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## Genetic variability studies on yield and yield contributing traits in blackgram (*Vigna mungo* (L.) Hepper

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**Abstract**

An experiment was conducted to estimate the genetic variability on twenty-eight genotypes of blackgram (seven parents and twenty-one  $F_1$ 's) during *kharif*- 2017 in RBD at Research cum Instructional Farm, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh. Variability was studied for twelve quantitative characters. From the present investigation it was found that all the characters showed significant variation for all the traits except for days to 50% flowering. GCV and PCV estimates were observed high for seed yield per plant followed by biological yield per plant and plant height.

**Keywords:** Blackgram, variability, GCV, PCV, heritability, genetic advance

**Introduction**

Blackgram (*Vigna mungo* (L.) Hepper) is one of the important pulse crops grown throughout India. It comes under the family Fabaceae. It is an important self-pollinating diploid grain legume (Naga *et al.*, 2006) [11] domesticated from *V. mungo* var. *silvestris* (Lukoki *et al.* 1980) [9]. It is consumed in the form of 'dal' (whole or split, husked and un-husked) or perched. It is used as nutritive fodder specially for milch animals. It is also green manuring crop. High values of lysine make blackgram an excellent complement to rice in terms of balanced human nutrition.

Blackgram is perfect combination of all nutrients, which includes proteins 25-26% carbohydrates (60%), fat (1.5%), minerals, amino acids and vitamins. It stands next to soybean in its dietary protein content (25-26%). It is rich in vitamin A, B<sub>1</sub>, B<sub>3</sub> and has small amount of thiamine, riboflavin, niacin and vitamin C in it. It contains 78% to 80% nitrogen in the form of albumin and globulin. The dry seeds are good source of phosphorus. It also has very high calorie content, 100 gm of blackgram has 347 calories (Panotra *et al.* 2016) [13]. Therefore, blackgram is the cheapest available source of protein for the poor and vegetarians.

Nature of gene action controlling economic trait plays important role in crop improvement programme and the exploring the gene action is essential (Titumeer *et al.*, 2014) [21]. Study of GCA helps for selection of good combiners with additive genes and the SCA are helpful for the effect for superior hybrid combination. Gene action is helpful for selection of breeding method for improvement of specific trait (Singh and Singh, 1974) [17]. Only additive type of gene action is fixable and essential to develop stable genotypes. Genetic variability study includes the parameter such as phenotypic, genotypic and environmental coefficient of variation, heritability and genetic advance are undeniably needed to start an efficient breeding method (Sarkar *et al.*, 2014) [16].

**Materials and methods**

Seven genotypes (TU-103, MASH-1008, INDIRA URD PRATHAM, PU-11-14, TU-94-2, LBG-623 and LBG-17) with their 21 cross combinations were studied in RBD design with two replications in individual row of 2 meter length at spacing of 45 x 10 cm. at experimental field of IGKV, Raipur. All the recommended practices were followed throughout the growth period of crop.

For observation five random plants from each replication were selected. Observation were recorded for twelve polygenic characters. Seed index was recorded by weighing of 100 seeds from randomly selected five plant in each replication. The protein was estimated according to the modified Kjeldahl's method (Piper, 1966) [14]. Standard statistical procedures were followed for comparing of means of genotypes.

## Results and discussion

The analysis of variance showed high significant difference among the seven parents and 21 cross combinations for 12 quantitative traits (Table 1). All the genotypes showed highly significant variation for almost all the traits. Highly significant variation was observed for days to maturity, plant height, number of pods per plant, pod length, number of seeds per pod, 100 seed weight, biological yield, seed yield per plant, harvest index and protein content except for days to 50% flowering and number of branches per plant. Minimal influence of environmental on treatment was determined by small degree of error mean sum of squares of all the traits.

Variability for traits days to 50% flowering and number of branches per plant was ranged from 44 days to 52 with mean of 47.82 and 2 to 5.5 with mean 3.75 respectively. Yield per plant was ranged from 6.06 to 45.10 g and overall means was 12.42 g. Protein content in the population was recorded between 16.35 to 27.80% with mean of 20.86. these results showed huge variability for yield and yield contributing traits. Among all the traits under observed in this experiment biological yield per plant (411.56), plant height (266.82), number of pods per plant (186.18), seed yield per plant (65.99) showed high amount of treatment mean sum of square. Variability present in number of pods per plant can help in selection for high yield.

