The Andhra Agric. J 72 (4): 457-460, 2025
doi :10.61657/aaj.2025.237

Genetic variability studies in blackgram [*vigna mungo* (L.) Hepper] genotypes

D Priyanka Bai, J Sateesh babu, N Satyanarayana and V Roja
Department of Genetics and Plant Breeding, Acharya N G Ranga Agricultural University,
Agricultural College, Bapatla-522101, Andhra Pradesh, India

ABSTRACT

The present study was undertaken to assess the magnitude of genetic variability, heritability, and genetic advance for seed yield and its associated traits in 45 blackgram genotypes during *rabi,* 2024-25 at Regional Agricultural Research Station, Lam, Guntur, Andhra Pradesh. The analysis of variance revealed significant differences among the genotypes for all characters studied, suggesting the presence of considerable genetic variation on the present study.On the present studies high heritability coupled with high genetic advance was recorded for seed yield per plant, number of branches per plant, clusters per plant, pods per plant, seeds per pod and pod length suggesting the predominance of additive gene action and the possibility of effective direct selection for these traits. These results also emphasized and suggested the potential for genetic improvement through direct selection in blackgram breeding programs.

Keywords: *Blackgram, Genetic advance, Heritability, PCV and GCV*

Blackgram (*Vigna mungo* (L.) Hepper), belonging to the family Fabaceae (Leguminosae), is an important pulse crop of the Indian subcontinent, commonly known as blackgram, urad bean, or urad dal, with a chromosome number of 2n = 22. It is a short-duration (70–90 days) self-pollinated annual legume grown mainly as a kharif and summer crop, preferring a warm and humid climate with an optimum temperature of 25–35 °C, and well-drained loam to clay loam soils with pH 6.5–7.5.. Agriculturally, it improves soil fertility through biological nitrogen fixation (30–40 kg N/ha), enhances soil structure and microbial activity, and fits well in crop rotation, intercropping, and mixed cropping systems as a catch crop.

Economically, it is highly valuable to small and marginal farmers due to it's low input requirement and high market demand, while ecologically it supports sustainable agriculture by reducing chemical fertilizer use and preventing soil erosion. Blackgram is widely used as dal, flour, and split pulse in foods such as idli, dosa, vada, papad, and traditional sweets, its residues serve as nutritious cattle feed and green manure, and it also has medicinal importance in traditional systems for improving digestion, vitality, bone strength.

The success of crop improvement relies on understanding genetic variability, heritability, and genetic advance, which indicate the scope for selection and genetic gain. High heritability coupled with high genetic advance suggests the predominance of additive gene action, favorable for selection-based breeding. India, the major producer and consumer of blackgram, mainly grows in the *rabi* and summer seasons under arid and semi-arid conditions. India continues to lead the world in both the production and consumption of blackgram. In the 2023–2024 period, Andhra Pradesh stood out as a key producer, with the second advance estimates reporting a production of 3.84 lakh tonnes from 3.08 lakh hectares, achieving an impressive average productivity of 1247 kg per hectare during 2023–2024 (IIPR, Annual Report 2023–24).

Despite its adaptability and importance, productivity remains low due to limited genetic variability and various biotic and abiotic stresses. Hence, assessing genetic diversity and utilizing improved breeding strategies are essential to enhance yield potential and stability in blackgram.

MATERIAL AND METHODS

The experiment material consisted of 45 blackgram genotypes were evaluated in a field trial during *rabi*, 2024-25 in alpha lattice design with five blocks and three replications at RARS, Lam, Guntur, Andhra Pradesh. Observations were recorded on 11 quantitative traits *viz*; days to 50% flowering, days to maturity, plant height (cm), number of branches per plant, number of clusters per plant, number of pods per plant, number of seeds per pod, pod length(cm), test weight(g), seed yield per plant(g). Standard statistical procedures were used to compute the phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in broad sense (h^2), and genetic advance as per cent of mean (GAM). Days to 50% flowering, days to maturity are recorded on plot basis and remaining all the traits are recorded on five plant basis. The analysis of variance for each character was calculated as per the standard statistical procedure given by Johnson *et al*. (1955). The phenotypic and genotypic coefficients of variation were calculated by using the formula given by Burton (1952).

