



STUDIES ON GENETIC DIVERSITY IN BLACKGRAM (*Vigna mungo* L. Hepper) GERMPLASM

Y.Vinod Kumar Reddy*, Sapna S.Lal and Gabriel M.Lal

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

* Corresponding author email: yaramvinodreddy@gmail.com

ABSTRACT

The present experiment was conducted at Field Experimentation Centre, Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture Technology and Sciences, Allahabad during kharif 2016 in Randomized Block Design with three replications. The present investigation was conducted to examine the 40 blackgram genotypes along with one check (T-9) to study the genetic diversity. Analysis of variance showed highly significant differences among 40 blackgram genotypes for 13 quantitative characters studied. Maximum genotypic and phenotypic variance was recorded for biological yield/plant, plant height and harvest index. Maximum GCV and PCV were recorded for number of branches/plant, biological yield/plant and seed yield /plant. High heritability was recorded for biological yield/plant, days to maturity, seed/pod, number of branches/plant and seed yield/plant. High heritability coupled with high genetic advance as percent of mean was recorded for biological yield/plant. Genetic diversity estimated in 40 blackgram genotypes using Mahalanobis's D^2 statistic. Forty genotypes were grouped into seven clusters by tocher method (Mahalanobis Euclidean Distance) cluster analysis. The maximum inter-cluster distance was observed between cluster 2 and cluster 5. The maximum intra-cluster distance was observed in cluster 1. Cluster 4 showed maximum cluster mean value for seed yield per plant among all the characters, biological yield/plant, seed yield/plant and seeds/pod contributes maximum.

KEYWORDS - Blackgram, Genetic Diversity, D^2 statistic and cluster.

INTRODUCTION

Blackgram (*Vigna mungo* L. Hepper) popularly known as urdbean or mash, is a grain legume domesticated from *V. mungo* var. *silvestris* (Lukoki, 1980). It belongs to family leguminosae with chromosome number $2n=2x=22$. Blackgram is reported to be originated in India (Zukovskiji, 1962). India is the world's largest producer as well as consumer of blackgram. It produces about 1.5 to 1.9 million tons of blackgram annually from about 3.5 million hectares of area, with an average productivity of 500 kg per hectare. Blackgram output accounts for about 10% of India's total pulse production (*Ministry of Agriculture, Govt. of India*, 2015). In 2014-2015, 1.61 million tonnes Urd production in the country is largely concentrated in five states viz, Uttar Pradesh (UP), Maharashtra, Madhya Pradesh, Andhra Pradesh and Tamil Nadu. These five states together contribute for about 70% of total urd production in the country (*Ministry of Agriculture, Govt. of India*, 2015). In U.P. Blackgram is grown in about 3.91 lakh hectares with a total production of 1.72 lakh tones (Annual Report 2014-2015). Among the states of India, Orissa ranks first in area 777 thousand hectares and production 396 thousand tones. However Punjab is a leading state in productivity with 834.9 kg/hectare (Rajendra *et al.* 2002). It is a cheap source of dietary protein (24%). It also contributes 76% carbohydrate 3-5% Fibre, 1.74% Fat and a major portion of lysine in the vegetarian diet. It is the richest sources of phosphoric acid being 5-10 times richer than other crops. Besides, being used as food for inexpensive source of

