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EVALUATION OF GENETIC PARAMETERS FOR YIELD AND YIELD CONTRIBUTING TRAITS IN BLACKGRAM (*VIGNA MUNGO* L. HEPPER)

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ABSTRACT

The present study was conducted on fourteen blackgram genotypes along with four check varieties, namely Indira URD 1, KU 96-3, Pratap URD 1, and TPU 4, to assess genetic variability for yield and related traits. The experiment was laid out in a randomized complete block design and evaluated across four locations in Madhya Pradesh i.e., RVSKVV R.A.K. College of Agriculture, Sehore; RVSKVV College of Agriculture, Gwalior; Krishi Vigyan Kendra, Jhabua; and Krishi Vigyan Kendra, Barwani during the Kharif season of 2021. Ten morphological traits were recorded to estimate key genetic parameters, including phenotypic and genotypic coefficients of variation (PCV and GCV), heritability, and genetic advance. Analysis of variance revealed highly significant differences ($p < 0.01$) among genotypes for all studied traits, indicating the presence of substantial genetic variability. For all characters, PCV values exceeded the corresponding GCV values, suggesting the influence of environmental factors on trait expression. High estimates of PCV and GCV were observed for biological yield per plant and seed yield per plant, reflecting considerable genetic variation and strong potential for genetic improvement through selection. These traits, along with plant height, exhibited high heritability coupled with high genetic advance as a percentage of the mean, indicating the predominance of additive gene action. Overall, the substantial genetic variability observed for economically important traits suggests that direct phenotypic selection in advanced generations can be effectively exploited for improving yield components and enhancing overall seed productivity in blackgram.

Keywords: Genotype, traits, heritability, genetic advance and genetic variability.

Introduction

Black gram (*Vigna mungo* L. Hepper), commonly known as urdbean, is an important short-duration, self-pollinated pulse crop belonging to the family Fabaceae, with a diploid chromosome number of 2n = 22. It occupies a vital place in the traditional agricultural systems of South and Southeast Asia (Babu *et al.*, 2016). India is recognized as the primary center of origin, where it has been cultivated since ancient times for its nutritional value and soil health benefits (Vavilov, 1926). Owing to its short growth duration (60–90 days), drought tolerance, and wide adaptability, black gram is cultivated during Kharif, Rabi, and Zaid seasons under rainfed, semi-irrigated, and intercropping systems. The crop is highly nutritious, containing about 24% protein, 1.4% fat, 3.2% minerals, and 59.6% carbohydrates, with a calorific value of 347 kcal per 100 g (Parveen *et al.*, 2011). In addition to its dietary importance, black gram contributes to sustainable agriculture through biological nitrogen fixation and improvement of soil structure. It is widely grown as a sole crop, intercrop, and in rice fallow systems, ensuring efficient utilization of land and residual soil moisture (Yashoda *et al.*, 2016).

Despite its economic and ecological importance, productivity of black gram remains low due to various biotic and abiotic stresses such as diseases, drought, nutrient deficiency, poor harvest index, indeterminate growth habit, and asynchronous maturity (Priya *et al.*, 2018). Furthermore, the narrow genetic base arising from the repeated use of closely related genotypes has restricted genetic improvement and adaptability across environments.

Genetic improvement of black gram largely depends on the availability and effective utilization of genetic variability. Estimation of genetic parameters such as phenotypic and genotypic coefficients of variation, heritability and genetic advance provides valuable insights into the inheritance of yield and its components and helps in identifying superior genotypes for selection. Therefore, the present study was undertaken to assess these genetic parameters for yield and related traits in black gram, with the objective of identifying promising lines for future breeding programmes.

Materials and Methods

The experimental study comprised eighteen black gram genotypes, including four checks, namely Indira URD 1 (C), KU 96-3 (C), Pratap URD 1 (C), and TPU 4 (C) (Table 1). These genotypes were evaluated during the Kharif season of 2021 across four distinct locations in Madhya Pradesh, namely RVSKVV R.A.K. College of Agriculture, Sehore; RVSKVV College of Agriculture, Gwalior; Krishi Vigyan Kendra, Jhabua; and Krishi Vigyan Kendra, Barwani.

All genotypes were grown in six-row plots of 4 m length following a randomized complete block design (RCBD) with three replications. The rows were spaced 30 cm apart, with an intra-row spacing of 10 cm between plants. Standard agronomic practices and recommended packages were uniformly applied throughout the cropping period to ensure healthy crop growth.

