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Correlation, path-coefficient and genetic diversity in Blackgram [*Viginamungo* (L) Hepper]

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ABSTRACT

An experiment was carried out during the *Kharif*season of 2011-12 at the research field of RAK College of Agriculture, Sehore (M.P.) to assess the correlation, path coefficient and genetic diversity in 75 morphologically diverse accessions of Blackgram [*Vignamungo* (L) Hepper].In present study Plant height, Pods per plant, seeds per plant and 100-seed weight exhibited significant and positive correlation with seed yield bothat genotypic and phenotypic level. The degree of association was highest between seeds per plant and seed yield per plant followed by pods per plant, biological yield per plant, plant height and 100 seed weight. Correlation studies indicated that seed yield per plant showed significant positive correlation with seeds per plant, pods per plant, biological yield per plant, plant height and 100 seed weight. Path coefficient analysis revealed that highest positive direct effect was shown by seeds per plant followed by biological yield per plant on the seed yield both at phenotypic and genotypic levels.Seventeen clusters were formed using D^2 analysis and maximum of 13 genotypes were found in cluster thirteen. Clustering pattern revealed that genetic diversity was directly related to geographic diversity. Among the genotypes studied,RBU 38, CBG 757, NDU 5-3, COBG 761, TP```U 05-13, KKB 20055, KPU 07-06, RUG 1, PU 06-20 and VBG 04-008 had potential for higher yield based on the genetic merit of yield factors, and are selected for further study for eventual release as varieties for farmers. Additionally,These genotypes also can used in genetic enhancement program to generate trangressive segregants since they were genetically diverse lines.

Key words: Correlation, cluster analysis, Blackgram, path coefficient, variability

INTRODUCTION

Blackgram [*Vignamungo* (L) Hepper] is a self-pollinated crop with low percentage of natural out crossing. It belongs to family fabaceae. The center of origin of blackgram is in India. Its seeds are highly nutritious with protein (24-26%), carbohydrates (60%), fat (1.5%), minerals, amino acids and vitamins. The biological value improves greatly, when wheat or rice is combined with Blackgram because of the complementary relationship of the essential amino acids such as arginine, leucine, lysine, isoleucine, valine and phenylalanine etc. India is the largest producer and consumer of blackgram in the world. Blackgram has been distributed mainly in tropical to sub-tropical countries where it is mainly grown in India, Pakistan, Sri-Lanka, Burma, and some countries of South East Asia. Its annual production is 17.60 lakh tones from 32.60 lakh hectare area in India with an average

productivity of 534 kg/ha. In Madhya Pradesh, the annual production of blackgram is 2.31 lakh tones from an area of 5.92 lakh hectares. However average productivity is 390 kg/ha, which is very low, and thus its genetic yield potential in warranted (Source: - Project co-ordinates (MULLaRP) Report, IIPR, Kanpur 2011-2012).

Genetic variability and their assessment for qualitative and quantitative traits of economic importance are pre-requisite for any crop-improvement   programme. The knowledge of correlation and path analysis is important to understand the association between the yield and its contributing character to find out guidelines for better selection of quantitative traits. Success of yield improvement largely depends upon the magnitude and nature of genetic variability present in yield contributing traits. If the variability in among germplasm the

population is largely of genetic nature with least environmental influence, the probability of isolating genetically superior genotypes is high. Correlation studies also provide better understandings of yield components that help the plant breeder during selection (Robinson *et al*.1951 and Johnson *et al*.1955). The present study was carried out to understand genetic variability among 75 blackgram germ plasm collected from geographically diverse ecology of India, and to isolate superior genotypes to use in breeding programs.

MATERIALS AND METHODS

Experimental material

The experimental material consisted of seventy five accessions of blackgram collected from IIPR, Kanpur; CSAU, Kanpur; NDUAT, Faizabad, HAU, Hisar; GBPUAT, Pantnagar; BARC,Mumbai; Ludhiana;RARS, Shillongani; TNAU, Coimbatore; Akola; ARS, Kota; Coimbatore; Nirmal Seeds Pvt. Ltd., Jalgaon; Vamban; RAU,Banswara;   ARS,Durgapura;   Bandanapur; Berhampur; Dharwad; Durgapura; Gwalior; GKV, Raipur; Killikulam; RARS, Lam; Sehore and SVBPUAT, Meerut gene stocks of All India Co-ordinate Research Project on MULLaRP at R.A.K. College of Agriculture, Sehore.

