenotypic variation, Genotypic Coefficient of Variation (GCV), Phenotypic Coefficient of Variation (PCV), heritability (h^2) in the broad sense, genetic advance and genetic advance as percent of the mean. This would be of great help to the breeder in evolving a selection programme for genetic improvement of crop plant. The estimates of mean Genotypic Coefficient of Variation (GCV), Phenotypic Coefficient of Variation (PCV), heritability (h^2) in broad sense, Genetic advance and Genetic advance as percent of mean for all the thirteen characters studied have been boxed in Table and fig explained here as under.

Phenotypic and genotypic coefficient of variation: To evaluate the genetic variability statistics has offered various analytical techniques. A genotypic and phenotypic coefficient of variation is one of them which offer to estimate the extent of variability in material under investigation. The estimation of genotypic and phenotypic components of variation gives us an idea of relative extent of heritable and non heritable variation. Thus, the components of variation such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were estimated. The phenotypic coefficients of variation were marginally higher than the corresponding genotypic coefficient of variation. Verma and Katna (1998) demonstrated the influence of environment on the expression of the character under study. Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are categorized as low (less than 10%), Moderate (10-20%) and high (more than 20%) as suggested by Sivasubramanian and Madhavamnen (1973). The estimated GCV and PCV helped in getting a clear understanding of the variability present among the various genotypes.

Genotypic coefficient of variation

The GCV was high for biological yield (27.20%) followed by harvest index (26.38%), seed yield per plant (25.18%), primary branches per plant (22.33%), clusters per plant (20.21%). The GCV was moderate for pods per plant (19.02%), plant height (15.41%) and seed index (12.22%). The GCV was low for rest of the characters like days to 50% flowering (7.40%) days to 50% pod setting (7.68%), pod length (6.83%), days to maturity (4.86%) and seeds per pod (2.77%).

Phenotypic coefficient of variation

The PCV was high for harvest index (29.36%) followed by, biological yield (28.60%), seed yield per plant (26.47%), primary branches per plant (25.74%), clusters per plant (23.84%) and pods per plant (22.10%). The PCV was moderate for plant height (16.28%) followed by, seed index (15.73%), pod length (10.25%). The PCV was low for rest of the characters like 50% pod setting (9.45%), days to 50% flowering (7.84%), days to maturity (7.04%) and seeds per pod (4.94%). In present study genotypic coefficient of variation (GCV) for biological yield per plant, harvest index, seed yield per plant and primary branches per plant was noted high which suggest good scope for yield improvement through direct selection. However, pods per plant, plant height and seed index has considerable genetic variability which can be further exploited for yield improvement. Magnitude of phenotypic coefficient of variation (PCV) for harvest index, biological yield, seed yield per plant, primary branches per plant was noted high and indicating the influence of environmental factors on seed yield and its component traits. Hence estimation of GCV will be more reliable.

Heritability and genetic advance

Heritability governs the resemblance between parents and their progenies whereas the genetic advance provides the knowledge about expected gain for a particular character after selection. Heritability suggests the relative role of genetic factors in expression of phenotypes and also acts as an index of transmissibility of a particular trait to its offsprings. However, the knowledge of heritability alone does not help in formulating concrete breeding programme, genetic advance along with heritability helps to ascertain the possible genetic control for any particular trait. The nature and extent of the inherent ability of a genotype for a character is an important parameter determining the extent of improvement of any crop species. Heritability and genetic advance are the important genetic parameters for selecting a genotype that permit greater effectiveness of selection by separating out environmental influence from total variability.

Heritability estimates along with genetic advance are normally more useful in predicting the gain under selection than that of heritability alone. However, it is not necessary that a character showing high heritability will also exhibit high genetic advance (Johnson *et al.* 1955). An attempt has been made in the present investigation to estimate heritability in broad sense and categorized as low (<50%), moderate (50-70%) and high (>70%) as suggested by Robinson (1966).