dietary protein it is better to use for bean sprouts than mungbean for its longer shelf life (Mishra and Khan, 2001). The productivity of pulse crop is very low when compared to cereals, which have been selected for high grain yield under high input conditions, while the selection pressure in case of pulses have been focused on the adaptation to both biotic and abiotic stresses. The reason for low yield is i) adaption of crop to marginal lands of rainfed nature. The crop has been traditionally cultivated under less fertile soils with least inputs, ii) unavailability of cultivars with high potential, iii) stress to diseases insects and environmental fluctuations, etc. Hence, large parts of the genetic variability for yield contributing characters were lost during the course of evolution. Yield are a complex trait determined by several component traits; hence selection for yield should take into account related traits as well. So the knowledge of correlation between yield and its component traits is essential for seed yield improvement through selection programmes. (Kumar *et al.* 2015). Among pulses, blackgram 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 polygene 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 study of correlation coefficient gives a measure of the relationship between traits and provides the degree to which various characters are associated with productivity. The systematic collection of blackgram 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 (Souframanien and Gopalakrishnan, 2004). In order to improve yield and other polygenetic characters, mutation breeding can also be effectively utilized (Deepalakshmi and Anandakumar, 2004). Therefore genetic variability is the basic requirement for making progress in crop breeding (Appalaswamy and Reddy, 2004). An assessment of the genetic diversity of pulses is an important first step in a programme to improve crop yield. The proper estimate of nature and magnitude of diversity in a crop is essential to information about extent of variation available for yield and its component traits. Seed 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). The study of inheritance of various developmental and productive traits through the estimation of different genetic parameters like components of variances, genotypic and phenotypic coefficients of variability, heritability and genetic advance is helpful for framing the effective breeding programme.

MATERIALS & METHODS

The present experiment was undertaken at Field of Department of Genetics and Plant Breeding, Naini Agriculture Institute, Sam Higginbottom University of Agriculture, technology and Sciences Allahabad, U.P. during kharif 2016. 40 genotypes of urd bean were grown in this experiment. Experiment was done according to randomized block design with three replications, and recommended package of practices were followed to raise

the crop. Seeds were sown with row to row spacing of 30 cm and plant to plant spacing of 10 cm. The data were recorded on five randomly selected plants of each replication for all characters but in case of days to 50% flowering and days to maturity, the observations were recorded on plot basis, pre harvest observations are Days to 50% flowering, Days to 50% pods setting, Plant height (cm), Number of primary branches per plant, Number of clusters per plant, Number of pods per plant, Days to maturity and Post harvest observations are No. Of seeds per pod, Pod length (cm), Seed index (g), Biological yield (g) and Seed yield per plant (g). Mean values were computed and data were analyzed for analysis of variance as suggested Fisher (1936) given in table :1. Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were given by Burton (1952). Heritability in broad sense was given by Lush (1949) and Burton and Devane (1953). Genetic advance was given by Lush (1949) and Johnson *et al.* (1955). Genetic divergence was given by Mahalanobis (1936).

RESULTS & DISCUSSION

The mean sums of squares of 13 different traits are presented in [Table-2]. High significant differences for all characters under study among the 40 blackgram genotypes were found in analysis of variance, at 1 % and 5 % level of significance indicating the presence of sufficient variability among different genotype. Maximum seed yield per plant was recorded for SHEKHAR 3, (17.33g) followed by AZAD-1(21.46 g), Genotypic coefficient of variation (GCV) ranged from 1.6 % to 63.79 %. Higher magnitude of GCV was recorded for number of Seed yield per Plant (63.79%) followed by plant height (18.24%) and biological yield (18.46%), while estimates for GCV were low for Days to 50% pod setting (1.36%), followed by Days to 50% flowering (1.6%), pod length (1.60%). Phenotypic coefficient of variation (PCV) ranged from 2.95% to 69.01 %. Maximum PCV was recorded for number of Seed yield/ plant (69.01%) followed by number of Primary branches/Plant (29.85%) while estimates for PCV were low for Days to 50% pod setting (2.95%) followed by days to 50% flowering (4.40%). All characters show maximum heritability in 40 genotypes (table: 3). the estimates of heritability (%) in broad sense for 13 characters studied, which range from 17% to 99%. Maximum heritability was recorded for characters i.e., Biological yield/plant (99%) followed by pod length (98%), plant height (95%), whereas minimum heritability (%) was recorded for Days to 50% flowering (17%). The genetic advance (as percent per mean) varied from 1.28 to 37.93%. Maximum genetic advance was recorded for biological yield (37.93%) followed by Plant height (25.87%), whereas minimum genetic advance was recorded for Days to maturity (1.37%) followed by Days to 50% pod setting (1.28%). In Genetic diversity (Mahalanobis D^2 statistics) In the present study, 40 genotypes were grouped into seven clusters (fig 1) by Non-Hierarchical Euclidean cluster analysis (table 4), maximum clusters are found in Cluster IV comprised nine genotypes (UH82-15 , UH82-83 , UG-27, UH-85-5 , IC-456048 , PKG-U3, U-9, UTTARA , PANT-U-30) evolving the maximum genotype, followed by clusters V

