Plant Archives Vol. 26, No. 2, 2026 pp. 1989-1994 e-ISSN:2581-6063 (online), ISSN:0972-5210

Plant Archives

Journal homepage: http://www.plantarchives.org

DOI Url : https://doi.org/10.51470/PLANTARCHIVES.2026.v26.no.2.273

GENETIC VARIABILITY STUDIES FOR YIELD COMPONENTS IN BLACK GRAM (*Vigna mungo* L. Hepper)

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(Date of Receiving-29-07-2026; Date of Revision-21-09-2026; Date of Acceptance-03-10-2026)

ABSTRACT

Genetic improvement in self-pollinated pulse crops relies directly on the magnitude and nature of genetic variability available in the germplasm. The present investigation evaluated 24 diverse black gram genotypes in a Randomized Block Design with two replications during *Rabi* 2021–2022 at Research and Education Farm, Department of Agril. Botany, College of Agriculture, Dapoli, Maharashtra, across 15 quantitative characters. Analysis of variance indicated highly significant differences among the genotypes for all traits. Phenotypic coefficient of variations (PCV) was marginally higher than their corresponding genotypic coefficient of variations (GCV), with the highest values recorded for number of pods per plant (41.72% and 40.70%), plant height (37.29% and 37.04%) and grain yield per plant (35.59% and 34.44%). Broad-sense heritability (h^2_b) was very high across most traits, ranging up to 98.75% for number of branches per plant, 98.69% for plant height, and 98.32% for number of clusters per plant. High heritability coupled with high genetic advance as percent of mean (GAM) was recorded for number of pods per plant (h^2_b - 95.19%, GAM- 81.81%), plant height (h^2_b - 98.69%, GAM- 75.81%), grain yield per plant (h^2_b - 93.61%, GAM- 68.63%), number of clusters per plant (h^2_b - 98.32%, GAM- 62.15%) and number of branches per plant (h^2_b - 98.75%, GAM - 61.22 %). These findings demonstrate the predominance of additive gene action, indicating that simple phenotypic selection would be effective for genetic yield enhancement in black gram. Thus, the genotypes KKVVM-18 followed by KKVVM-20 and KKVVM-9 were observed as best performers in the genotypes studied.

Key words : *Vigna mungo*, Genetic variability, GCV, PCV, Broad-sense heritability, GAM.

Introduction

Pulses, also known as grain legumes, are a wonderful gift from nature and an essential addition to the diet that primarily consists of cereal. They are the main source of protein in Asia. (Sahoo and Jaiwal, 2008). Pulses are sporadically grown on marginal lands with low fertility and moisture stress, so genotypes are more adaptable to poor management that registers yield limitations. This does not indicate low genetic potential however, they may have higher genetic potential than cereals (Jain, 1978). Pulses are among the best crops in the world; their availability and production take on a special significance for the nutritional security of the people. India is a unique nation that cultivates a wide range of pulse crops that are grown nowhere else in the world.

Black gram [*Vigna mungo* (L.) Hepper] is an important pulse crop that provides protein to vegetarians while also enriching soil through biological nitrogen fixation. Among pulses, black gram is widely consumed and cultivated throughout India. Black gram has a unique position in Indian agriculture and it is widely grown throughout the year in India.

Blackgram is an excellent source of protein (25-26%), carbohydrates (60%), fat (1.5%), minerals, amino acids, and vitamins (Malik, 1994). In terms of dietary protein content, it ranks second only to soybean. It contains vitamin A, B1, B3 and a trace of thiamine, riboflavin, niacin and vitamin C. It has the highest phosphoric acid content of any pulse. It contains about 78 - 80% nitrogen in the form of albumin and globulin. The dry seeds are

high in phosphorus. Black gram has 347 calories per 100 gm. As a result, black gram is the most affordable source of protein for the poor and vegetarians (Tharanathan and Mahadevamma, 2003).

The success of any targeted breeding programme is governed by the nature and extent of genetic variability present in the base population. Because observed phenotypic variation encompasses both heritable genotypic effects and non-heritable environmental fluctuations, evaluating biometric indicators specifically genotypic and phenotypic coefficients of variation, broad-sense heritability and genetic advance is essential. These parameters help determine whether trait expression is driven by additive or non-additive gene effects, ensuring effective parental selection and generation advancement. Effective breeding therefore requires partitioning total phenotypic variance into its genotypic, phenotypic, and environmental components. Evaluating the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad-sense heritability (h^2_b) and expected genetic advance as percent of mean (GAM) illuminates the heritable portion of variation and identifies whether traits are governed by additive or non-additive gene action. Establishing these genetic parameters across diverse germplasm collections provides the foundation needed to select superior donor parents and devise efficient hybridization and selection strategies for black gram improvement.