In present investigation high heritability recorded for seed yield per plant (90.00%), primary followed by biological yield per plant (90.00%), plant height (90.00%), harvest index (81.00%), days to 50% pod setting (81.00%), primary branches per plant (75.00%), pods per plant (74.00%), clusters per plant (72.00%), and moderate heritability recorded for days to maturity (67.00%), days to 50% flowering (65.00%), 100-seed weight (60.00%), pod length (44.00%). Kumar and Reddy (1986) also reported low to moderate heritability for 100-seed weight in black gram. It reveals that the character under improvement is highly influenced by environmental effects and genetic improvement through selection would not be rewarded due to masking effect of the environment on the genotypic effect.

The heritability value alone however, provides no indication of the amount of genetic improvement that would result from selection of superior genotypes. The heritability estimates would be reliable if it is limited in a broad sense, additive and non additive gene effects are accompanied with high genetic advance. To facilitate the comparison of progress in various characters of different genotypes genetic advance was calculated as percentage of mean. The magnitude of genetic advance as percentage of mean was categorized as high (> 20%), moderate (20% - 10%) and low (< 10%).

Genetic advance as percentage of mean was observed high in biological yield per plant (53.29%), followed

by seed yield per plant (49.34%), harvest index (48.82%), primary branches per plant (39.90%), clusters per plant (35.90%), pods per plant (33.72%) and plant height (30.04%). It may be concluded that, if the value of genetic advance is high, then the character is governed by additive genes and selection will be rewarding for improvement of such traits. Genetic advance as percentage mean was recorded moderate for 100 seed weight (19.56%), days to 50% pod setting (14.20%) and days to 50% flowering (12.26%).

However, it was recorded low for the character pod length (9.38%), days to maturity (8.21%) and seeds per pod (1.77%). The above findings were in agreement with the findings of Sharma and Ahmed (1997) and Isaacs *et al.* (2000) who reported moderate genetic advance and Verma and Katna (1998) reported low genetic advance in black gram. Low magnitude of genetic advance reveals the presence of dominance or epistatic variances in the control of aforesaid characters. The low value of genetic advance suggests influence of environment

and hence selection for these traits would be worthwhile in later generations because the character is governed by non-additive genes and heterosis breeding may be useful.

High heritability values coupled with high genetic advance as percent of mean showing high to high heritability estimates were observed for the characters *viz.*, biological yield (90.00%, 53.29%), seed yield per plant (90.00%, 49.34%), plant height (90.00%, 30.40%), harvest index (81.00%, 48.82%), days to 50% pod setting (81.00%, 14.20%), primary branches per plant (75.00%, 39.90%), pods per plant (74.00%, 33.72%) and clusters per plant (72.00%, 35.90%). Characters showing high to low heritability estimates coupled with medium to low genetic advance as percentage of mean indicating greater contribution of dominance and epistatic variance in the expression of the characters. The above findings are of confirming with the Veeraswamy *et al.* (1973), Goutet *et al.* (1978), Shrivastava (1985) and Rao (1986) who reported similar findings in black gram.