Experimental layout

The experiment was laid out following RBD in two replications in single row length was 3 meter keeping standard row spacing of 30 cm. and a plant distance was maintained at 10 cm.   Site-specific recommended fertilizer dose of 25 kg N + 50 kg P2O5 + 25 kg K2O + 20 kg S/ha was applied uniformly and recommended package of practices were adopted for optimum crop growth and plant protection. Six randomly selected plants from each row were harvested to record data on morphological and yield traits. A random selection of six plants from each row was made and the observations were recorded on each selected plant. The mean values of each character under study were computed on the basis of six plants for each genotype in each replication

Recording of data

The data were recorded on eleven quantitative traits, viz. days to 50% flowering, day to   maturity, primary branches/plant, secondary branches/plant, pods/ plant, plant height, seeds pod/plant, seed yield (g), biological yield (g), 100-seed weight (g) and harvest index (%).

Statistical analysis

ANOVA was   carried out   as   per standard analysis

protocaol. The correlation coefficient values(r) were calculated at genotypic, phenotypic and environmental levels according to the formula given by Johnson *et al* (1955a) and described by Singh and Choudhary (1985). Path coefficient analysis was utilized to partition the phenotypic and genotypic correlation coefficient into the direct effects and indirect effects along with residual effects. The analysis was carried out as per the equation suggested by Dewey and Lu (1959) originally proposed by Wright (1921) and described by Singh and Choudhary (1985).

RESULTS

Analysis of variance and parameters of genetic variability

The mean sum of squares due to genotypes were highly significant at 1% level of significance for days to 50% flowering, days to maturity, plant height, pods per plant, biological yield per plant, seeds per pod, seeds per plant, seed yield per plant, and the mean sum of squares due to genotypes were significant at 5% level of significance for the traits primary branches per plant and harvest index. This indicated the existence of considerable variability for all studied characters in the germplasm. Hence, it offers a better scope for further improvement of breeding material by the selection of promising genotypes in Bllackgram breeding programme, however the character 100-seed weight was found insignificant. The mean sum of squares of various characters is presented in Table 1.

Parameters of genetic variability

The parameters of genetic variability such as mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance as percentage of mean (GA) were estimated for all the quantitative characters are presented in Table 2.The high range was observed for seeds per plant (86-342) with the mean of 188 followed by plant height (21-59) with mean of 36, pods per plant (15-51) with mean of 28, biological yield per plant (7-33) with mean of 17, harvest index (24-55) with mean of (41), days to maturity (66-83) with mean of 75 and seed yield per plant (3-13) with the mean of 7 which indicates that sufficient variability is present in the germplasm for above characters while low range was recorded for days to 50% flowering (36-42), branches per plant (1-4), seeds per pod (6-9) and 100 seed weight (3-5)

Heritability

The heritability estimates in broad sense was recorded from 28.8% to 86.0% for various characters. The highest

Table 1. Analysis of variance for seed yield & its contributing characters in Blackgram germplasm

Source of variance	D.F.	Days to flowering	Days to maturity	Plant height (cm)	Branches per plant	Pods per plant	Seeds per pod	Seeds per plant	Biological yield per plant	100 seed weight (g)	Harvest index (%)	Seed yield per plant
				Mean sum of square								
Replication	1	1.92	1.93	7.84	0.015	0.054	0.54	72.50	27.21	0.23	32.56	0.21
Genotypes	74	6.31**	25.76**	196.06**	0.62*	35.37**	1.31**	6592.24**	85.87**	0.47	113.81*	11.52**
Error	74	1.94	1.94	32.26	0.29	26.12	0.49	873.22	9.36	0.26	51.28	1.50

Table 2. Genetic parameters for yield and its contributing traits.

