



Research Note

Genetic variability for yield and yield attributing traits in F_3 generation of blackgram

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Abstract

The present investigation was carried out in the F_3 population of three black gram crosses viz., LBG-787 x LBG-752, TU-94-02 x KU-1006, and TU-94-02 x LBG-752 along with their parents. High PCV and GCV were recorded for plant height, the number of clusters per plant, the number of pods per plant and seed yield per plant in two crosses, LBG-787 x LBG-752 and TU-94-02 x KU-1006 indicating the existence of wide variability for these traits in the progenies of these crosses. High heritability coupled with high genetic advance as per cent of mean were recorded for plant height, the number of clusters per plant, the number of pods per cluster, the number of pods per plant and seed yield per plant in the cross LBG-787 x LBG-752 and for plant height, the number of branches per plant, the number of clusters per plant, the number of pods per cluster, the number of pods per plant and seed yield per plant in the cross TU-94-02 x KU-1006, respectively. This indicates the scope of selection for these traits in a particular population since there is a wide range of variation and additive gene action for the traits.

Keywords

F_3 population, Progenies, Heritability, Genetic advance, Yield attributes

Black gram (*Vigna mungo*(L).Hepper) is popularly known as urd bean. It is a self-pollinating, short-duration legume that belongs to family *Fabaceae* with a chromosome number of $2n=22$. It is mainly grown for its seeds which are used as whole or splits (dhal). The critical position of pulse production particularly black gram against the increased population poses a challenge on the part of the breeders to develop a high yielding, short duration, bold-grained and disease-resistant varieties.

In order to improve the yield through selection, it is essential to have a thorough knowledge of the genetic variability available in the germplasm and the extent to which the desirable traits are heritable, which requires an insight of the ancillary characters for better selection. Therefore, the present study was aimed at finding out nature and magnitude of genetic variability present in segregating populations of the black gram for seed yield and other yield component traits that can be used in the further breeding program.

Genetic parameters such as the genotypic coefficient of

variation (GCV) and the phenotypic coefficient of variation (PCV) are useful in detecting the amount of variability present in germplasm. Burton (1952) suggested that the GCV along with heritability estimate could provide better picture of the advance to be expected by phenotypic selection. Heritability values along with genetic advance would be more reliable and helpful in predicting the gain under selection than heritability estimate alone. With these parameters, the present investigation was undertaken for the genetic improvement of black gram.

The present investigation was carried out at dryland farm of Sri Venkateswara Agricultural College, Tirupati. The experimental material consisted of three F_3 populations generated from LBG-787 x LBG-752, TU-94-02 x LBG-752, TU-94-02 x KU-1006, and their parents i.e., LBG-787, TU-94-02, LBG-752 and KU-1006. The experiment was laid out in a Compact Family Block Design with four replications during Kharif, 2018. Each cross along with its parents constitutes a family.

A total of ten F_3 progenies and parents of each cross were grown in 2 rows of 3m length. The parents and the F_3 populations were sown following a spacing of 30cm between the rows and 10cm between the plants within a row. Five plants in each row were tagged randomly for recording the observations. Data was recorded for yield and yield attributing traits viz., days to 50% flowering, days to maturity, plant height, the number of branches per plant, the number of clusters per plant, the number of pods per cluster, the number of pods per plant, pod length, the number of seeds per pod, test weight and seed yield per plant. The mean values obtained for each character were subjected to analysis of variance using Compact Family Block Design as described by Chandel (1964). The analysis was carried out in two stages by taking crosses as families. Before making the comparison, a test of homogeneity of error variance for progenies was carried out for each character by applying Bartlett's test of homogeneity as described by

Panase and Sukhatme (1985).

Phenotypic and genotypic coefficients of variation (PCV and GCV) were computed according to Burton (1952). Heritability in a broad sense [$h^2_{(bs)}$] was calculated by the formula given by Lush (1940). From the heritability estimates, the genetic advance was estimated by the formula given by Johnson *et al.* (1955).