Table 1. Analysis of variance for 13 quantitative characters in Blackgram

S.N	Character	Replic ations d.f=2	Treatments d.f=37	Hybrids d.f=21	Parents d.f=13	Hybrids vs.Parents	Checks	Checks vs.Hybrids	Checks vs.Parents	Error	Total
1.	Days to 50% Flowering	6.16	30.95**	19.07**	10.08*	227.05**	20.16*	504.37**	240.00**	4.76	13.37
2.	Days to 50% Pods Setting	12.79*	48.00**	44.71**	16.93**	374.24*	0.66	431.30**	142.37**	3.56	18.28
3.	Days to Maturity	7.41	38.12**	49.03**	30.04*	7.67	0.16	12.83	5.32	5.31	16.09
4.	Plant Height (cm)	25.98	253.50**	341.58**	38.20**	1454.74**	3.37	1198.78**	298.82**	9.47	89.69
5.	Number of Primary branches Per Plant	0.03	1.47**	0.86**	0.21**	30.14**	0.06	1.44**	13.05**	0.14	0.57
6.	Number of Clusters Per Plant	4.10	11.44**	9.50**	7.86**	47.99**	9.62**	90.45**	39.93**	1.32	4.68
7.	Number of Pods Per Plant	14.45	82.54**	87.58**	56.72**	71.34*	25.21	356.51**	500.30**	8.61	32.93
8.	Number of Seeds Per Pod	0.26	0.39	0.47	0.28	0.55	0.24	0.64	0.21	0.30	0.33
9.	Pod Length (cm)	0.14	0.34**	0.28**	0.18**	3.97**	0.00	0.17	1.66**	0.10	0.18
10.	100 Seed Weight (g)	0.28	0.86**	0.29**	1.07**	8.98**	0.04	0.60	4.39**	0.15	0.39
11.	Biological Yield	0.19	81.59**	131.79**	13.68**	259.13**	0.29	7.45	19.61**	2.77	28.54
12.	Harvest Index (%)	11.51	309.74**	456.51**	156.26**	234.67*	4.25	107.96*	12.07	22.86	116.64
13.	Seed Yield Per Plant (g)	0.16	8.74**	9.35**	7.68**	39.08**	0.40	2.31**	0.78	0.29	3.06

** and * Significant at 1% and 5% level of significance respectively

Table 2. Genetic parameters for 13 characters of 39 blackgram genotypes

S. No	Character	Genotypic Variance (Vg)	Phenotypic Variance (Vp)	Genotypic Coefficient of variation (%)	Phenotypic Coefficient of variation (%)	Heritability (h ²) (%) (broad sense)	Genetic advancement (1%)	Genetic advance as per cent of mean (5%)
1.	Days to 50% flowering	8.73	13.50	7.40	9.20	0.65	6.27	4.90
2.	Days to 50% Pods Setting	14.81	18.38	7.68	8.56	0.81	9.12	7.12
3.	Days to maturity	10.94	16.25	4.86	5.92	0.67	7.16	5.59
4.	Plant height	81.34	90.82	15.41	16.28	0.90	22.53	17.58
5.	Number of Primary branches per plant	0.44	0.59	22.33	25.74	0.75	1.53	1.19
6.	Number of Clusters per plant	3.37	4.70	20.21	23.84	0.72	4.11	3.21
7.	Number of Pods per plant	24.64	33.26	19.02	22.10	0.74	11.28	8.80
8.	Number of Seeds per pod	0.03	0.33	2.77	8.93	0.10	0.15	0.11
9.	Pod length	0.08	0.18	6.83	10.25	0.44	0.50	0.39
10.	100-seed weight	0.24	0.39	12.22	15.73	0.60	1.00	0.78
11.	Biological yield	26.27	29.05	27.20	28.60	0.90	12.87	10.04
12.	Harvest index	95.63	118.49	26.38	29.36	0.81	23.19	18.10
13.	Seed yield per plant	2.82	3.11	25.18	26.47	0.90	4.21	3.29

Table 3 (a). Mean performance of 39 genotypes of Blackgram for yield and component characters