Character	Mean	Range		SEm±	GCV	PCV	h^2	GA as % of mean	GA
		Min.	Max.						
Days to 50% flowering	40.06	36.00	42.00	1.39	03.69	05.07	53.0	5.54	02.22
Days to maturity	75.27	66.00	83.00	1.39	04.58	04.94	86.0	8.68	06.59
Plant height (cm)	35.91	21.00	58.85	5.68	25.20	29.75	71.7	44.16	15.79
Branches per plant	02.26	1.00	4.00	0.54	17.87	29.93	35.6	22.12	0.50
Pods per plant	28.40	15.00	51.00	5.11	26.02	31.64	67.7	44.08	12.52
Seeds per pod	06.67	5.50	8.50	0.70	09.58	14.28	45.0	.13.19	0.88
Seeds per plant	187.80	86.50	342.0	29.55	28.47	32.53	76.6	51.34	96.42
Seed yield per plant (g)	06.93	3.08	12.67	1.22	32.28	36.83	76.8	58.29	04.04
Biological yield per plant (g)	17.37	6.56	32.67	3.05	35.60	39.72	80.3	65.74	11.42
100 seed weight (g)	03.69	2.61	5.10	0.51	08.84	16.47	28.8	9.75	0.36

Table 3. Phenotypic correlation coefficients among different characters of Black gram Germplasm.

Character	Days to maturity	Plant height (cm)	Branches per plant	Pods per plant	Seeds per pod	Seeds per plant	Biological yield per plant	100 seed weight (g)	Harvest index (%)	Seed yield per plant
Days to 50% flowering	0.702**	0.486**	-0.213	0.203	0.000	0.180	0.128	0.00	0.031	0.175
Days to maturity		0.520**	-0167	0.133	0.050	0.120	0.075	0.109	0.163	0.160
Plant height (cm)			-0.166	0.582**	-0.067	0.493**	0.456**	0.311**	0.175	0.578**
Branches per plant				0.319**	-0.094	0.242*	0.119	-0.079	0.091	0.186
Pods per plant					-0.133	0.846**	0.684**	0.168	0.166	0.832**
Seeds per pod						0.249*	0.273*	0.019	-0.173	0.209
Seeds per plant							0.757**	0.072	0.119	0.895**
Biological yield per plant								0.288**	-0.371**	0.811**
100 seed weight (g)									0.262*	0.465**
Harvest index (%)										0.200

** = significant at 1% level of significance.
*   = significant at 5% level of significance

heritability was found in days to maturity (86.0%) followed by biological yield per plant (80.3%) and seed yield per plant (76.8%). The lowest heritability was recorded in 100-seed weight (28.8%).

Genetic advance (%)

The genetic advance as percent of mean ranged from 5.54% to 65.74%. The highest genetic advance as percent of mean was recorded in biological yield per plant (65.74%), followed by seed yield per plant (58.29%) and seeds per plant (51.34%).

Correlation analysis

Correlation coefficient is a statistical measure, which is used to find out the degree and direction of relationship between two or more variables. The values of phenotypic and genotypic correlation coefficient among yield and it attributes are presented in Table 2 and 3.

Correlation with seed yield

In present investigation, seeds per plant (0.895**), pods per plant (0.832**), plant height (0.578**) and 100 seed weight (0465**) were significantly and positively associated with seed yield per plant both at phenotypic and genotypic levels. The degree of association was highest between seed yield per plant and seeds per plant (0.895**) followed by pods per plant (0.832**), biological yield per plant (0.811**), plant height (0.578**) and 100 seed weight (0.465**) whereas days to 50% flowering, days to maturity, primary branches per plant, seeds per pod and harvest index were not significant. They presented in Table 3 and 4.

Correlation between other characters

Days to 50% flowering had the highly significant and positive association with days to maturity (0.702**) and plant height (0.486**). Days to maturity was found significant and positive correlation with only plant height (0.520**) while other all characters were not correlated significantly with maturity. Plant height had highly significant and positive correlation with pods per plant (0.582**), seeds per plant (0.493**), biological yield per plant (0.456**), 100 seed weight (0.311**) and seed yield per plant (0.578**). Branches per plant were significant and positive correlation with pods per plant (0.319**), seeds per pod (0.242**). Pods per plant was observed highly significant and positive association with seeds per plant (0.846**), biological yield per plant (0.684**) and seed yield per plant (0.832**). Seeds per pod were significantly associated with biological yield per plant (0.273**) and seeds per plant (0.249*). Seeds per plant had highly significant and positive correlation with seed yield per plant (0.495**) and biological yield per plant (0.757**) whereas 100 seed weight and harvest index were recorded non significant association with seeds per plant. Biological yield per plant exhibited highly

Table. 4. Genotypic correlation coefficients among different characters of the genotrypic variation.