Analysis of variance (ANOVA) was done to know the variations among the progenies based on the 11 morphological traits. The analysis of variance for all the characters studied in three crosses of black gram was presented in **Table 1**. The analysis of variance between families revealed that the mean squares due to crosses were significant for all the characters. Bartlett's test for homogeneity of error variances for three crosses indicated that the error variances were homogeneous for all the characters except for the number of clusters per plant, the number of pods per plant and test weight.

Table 1. Analysis of variance (mean squares) between families and between progenies within families of three crosses for different characters in black gram

Source of variation	Degrees of freedom	DF	DM	PH	NB	NCP	NPC	NPP	PL	NSP	SY	TW
Analysis of variance between families												
Replications	3	0.10	0.13	5.83*	0.07**	3.93*	0.03	12.6*	0.05**	0.06*	0.78**	0.011
Crosses	2	5.52**	2.66**	51.27**	0.67**	22.67**	0.21**	55.06**	0.12**	0.67**	14.12**	0.11**
Error	6	0.05	0.08	0.90	0.01	0.43	0.01	2.25	0.01	0.01	0.07	0.01
Bartlett's test		NS	NS	NS	NS	S	NS	S	NS	NS	NS	S
Analysis of variance between progenies of different families												
LBG-752 x LBG-787												
Replications	3	0.52	3.02*	63.67**	0.37	34.55**	0.36**	134.39**	0.15	0.07	5.04	0.01**
Progenies	11	11.47**	7.52**	414.58**	2.57**	193.64**	2.32**	796.33**	1.77**	1.90**	43.65**	0.27**
Error	33	0.27	0.79	12.7	0.15	6.19	0.07	25.75	0.03	0.03	2.02	0.01
Bartlett's test		NS	NS	NS	NS	S	NS	S	NS	NS	NS	NS
TU-94-02 x KU-1006												
Replications	3	2.02*	0.29	7.87	0.08	6.92	0.02	21.46*	0.30	0.26	1.04	0.04
Progenies	11	5.27**	9.88**	236.35**	1.87**	121.58**	0.90**	429.06**	1.27**	1.29**	26.79**	0.13
Error	33	0.55	1.91	6.05	0.07	3.81	0.03	7.05	0.22	0.19	0.73	0.05
Bartlett's test		NS	NS	NS	NS	NS	S	S	NS	NS	NS	NS
TU-94-02 x LBG-752												
Replications	3	0.16	0.13	20.18	0.55	1619	0.12	49.33	0.35	0.64	5.18	0.12
Progenies	11	23.81**	15.65**	146.84**	2.21**	63.64*	0.67**	136.75*	1.56**	1.51*	27.72**	0.40**
Error	33	0.22	0.46	30.88	0.56	23.59	0.20	52.54	16.18	0.69	6.36	0.08
Bartlett's test		NS	NS	NS	NS	S	NS	S	NS	NS	NS	NS

* - Significant at 5 % level; ** - Significant at 1%level

S - significant; NS - nonsignificant

DF - Days to 50% flowering
NB - No. of branches
NPP - Number of pods per plant
TW - Test weight (g)

DM - Days to maturity
NCP - No. of clusters per plant
PL - Pod length (cm)
SY - Seed yield per plant (g)

PH - Plant height (cm)
NPC - No. pods per cluster
NSP - No. seeds per pod

The analysis of variance among progenies within each family indicated significant differences among progeny means for all the characters in all the crosses except for

test weight in cross TU-94-02 x KU-1006. Bartlett's test for homogeneity of error variances for the progenies within each cross indicated that the error variances were

homogeneous for all the characters except for the number of clusters per plant, the number of pods per plant in the crosses, LBG-787 x LBG-752, TU-94-02 x LBG-752, and for the number of pods per cluster and the number of pods per plant in the cross TU-94-02 x KU-1006. Segregation, by allowing allelic recombination, increases the variability among the population. The estimates

of genetic parameters viz., phenotypic and genotypic coefficient of variation (PCV and GCV), heritability in a broad sense, genetic advance and genetic advance as per cent of mean were computed for eleven characters in three crosses of black gram and were presented in **Table 2.**

Table 2. Genetic variability and selection parameters estimated for grain yield and its components in F₃ populations of three black gram crosses

Character	Cross	Mean	PV	GV	PCV	GCV	h ² (bs)	GA	GAM
Days to 50% flowering	LBG-787 x LBG-752	37.35	3.08	2.80	4.70	4.48	71.0	3.29	8.80
	TU-94-02 x KU-1006	36.31	1.73	1.18	3.63	2.99	68.2	1.85	5.09
	TU-94-02 x LBG-752	35.00	6.13	5.90	7.07	6.94	96.3	4.91	14.03
Days to maturity	LBG-787 x LBG-752	81.52	2.48	1.68	1.93	1.59	47.9	2.20	2.70
	TU-94-02 x KU-1006	81.35	3.91	1.99	2.43	1.73	50.9	2.07	2.55
	TU-94-02 x LBG-752	82.85	4.26	3.80	2.49	2.35	89.1	3.79	4.57
Plant height (cm)	LBG-787 x LBG-752	26.51	113.18	100.47	40.13	37.81	68.8	19.46	73.39
	TU-94-02 x KU-1006	33.41	63.63	57.57	23.87	22.71	90.5	14.87	44.50
	TU-94-02 x LBG-752	31.61	59.88	28.99	24.48	17.04	48.4	7.72	24.42
No. of branches per plant	LBG-787 x LBG-752	2.87	0.76	0.61	30.36	27.07	59.5	1.43	49.73
	TU-94-02 x KU-1006	3.65	0.53	0.45	19.93	18.36	84.9	1.27	34.84
	TU-94-02 x LBG-752	3.51	0.98	0.41	28.19	18.33	42.3	1.86	24.55
No. of clusters per plant	LBG-787 x LBG-752	18.86	53.06	46.86	38.62	36.29	68.3	13.25	70.27
	TU-94-02 x KU-1006	22.58	33.26	29.44	25.54	24.03	88.5	10.52	46.57
	TU-94-02 x LBG-752	23.29	33.61	10.01	24.89	13.58	29.8	3.56	15.27
No. of pods per cluster	LBG-787 x LBG-752	2.06	0.64	0.56	38.61	36.36	68.7	1.46	70.54
	TU-94-02 x KU-1006	2.52	0.26	0.22	20.06	18.44	84.5	1.88	34.92
	TU-94-02 x LBG-752	2.25	0.32	0.12	25.13	15.17	36.4	1.43	18.86
No. of pods per plant	LBG-787 x LBG-752	39.06	218.40	192.65	37.84	35.54	68.2	26.85	68.75
	TU-94-02 x KU-1006	46.01	112.56	105.50	23.06	22.32	93.7	20.49	44.52
	TU-94-02 x LBG-752	40.28	73.60	21.05	21.30	11.39	28.6	5.06	12.55
Pod length (cm)	LBG-787 x LBG-752	4.71	0.47	0.44	14.53	14.03	93.2	1.31	17.89
	TU-94-02 x KU-1006	4.98	0.48	0.26	13.97	10.30	54.4	1.78	15.65
	TU-94-02 x LBG-752	5.03	0.76	0.27	17.30	10.28	35.3	1.63	12.58
No. of seeds per pod	LBG-787 x LBG-752	5.75	0.50	0.47	12.32	11.91	93.5	1.36	13.72
	TU-94-02 x KU-1006	5.93	0.47	0.28	11.59	8.84	58.2	1.82	13.90
	TU-94-02 x LBG-752	6.53	0.90	0.20	14.52	6.91	22.6	1.44	6.78
Test weight (g)	LBG-787 x LBG-752	4.69	0.07	0.07	5.69	5.59	76.3	1.53	11.29
	TU-94-02 x KU-1006	4.76	0.07	0.02	5.71	3.10	29.6	1.17	3.48
	TU-94-02 x LBG-752	5.01	0.16	0.08	8.01	5.67	50.1	1.41	8.26
Seed yield per plant (g)	LBG-787 x LBG-752	8.95	12.43	10.41	39.39	36.04	83.7	6.08	67.92
	TU-94-02 x KU-1006	10.42	7.25	6.52	25.84	24.50	89.9	4.99	47.86
	TU-94-02 x LBG-752	12.68	11.71	5.34	26.98	18.22	45.6	3.22	25.35