S.No	Genotypes	Days to 50% Flowering	Days to 50% Pods Setting	Days to maturity	Plant height	Number of primary branches per plant	Number of Clusters per plant	Number of Pods per plant	Number of Seeds per pod	Pod length	100 seed weight	Biological Yield	Harvest index	Seed yield per plant
1.	PU-31 × LBG-648	40.00	52.33	72.33	61.1	2.60	6.66	31.86	6.20	4.10	3.98	17.03	46.62	7.91
2.	PU-31 × MU-44	39.33	49.33	68.33	60.6	3.60	8.13	31.06	6.33	4.66	3.58	22.11	37.28	8.19
3.	PU-31 × KU-13-01	49.00	51.66	74.00	60.9	3.40	7.60	19.60	6.26	4.06	4.25	20.04	38.14	7.57
4.	PU-31 × KPU-13-192	39.66	50.66	72.00	64.1	3.80	12.33	30.40	6.26	4.33	4.17	27.81	31.19	8.64
5.	PU-31 × KPU-63-189	37.00	51.66	71.33	70.2	3.60	5.86	30.46	7.00	4.36	3.47	19.94	41.07	8.08
6.	PU-31 × KU-96-7	38.66	48.66	68.66	63.4	2.60	9.20	31.46	5.33	3.90	3.85	20.64	35.73	7.28
7.	PU-31 × MU-06	36.00	46.66	64.00	75.4	4.26	10.80	75.66	6.40	4.73	4.04	33.93	26.60	8.99
8.	PU-38 × T4	36.33	47.00	69.00	60.9	3.06	7.00	34.46	6.66	4.63	3.64	18.63	54.20	10.04
9.	PU-38 × LBG-648	39.33	47.33	71.33	39.1	2.33	6.73	25.73	6.80	4.66	3.53	28.53	18.56	5.27
10.	PU-38 × KPU-13-192	36.66	44.66	66.00	65.2	4.20	5.00	14.40	6.66	4.70	2.86	30.17	14.72	4.44
11.	PU-38 × PU-31	39.33	44.00	71.66	68.8	3.80	10.40	30.60	6.53	4.00	3.93	16.66	45.95	7.41
12.	MASH-338 × PU-38	42.33	50.33	70.00	62.4	3.66	7.46	21.20	7.00	4.16	3.67	14.29	54.47	7.78
13.	MASH-338 × T4	43.66	56.33	75.33	68.4	3.06	9.80	28.60	6.00	4.33	4.11	16.88	53.67	9.03

14.	MASH-338 × VBG-11-	44.66	42.33	64.66	48.2	3.93	7.66	28.46	6.40	4.80	3.68	15.59	43.74	6.80
15.	MASH-338 ×	44.40	51.66	71.33	72.6	3.20	8.33	24.33	6.06	4.36	3.49	13.98	39.88	5.53
16.	MASH-338 × PU-11-14	36.66	46.33	62.33	67.8	2.73	10.33	22.27	6.66	3.96	4.01	17.41	46.72	8.10
17.	MASH-338 × IU-02-1-	34.66	42.00	64.66	43.7	3.73	7.80	26.26	6.66	3.76	3.76	14.95	39.83	5.95
18.	PU-11-14 × KU-13-01	35.33	44.00	63.00	69.0	3.40	8.93	17.33	6.00	4.33	3.69	14.26	78.25	4.03
19.	PU-11-14 × MU-06	34.66	43.33	61.00	51.2	2.86	9.33	22.46	5.86	4.00	3.55	10.41	45.77	4.68
20.	PU-11-14 × UTTARA	39.00	48.33	66.00	83.6	3.66	6.86	24.00	6.40	4.33	3.80	32.66	14.31	4.66
21.	PU-11-14 × PU-31	40.66	52.00	68.66	70.5	3.60	8.80	32.66	6.66	4.66	4.01	17.57	51.92	9.10

Table 3 (b). Mean performance of 39 genotypes of Blackgram for yield and component characters