Character	Days to maturity	Plant height (cm)	Branches Per plant	Pods per plant	Seeds per pod	Seeds per plant	Biological yield per plant	100 seed weight (g)	Harvest index (%)	Seed yield per plant
Days to 50% flowering	0.660**	0.667**	-0.228	0.456**	0.007	0.343**	0.280*	0.000	0.056	0.334**
Days to maturity		0.610**	-0.190	0.224	0.084	0.173	0.126	0.219	0.280*	0.222
Plant height (cm)			-0.301**	0.767**	0.024	0.624**	0.614**	0.656**	0.186	0.726**
Branches per plant				0.049	0.353**	0.157	0.174	-0.510**	-0.323**	0.061
Pods per plant					0.196	0.909**	0.880**	0.433**	0.021	0.962**
Seeds per pod						0.575**	0.369**	-0.005	0.040	0.455**
Seeds per plant							0.848**	0.221	0.043	0.957**
Biological yield per plant								0.466**	-0.404**	0.912**
100 seed weight (g)									-0.073	0.492**
Harvest index (%)										-0.006

** = significant at 1% level of significance.
*   = significant at 5% level of significance.

Table 5. Direct and indirect effects of yield components on seed yield in black gram germplasm.

Character	Days to 50% flowering	Days to maturity	Plant height (cm)	Branches Per plant	Pods per plant	Seeds per pod	Seeds per plant	Biological yield per plant	100 Seed weight (g)	Harvest index (%)	Correlation with seed yield
Days to 50% flowering	0.036	-0.018	-0.001	-0.001	0.018	0.000	0.079	0.054	0.000	0.007	0.175
Days to maturity	0.026	-0.026	-0.001	-0.001	0.012	0.002	0.053	0.032	0.026	0.039	0.160
Plant height (cm)	0.018	-0.014	-0.003	-0.001	0.053	-0.002	0.218	0.193	0.074	0.041	0.578**
Branches per plant	-0.008	0.004	0.000	0.003	0.029	-0.003	0.107	0.050	0.019	0.021	0.186
Pods per plant	0.007	-0.003	-0.001	0.001	0.090	-0.004	0.374	0.290	0.040	0.039	0.832**
Seeds per pod	0.000	-0.001	0.000	0.000	-0.012	0.034	0.110	0.116	0.005	-0.041	0.209
Seeds per plant	0.007	-0.003	-0.001	0.001	0.076	0.008	0.442	0.320	0.017	0.028	0.895**
Biological yield per plant	0.005	-0.002	-0.001	0.000	0.062	0.009	0.334	0.423	0.068	-0.088	0.811**
100 seed weight (g)	0.000	-0.003	-0.001	0.000	0.015	0.001	0.032	0.122	0.237	0.062	0.465**
Harvest index (%)	0.001	-0.004	0.000	0.000	0.015	-0.006	0.053	-0.157	0.062	0.236	0.200

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Table 6. Direct and indirect effects of different components on biological yield in genotypes of black gram.

Character	Days to 50% flowering	Days to maturity	Plant height (cm)	Branches Per plant	Pods per plant	Seeds per pod	Seeds per plant	Seed yield per plant	100 seed weight(g)	Harvest index (%)	Correlation with biological yield
Days to 50% flowering	**-0.069**	0.038	0.014	0.001	0.008	0.000	-0.001	0.155	0.000	-0.018	0128
Days to maturity	-0.049	**0.054**	0.015	0.001	0.005	0.000	0.000	0.141	0.001	-0.092	0.075
Plant height (cm)	-0.034	0.028	**0.029**	0.001	0.022	0.000	-0.001	0.510	0.002	-0.099	0.456**
Branches per plant	0.015	-0.009	-0.005	**-0.006**	0.012	0.000	-0.001	0.164	0.000	-0.051	0.119
Pods per plant	-0.014	0.007	0.017	-0.002	**0.037**	0.001	-0.002	0.734	0.001	-0.094	0.684**
Seeds per pod	0.000	0.003	-0.002	0.001	-0.005	**-0.005**	-0.001	0.185	0.000	0.098	0.273*
Seeds per plant	-0.012	0.006	0.014	-0.001	0.031	-0.001	**-0.003**	0.790	0.000	-0.068	0.757**
Seed yield Per plant	-0.012	0.009	0.016	-0.001	0.031	-0.001	-0.003	**0.883**	0.002	-0.113	0.811**
100 seed weight (g)	0.000	0.006	0.009	0.000	0.006	0.000	0.000	0.410	**0.005**	-0.148	0.288**
Harvest index (%)	-0.002	0.009	0.005	-0.001	0.006	0.001	0.000	0.177	0.001	**-0.566**	-0.37