Observations were recorded on a plot basis for days to 50% flowering, days to maturity, and harvest index (%). For plant height at maturity (cm), number of branches per plant, number of pods per plant, number of seeds per pod, 100-seed weight (g), biological yield per plant (g), and seed yield per plant (g), data were recorded from five randomly selected plants in each plot, and their mean values were used for analysis. The recorded data were subjected to analysis of variance (ANOVA) to assess the significance of differences among genotypes. Furthermore, genetic parameters, including genotypic and phenotypic coefficients of variation, heritability, and genetic advance, were estimated using R software (version 3.4.1).

Table 1: List of blackgram genotypes

S. No.	Genotypes	S. No.	Genotypes	S. No.	Genotypes
1.	RVSTU 22-1	7.	RVSU 22-7	13.	Indira URD 1(C)
2.	RVSTU 22-2	8.	RVSU 22-8	14.	KU 96-3 (C)
3.	RVSTU 22-3	9.	RVSU 22-9	15.	Pratap URD 1(C)
4.	RVSTU 22-4	10.	RVSU 22-10	16.	IU 92-14
5.	RVSU 22-5	11.	RVSU 22-11	17.	IU 94-1
6.	RVSU 22-6	12.	RVSU 22-12	18.	TPU 4 (C)

Results and Discussion

In the present investigation, ten yield and yield-related traits were evaluated in fourteen advanced breeding lines of black gram along with four check varieties. The analysis of variance revealed highly significant differences among the genotypes for all the studied traits (Table 2), indicating the presence of substantial genetic variability within the experimental material. Such variability provides a strong basis for the reliable estimation of genetic parameters and effective selection in breeding programs. The present findings are in close agreement with earlier reports in black gram by Senthilkumar and Chinna (2012) and Natarajan (2001).

The mean and range performance for ten yield and yield-related traits among the blackgram genotypes are shown in Table 3. Advanced breeding lines of blackgram showed considerable variation in mean value for the yield and its attributing traits across the population. The evaluated genotypes exhibited wide ranges for days to 50% flowering (36–50 days), days to maturity (68–88 days), plant height (35.78–46.26 cm), number of branches per plant (1–5), number of pods per plant (15–47), number of seeds per pod (5.50–7.79), hundred seed weight (3.49–4.17 g), biological yield per plant (8.57–30.55 g), seed yield per plant (4.04–15.61 g) and harvest index (16.72–26.20 %).

Table 2: Analysis of variance for yield and yield attributing traits in eighteen genotypes including four checks of blackgram

Source of variance	Mean sum of Square (MSS)		
	Replication (DF=8)	**Genotypes (DF=17)**	**Error (DF=136)**
DTF	1.46	4.82*	1.40
DTM	2.14	6.93*	1.36
PH	0.96	36.68**	2.12
NB/P	0.73	1.09*	0.47
NPO/P	2.43	34.31**	1.42
NS/P	0.77	0.66*	0.47
HSW	0.04	0.41*	0.03
BY/P	28.56	85.21**	9.36
SY/P	68.51	92.10**	6.58
HI	3.62	23.58*	2.918

Note: DTF: Days to 50% flowering; DTM: Days to maturity; PH: Plant height; NB/P: Number of branches per plant; NPO/P: Number of pods per plant; NS/P: Number of seeds per pod; HSW: Hundred seed weight; BY/P: Biological yield per plant; SY/P: Seed yield per plant; HI: Harvest index

Table 3: Mean, Range, PCV, GCV, heritability, genetic advance and genetic advance as percentage of mean for all the yield and yield related traits in blackgram

Sr. No.	Characters	Mean	Range		PCV (%)	GCV (%)	h^2 (%)	GA (5%)	GA as % of mean
			Min.	Max.					
1.	Days to 50 % flowering	40.71	36.00	50.00	5.77	1.58	53	4.43	6.89
2.	Days to maturity	77.68	68.00	88.00	3.86	1.42	86	5.80	8.08
3.	Plant height	41.29	35.78	46.26	12.21	6.71	71	15.23	41.60
4.	No. of branches per plant	3.48	1.00	5.00	20.79	3.73	35.6	18.10	43.37
5.	No. of pods per plant	28.39	15.00	47.00	25.20	13.82	67.45	3.02	15.61
6.	No. of seeds per pod	6.03	5.50	7.75	21.32	2.85	45.21	2.94	13.52
7.	100 seed weight (g)	3.80	3.49	4.17	13.98	4.05	76.62	3.89	7.42
8.	Biological yield per plant (g)	19.68	8.57	30.55	39.78	31.26	80.22	11.42	63.21
9.	Seed yield per plant (g)	9.91	4.04	15.61	36.52	30.14	76.58	10.88	57.23
10.	Harvest index (%)	21.24	16.72	26.20	20.67	10.18	74.12	8.96	10.33