with seven genotypes (PLU-710, IPU-96-1, IC-250190, IPU-199-60, U-5, STPN2, IC-106194), and VI cluster with seven genotypes (IPU 96-1, IC-250107, T-9, SPS-33, IC-56048, IPU 94-10, PLU 826), clusters II with six genotype (NDU-5-7, SHEKHAR-3, P-1, IPU-7-3, IC-91567, UH-81-89), cluster III with five genotype (IC-250188, PLU-648, UH-10, UH-82-85, PU-31), cluster I comprised also three genotype (IC-24129, PGRV-99022, IC-140016), and cluster 7 comprise also three genotype (PLU-277, AZAD-1, IPU99-16), the pattern of group constellation proved the existence of significant amount of variability. The maximum intra-cluster (D^2) was registered for, Cluster I (215.881), followed Cluster III (182.631), cluster 7 (161.748), Cluster V (128.352), Cluster IV (127.216), and Cluster II (82.517). Inter-cluster distance

(D^2) was found maximum between cluster V (1009.307) followed by Cluster III (950.981). Minimum inter-cluster distance was found between Cluster I (341.205) (table 5 & 6). The results indicated that there is close genetic similarity between the cultivars of black gram based on the study. Where as the percent contribution of thirteen characters towards total genetic divergence has the highest contribution in the manifestation of genetic divergence was exhibited by biological yield (65.26%) followed Pod Length cm by (22.56%), Plant Height cm (8.46%) and Seed Yield/ Plot (2.05%) suggesting scope for improvement in these characters. (table7) In other words, selection for these characters may be rewarding. Similar results were reported by Pandey and Anurag (2010) for biological yield and test weight.

TABLE 1: Analysis of variance for 13 different quantitative characters in 40 genotypes of blackgram

S. No.	Characters	Mean sum of squares		
		Replications (d.f.=2)	Treatments (d.f.= 39)	Error (d.f.= 78)
1	Days to 50% flowering	0.85	5.10	3.17
2	Days to 50% pod setting	0.075	4.21**	2.33
3	Plant height	1.83	14.45**	2.55
4	Number of branches per plant	0.32	1.26**	0.4
5	Number of clusters per plant	0.05	0.98*	0.5
6	Pods per plant	2.70	19.90*	1.13
7	Pod length	0.018	0.27**	0.02
8	Number of seeds per pod	0.77	1.48**	0.34
9	Days to maturity	0.97	9.23**	5.68
10	Seed index	0.35	1.19**	0.47
11	Harvest index	11.92	24.24**	15.10
12	Biological yield	0.52	262.04**	0.47
13	Seed yield per plant	4.09	92.65**	4.98