S.No	Genotypes	Days to 50% Flowering	Days to 50% Pods Setting	Days to maturity	Plant height	Number of primary branches per plant	Number of Clusters per plant	Number of Pods per plant	Number of Seeds per pod	Pod length	100 seed weight	Biological Yield	Harvest index	Seed yield per plant
22.	PU-31	42.00	53.00	69.66	64.9	1.86	8.60	20.20	6.46	3.70	3.83	14.82	34.56	5.02
23.	LBG-648	43.66	53.00	75.66	51.8	2.93	12.33	34.40	5.80	3.96	5.71	12.17	25.65	3.06
24.	MU-44	41.66	51.00	64.33	64.4	2.43	11.13	23.66	6.33	4.30	5.33	19.10	36.79	7.02
25.	KU-13-01	39.33	48.00	62.33	65.8	2.26	8.00	21.26	6.66	3.83	3.72	17.10	25.17	4.28
26.	KPU-13-192	38.66	49.33	64.00	60.2	2.06	9.93	23.60	6.33	4.40	3.98	18.52	24.70	4.58
27.	KPU-63-189	38.33	47.00	69.33	51.8	2.26	11.60	29.13	6.66	4.20	4.32	17.85	40.78	7.22
28.	T4	38.66	50.33	64.33	69.2	2.00	12.73	21.60	7.00	3.53	4.27	18.79	43.58	8.17
29.	MU-06	42.33	50.66	67.66	54.0	2.33	8.13	20.80	6.53	3.83	3.90	17.53	27.92	4.88
30.	MASH-338	42.00	53.66	68.66	49.6	2.66	9.33	26.46	6.26	4.10	4.34	18.56	41.84	7.75
31.	PU-38	41.33	54.66	67.33	47.6	2.40	9.86	28.26	7.00	3.86	4.64	17.15	36.14	6.13
32.	VBG-11-14	43.00	54.33	69.33	65.8	2.00	8.26	29.60	6.93	4.00	4.40	19.52	35.97	7.02
33.	Vallabh Urd	40.66	52.00	68.33	62.9	2.53	7.60	20.13	6.33	4.10	3.88	16.11	31.12	5.01
34.	PU-11-14	39.66	51.66	66.66	67.1	2.46	8.66	21.46	6.53	3.53	4.01	18.92	46.50	8.78
35.	IU-02-1-3	40.33	51.66	70.66	59.5	2.40	9.95	27.93	6.33	4.10	4.01	14.46	46.61	6.76
36.	Uttara	42.00	53.66	68.66	67.8	2.46	10.40	27.23	6.66	3.63	5.23	18.47	37.09	6.83
37.	KU-96-7	44.33	55.33	68.33	66.5	2.26	8.06	19.93	6.66	3.86	3.85	14.24	34.59	4.84
38.	T9	46.00	56.66	66.66	46.7	3.86	13.66	32.36	6.53	4.50	3.35	18.78	33.22	6.21
39.	AZAD	49.66	57.33	67.00	48.2	3.93	11.13	36.46	6.93	4.50	3.62	19.22	34.90	6.73
	Mean	39.91	50.10	68.06	58.51	2.98	9.08	26.09	6.46	4.17	3.98	18.84	37.06	6.66
	C.V.	5.47	3.76	3.38	5.26	12.79	12.65	11.24	8.49	7.63	9.89	8.83	12.89	8.15
	F ratio	6.49	13.45	7.17	26.75	10.13	8.65	9.58	1.32	3.40	5.57	29.43	13.54	29.57
	S.E.	1.26	1.09	1.33	1.77	0.22	0.66	1.69	0.31	0.18	0.22	0.96	2.76	0.31

	C.D. 5%	3.55	3.07	3.74	5.00	0.62	1.87	4.77	-----	0.51	0.64	2.70	7.77	0.88
	C.D. 1%	4.71	4.07	4.97	6.64	0.82	2.48	6.33	-----	0.68	0.85	3.59	10.31	1.17
	Range Lowest	34.66	42.00	61.00	39.13	1.86	5.00	14.40	5.33	3.53	2.86	10.41	14.31	3.06
	Range Highest	49.66	57.33	75.66	83.63	4.26	13.66	36.46	7.00	4.80	5.71	33.93	54.47	10.04

CONCLUSION

It was concluded from the present investigation that among 21 crosses of blackgram on the basis of mean performance and heterosis the crosses PU-38×T4 recorded the high performance for seed yield per plant followed by PU-11-14×PU-31 and MASH-338×T4, PU-31 □ LBG-648, PU-31 □ MU-06, PU-31 □ KPU-13-192 was found to be superior crosses these performed maximum seed yield. Biological yield, harvest index, seed yield per plant, exhibited high GCV, PCV and genetic parameters revealed that heritability (broad sense) and genetic advance as % of mean values were high for seed yield per plant indicating that selection would be fruitful for improvement of these traits.

REFERENCES

Appalaswamy, A. and Reddy. (2004) Genetic divergence and heterosis studies of mungbean (*Vignaradiata* L. Wilczek). *Legume Research.* 21: 115-118.