RESULTS AND DISCUSSION

The analysis of variance revealed highly significant differences among the genotypes for all the characters studied, indicating the existence of sufficient variation among the genotypes studied Table 1. The estimates of variability, heritability and genetic advance as per cent of mean were detailed in the Table 2. Genetic variability revealed significant genotypic differences for all the traits indicating ample variability. High PCV and GCV values were recorded for traits like seed yield per plant which suggest considerable scope for selection. These results were in conformity with the Bhanuprasad *et al*. (2022), and Gnanasekaran *et al*. (2023). Moderate genotypic and phenotypic coefficients of variation were recorded for plant height, clusters per plant, seeds per pod, pod length, pods per cluster and pods per plant. These results were in conformity with Yergude *et al*. (2021) and Karthik *et al*. (2022) for plant height, Deekshit *et al*. (2022) and Mukesh *et al*. (2024) for clusters per plant, Nagamani *et al*. (2025) for seeds per pod, pods per plant and pods per cluster and Sathees *et al*. (2019) for pod length.

Low phenotypic and genotypic coefficients of variation were recorded for days to 50% flowering and days to maturity. These results were in conformity with Mukesh *et al*. (2024) for days to 50% flowering, Sindhu *et al*. (2023) for days to maturity. The narrow difference between PCV and GCV for most traits indicated that environmental influence was minimal.

High heritability and high genetic advance was observed for seed yield per plant (81.29%, 44.75%), pod length (84.30%, 25.97%), seeds per pod (74.18%, 23.03%), pods per plant (69.80%, 20.17%), clusters per plant (70.64%, 24.62%), and

Table 1. Analysis of variance for seed yield and yield contributing traits in blackgram [*Vigna mungo* (L.) Hepper]

Source of variations	D.F	Days to 50% flowering	Days to maturity	Plant height (cm)	Branches per plant	Clusters per plant	Pods per cluster	Pods per plant
Replications	2	0.033	0.071	0.025	0.014	0.256	0.058	0.31
Treatments (unadjusted)	44	2.506**	4.486*	22.119**	0.191**	1.091**	0.439**	2.43**
Blocks within Replicated (adj)	12	1.024	1.152	1.923	0.013	0.099	0.067	0.424
Intrablock error	76	0.891	2.859	3.544	0.010	0.133	0.086	0.306

Source of variations	D.F	Seed per pod	Pod length(cm)	Test weight(g)	Seed yield per plant(g)
		Mean sum of squares			
Replications	2	0.495	0.09	0.204	0.032
Treatments (unadjusted)	44	1.718**	0.946**	0.295*	0.415**
Blocks within Replicated (adj)	12	0.126	0.078	0.128	0.039
Intrablock error	76	0.179	0.055	0.171	0.03

Table 2. Estimation of variability parameters for seed yield and yield contributing traits in blackgram [*Vigna mungo* (L.) Hepper]

S. No.	Character	Mean	Range		Coefficient of		Heritability (broad sense) (%)	Genetic advance as % of mean
			Minimum	Maximum	GCV (%)	PCV (%)		
1	Days to 50 % flowering	36.84	35.33	39.34	1.99	3.25	37.65	2.52
2	Days to maturity	67.36	65.66	71	1.09	2.74	15.94	0.9
3	Plant height (cm)	21.96	18.2	27.6	11.33	14.21	63.6	18.62
4	Branches per plant	1.29	1	1.87	19.11	20.61	85.94	36.49
5	Clusters per plant	3.98	3.07	5.87	14.22	16.92	70.64	24.62
6	Pods per cluster	3.24	2.47	3.93	10.59	13.92	57.83	16.58
7	Pods per plant	7.18	6	9.27	11.72	14.03	69.8	20.17
8	Seeds per pod	5.52	4.17	7.21	12.98	15.07	74.18	23.03
9	Pod length (cm)	3.97	3.07	6.87	13.73	14.96	84.3	25.97
10	Test weight (g)	4.01	3.19	4.6	5.07	11.51	19.42	4.6
11	Seed yield per plant (g)	1.49	0.92	2.37	24.09	26.72	81.29	44.75

PCV- Phenotypic Coefficient of Variation **GCV- Genotypic Coefficient of Variation**

branches per plant (85.94%, 36.49%). This indicated strong preponderant additive gene action and suggesting that these traits are amenable for improvement through direct selection. These results were in conformity with Gnanasekaran *et al*. (2023), Mukesh *et al*. (2024) for seed yield per plant, Sathees *et al*. (2019) for pod length, Nagamani *et al*. (2025) for seeds per pod, pods per plant, clusters per plant and branches per plant.