Materials and Methods

The experiment was conducted during *Rabi* 2021–2022 at the Educational and Research Farm, Department of Agricultural Botany, College of Agriculture, Dapoli, Ratnagiri, Maharashtra (17°45' N latitude, 73°12' E longitude; 250 m AMSL; lateritic soil with pH 5.6–8.0). The genetic material comprised 24 black gram genotypes, including 23 local collections from diverse agro-climatic locations across Maharashtra (KKVVM-1 to KKVVM-23) and one released check variety, KKVVM-24 (PDKV Black Gold from PDKV, Akola).

The trial was arranged in a Randomized Block Design (RBD) with two replications. Seeds were dibbled at a spacing of 30 cm between plants and 20 cm between rows in plots measuring 3 m × 1 m (5 rows per genotype with 10 plants per row; 50 plants per replication). Standard crop management practices and a recommended fertilizer schedule of 25 kg N: 50 kg P_2O_5 per hectare (half nitrogen at sowing, half at 30 days after sowing) were applied. Five randomly tagged representative plants per genotype per replication were evaluated for 15 quantitative traits: Days to Initiation of Flowering (Calendar days from sowing to the opening of the first flower in a plot), Days to 50% Flowering (Days from sowing until 50% of the plants in a plot flowered), Days to Maturity (Days from sowing until over 90% of pods turned mature and dry), Plant Height (cm) (Main stem length from ground level to the apex at harvest), Number of Primary Branches/ Plant (Count of productive branches on the main axis), Number of Clusters/Plant (Total pod-bearing clusters per tagged plant), Number of Pods/Cluster (Average pods per cluster {total pods divided by total clusters}), Number of Pods/Plant (Total count of well-developed mature pods harvested per plant), Number of Grains/Pod (Average seed count obtained from representative pods), Pod Length (cm) (Average length from base to beak across representative mature pods), Hundred Seed Weight (g) (Weight of 100 randomly sampled, clean dry seeds), Grain Yield/Plant (g) (Total weight of clean, dried seeds harvested per plant), Dry Matter/Plant (g) (Above-ground plant biomass dried to constant weight), Harvest Index (%) (Ratio of grain yield to total dry matter {Grain Yield / Dry Matter} \100), Protein Content (%) (Total nitrogen determined via micro-Kjeldahl digestion and multiplied by 6.25).

Analysis of variance (ANOVA) was performed according to Panse and Sukhatme (1985). Environmental variance was calculated as σ^2_e = EMS, genotypic variance as σ^2_g = GMS – EMS/r and phenotypic variance as $\sigma^2_p = \sigma^2_g + \sigma^2_e$. Phenotypic and genotypic coefficients of variation were computed and classified as per Sivasubramanian and Menon (1973; Low: <10%, Moderate: 10-20 %, High: >20%). Broad-sense heritability (h^2_b) was derived *via* Lush (1949) and expected genetic advance (GA) along with genetic advance as percent of mean (GAM) at a 5% selection intensity (k = 2.06) were computed and categorized using the scales of Johnson *et al*. (1955) (Low: <10%, Moderate: 10 -20%, High: >20%).

Results and Discussion

Analysis of Variance and Mean performance

The analysis of variance revealed highly significant ($p < 0.01$) differences among the 24 genotypes for all 15 evaluated quantitative traits, establishing the presence of wide genetic variability (Table 1). The treatment mean sum of squares was widest for plant height (184.870), harvest index (127.720), days to maturity (59.605), number of pods per plant (57.059), and days to 50% flowering (49.812).

Trait means showed wide variation across the germplasm. Days to initiation of flowering ranged from 33.00 (KKVVM-14) to 48.50 days (KKVVM-13, KKVVM-19), days to 50% flowering varied from 42.50

Table 1 : Estimates of phenotypic (σ^2_p), genotypic (σ^2_g) and environmental (σ^2_e) variances for 15 quantitative characters of black gram.

