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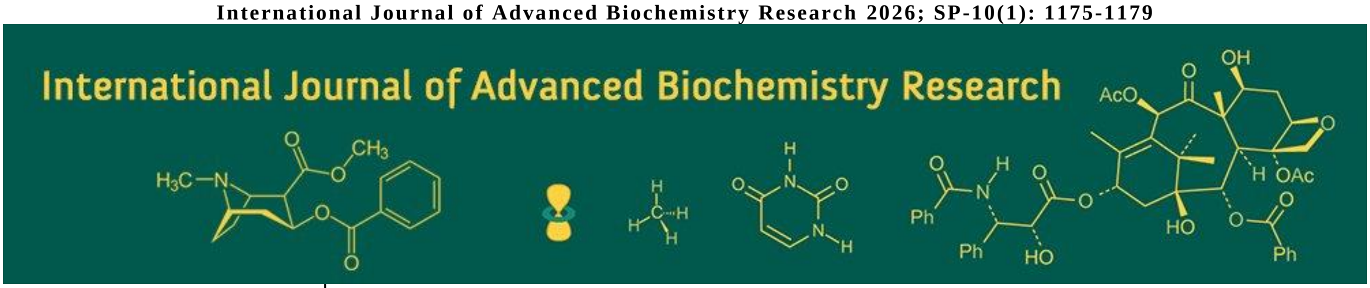

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Pushpa Reni Y
Regional Agricultural Research Station, Acharya N.G. Ranga Agricultural University, Lam, