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## Genetic variability studies in blackgram

**A Kavitha Reddy, M Shanthi Priya, D Mohan Reddy and B Ravindra Reddy****Abstract**

Genetic variability analysis was carried out for yield, yield components and water use efficiency characters in 30 blackgram genotypes. The study indicated existence of considerable amount of variability for all the characters. High heritability estimates were recorded for relative water content, SLA at 50 DAS, number of pods per plant, plant height, days to 50% flowering, seed yield per plant and number of clusters per plant. Number of clusters per plant, number of pods per plant, seed yield per plant and number of primary branches per plant exhibited high genetic advance as percent of mean. High heritability coupled with high genetic advance as percent of mean was recorded for number of pods per plant, seed yield per plant and number of clusters per plant indicating preponderance of additive gene action. Therefore, selection for the above traits would be more rewarding to bring improvement in black gram.

**Keywords:** Black gram, broad sense heritability, genetic advance, GAM, variability

**Introduction**

Blackgram [*Vigna mungo* (L.) Hepper] ( $2n=22$ ) is one of the highly prized pulses of India. Blackgram is said to have originated in India, where it has been in cultivation from ancient times. Blackgram is a widely grown grain legume and belongs to the family fabaceae and assumes considerable importance from the point of food and nutritional security.

The yield potential of blackgram is very low because of the fact that, the crop is mainly grown in rainfed conditions with poor management practices and the other constraints of blackgram production include non availability of location specific varieties, susceptibility to moisture stress, insect pests and diseases.

Water use efficiency is one of the genetic characters which can contribute to higher productivity under scarce water resources. Moisture stress at flowering and pod filling stages reduces seed yield and harvest index significantly. Hence, identification of high yielding genotypes with higher water use efficiency is the research priority.

Knowledge of variability, heritability, genetic advance and diversity of yield and yield component traits of blackgram indicates the scope of improvement through selection (Deepalakshmi *et al.*, 2004, Kumar and Mishra 2004, Veeramani *et al.*, 2005) <sup>[3, 11, 20]</sup>. The present investigation was taken up among thirty genotypes of blackgram to assess the amount of genetic variability for yield, yield component and water use efficiency traits.

**Material and Methods**

The present investigation was carried out among 30 blackgram genotypes during *Kharif*, 2017 at dry land farm of Sri Venkateswara Agricultural College, Tirupati using Randomized Block Design with three replications.

Observations were recorded on five randomly selected plants in each genotype for plant height, number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length, number of seeds per pod, 100 seed weight, harvest index, SPAD chlorophyll meter reading at 35 DAS, SPAD chlorophyll meter reading at 50 DAS, Specific leaf area 35 DAS, Specific leaf area 50 DAS, relative water content and seed yield per plant, whereas for days to 50% flowering and days to maturity observations were recorded on plot basis.

The variation among 30 genotypes for different characters was tested for significance by using analysis of variance technique as given by Panse and Sukhatme (1961) <sup>[17]</sup>. The genotypic (GCV) and phenotypic (PCV) coefficient of variation was calculated by the formulae given by

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Burton (1952) [2]. Heritability in broad sense [h<sup>2</sup>b] was calculated by the formula given by Lush (1940) [13] and genetic advance as given by Johnson *et al.* (1955a) [9].

## Results and Discussion

The analysis of variance carried out for 17 yield, yield component and water use efficiency traits revealed highly significant (1%) differences among the genotypes for the characters *viz.*, days to 50% flowering, days to maturity, plant

height, number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length, number of seeds per pod, 100 seed weight, harvest index, seed yield per plant, SCMR at 35 DAS, SCMR at 50 DAS, SLA at 35 DAS, SLA at 50 DAS and relative water content (Table 1). These results indicated the presence of considerable amount of genetic variation for all the 17 traits in the experimental material under inorganic fertilizer management.

**Table 1:** Analysis of variance for 17 characters in 30 blackgram genotypes

S. No	Characters	Mean sum of squares		
		Replications (df=2)	Treatments (df=29)	Error (df=58)
1	Days to 50% flowering	1.87	9.71**	1.88
2	Days to maturity	6.94	11.35**	2.59
3	Plant height (cm)	7.70	34.09**	4.03
4	No. of primary branches per plant	0.04	0.47**	0.14
5	No. of clusters per plant	0.30	12.78**	1.82
6	No. of pods per cluster	0.008	0.27**	0.08
7	No. of pods per plant	11.38	95.37**	9.70
8	Pod length (cm)	0.09	0.24**	0.05
9	No. of seeds per pod	0.02	0.78**	0.36
10	100 seed weight (g)	0.17	0.56**	0.09
11	Seed yield per plant (g)	4.26	17.88**	6.61
12	Harvest index (%)	0.31	1.74**	0.22
13	SPAD chlorophyll meter reading at 35DAS	36.69	27.03**	11.87
14	SPAD chlorophyll meter reading at 50DAS	22.43	26.96**	9.03
15	Specific leaf area at 35DAS (cm <sup>2</sup> g <sup>-1</sup> )	1577.66	1714.54**	487.25
16	Specific leaf area at 50DAS (cm <sup>2</sup> g <sup>-1</sup> )	71.07	971.77**	29.13
17	Relative water content (%)	0.89	38.17**	0.92

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

## Variability studies

The estimates of genetic parameters *viz.*, phenotypic and genotypic coefficient of variation, heritability in broad sense,

genetic advance and genetic advance as percent of mean computed for seventeen characters in thirty genotypes are presented in Table 2.

