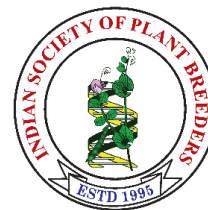


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## Research Note

### Estimation of genetic variability in blackgram [*Vigna mungo*(L.) Hepper]

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#### Abstract

An investigation was carried out during *kharif*, 2018 in Randomized Block Design to estimate the variability parameters in blackgram using thirty five genotypes including two checks *viz.*, Pratap Urd-1 and Pant Urd-31. The results of ANOVA showed that the genotypes varied significantly for all the traits. The high GCV and PCV estimates were recorded for seed yield per plant, plant height, harvest index and 100-seed weight. High magnitude of heritability combined with the high genetic gain was found for traits *viz.*, plant height, the number of pods per cluster and 100-seed weight. Therefore, direct selection for the traits like, plant height, harvest index, 100-seed weight and the number of pods per cluster would be useful for increasing seed yield in blackgram.

#### Key words

Blackgram, Genetic Advance, Heritability, Variability.

Blackgram [*Vignamungo* (L.) Hepper] is an important grain legume crop related to the family *Leguminosae*. Among pulses, blackgram is an important short duration pulse crop extensively cultivated on marginal and poor soils with a low input in India. It has nutritious value hence being a cheap source of dietary protein. Its 100 gram of seed contains 25g seed protein, 60g carbohydrate, 1.5g fat, 0.9g fiber, 3.2g minerals (*i.e.* phosphorus, calcium and iron). It is also a good source of amino acids & vitamins *viz.*, vitamin A (retinol), B<sub>1</sub> (thiamine), B<sub>2</sub> (riboflavin), B<sub>5</sub> (niacin) and vitamin C and its calorific value is very high *i.e.* 347 calories per 100 gram of blackgram seeds. Blackgram has symbiotic association with *rhizobium* bacteria therefore, it ameliorate the soil fertility by symbiotic nitrogen fixation as it possess root nodules in their roots.

Productivity of blackgram is low because of various constraints including lower genetic potential of existing genotype. Therefore, it is essential to enhance the yield of blackgram by studying the genetic architecture of the crop. The efficiency of selection for a trait is greatly relying on

the amount of variability exists in the genotypes. Hence, prior to initiating any crop improvement program the knowledge of the inheritance of yield and its component traits through estimation of genetic variability parameters *viz.*, GCV (genotypic coefficient of variation), PCV (phenotypic coefficient of variation), h<sup>2</sup> (heritability), GA (genetic advance) and GG (genetic gain) is prerequisite. Therefore, this investigation was conducted with a set of blackgram accessions to study the various variability parameters.

Thirty five accessions of blackgram along with two checks *viz.*, Pratap Urd-1 and Pant Urd-31 were planted at Instructional Research Farm, Department of Genetics and Plant breeding, Rajasthan College of Agriculture, MPUAT, Udaipur during *kharif*, 2018. The experimental material was raised in RBD (Randomized Block Design) with three replications with a row and plant spacing of 30×10cm, respectively. The agronomical practices were adopted according to the package of practices of Zone IVA throughout the period of crop growth.

The data was taken from each plot, on five randomly selected plants for fourteen traits viz., plant height (cm), the number of branches per plant, the number of clusters per plant, the number of pods per plant, the number of pods per cluster, pod length (cm), the number of seeds per pod, seed yield per plant (g), biological yield per plant (g), harvest index (%), 100-seed weight (g) and seed protein content (%) whereas for remaining two traits viz., days to 50 per cent flowering and days to 75 per cent maturity were taken on whole plot basis. Further statistical analysis was carried out by using the mean value of five plants.

Analysis of variance (ANOVA) was done by Panse and Sukhatme (1985). Estimation of variability parameters, GCV and PCV was done using procedure suggested by Burton (1952), method given by Burton and Devane (1953) was used for the estimation of heritability and genetic advance was determined by adopting the procedure given by Johnson *et al.* (1955).

Knowledge about genetic variability is a prime need for deciding the efficiency of selection in any crop improvement program. Its existence is vital for biotic and abiotic stress resistance and wide adaptability. Results of ANOVA showed that the genotypes involved in the study had a significant difference for all the traits which distinctly endorsed the validation of studying genetic variability using these genotypes. The variability

parameters are worked out for fourteen traits in blackgram are presented in **Table 1**. The magnitude of PCV was greater than their corresponding GCV for all the traits studied representing that the environment significantly influenced the expression of these traits. These outcomes are in agreement with the results of Reddy *et al.* (2011), Panigrahi *et al.* (2014), Priyanka *et al.* (2016) and Panwar *et al.* (2019). The magnitude of different variability parameters was categorized on the basis of mean plus/minus half standard deviation. Values more than (mean + 1/2SD) categorized as high, equal to (mean + 1/2SD)/(mean - 1/2SD) as medium and it is less than (mean - 1/2SD) as low (Diwakar *et al.*, 2016).