Significant at 5%* & 1%** level of significance

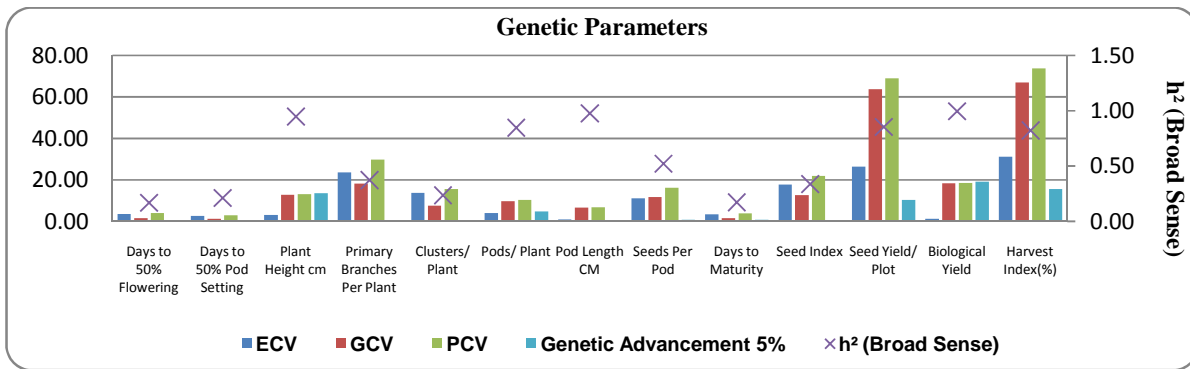
TABLE 3: Genetic parameters for 13 biometrical characters of 40 blackgram genotypes

S.No.	Characters	Genotypic Coefficient of variation	Phenotypic coefficient of variation	Heritability (%) (broad sense)	Genetic advance	Genetic advance as % of mean
1	Days to 50% flowering	1.6	4.40	17	0.68	1.40
2	Days to 50% pod setting	1.36	2.95	21	0.75	1.28
3	Days to maturity	12.90	3.86	17	0.93	1.37
4	Plant height	18.24	13.25	95	13.59	25.87
5	Number of branches/ plant	7.61	29.85	37	0.65	22.97
6	Cluster /plant	9.66	15.68	24	0.40	7.60
7	Pods /plant	6.69	10.50	85	4.47	18.32
8	Seed /pod	11.72	16.23	52	0.91	17.43
9	Pod length	1.60	6.76	98	0.61	13.62
10	Biological yield /plant	18.46	18.51	99	19.18	37.93
11	Harvest index	66.94	38	82	15.59	25.02
12	100-seed weight	12.68	21.85	34	0.59	15.55
13	Seed yield /plant	63.79	69.01	85	10.59	18.32

TABLE 4: Distribution of 40 blackgram genotypes into different clusters

S. No.	Cluster No.	No. of genotypes	Genotypes included
1	I	3	IC-24129, PGRV-99022, IC-140016
2	II	6	NDU-5-7, SHEKHAR-3, P-1, IPU-7-3, IC-91567, UH-81-89
3	III	5	IC-250188, PLU-648, UH-10, UH-82-85, PU-31
4	IV	9	UH82-15, UH82-83, UG-27, UH-85-5, IC-456048, PKG-U3, U-9, UTTARA, PANT-U-30
5	V	7	PLU-710, IPU-96-1, IC-250190, IPU-199-60, U-5, STPN2, IC-106194
6	VI	7	IPU 96-1, IC-250107, T-9, SPS-33, IC-56048, IPU 94-10, PLU 826
7	VII	3	PLU-277, AZAD-1, IPU99-16

Studies on genetic diversity in blackgram



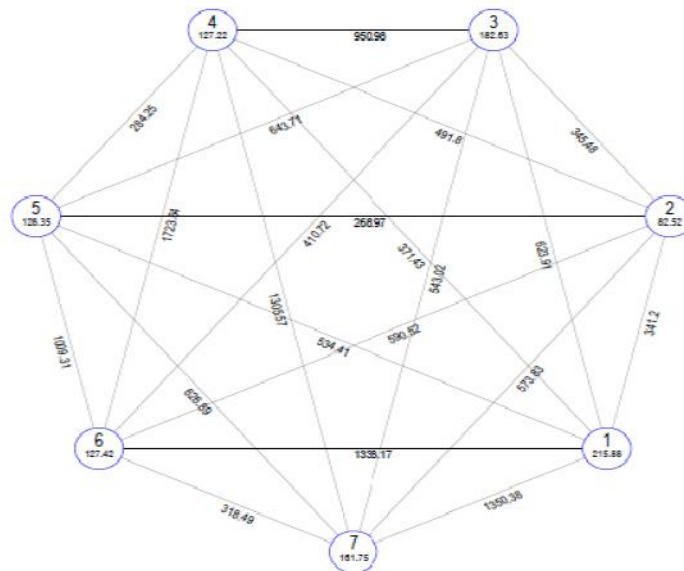
Histogram depicting estimates of genetic parameters for 13 important agro-economic traits in blackgram