S. no.	Characters	σ^2p	σ^2g	σ^2e
1	Days to initiation of flowering	16.486	11.022	5.464
2	Days to 50 per cent flowering	27.681	22.130	5.551
3	Days to maturity	32.317	27.288	5.029
4	Number of branches per plant	0.275	0.271	0.003
5	Number of clusters per plant	2.953	2.904	0.050
6	Number of pods per cluster	0.139	0.120	0.018
7	Number of pods per plant	29.232	27.827	1.405
8	Number of grains per pod	0.703	0.570	0.133
9	Pod length (cm)	0.077	0.041	0.036
10	Hundred seed weight (g)	0.345	0.290	0.055
11	Plant height (cm)	93.042	91.826	1.216
12	Grain yield per plant (g)	0.560	0.524	0.036
13	Dry matter per plant (g)	1.419	1.375	0.044
14	Harvest index (%)	64.776	62.940	1.836
15	Protein content (%)	5.481	4.644	0.837

(KKVVM-14) to 63.50 days (KKVVM-13) and days to maturity extended from 85.50 (KKVVM-14) to 108.50 days (KKVVM-13). Plant height ranged between 14.70 cm (KKVVM-15) and 46.30 cm (KKVVM-13). Yield components displayed marked differences: number of branches per plant ranged from 1.10 (KKVVM-17) to 3.10 (KKVVM-18); number of clusters per plant varied between 4.20 (KKVVM-10, KKVVM-12) and 12.00 (KKVVM-18); number of pods per cluster ranged from 1.93 (KKVVM-17) to 3.48 (KKVVM-24); number of pods per plant ranged from 7.07 (KKVVM-5) to 33.05 (KKVVM-18); and hundred seed weight ranged from 2.18 g (KKVVM-10, KKVVM-12) to 4.15 g (KKVVM-1). Grain yield per plant ranged from 1.04 g (KKVVM-5) to 4.36 g (KKVVM-18). Dry matter per plant varied from 3.52 g (KKVVM-5) to 9.00 g (KKVVM-18), harvest index ranged from 25.19% (KKVVM-4) to 48.45% (KKVVM-18), and seed protein content spanned 17.68% (KKVVM-17) to 24.68% (KKVVM-10).

Components of variation

The total variation between the genotypes were subdivided into genotypic, phenotypic and environmental variance. The estimates of variance due to these three components for fifteen characters among 24 genotypes of black gram are given in Table 1. The phenotypic, genotypic and environmental variances for various characters varied from 0.077 (pod length) to 93.042 (plant height) for phenotypic, 0.041 (pod length) to 91.826 (plant height) for genotypic and 0.003 (number of branches per plant) to 5.551 (days to 50 per cent flowering) for environmental variance. The magnitude of phenotypic variance was higher than genotypic variance for all the characters under study. The phenotypic variance was maximum for plant height (93.042) followed by harvest index (64.776) and days to maturity (32.317) whereas it was minimum for pod length (0.077) followed by number of pods per cluster (0.139), number of branches per plant (0.275), hundred seed weight (0.345), grain yield per plant (0.560), number of grains per pod (0.703) and dry matter per plant (1.419). The characters, *viz*., number of clusters per plant (2.953), protein content (5.481), days to initiation of flowering (16.486), days to 50 per cent flowering (27.681), number of pods per plant (29.232), days to maturity (32.317) recorded moderate result of phenotypic variance.

The genotypic variance was higher in magnitude over environmental variance. The highest genotypic variance was noticed in plant height (91.826) followed by harvest index (62.940), number of pods per plant (27.827), days to maturity (27.288) and days to 50 per cent flowering (22.130). The lowest magnitude of genotypic variances was observed in pod length (0.041) followed by number of pods per cluster (0.120), number of branches per plant (0.271), hundred seed weight (0.290), grain yield per plant (0.524) and number of grains per pod (0.570). The moderate genotypic variance was noted for dry matter per plant (1.375), number of clusters per plant (2.904), protein content (4.644) and days to initiation of flowering (11.022).

The magnitude for environmental variance was higher for days to 50 per cent flowering (5.551) followed by days to initiation of flowering (5.464), days to maturity (5.029) and it was lowest for number of branches per plant (0.003) followed by number of pods per clusters (0.018) and pod length (0.036).

Similar results were in confirmed by Dharmendra *et al*. (2014) and Anu *et al.* (2017) for plant height and pod length. Hemalatha *et al*. (2017) for plant height, Gowsalya *et al*. (2016) for plant height, pod length, number of branches per plant and hundred seed weight.

Coefficient of variation

The estimates of genotypic and phenotypic coefficient of variation estimated for 15 characters of black gram under study are presented in Table 2.