The highest GCV was found for seed yield per plant followed by harvest index, plant height and 100-seed weight which suggested the possibility of improvement through selection in these traits since they had abundant genetic variation among genotypes. Similar results were also obtained by Panigrahi *et al.* (2014), Babu *et al.* (2016), Aftab *et al.* (2018), Panwar *et al.* (2019) and Chaithanya *et al.* (2019) for seed yield per plant, plant height and harvest index. The traits viz., the number of pods per cluster, the number of branches per plant, biological yield per plant and the number of clusters per plant were exhibited a moderate GCV. While, days to 50 per cent flowering, days to 75 per cent maturity and seed protein content were showed a low GCV estimates. This indicating the occurrence of low genetic variability

**Table 1. Mean value and Variability parameters for seed yield per plant and its attributing traits in blackgram**

Traits	Mean	GCV (%)	PCV (%)	ECV (%)	h <sup>2</sup> (%)	GA	GG (%)
DF	40.10	3.76	5.73	4.32	43.11	2.04	5.09
DM	72.63	2.84	3.42	1.91	68.75	3.52	4.84
PH	24.48	16.19	17.53	6.71	85.34	7.54	30.81
NB	8.52	14.59	16.39	7.47	79.24	2.28	26.76
NC	8.01	13.95	15.66	7.10	79.43	2.05	25.62
NP	19.91	11.09	13.91	8.39	63.58	3.63	18.21
NPC	2.53	14.75	16.72	7.88	77.81	0.68	26.81
PL	4.44	13.56	14.68	5.64	85.26	1.15	25.79
NS	5.38	13.57	18.00	11.82	56.86	1.13	21.08
SY	5.01	19.63	24.11	13.99	66.32	1.65	32.94
BY	16.74	14.16	17.41	10.13	66.15	3.97	23.73
HI	30.22	17.63	22.24	13.56	62.84	8.70	28.78
SI	5.00	15.68	16.78	5.99	87.26	1.51	30.16
SPC	23.08	4.81	5.83	3.30	68.05	1.89	8.18

DF, days to 50 per cent flowering; DM, days to 75 per cent maturity; PH, plant height (cm); NB, number of branches per plant; NC, number of clusters per plant; NP, number of pods per plant; NPC, number of pods per cluster; PL, pod length (cm); NS, number of seeds per pod; SY, seed yield per plant (g); BY, biological yield per plant (g); HI, harvest index (%); SI, 100-seed weight (g); SPC, seed protein content (%)

for these traits therefore, selection will not be useful for these traits.

Seed yield per plant followed by harvest index and the number of seeds per pod had high PCV estimates. This indicates that the expression of these traits considerably influenced by the environment. Aftab *et al.* (2018) and Chaithanya *et al.* (2019) were also found similar results for seed yield per plant and harvest index. Moderate PCV estimates were observed for plant height, the number of branches per plant, the number of pods per cluster, biological yield per plant and 100-seed weight.

Estimates of high heritability were reported for 100-seed weight followed by plant height, pod length, the number of clusters per plant, the number of branches per plant and the number of pods per cluster indicating a low environmental influence and high ability of these traits for transmission to next generations. Results are in harmony with some previous findings of Konda *et al.* (2009), Kuralarasan *et al.* (2017), Aftab *et al.* (2018) and Chaithanya *et al.* (2019) for the number of clusters per plant, plant height and the number of branches per plant. The traits *viz.*, days to 75 per cent maturity, seed yield per plant, biological yield per plant and seed protein content expressed moderate heritability. For predicting the effectiveness of selection, high  $h^2$  in combination with high GA would be more reliable. High heritability as well as high genetic advance was observed for plant height suggested that this character was controlled by additive gene effect hence the selection will be more valuable for yield enhancement. Results are found in accordance with Kant and Srivastava (2011) and Singh *et al.* (2014) for plant height.

The highest genetic gain was reported for seed yield per plant followed by plant height, 100-seed weight, harvest index and the number of pods per cluster representing that these traits are controlled by additive genetic variance to a large extent and improvement of these traits through selection would be rewarding. These findings are in agreement with the results of Aftab *et al.* (2018) and Chaithanya *et al.* (2019) for seed yield per plant. Moderate genetic gain was observed for the number of branches per plant, pod length, the number of cluster per plant, the number of pods per plant, the number of seeds per pod and biological yield per plant.

The current study revealed that an adequate genetic variability was present between genotypes. Selection based on seed yield per plant, harvest index, plant height and 100-seed weight would be effective as these traits had high GCV. The traits *viz.*, plant height, 100-seed weight and the number of pods per cluster had a high heritability combined with high genetic gain while seed yield per plant expressed moderate heritability with high genetic gain therefore, direct selection for above traits would be helpful in yield enhancement for future breeding programs.

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