**Table 2:** Mean, range, coefficient of variation, heritability (broad sense) and genetic advance as percent of mean for 17 characters in 30 blackgram genotypes

S. No.	Character	Mean	Range		Variance		Coefficient of Variation		Heritability (Broad sense) (%)	Genetic advance (GA)	Genetic advance as percent of mean (%)
			Min.	Max.	Genotypic	Phenotypic	Genotypic	Phenotypic			
1	Days to 50% flowering	40.66	37.00	44.33	2.84	4.03	4.15	4.94	70.51	2.92	7.17
2	Days to maturity	70.04	65.67	74.00	2.92	5.52	2.44	3.35	52.88	2.56	3.65
3	Plant height (cm)	41.69	35.33	52.07	10.02	14.06	7.59	8.99	71.30	5.51	13.21
4	No. of primary branches per plant	1.95	1.27	2.73	0.11	0.25	17.26	25.64	45.33	0.47	23.95
5	No. of clusters per plant	8.96	5.33	13.60	3.65	5.48	21.32	26.10	66.73	3.22	35.88
6	No. of pods per cluster	2.90	2.33	3.87	0.06	0.15	8.45	13.30	40.33	0.32	11.05
7	No. of pods per plant	26.78	16.13	40.73	28.56	38.26	19.96	23.10	74.64	9.51	35.52
8	Pod length (cm)	4.44	3.97	5.13	0.06	0.12	5.64	7.67	54.11	0.38	8.54
9	No. of seeds per pod	6.04	4.93	7.20	0.14	0.51	6.23	11.76	28.03	0.41	6.79
10	100 seed weight (g)	4.37	3.87	5.22	0.09	0.18	6.80	9.71	49.04	0.43	9.81
11	Harvest index (%)	21.56	16.29	28.76	3.76	10.37	7.03	11.69	36.20	2.40	8.72
12	Seed yield per plant (g)	4.99	3.48	6.44	0.51	0.73	14.24	17.12	69.11	1.22	24.38
13	SPAD chlorophyll meter reading at 35 DAS	41.28	33.27	47.53	5.05	16.93	5.45	9.97	29.84	2.53	6.13
14	SPAD chlorophyll meter reading at 50 DAS	47.61	42.33	55.60	5.98	15.01	5.14	8.14	39.82	3.18	6.68
15	Specific leaf area at 35 DAS (cm <sup>2</sup> g <sup>-1</sup> )	285.37	221.17	321.74	409.10	896.35	7.09	10.49	45.64	28.15	9.86
16	Specific leaf area at 50DAS (cm <sup>2</sup> g <sup>-1</sup> )	185.28	144.91	214.61	314.21	343.35	9.57	10.00	91.51	34.93	18.85
17	Relative water content (%)	75.13	63.57	84.29	12.42	13.34	5.85	6.07	93.09	7.00	11.63

Phenotypic co-efficient of variation was of high magnitude than the genotypic co-efficient of variation for all the characters indicating the influence of environment in the expression of these traits. Similar results have been recorded by Konda *et al.* (2009) <sup>[10]</sup>, Meshram *et al.* (2012) <sup>[14]</sup>, Deepshika *et al.* (2014) <sup>[4]</sup>, Dharmendra *et al.* (2017) <sup>[5]</sup> and Patidar *et al.* (2018) <sup>[18]</sup>.

Number of clusters per plant showed higher estimates of variability indicating the ample variation among the genotypes for the trait. Therefore, simple selection would be effective for further improvement of number of clusters per plant.

Higher PCV and GCV estimates for number of clusters per plant was in accordance with the results obtained by Gupta *et al.* (2006) <sup>[7]</sup>, Priyanka *et al.* (2016) <sup>[19]</sup>, Hemalatha *et al.* (2017) <sup>[8]</sup>, Kuralarasan *et al.* (2017) <sup>[12]</sup>.

The characters, SLA at 50 DAS, SCMR at 35 DAS, 100 seed weight, plant height, SCMR at 50 DAS, pod length, relative water content, days to 50% flowering and days to maturity exhibited lower estimates of both GCV and PCV.

Lower estimates of PCV and GCV obtained for days to 50% flowering, days to maturity, hundred seed weight and pod length were in accordance with the results obtained by Gupta *et al.* (2006), Konda *et al.* (2009) <sup>[10]</sup>, Panigrahi and Baisakh (2014) <sup>[16]</sup> and Anu *et al.* (2017) <sup>[1]</sup>. Patidar *et al.* (2018) <sup>[18]</sup> also noted lower PCV and GCV values for days to 50% flowering, days to maturity and pod length.