The results showed that, phenotypic coefficient of variation (PCV) was greater in magnitude than the respective genotypic coefficient of variation (GCV). The characters *i.e.*, number of pods per plant (41.72%), plant height (37.29%), grain yield per plant (35.59%), number of clusters per plant (30.69%) showed highest phenotypic

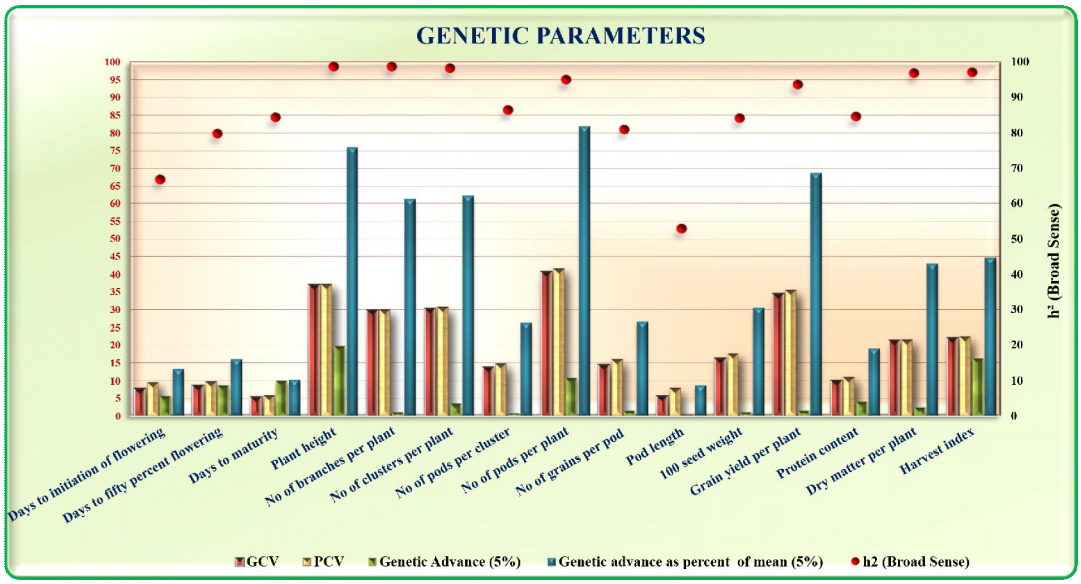


Fig. 1 : Comparison of Genetic Parameters across traits.

coefficient of variation. The least magnitude of phenotypic coefficient of variation was reported in days to maturity (5.86%) followed by pod length (7.87%), days to initiation of flowering (9.54%) and days to 50 per cent flowering (9.73). The remaining characters like Protein content (10.93%), number of pods per cluster (14.73%), number of grains per pod (15.88%),100seed weight (17.61%) and dry matter per plant (21.57%) indicated moderate phenotypic coefficient of variation.

The amount of genetic variation present in the 24 genotypes was worked out in terms of genotypic coefficient of variation (GCV). The highest genotypic coefficient of variation was recorded in number of pods per plant (40.70%), followed by plant height (37.04%) and grain yield per plant (34.44%) whereas least GCV was seen in days to maturity (5.39%), followed by pod length (5.73%), days to initiation of flowering (7.80%), days to 50 per cent of flowering (8.70%) and protein content (10.07%). The moderate GCV was observed in remaining traits, *viz*., number of pods per cluster (13.71%), number of grains per pod (14.30%), hundred seed weight (16.15%), dry matter per plant (21.24%), harvest index (22.02%), number of branches per plant (29.90 %) and number of clusters per plant (30.43%).

Such kind of results were reported by Gowsalya *et al*. (2016), Priyanka *et al*. (2016), Dharmendra *et al*. (2014), Jyothsna *et al*. (2016), Sateesh *et al*. (2016), Yashoda *et al*. (2016), Anu *et al*. (2017), Bal and Lal (2021).

This classification (GCV and PCV) was done based on the standard scale given by the Sivasubramanian and Menon (1973).

Heritability and genetic advance

The estimate of heritability and genetic advance for 15 different characters are presented in Table 2.