Days to maturity was ranged from 66 to 80 days, with a mean performance of 72.82 days. Mainly the parental varieties INDIRA URD PRATHAM, PU-11-14 and LBG-623 observed for the early maturity with one cross combination TU-103 x TU-94-2 (70 days). Similar findings were reported by Thamodharan *et al.*, (2017)<sup>[20]</sup> and Yashodha *et al.*, (2016)

<sup>[22]</sup>. Number of pods per plant ranged from 11-46 with a mean performance of 29.04. Highest number of pods per plant was recorded in crosses LBG-623 x LBG-17 (46) with reference to other researchers the results are in general agreement with Zuge *et al.*, (2019)<sup>[23]</sup> and Sushmitharaj *et al.*, (2018)<sup>[18]</sup>. Pod length ranged from 3.25 cm to 4.75 cm with a mean performance of 4.32 cm. The maximum length of pods was recorded for TU-103 x INDIRA URD PRATHAM (4.75 cm) and TU-103 x TU-94-2 (4.75 cm) Pod length is an important trait for yield enhancement as increase in pod length will also help in increasing number of seeds per pod. More the seeds per pod, more the yield per plant. Number of seeds per pod ranged from 5.5 to 8.5, with a mean performance of 6.52. Maximum number of seeds per pod was 9 and recorded in cross INDIRA URD PRATHAM x LBG-623. Selection for more number of seeds per pod will be beneficial for yield improvement. These results are similar to the previous results as reported by Tank *et al.*, (2018)<sup>[19]</sup>, Hemlatha *et al.*, (2017) and Punia *et al.*, (2013). 100 seed weight ranged from 2.03 g to 4.74 g, with a mean performance of 3.62 g. Cross MASH-1008 x PU-11-14 recorded for highest 100 seed weight (4.74 g) and TU-103 x Indira URD Pratham (4.07 g). In blackgram test weight (100 seed weight) is an important yield contributing trait which can indicates the boldness of seed and market preference. Harvest index (%) ranged from 22.60% to 39.04%, with a mean performance of 32.90%. Biological yield per plant was ranged from 10.55 g to 61.55 g, with a mean performance of 36.94 g. Highest biological yield per plant was recorded in Indira URD Pratham x TU-94-2 (61.55 g), similar findings were reported by Tank *et al.*, (2018)<sup>[19]</sup> and Hemlatha *et al.*, (2017).

**Table 1:** Analysis of variance for eleven characters of Blackgram genotypes

S. No.	Character	Mean	Range	Mean sum of square			CV
				Treatment (d.f=27)	Replication (d.f=1)	Error ( $\pm$ ) (d.f=27)	
1	Days to 50% flowering	47.82	44-52	4.79	14.00	2.93	3.80
2	Days to maturity	72.82	66-80	17.12**	8.64	6.57	3.52
3	Plant height (cm)	38.09	16-59	266.82**	36.16	16.83	10.77
4	No. of branches per plant	3.75	2-5.5	1.65	0.00	1.19	29.03
5	No. of pods per plant	29.04	14-46	186.18**	4.57	57.42	26.10
6	Pod length (cm)	4.32	3.25-4.75	0.27**	1.14	0.11	7.53
7	No. of seeds per pod	6.52	5.5-8.5	0.98**	0.88	0.32	8.67
8	100 seed weight (g)	3.62	2.03-4.74	0.40**	0.07	1.56	34.51
9	biological yield	36.94	10.55-61.55	411.56*	666.26	221.10	40.26
10	Seed yield per plant (g)	12.42	6.06-45.10	65.99*	98.21	32.66	46.02
11	Harvest index (%)	32.90	22.60-39.04	31.20**	3.41	9.14	9.19
12	Protein content (%)	20.86	16.35-27.80	11.78**	0.01	0.01	0.41

Variability estimate in a population is a pre-requisite for trait improvement in breeding programme aimed at improving yield and quality characters under consideration. Without a major portion of variation is heritable in nature, selection for such trait will be misleading. Hence, heritability combined with genetic advance is an important measure for selection. The estimates of GCV, PCV, heritability, genetic advance and genetic advance as percent of means was given in Table 2.

In the outcome of present study, it found that PCV was relatively higher than GCV for all the characters except for plant height (cm) and number of branches per plant. However, the degree of difference between PCV and GCV values were low for most of the characters except for number of branches per plant, biological yield and seed yield per plant, which indicates the less environmental influence on most of the characters and moderate influence on the above stated characters.

The phenotypic coefficient of variation was high for seed yield per plant (56.55), biological yield (48.15), number of pods per plant (38.01) and plant height (29.35) while, maximum genotypic coefficient of variation was recorded for seed yield per plant (32.87), number of branches per plant (31.74), plant height (31.27), number of pods per plant (27.36) and biological yield (26.42) which indicates the scope of selection for early maturity, number of branches per plant and seed yield per plant. These results are in agreement with the results of previous workers *viz.*, Gandhi *et al.*, (2018), Mehta and Lal (2018)<sup>[10]</sup> and Sushmitharaj *et al.*, (2018)<sup>[18]</sup>.