TABLE 5: Intra and inter cluster averages distances in blackgram genotypes

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	215.881	341.205	623.914	371.428	534.407	1338.172	1350.383
Cluster II		82.517	345.478	491.803	268.965	590.517	573.831
Cluster III			182.631	950.981	643.707	410.724	543.019
Cluster IV				127.216	284.247	1723.638	1305.568
Cluster V					128.352	1009.307	626.887
Cluster VI						127.425	318.493
Cluster VII							161.748

TABLE 6: Cluster mean values for different component characters in blackgram

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Days to 50 % Flowering	49.30	47.66	48.22	47.94	48.57	46.33	50.00
Days to 50 % Pod Setting	58.63	58.18	57.00	58.83	58.81	57.33	58.86
Plant height	54.87	52.69	55.68	49.84	49.76	43.63	53.86
Primary Branches/ Plant	2.86	2.85	2.72	2.94	3.04	1.66	2.66
Clusters/ Plant	5.20	5.07	5.22	5.22	5.19	5.33	6.66
Pods/ Plant	26.40	26.25	26.88	25.61	25.09	26.33	18.00
Pod Length	4.67	4.49	4.21	4.45	4.69	3.80	3.69
Seeds/ Pods	5.13	5.44	5.27	5.22	5.28	4.33	5.33
Days to Maturity	68.63	67.11	68.38	67.38	67.76	65.33	68.33
Seed index	3.58	3.77	3.62	4.05	3.99	3.74	4.19
Harvest index	11.04	12.78	11.48	9.90	15.71	28.60	6.47
Biological Yield/ Plant	56.24	38.07	52.57	63.62	44.45	47.33	62.33
Seed Yield/ Plant	9.46	6.79	9.21	7.36	9.38	13.83	4.23



Euclidean² Distance (Not to the Scale)

FIGURE1: cluster diagram depicting intra and inter distances

TABLE 7: Percent contribution of 13 characters to genetic divergence:

S.No.	Characters	Contribution %
1	Days to 50% Flowering	0.01
2	Days to 50% Pod Setting	0.01
3	Plant Height cm	8.46
4	Primary Branches Per Plant	0.13
5	Clusters/ Plant	0.13
6	Pods/ Plant	1.03
7	Pod Length CM	22.56
8	Seeds Per Pod	0.01
9	Days to Maturity	0.13
10	Seed Index	0.01
11	Seed Yield/ Plot	2.05
12	Biological Yield	65.26
13	Harvest Index (%)	0.26

CONCLUSION

On the basis of results of the experiment it can be concluded that, the genotypes **SHEKHAR-3**, followed by **AZAD-1**, were identified as the genotypes for seed yield at Allahabad region. The present investigation registered high along with high genetic advance as a 5 % of mean for seed yield per plant which should be given top priority for effective selection, the present investigation further revealed that Cluster IV and Cluster VII are most divergence to each other. Therefore genotypes present in these clusters are suggested to provide broad spectrum variability in segregating generations and may be used as parents for future hybridization programme to develop desirable types of recombination.