Heritability in broad sense varied from 53.04% (pod length) to 98.75% (number of branches per plant). High heritability was observed for number of branches per plant (98.75%) followed by plant height (98.69%), number of clusters per plant (98.32%), harvest index (97.17%), dry matter per plant (96.91%), number of pods per plant (95.19%), grain yield per plant (93.61%), number of pods per cluster (86.65%), protein content (84.74%), days to maturity (84.44%), hundred seed weight (84.15%), number of grains per pod (81.07%) and days to 50 per cent flowering (79.95%). Moderate heritability was observed for days to initiation of flowering (66.86%) and pod length (53.04%).

The genetic advance ranged from 0.30 (pod length) to 19.61 (plant height). Plant height (19.61) reported highest magnitude of genetic advance followed by harvest index (16.11) and number of pods per plant (10.60) while lowest magnitude of genetic advance was exhibited by pod length (0.30) followed by number of pods per cluster (0.66), hundred seed weight (1.02) and number of branches per plant (1.07). Moderate estimates of genetic advance were noted in days to maturity (9.89), days to 50% flowering (8.67), days to initiation of flowering (5.59), protein content (4.09), number of clusters per plant (3.48) and dry matter per plant (2.38).

The genetic advance as per cent of mean (GAM) was varied from 8.60% (pod length) to 81.81% (number of pods per plant). The highest GAM was reported in number of pods per plant (81.81%) followed by plant

Table 2 : Estimates of genetic parameters for 15 quantitative characters in black gram.

S. no.	Characters	PCV(%)	GCV(%)	ECV(%)	h^2b(%)	GA	GAM(%)
1	Days to initiation of flowering	9.54	7.80	5.49	66.86	5.59	13.13
2	Days to 50 per cent flowering	9.73	8.70	4.36	79.95	8.67	16.02
3	Days to maturity	5.86	5.39	2.31	84.44	9.89	10.20
4	Number of branches per plant	30.09	29.90	3.37	98.75	1.07	61.22
5	Number of clusters per plant	30.69	30.43	3.98	98.32	3.48	62.15
6	Number of pods per cluster	14.73	13.71	5.38	86.65	0.66	26.29
7	Number of pods per plant	41.72	40.70	9.15	95.19	10.60	81.81
8	Number of grains per pod	15.88	14.30	6.91	81.07	1.40	26.52
9	Pod length (cm)	7.87	5.73	5.39	53.04	0.30	8.60
10	Hundred seed weight (g)	17.61	16.15	7.01	84.15	1.02	30.52
11	Plant height (cm)	37.29	37.04	4.26	98.69	19.61	75.81
12	Grain yield per plant (g)	35.59	34.44	9.00	93.61	1.44	68.63
13	Dry matter per plant (g)	21.57	21.24	3.79	96.91	2.38	43.07
14	Harvest index (%)	22.34	22.02	3.76	97.17	16.11	44.71
15	Protein content (%)	10.93	10.07	4.27	84.74	4.09	19.09

height (75.81%), grain yield per plant (68.63%), number of clusters per plant (62.15%), number of branches per plant (61.22%), harvest index (44.71%), dry matter per plant (43.07%), hundred seed weight (30.52%), number of grains per pod (26.52%) and number of pods per cluster (26.29%). The minimum magnitude of GAM was recorded for pod length (8.60%) followed by days to maturity (10.20%) and days to initiation of flowering (13.13%). The moderate estimate of GAM was recorded in days to 50% flowering (16.02%) and protein content (19.09%). Similar kind of results were obtained by Pushpa *et al.* (2013), Punia *et al*. (2014), Gowasalya *et al*. (2016), Priyanka *et al.* (2016), Sateesh *et al*. (2016) and Jyothsna *et al*. (2016).

This classification of (Heritability, Genetic advance and GAM) was done based on the standard scale given by the Johnson *et al*. (1955).

Conclusion

Broad range of variability was present between the genotypes studied for the different quantitative characters. High heritability coupled with high genetic advance per cent mean was observed for number of pods per plant, plant height, grain yield per plant (g) and number of clusters per plant. The higher estimates of heritability coupled with high genetic advance as percent of mean shows additive gene action and make in suitable for direct selection.

Thus, the genotypes KKVVM-18 followed by KKVVM-20 and KKVVM-9 were observed as best performers in the genotypes studied. These had the highest seed yield per plant and also maximum yield attributing characters. The genotype KKVVM-1 had maximum hundred seed weight, KKVVM-18 had maximum number of pods per plant, number of branches per plant and pod length. The genotype KKVVM-10 had highest protein content and KKVVM-13 had maximum plant height. All the genotypes mentioned above have the potential to be used as promising genetic material in future breeding programmes.

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