significant and positive correlation with seed yield per plant (0.811**), 100 seed weight (0288**) and it also showed significant and negative correlation with harvest index and 100 seed weight showed significant and positive correlation with seed yield per plant (0.465**), harvest index (0262**).

(**Note: ** Significant at 1% level of significance**)

Path coefficient analysis

Simple correlation does not provide the true relationship amongst characters. The total phenotypic and genotypic correlation coefficients were further partitioned into direct and indirect effects, both at phenotypic and genotypic levels.

Seed yield with other yield traits

Seeds per plant (0.442) exhibited highest positive direct effect on seed yield followed by biological yield per plant (0.423) and 100 seed weight (0.237) whereas plant height (-0.003) showed the negative direct effect on the seed yield. Characters which show direct and indirect effect on seed yield are presented in table 5.The highest direct effect and positive association of seeds per plant (0.442) was observed on seed yield. High indirect effect of seeds per pod was recorded through biological yield per plant (0.320) followed by pods per plant (0.076), harvest index (0.028) and 100 seed weight (0.017) on seed yield per plant. Pods per plant (0.090) had direct vary low positive effect but significant association with seed yield per plant was found because indirect effects via., seeds per plant (0.374) followed by biological yield per plant (0.290), 100 seed weight (0.040) and harvest index was observed on seed yield. Biological yield per plant showed positive and highly significant association with seed yield per plant because of its high direct effect (0.423) and indirect effect through seeds per plant (0.334) followed by 100 seed weight (0.068) and pods per plant (0.062) was found on seed yield.Plant height showed positive and significant association

Table 7. Clustering pattern of genotypes

Clusters	Number of genotypes	Genotypes
I	11	COB 6-671, KUG 216, KU 96-3 (ch), VBG 04-003, IPU 07-3, UH 04-04, IPU 09-18, UH 07-13,KU 010-1, IPU 09-16, UH 07-06
II	02	IPU 07-19, NDU 7-22.
III	05	KU 99-22, PU 04-10, TU 80, TU 26, NDUK 10-50
IV	02	SBG 40, NDU 07-25.
V	02	PU 04-25, NDU 7-24.
VI	08	KUG 212, TPU 02-1, KU 99-21, IPU 02-33, KUG 502, UH 07-16, NDU 9-15, IPU 8-25.
VII	09	IPU 2006-02, SB 22-19, KU 99-19, KUG 531, IPU 8-18, RVSU 51, RVSU 54, VBG 04-014, RUG 10.
VIII	02	UH 04-06, NUL 138.
IX	03	CBG 757, TPU 05-13, TU 26-1.
X	02	NDU 5-3, KU 99-26.
XI	02	KPU 07-06, KPU 07-08.
XII	10	NUL 7, KU 32-3, PU 04-29, KU 99-33, KUG 479, AKU 07-4, BDU 1, IGKU 03-16, PU 08-2,NDUK 10-52.
XIII	13	OBG 33, AKU 9804, TPU 4 (ch), RBU 38 (ch), CBG 703, PU 06-20, KKB 20055, VBG 04-008, DU 4, RUG 1, UH 07-17, COBG 761, AKU 07-1.
XIV	01	VALLABH 1.
XV	01	RBU 03-14.
XVI	01	IPU 2006-1.
XVII	01	SB 121-36.

with seed yield per plant because of its high indirect effect via. Seeds per plant (0.218) followed by biological yield per plant (0.193), 100 seed weight (0.074), pods per plant (0.053) and harvest index (0.041) was recorded on seed yield.100 seed weight exhibited positive and significant association with seed yield per plant due to its high direct effect (0.237) and indirect effect through biological yield per plant (0.122) followed by harvest index (0.062), seeds per plant (0.032) and pods per plant (0.015) was observed on seed yield.