Moderate heritability coupled with moderate genetic advance was observed for pod per cluster (57.83%, 16.58%) indicating environmental influence and a moderate response to selection. Days to 50% flowering (37.65%, 2.52%) exhibited high to moderate heritability but low genetic advance, suggesting non-additive gene effects or strong environmental influence, making direct selection for yield based and less effective on above traits.

CONCLUSION

The present study revealed that traits like for seed yield per plant , pod length, seeds per pod, pods per plant, clusters per plant and branches per plant showed high heritability and genetic advance, indicating the predominance of additive gene action and potential for improvement through selection. Traits with moderate to low genetic advance despite high heritability may require different breeding strategies such as hybridization followed by selection. Seed yield per plant showed highest heritability and a very high genetic advance, along with other yield components such as branches per plant and pods per plant suggesting their potential for improvement through selection. These findings provide valuable insights for blackgram improvement programs aiming for higher production and productivity.

LITERATURE CITED

Bhanuprasad P, Lavanya G R, Reddy B M and Ramesh B 2022. Genetic parameters and diversity analysis in blackgram (*Vigna mungo* L. Hepper) for seed yield characters. *International Journal of Plant & Soil Science*, 34(24): 340-347.

Burton G W 1952. Quantitative inheritance in grasses. *Proceedings of the 6th International Grassland Congress*. 277-283.

Deekshith K S, Venkanna V, Devi K R, Naik DS and Kumar CS 2022. Genetic variability, heritability and genetic advance in blackgram (*Vigna mungo* L.). *Biological Forum-An International Journal*. 14(12): 583-588.

Gnanasekaran M, Gunasekaran M and Thiyagu K 2023. Genetic variability, heritability, genetic advance and association studies in blackgram [*Vigna mungo* (L.) Hepper]. *Legume Research-An International Journal*.

Johnson H W, Robinson H F and Comstock R E 1955. Estimates of genetic and environmental variability in soybean. *Agronomy Journal* 47: 314-318.

Karthik U, Lal G M, Bara B M, Yajavathi C and Gangadhar L 2022. Direct and indirect effects of yield contributing characters on seed yield in blackgram (*Vigna mungo* (L.) Hepper). *International Journal of Environment and Climate Change* 12(11) :2016-2027.

Mukesh,Yumnam S, Laishram P, Kumar H, Senjam P, Singh L, Gopimohan N and Jat J K 2024. Genetic basis of yield variation in spring mung Bean (*Vigna radiata* (L).): A correlation and path analysis study. *International Journal of Bio-Resource & Stress Management*,*15*-(16).

Nagamani N, Shashikala S, Manjunatha B, Sadashiv N and Usha T 2025. Studies on genetic variability and screening of yellow vein mosaic virus (YVMV) resistance in mutant lines of blackgram (*Vigna mungo* (L). Hepper) under field condition. *Contemporary Research and Perspectives in Biological Science.*

Sathees N, Shoba D, Saravanan S, Kumari S M P and Pillai M A 2019. Studies on genetic variability, association and path coefficient analysis in blackgram (*Vigna mungo* L. Hepper). *International Journal of Current Microbiology and Applied Sciences*. 8(6): 1892-1899.

Sindhu N, Macwana S S, Boddu S and Surakanti S 2023. Assessment of genetic variability, character association and path analysis for yield and yield attributes in blackgram (*Vigna mungo* (L.) hepper). *Environment and Ecology.* 41(2): 765-771

Yergude P, Rakshe M B and Ujjainkar V V 2021. Genetic varability analysis in blackgram (*Vigna mungo* L. Hepper). *The Pharma Innovation Journal*. 10(9): 1447-1451.

Received on 10.10.2025 and Accepted on 12.11.2025