REFERENCES

- Al-Jibouri, H.A., Mullar P.A., and Rabinsion, H.F. (1958) Genetic and environmental variances and co-variances in an upland cotton cross of inter specific origin. *Journal of Agronomy*, 50:633-636.
- Appalaswamy, A. and Reddy (2004) Genetic divergence and heterosis studies of mungbean (*Vignaradiata* L. Wilczek). *Legume Research*, 21: 115-118.
- Asrat, A., Yadav, O.P. and Tomer, Y.S. (2001) Genetic divergence in blackgram. *Haryana Agriculture. University Journal Research*, 31(1/2): 13-17.
- Anonymous (2011) Agriculture Statistics at a glance. Directorate of Economics and Statistics, New Delhi.
- Bhattacharya, A. (2002) Effect of yield attributing traits on seed yield of mungbean and urdbean. *Indian journal Pulses Research*, 15(1): 23-27.
- Burton, G.W. and De Vane, E.M. (1953) Estimating heritability in tall fesses from replicated cloned material. *Journal of Agronomy*, 45(3): 474-481.
- Das, S., Das S.S. and Ghosh P. (2014) Analysis of genetic diversity in some blackgram cultivars using ISSR. *European Journal of Experimental Biology*, 4(2):30-34.
- Deepalakshmi, A.J. and Anandakumar, C.K. (2004) Creation of genetic variability for different polygenic traits in blackgram (*Vignamungo* L. Hepper) through induced mutagenesis. *Legume Research*, 3: 188-192.
- Deepshikha, Lavanya, G.R. and Kumar Sujeet. (2014) Assessment of Genetic Variability for Yield and Its Contributing Traits in Blackgram. *Trends in Biosciences*, 7(18): 2835-2838.
- Devi, M.S., Kumar M.H. and Sekhar, M.R. (2011) Divergence studies for morphological and biochemical characters in blackgram. *Annals of Biology*, 27 (1): 51-56.
- Donald, CM. and Hamblin, J. (1976) The biological yield and harvest index of cereals as agronomic and plant breeding criteria. *Advance Agronomy*, 28: 61-83.
- Fisher, R.A. (1936) Statistical tables for biological, agricultural and mendelian inheritance. *France Royal Society of Edinburgh*, 52: 399- 433.
- FetemehAbna, FaruqGolam* and SubhaBhassu(2011) Estimation of genetic diversity of mungbean (*Vigna radiata* L. Wilczek) in Malaysian tropical environment. University of Malaya, 50603, *African Journal of Microbiology*.
- Ghafoor, A., Sharif, A., Ahamad, Z., Zahid , M.A. and Rabbani, M.A. (2001) Genetic diversity in blackgram (*Vignamungo* L. Hepper). *Field crops Research*, 69: 183-190.
- Jayamani, P. and Sathya, M. (2013) Genetic diversity in pod characters of blackgram (*Vigna mungo* L. Hepper). *Legume Research*, 36 (3): 220-223.
- Johnson, H.W., Robinson, H.F. and Comstock. R.E. (1955) Genotypic and Phenotypic Correlations in Soybean and their implications in selection. *Agronomy journal*, 47: 477-438.
- Katiyar, P.K. & Dixit, G.P. (2011) Assessment of genetic divergence in greengram (*Vigna radiata*) germplasm. *Indian Journal of Agriculture Science*, 81(1): 79-81.
- Konda C.R., Salimath P.M. and Mishra M.N. (2009) Genetic variability studies for productivity and its components in blackgram(*vigna mungo* L. Hepper). *Indian journal Genetics*, 62(4):345-346.