CV : Coefficient of Variation PCV : Phenotypic Coefficient of Variation GA : Genetic Advance
 PV : Phenotypic Variance GCV : Genotypic Coefficient of Variation GAM : Genetic Advance as percent
 GV : Genotypic Variance h² (bs) : Heritability in Broad Sense of Mean

The analysis revealed that the phenotypic coefficient of variation (PCV) was slightly higher than the genotypic coefficient of variation (GCV) for all the characters, so it is evident that expression of the characters is mainly governed by the genotypes itself along with the meager

effect of environment. This finding also gets corroborated with Meshram *et al.* (2013) and Ramya *et al.* (2014) and Deepshikha *et al.* (2014) in black gram.

In the present study, high PCV and GCV was recorded for plant height, the number of branches per plant, the

number of clusters per plant, the number of pods per cluster, the number of pods per plant and seed yield per plant in the cross, LBG-787 x LBG-752 while it was for the number of clusters per plant, the number of pods per plant and seed yield per plant in the cross TU-94-02 x KU-1006. This indicates the existence of wide variability for these traits in the progenies of these crosses. On contrary the cross TU-94-02 x LBG-752, no character has shown a high GCV and PCV. These findings were in accordance with Sharma *et al.* (2006) and Reddy *et al.* (2011) for plant height and the number of pods per plant; Sharma *et al.* (2006) for the number of branches per plant; Hemalatha *et al.* (2017) for the number of clusters per plant; and Vijay *et al.* (2015) and Reddy *et al.* (2011) for seed yield per plant.

In cross LBG-787 x LBG-752, high heritability and the high genetic advance were observed for plant height, the number of clusters per plant, the number of pods per cluster, the number of pods per plant and seed yield per plant. In cross TU-94-02 x KU-1006, high heritability coupled with high genetic advance was observed for plant height, the number of branches per plant, the number of clusters per plant, the number of pods per cluster, the number of pods per plant and seed yield per plant. This suggests that high heritability most likely due to additive gene effect. Hence, these traits may be subjected to any selection scheme to develop stable genotypes in particular crosses. Similar results have been reported by Panigrahi *et al.* (2014) for the number of branches; Sharma *et al.* (2006) for plant height; Gowsalya *et al.* (2016), Hemalatha *et al.* (2017) and Panda *et al.* (2017) for the number of clusters per plant, the number of pods per plant and seed yield per plant; Sowmini and Jayamini (2013) for the number of pods per cluster; and Rolaniya *et al.* (2017) for biomass per plant.

High heritability with moderate genetic advance as per cent of mean was recorded by pod length, the number of seeds per pod and test weight in the cross LBG-752 x LBG-787 and by days to 50% flowering in the cross TU-94-02 x LBG-752 indicating the presence of additive as well as non-additive gene action in their genetic control. These results were in accordance with the earlier findings by Deepshikha *et al.* (2014) for pod length and the number of seeds per pod.

In cross TU-94-02 x LBG-752, low heritability and low genetic advance was shown by the number of seeds per pod. It indicates that the above character was highly influenced by the environmental effects and selection for such traits would be ineffective in this cross. This trait improvement can be made opting the two to three cycles of recurrent selection followed by either pedigree or single seed descent method of breeding.

The existence of variability among the black gram progenies in F_3 populations of three crosses indicates that the selection will be effective in enhancing the seed yield by progeny selection. Emphasis shall be given for traits, plant height, the number of clusters per plant, the number of pods per cluster, the number of pods per plant and

seed yield per as they have expressed high estimates of variability, heritability and genetic advance as per cent of mean.

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