### Heritability

High heritability estimates were recorded for relative water content, SLA at 50 DAS, number of pods per plant, plant height, days to 50% flowering, seed yield per plant and number of clusters per plant indicating the least influence of environment on these characters. The characters *viz.*, pod length, days to maturity, 100 seed weight, SLA at 35 DAS, number of primary branches per plant, number of pods per cluster, SCMR at 50 DAS and harvest index showed moderate heritability estimates, while SCMR at 35 DAS and number of seeds per pod exhibited lower heritability estimates.

### Genetic advance

All the characters *viz.*, number of pods per plant, relative water content, plant height, number of clusters per plant, SCMR at 50 DAS, days to 50% flowering, days to maturity, SCMR at 35 DAS, harvest index, seed yield per plant, number of primary branches per plant, 100 seed weight, number of seeds per pod, pod length, number of pods per cluster and exhibited low genetic advance except SLA at 35 DAS and SLA at 50 DAS which registered high genetic advance.

### Genetic advance as percent of mean

The characters, number of clusters per plant, number of pods per plant, seed yield per plant and number of primary branches per plant exhibited high genetic advance as percent of mean. Moderate estimates of genetic advance as percent of mean were exhibited by SLA at 50 DAS, plant height, relative water content, number of pods per cluster. The traits that recorded lower values of genetic advance as percent of mean were days to 50% flowering, days to maturity, pod length, number of seeds per pod, 100 seed weight, harvest index, SCMR at 35 DAS, SCMR at 50 DAS and SLA at 35 DAS.

High heritability coupled with high genetic advance as percent of mean was recorded for number of pods per plant, seed yield per plant and number of clusters per plant indicating preponderance of additive gene action and hence

phenotypic selection would be more effective for improvement of these characters.

High heritability coupled with high genetic advance as percent of mean for number of pods per plant, seed yield per plant and clusters per plant was earlier reported by Gupta *et al.* (2006) <sup>[7]</sup>, Kuralarasan *et al.* (2017) <sup>[12]</sup>, Gowsalya *et al.* (2016) <sup>[6]</sup>, Hemalatha *et al.* (2017) <sup>[18]</sup> and Panda *et al.* (2017) <sup>[15]</sup>.

Moderate heritability coupled with high genetic advance as percent of mean was recorded for number of primary branches per plant. Improvement can be brought about in this trait through simple pedigree method of breeding and phenotypic selection would be effective.

High heritability coupled with low genetic advance as percent of mean recorded for days to 50% flowering indicates the presence of non-additive gene action. The high heritability is being exhibited due to favourable influence of environment rather than the genotype and selection for this trait may not be rewarding.

High heritability coupled with low genetic advance recorded for days to 50% flowering is in accordance with the results obtained by Vijay *et al.* (2015) <sup>[21]</sup>, Priyanka *et al.* (2016) <sup>[19]</sup> and Panda *et al.* (2017) <sup>[15]</sup>.

High heritability coupled with moderate genetic advance as percent of mean recorded for plant height, SLA at 50 DAS and relative water content indicated the presence of non-additive gene action. The high heritability is being exhibited due to favourable influence of environment rather than the genotype and selection for such traits may not be rewarding. This finding obviates simple selection and necessitates recombination breeding with postponement of selection at later generations.

The estimates of high heritability along with moderate genetic advance for plant height was in accordance with the results obtained by Dharmendra *et al.* (2017) <sup>[5]</sup> and Panda *et al.* (2017) <sup>[15]</sup>. Results of low heritability and low genetic advance for number of seeds per pod were in consonance with the results presented by Konda *et al.* (2009) <sup>[10]</sup>, Vijay *et al.* (2015) <sup>[21]</sup>, Anu *et al.* (2017) <sup>[1]</sup> and Panda *et al.* (2017) <sup>[15]</sup>.

The results showed that number of clusters per plant registered high GCV, heritability and genetic advance as percent of mean suggesting that this character can be easily improved through selection. Seed yield per plant recorded moderate GCV, high heritability and high genetic advance.

Among the water use efficiency traits, SCMR at 35 DAS exhibited low GCV, low heritability and low genetic advance while SCMR at 50 DAS recorded low GCV, moderate heritability and low genetic advance. SLA at 35 DAS exhibited low GCV, moderate heritability and low genetic advance; SLA at 50 DAS recorded low GCV, high heritability and moderate genetic advance.

This indicates that environment is playing a significant role in the expression of these traits.

Relative water content registered low GCV, high heritability and moderate genetic advance. This condition is an indicative of non-additive gene action. The high heritability is being exhibited due to favourable effect of environment rather than genotype and direct selection for such a trait may not be rewarding.

### Conclusion

High heritability coupled with high genetic advance as percent of mean was observed for number of pods per plant, seed yield per plant and number of clusters per plant

indicating the preponderance of additive gene action and selection may be rewarding.

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