TABLE: 2 (a) Mean performance of 40 blackgram genotypes for 13 quantitative characters

No	Character	Days to 50% Flowering	Days to 50% Pods Setting	Plant Height (cm)	Branches /Plant	Cluster s/Plant	Pods/Plant	Pod Length (cm)	Seeds/ Pod	Days to Maturity	Seed Index (g)	Seed Yield/Plant (g)	Biologica l Yield (g)	Harvest Index (%)
1	IC-24129	50.00	58.00	53.86	2.66	6.66	18.00	3.69	5.33	68.33	4.19	4.23	62.33	6.47
2	IC-250188	48.33	60.00	52.13	1.33	4.66	22.00	4.58	5.33	68.66	3.07	2.90	63.33	5.02
3	IPU96-1	48.00	57.00	40.50	4.00	5.33	25.33	4.72	5.66	67.33	3.89	5.36	42.83	5.45
4	PLU-277	49.00	59.00	37.63	3.33	5.33	27.33	4.27	5.66	68.00	3.33	4.70	45.91	9.42
5	PGRV-99022	46.33	57.33	43.63	1.66	5.33	26.33	3.80	4.33	65.33	3.74	13.83	47.33	28.60
6	NIDU-5-7	45.66	60.33	55.90	2.66	5.66	28.66	4.25	4.00	67.33	4.20	5.36	65.90	7.45
7	PLU-710	50.33	58.66	56.53	1.33	5.33	30.00	4.16	4.33	69.66	3.54	4.76	53.53	6.13
8	IC-250187	51.33	60.33	52.56	4.66	5.33	22.00	4.32	5.33	70.33	3.68	2.33	61.16	2.90
9	SHEKHAR-3	47.33	56.33	53.40	2.66	5.00	24.33	4.34	5.66	66.66	3.63	17.33	47.55	30.89
10	P-1	47.00	57.33	52.60	3.00	5.66	27.00	4.30	5.66	65.33	5.67	14.63	64.85	18.71
11	PLU-648	50.66	60.00	55.63	3.33	5.33	26.33	4.15	5.33	72.00	3.35	5.33	56.70	8.26
12	IPU-7-3	48.66	58.00	57.16	2.66	5.33	28.00	4.25	5.33	64.66	5.13	12.90	37.66	27.99
13	IPU-96-1	47.66	57.66	56.26	2.66	5.66	27.33	4.36	5.00	67.00	3.33	4.53	35.76	8.27
14	IC-140816	46.66	57.33	42.90	2.33	5.66	27.66	4.31	6.00	66.33	5.03	25.96	44.66	41.44
15	T-9	47.00	59.33	46.90	3.33	5.33	25.33	4.42	6.33	66.66	3.38	5.66	35.26	14.79
16	AZAD-1	48.33	58.00	48.30	3.00	6.66	27.00	4.46	5.66	66.66	5.75	21.46	55.96	23.79
17	SPS-33	48.00	59.00	43.60	3.00	5.00	23.00	4.45	5.66	67.66	4.11	3.36	39.28	8.33
18	UH82-15	49.33	59.66	57.26	3.33	4.66	19.66	4.80	5.66	69.33	4.76	4.133	44.00	10.72
19	UH82-83	48.66	58.66	63.03	2.66	3.66	23.00	4.74	3.33	68.00	3.10	3.40	57.66	4.48
20	UG-27	49.00	58.33	61.23	2.66	4.66	24.00	4.90	5.66	65.00	4.00	5.73	43.31	11.82
21	IC-250190	48.33	58.33	60.46	2.66	5.00	25.00	4.19	6.00	69.33	3.59	3.00	43.00	12.29
22	UH-85-5	48.00	57.33	48.66	2.66	3.66	26.66	4.76	5.33	71.66	4.03	6.03	38.00	14.94
23	IPU-199-60	46.33	56.00	57.33	3.33	4.66	25.66	4.26	5.33	65.33	3.65	3.56	49.00	7.14
24	IC-91567	47.66	57.00	55.50	2.66	5.33	25.66	4.19	5.33	71.66	3.56	3.36	51.86	6.11

TABLE: 2 (b) Mean performance of 40 blackgram genotypes for 13 quantitative characters