Genetic divergence

D^2 statistics measures the degree of diversification. It measures the forces of differentiation at two levels, i.e. intra-cluster and inter-cluster levels. . Analyses of covariance for all possible combination of characters were done for genetic divergence. All the seventy five genotypes grouped into seventeen clusters. The varietal composition of the clusters I, II, III, IV, V, VI, VII, VIII, IX,X, XI, XII, XIII, XIV, XV, XVII and XVII had 11, 2, 5, 2, 2, 8, 9, 2, 3, 2, 2, 10, 13, 1, 1, 1 and 1 genotypes respectively. The maximum number of genotypes (13) fell in XIII cluster followed by 11 genotypes in I cluster while the cluster XIV, XV, XVII and XVII had only one genotype each which indicate that these four genotypes are vary diverge from other genotypes. Clustering pattern of genotypes has been given in Table 7.

DISCUSSION

The aim of the present investigation was to study the genetic divergence in 75 genotypes on eleven characters of Blackgram. It will give an effective means to assess the extent of available variability, which would be useful for select superior genotypes on the basis of their phenotypic expression so as to use them in breeding programme to improve the commercially important characters. The discussion pertaining to the different aspects of present investigation.

Genetic parameter and association analysis

1) **Analysis variance**2) **Parameters of genetic variability** 3) **Correlation analysis** 4)**Path analysis**

Genetic variability in any crop is an essential pre requisite for an efficient crop improvement programme. The technique for adopting any breeding programme depends upon the nature and magnitude of variability present in the available genotypes. Assessment of genetic variability of yield and its contributing traits in the available population was an important purpose of the present investigation. Phenotype of an individual reflects the genotypic contribution interacting with the environment. Phenotypic and genotypic coefficients of variation play an important role in understanding the extent and nature of genetic variability in the population studied. The mean sum of squares due to genotypes were highly significant for the characters such as days to 50% flowering, days to maturity, plant height, pods per plant, biological yield per plant, seeds per pod, seeds per plant, seed yield per plant. It indicates the presence of considerable amount of genetic variability among the genotypes for these characters. Variation amongst genotypes is due to their collection area, the different

geographical area from where germplasms collected. Existence of high genetic variability for seed yield and its contributing traits provide better scope for utilization in further breeding programme. These finding are in agreement with the results obtained by Gowda *et al.* (1997) for grain yield per plant, pods per plant, branches per plant and plant height; Sinhamahapatra (2006) for plant height , number of pods per plant , number of seeds per pod, days to maturity, harvest index, biological yield and seed yield; Svaithramma *et al (1999),* Sharma *et al.* (2006), Pervin *et al.* (2007) and Shafique *et al* (2011) for plant height, pods per plant and branches per plant in black gram.

Parameters of genetic variability

The range for the characters seeds per plant, seed yield per plant, biological yield per plant, pods per plant and plant height showed high which indicates that high variability is present for these characters hence selection may be done for these characters to obtained desirable genotypes. These findings are similar to results obtained byGowda *et al.* (1997) reported sufficient variability for grain yield per plant, pods per plant, branches per plant and plant height in black gram. The estimation of PCV was higher than GCV for all the characters studied indicating there is an influence of environment on expression of these characters. The difference between PCV and GCV was of lower magnitude for the traits like days to maturity, days to 50 % flowering. It indicates that there is little influence of environment on the expression of these characters. Selection for improvement of such characters should be avoided. These finding are in agreement with the results obtained by Kumar *et al.* (1998) Sarkar *et al.* (2006), Pervin *et al.* (2007) for pods per plant and plant height in black gram. The characters viz. seed yield per plant, seeds per plant, Pods per plant, plant height showed high PCV and GCV estimates. This suggests that the selection based on these characters would facilitate successful isolation of desirable types. These finding are in agreement with the results obtained by Gowda *et al.* (1997), Shafique *et al* (2011) and Sarkar *et al.* (2006) for seed yield, biological yield and branches per plant in blackgram.