Heritability is that portion of variation which is transferable to the next generation which measures the variability that is due to genetic cause and is the ratio of genotypic variance to the total phenotypic variance. Environmental variation plays major role on heritability of character in addition to genetic cause. Difference in the estimates of heritability can occur due

to genetic as well as environmental variance. The heritability ( $H^2$  bs) have been classified into three classes as low (<50%), medium (50-70%) and high (>70%) as per classes suggested by Burton (1952).

Heritability in broad sense was calculated for all the twelve characters studied. Protein content showed the highest heritability (99.88%) followed by 100 seed weight (95.92%) and plant height (88.13%). High heritability indicates that these characters are highly heritable and governed by additive gene effects. Similarly, Arunbalachandran *et al.*, (2010)<sup>[1]</sup> and Lad *et al.*, (2010)<sup>[8]</sup> have also reported high heritability for plant height, 100 seed weight, protein content *etc.*

Heritability estimates are used to calculate the genetic advance from selection is additionally beneficial for quantitative characters. The heritability alone is not sufficient to predict the selective advantage for any trait and also unable to provide any indication for genetic improvement that would result from selecting the best individuals. The genetic advance was high for plant height (21.62) while moderate for number of pods per plant (12.02) and biological yield per plant (11.03). High heritability coupled with high genetic advance was recorded for only plant height. These findings are accordance with the findings of Jyothisna *et al.*, (2016)<sup>[7]</sup> and Neelavathi and Govindarasu (2010)<sup>[12]</sup>. Moderate heritability

with moderate genetic advance was observed in number of pods per plant whereas, the lowest value of heritability coupled with low genetic advance was observed in seed yield per plant, days to maturity, days to 50% flowering, number of branches per plant and pod length, direct selection for these traits may give poor response in blackgram. Similar results were also reported by Punia *et al.*, (2014)<sup>[15]</sup> and Asha (2013)<sup>[2]</sup>.

The range of genetic advance as percentage of mean was suggested by Johnson *et al.* (1955)<sup>[6]</sup> and classified as low (<10%), moderate (10-20%) and high (>20%). Plant height (56.77) showed highest genetic advance as percent of mean followed by number of pods per plant (41.39), seed yield per plant (39.37), biological yield (29.86), 100 seed weight (24.69) and protein content (23.94). High heritability with moderate genetic advance as percentage of mean was observed for harvest index (54.70, 15.38) and number of seeds per pod (50.86, 12.96). Moderate heritability with high genetic advance as percentage of mean was observed for number of pods per plant (52.86, 41.39). Based on the combined estimates of heritability and genetic advance (per cent) only plant height was found to be governed by additive gene action. While all the remaining traits were governed by non-additive gene action.

**Table 2:** Coefficient of Variation, Heritability and Genetic Advance for 12 yield contributing characters of 28 Blackgram genotypes.

S. No.	Character	$\sigma^2g$	$\sigma^2p$	$\sigma^2e$	Coefficient of variation		h <sup>2</sup> (%)	GA	GA (% of mean)
					GCV	PCV			
1	Days to 50% flowering	0.74	4.04	3.30	1.80	4.20	18.43	0.76	1.60
2	Days to maturity	5.28	11.84	6.57	3.15	4.73	44.54	3.16	4.34
3	Plant height (cm)	124.99	141.82	16.83	31.27	29.35	88.13	21.62	56.77
4	Number of branches per plant	0.23	1.42	1.19	31.74	12.83	16.34	0.40	10.68
5	Number of pods per plant	64.38	121.80	57.42	27.63	38.01	52.86	12.02	41.39
6	Pod length (cm)	0.08	0.19	0.11	6.57	9.99	43.26	0.38	8.91
7	No. of seeds per pod	0.33	0.65	0.32	8.82	12.37	50.86	0.84	12.96
8	100 seed weight (g)	0.20	0.20	0.01	12.24	12.50	95.92	0.89	24.69
9	biological yield	95.23	316.33	221.10	26.42	48.15	30.10	11.03	29.86
10	Seed yield per plant	16.67	49.33	32.66	32.87	56.55	33.79	4.89	39.37
11	Harvest index (%)	11.03	20.17	9.14	10.10	13.65	54.70	5.06	15.38
12	Protein content (%)	5.89	5.89	0.01	11.63	11.64	99.88	4.99	23.94

### Authors contributions

Conceptualization of research work and designing of experiments (TNA, NHC); Execution of field/lab experiments and data collection (TNA, ZSS); Analysis of data and interpretation (NSK, TNA); Preparation of manuscript (TNA, NSK).

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