Burton, G.W.(1952). Quantitative inheritance in grasses Proc. 6th int. Grassland cong.1:227-283.

Burton, G.W., and DeVane, E.M. (1953). Estimating heritability in tall fasses from replicated cloned material. *Journals of Agronomy.* 45(3): 474-481.

Deepalakshmi, A.J. and Anandakumar, C.K.(2004).Creation of genetic variability for different polygenic traits in black gram (*Vignamungo* (L.)Hepper) through induced mutagenesis. *Legume Research.* 3:188-192.

Delannay, X., Rodgers, D.M. and Plamer, R.G. (1983). Relative genetic contribution among ancestral lines to North America soybean cultivars. *Crop Sci.* 23: 944-949

Falconer, D.S. (1981).Introduction to Quantitative genetics, 3rd ed. Longman, New York. 340

Fisher, R.A. (1938). Statistical tables for biological, agricultural and mendelian inheritance. France Royal Society of Edinburgh.52:399- 433.

Gout, J. V., Viraktanath, B.C. and Laxmi, P. V. (1978).Variability and correlation studies in black gram (*Phaseolusmungo* L.).*Mysore J. Agric. Sci.*, 11 (3): 322-325.

Isaacs, S. M., Jebaraj, S. and Ganesh, S. K. (2000).Estimates of genetic variability and heritability in black gram [*Vignamungo* (L.)Hepper].*Res. on Crops.* 1 (1): 37-39.

Johnson, H.W., Robinson, H.F. and Comstock, R.E.(1955).Genotypic and Phenotypic Correlations in Soybean and their implications in selection.*Agronomy.*47:477-438.

Kumar, M. H. and Reddy, P. N. (1986).Variability and heritability in F3 progenies of black gram (*Vignamungo* L. Hepper).*J. Res. APAU.* 14: 14-17.

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

Rao, S. S. (1986). Genetic analysis of yield and its components in black gram (*Vignamungo* (L.)Hepper) Ph.D. Thesis, Jawaharlal Nehru KrishiVishwavidyalaya, Jabalpur.

Robinson, H.F. (1966). Quantitative genetics in relation to breeding on the centennial of mendelism. *Indian Journal of Genetics.* 26: 171 - 187.

Roopalakshmi, K., Kajjidoni, S.T. and Salimath, S.M.(2003). Effect of irradiation and matting schemes on native of association of seed yield and its components in black gram.*Legume Research.*26(4):288-291.

Sharma, Debojit and Ahmad, N.U.(1997). Genetics and combining ability studies for yield and its components in black gram [*Vignamungo* (L.)Hepper].*J. Agric. Sci. Soc. North East India.* 10 (1): 19-24.

Shrivastava, D. K. (1985).Genetic analysis of yield and its components in urd (*Vignamungo* L. Hepper). M. Sc. Thesis, Jawaharlal Nehru KrishiVishwavidyalaya, Jabalpur.

Singh, I. P., Singh, S.K., and Singh, K. P. (2007) Genetic variation, character association and path analysis between grain yield and its component in black gram [*Vignamungo* (L.) Hepper].*Progressive Agriculture.*7(1/2):113-115.

Sivasubramanian, S. and Madhavamenon, P. (1978).Genotypic and phenotypic variability in rice.*Madras Agric. J.* 60: 1093-1096.

Soufmanien, J. and Goplalakrishnan, T. (2004).A comparative analysis of genetic diversity of black gram genotype using RAPD and ISSR markers.*The Applied Genetics.*109:1687-1693.

Veeraswamy, R., Paloniswamy, G. A. and Swamy, R. (1973). Yield attributes and heritability in some varieties of black gram (*Phaseolusmungo*L.Hepper). *Madras Agric. J.*, 60: 183- 185.

Verma, S. and Katna, G. (1998). Variability studies in urdbean for intercrop and monocrop conditions. *Indian J. Pulses Res.*, 11 (1): 33-37.