No	Character	Days to 50% Flowering	Days to 50% Pods Setting	Plant Height (cm)	Branches / Plant	Cluster s/ Plant	Pods /Plant	Pod Length (cm)	Seeds/ Pod	Days to Maturity	Seed Index (g)	Seed Yield/ Plant (g)	Biological Yield (g)	Harvest Index (%)
25	IC-56048	48.00	57.66	62.93	3.33	5.00	25.00	4.78	5.66	65.33	3.14	10.33	52.66	12.43
26	PKG U3	48.66	59.33	58.21	2.66	5.33	25.66	4.88	3.00	66.66	3.00	2.03	47.33	1.79
27	UH-10	49.33	59.33	53.83	3.33	5.33	23.00	4.44	5.66	68.66	3.70	11.30	57.66	7.66
28	U-5	47.00	58.33	60.93	2.66	4.66	24.33	4.38	5.33	69.00	3.48	11.30	37.66	12.63
29	UH-82-35	49.00	56.66	52.13	2.33	5.00	25.00	4.60	5.66	68.00	3.74	6.03	51.96	10.28
30	IC56048	47.66	58.00	46.80	3.33	5.00	26.66	4.66	5.66	65.33	4.06	8.30	62.76	11.10
31	U-9	46.33	57.33	57.03	2.33	5.66	28.66	4.78	5.66	66.33	3.48	8.80	37.66	9.54
32	UTTARA	49.66	58.66	53.83	2.00	5.33	27.66	4.83	5.33	68.66	4.28	9.50	58.33	7.09
33	STPN2	49.66	59.00	59.66	2.66	5.66	27.66	4.64	4.0	68.33	3.75	12.36	61.43	16.42
34	IPU 94-10	50.00	58.66	45.53	2.33	5.33	27.33	4.64	5.33	69.66	3.78	6.60	52.70	10.97
35	IPU 99-16	47.66	57.00	39.03	2.66	5.00	27.33	4.62	5.33	67.33	3.66	10.63	63.70	14.18
36	PLU 826	48.00	58.33	43.20	3.66	5.33	26.33	4.84	4.33	66.66	3.43	5.56	38.33	6.20
37	UH 81-89	49.66	57.33	48.50	3.00	5.66	27.33	4.05	5.33	69.66	3.75	11.66	57.66	7.78
38	PANTH U-30	49.66	59.66	53.83	3.66	4.66	29.66	4.87	5.33	70.00	3.69	8.33	57.30	8.73
39	IC-106194	48.00	56.66	62.83	3.33	5.33	29.00	4.25	5.66	67.33	3.61	14.56	55.60	10.86
40	PU-31	49.33	60.33	50.63	3.00	5.33	28.66	4.93	5.33	69.66	3.92	17.76	43.11	29.23
	Mean	48.38	58.300	52.54	2.85	5.21	25.88	4.48	5.25	67.82	3.86	8.47	50.57	12.74
	C.V	3.68	2.62	3.30	23.62	13.70	4.11	1.01	11.23	3.51	17.80	26.33	1.35	31.15
	F.ratio	1.60	1.80	55.07	2.78	1.92	17.52	131.89	4.26	1.62	2.52	18.59	54.41	14.84
	F.Prob	0.03	0.01	0.00	0.01	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00
	SE	1.02	0.88	0.92	0.38	0.41	0.61	0.02	0.34	1.37	0.39	1.28	0.39	2.24
	C.D.5%	2.89	2.48	2.59	1.09	1.16	1.73	0.07	0.95	3.87	1.11	3.62	1.11	6.31
	C.D.1%	3.84	3.29	3.44	1.45	1.54	2.29	0.09	1.27	5.14	1.48	4.81	1.48	8.3
	Range lowest	45.66	56.00	37.63	1.33	3.66	18.00	3.59	3.00	64.66	3.00	2.03	35.26	1.79
	Range Highest	51.33	60.33	63.03	4.66	6.66	30.00	4.94	6.33	72.00	5.75	25.96	65.90	41.55