Heritability and genetic advance are important parameters for selection programme. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimate alone. However, it is not necessary that a character showing high heritability will also exhibit high genetic advance. These finding are in agreement with the results obtained by Johnson *et al.* (1955).Heritability is the heritable portion of phenotypic variance. It is a good index of the transmission of characters from parents to their offspring (Falconer, 1981).

Heritability in broad sense refers to the functioning of the whole genotypes as unit and is used in context of environmental effect. The heritability estimates in broad sense were classified by Robinson et al. (1951) as low (<50%), medium (50-70%) and high (>70%).

In the present investigation, high estimates of heritability and high genetic advance as percent of mean were observed for biological yield per plant, seed yield per plant and seeds per plant which indicating that these characters were under the influence of additive gene action. This result indicates that these characters were highly heritable and hence were less affected by the environment. The plant breeder, therefore, may make his selection safely on the basis of phenotypic expression of these characters. Plant height had high heritability coupled with moderate genetic advance while high heritability with low genetic advance was recorded for days to maturity. High heritability estimates coupled with high genetic advance have been reported by Ramprasad *et al.* (1989),Gowda *et al.* (1997), Sharma and Ahmed (1997), Yadav and Dahiya (2000), Isaacs *et al.* (2000), Patil*et al.* 2001), Ahmed and Salimath (2002), Patil and Salimath (2004), Led *et al.* (2010), Arulbalachandran *et al.* (2010), Devi *et al.* (2011), Reddy *et al.* (2011) and Singh and Khuble (2011) in blackgram.

Correlation analysis

Correlation studies provide better understandings of yield components that help the plant breeder during selection (Robinson *et al.*1951 and Johnson *et al.* 1955). Mass selection has been used to improve grain yield in several crops through indirect selection for highly heritable traits, which are associated with yield. In the present investigation correlation coefficient have been worked out for all the combination of eleven characters at genotypic and phenotypic levels. Phenotypic correlation can be directly observed and includes both genotypic and environment effects and therefore differs under different environmental conditions. Genotypic correlation refers to the inherent or heritable association between two variables. This type of correlation may be either due to pleitropic action of genes or due to linkage or more likely both. Environmental correlation is entirely due to environmental effects and this is not much importance to a breeder as it is not heritable and stable. Genotypic correlations are generally of lower magnitude than phenotypic correlation because of masking effect of environment. If genotypic and phenotypic correlations are of same magnitude, it indicates the lack of environmental influence and high heritability of the association. In present study plant height, pods per plant, seeds per plant and 100 seed weight exhibited significant and positive correlation with seed yield both at genotypic and phenotypic level. The degree of association was highest between seeds per plant and seed yield per plant

followed by pods per plant, biological yield per plant, plant height and 100 seed weight. This result is supported by findings of Raut*et al.* (1990), Govindaraj and Subramanaian (2001) and Gupta *et al* (2003) for plant height, number of branches per plant, number of pods per plant and number of seeds per pod; Raut*et al.* (1990),Yadav and Dahiya (2000) for pods per plant, seeds per plant and seed weight in blackgram.

The pods per plant were found positive and highly significant with seeds per plant both at phenotypic and genotypic levels. Highly positive correlation was observed between seeds per plant and biological yield, days to 50% flowering and days to maturity, plant height and pods per plant. All these traits except days to 50% flowering had positive relationship with seed yield indicating certain inherent relationship with seed yield. Selection for these characters simultaneously would bring improvement in black gram yield. These finding are in agreement with the results obtained by Chauhan *et al.* (2007), kumar and Mishra (2005), Singh *et al.* (2007) and Konda *et al.* (2008) for pods per plant, seeds per plant, seed weight, flowering, maturity and plant height; Malik *et al.* (2008), Reddy *et al.* (2011) and Shivade *et al.* (2011) for pod length, dry matter, seeds per plant, pods per plant in black gram.