Note: DTF: Days to 50% flowering; DTM: Days to maturity; PH: Plant height; NB/P: Number of branches per plant; NPO/P: Number of pods per plant; NS/P: Number of seeds per pod; HSW: Hundred seed weight; BY/P: Biological yield per plant; SY/P: Seed yield per plant; HI: Harvest index

The estimates of phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (broad sense), genetic advance, and genetic advance as a percentage of mean are presented in Table 3. The PCV and GCV values ranged from 3.86% to 39.78% and 1.42% to 31.26%, respectively. Based on the classification proposed by Sivasubramanian and Menon (1973), the coefficient of variation was categorized as low (<10%), moderate (10–20%), and high (>20%). High PCV and GCV were recorded for biological yield per plant (39.78% and 31.26%) and seed yield per plant (36.25% and 30.14%). High PCV with medium GCV was observed for number of pods per plant (25.20% and 13.82%) and harvest index (20.67% and 10.18%). High PCV coupled with low GCV was noted for number of branches per plant (20.79% and 3.73%) and number of seeds per pod (21.32% and 2.85%). Medium PCV and low GCV were observed for plant height (12.21% and 6.71%) and hundred seed weight (13.98% and 4.05%), respectively. In contrast, Low PCV and GCV values (<10%) were observed for days to 50% flowering (5.77% and 1.58%) and days to maturity (3.86% and 1.42%), indicating limited variability for these traits.

The wide range of PCV and GCV values indicated the presence of substantial variability among the genotypes for the studied traits. High PCV and GCV for biological yield and seed yield per plant suggested that these traits are largely governed by genetic factors and can be effectively improved through selection. Traits showing high PCV but comparatively lower GCV, such as number of pods per plant and harvest index, indicated considerable environmental influence. Similarly, traits with medium to low GCV values reflected limited genetic variability, suggesting slower genetic progress through direct selection. The present findings are in agreement with those of Gupta *et al.* (2012), Babu *et al.* (2016), Gowsalya *et al.* (2016) and Hemalatha *et al.* (2017).

Table 3 displays the estimated heritability and genetic advance values. Broad sense heritability estimates can be divided as low (<40 %), moderate (40-60 %) and high (>60 %). The heritability ranged from 35.6 % to 86 %. High heritability estimates have been observed for the traits., days to maturity (86 %), plant height (71 %), number of pods per plant (67.45 %), hundred seed weight (76.62 %), biological yield per plant (80.22 %), seed yield per plant (76.58 %) and harvest index (72.41%). Moderate value of heritability was recorded for days to 50% flowering (53 %) and number of seeds per pod (45.21 %) and low value of heritability for number of branches per plant (35.6 %) were observed. Similar results have also been reported by Panigrahi *et al.* (2014), Kumar *et al.* (2015) and Gowsalya *et al.* (2016).

The estimates for genetic advance as a percent of means were observed ranging from 6.89 % for days to 50% flowering to 63.21 % for biological yield per plant. Genetic advance as a percent of mean can be divided into 3 groups *viz*., low (<10%), moderate (10-20%) and high (>20%). Traits such as., Plant height (41.60%), number of branches per plant (43.37 %), biological yield per plant (63.21 %) and seed yield per plant (57.23 %) showed highest estimate of genetic advance as a percentage of mean. While, number of pods per plant (15.61 %), number of seeds per pod (13.52 %) and harvest index (10.33 %) showed moderate advance. In contrast days to 50% flowering (6.89 %), days to maturity (8.08 %) and hundred seed weight (7.42 %) showed less genetic advance. Similar results were also found by Gupta *et al.* (2012), Punia *et al.* (2013), Reni *et al.* (2013), Singh *et al.* (2014), Kumar *et al.* (2015), and Babu *et al.* (2016).

In addition to high heritability coupled with high genetic advance as percent of mean was observed for the traits like plant height (71 % and 41.60 %), biological yield per plant (80.22 % and 63.21 %) and seed yield per plant (76.58 % and 57.23 %) signifying the effectiveness of selection in enhancing major yield components and yield itself. Similar results for blackgram genotypes having higher heritability with the higher genetic advance were reported by Gupta *et al.* (2012) and Punia *et al.* (2013).

Therefore, the present study revealed sufficient genetic variability among the genotypes for all the traits under investigation. Traits such as., plant height, biological yield per plant, and seed yield per plant exhibited high heritability coupled with high genetic advance, indicating the predominance of additive gene action. These traits were less influenced by environmental factors and possessed high genetic variability, suggesting that they can be effectively improved through direct selection in future breeding programs.

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