Path analysis

As simple correlation does not provide the true contribution of the characters towards the yield, the total phenotypic and genotypic correlation coefficients were further partitioned into direct and indirect effects throughout path coefficient analysis. Path analysis revealed that both at phenotypic and genotypic levels the highest positive direct effect was shown by seeds per plant followed by bological yield per plant which appeared to be the true relationship, hence direct selection through these traits will be effective.

These results are in accordance with the findings of Sharma *et al.* (2005), Chauhan *et al.* (2007) and Konda *et al.* (2008) for pods per plant, seeds per pod and 100 seed weight; Yadav and Dahiya (2000), Raika *et al.* (2002) and kumar and Mishra (2005) biological yield in black gram. Seed yield per plant exhibited the highest direct effect and positive correlation with the biological yield while other characters plant height, pods per plant and 100 seed weight showed the negligible direct effect on the biological yield which shows that seed yield is directly correlated with biological yield. The highest indirect effect of seeds per plant was observed followed by pods per plant and plant height through seed yield per plant on biological yield per plant. The present finding is supported by findings of Chauhan *et al.* (2007) for plant height, flowering and branches per plant; Malik *et al.* (2008) for seed yield in black gram.

Genetic divergence

D^2 statistics helps in the selection of genetically diverse parents for their exploitation in hybridization programmes. The technique measures the degree of diversification. It measures the forces of differentiation at two levels i.e. intra cluster and inter cluster levels. It provides reliable estimates of genetic divergence and a large number of germplasm lines can be evaluated at time for genetic diversity by this technique. In the present investigation, seventy five genotypes were grouped into 17 clusters using D^2 method. The intra and inter cluster distance was calculated by using D^2 values. The maximum number of genotypes (13) was found in the cluster XIII followed by cluster I (11) and cluster XII (10). These results revealed that geographic diversity might not be an important factor in determining genetic divergence. These finding are supported with the results obtained by Manikannan *et al.* (2000) and Lad *et al.* (2005), Konda*et al.* (2007) and Majumdar *et al.* (2011) in black gram. The intra cluster distances were found higher than the inter cluster distance revealing a considerable amount of genetic diversity among the genotypes studied. The highest inter cluster distance was observed between cluster II and XII followed by cluster XI and XIV and cluster I and XIV. The genotypes grouped in these clusters can be used in breeding programme in order to get a wide spectrum of variability and trangressivesegregants. The minimum distance between clusters XVI and XVII indicated that they were genetically closure clusters. Selection of parents from such clusters may be avoided because it may result in narrow genetic base. This result is supported by findings of Venkatesan *et al.* (2003), Lad *et al.* (2005), Konda *et al.* (2007), Umadevi and Ganesan (2007) and Katna and Verma (2003) in black gram. The variance of cluster mean of different characters indicated that there is a significant variation for all the characters except 100 seed weight, branches per plant and pods per plant. Hence, characters like days to 50% flowering, days to maturity, plant height, pods per plant, seeds per plant, biological yield per plant, harvest index and seed yield per plant contributed more towards genetic divergence. These finding are in close harmony with the results obtained by Manikannan *et al.* (2000), Neelavathi and Govindarasu (2010) for pods per plant and biological yield; Elangaimannan *et al.* (2008) and Umadevi and Ganesan (2007) for branches per plant, seeds per plant and seeds per pod in black gram.

CONCLUSION

There was sufficient genetic variability among the genotypes for all the traits under study. Seed yield per plant and seeds per plant showed high heritability along with high genetic advance. Hence, these characters were less influenced by environments and posses high genetic

variability. Seeds per plant, pods per plant, biological yield per plant, plant height and 100 seed weight had highly significant and positive correlation with seed yield and also had positive association among themselves. Hence selection of these characters simultaneously would bring improvement in yield. Seeds per plant followed by biological yield per plant on the seed yield hence showed the highest direct effect, direct selection of these traits would be rewarding. Among the genotypes studied,RBU 38, CBG 757, NDU 5-3, COBG 761, TPU 05-13, KKB 20055, KPU 07-06, RUG 1, PU 06-20 and VBG 04-008 had potential for higher yield based on the genetic merit of yield factors. These genotypes can be further tested over years across locations to select for direct release as varieties. Besides, these genotypes can be used in cross-breeding programs to generate trangressivesegregants for each traits further selection.

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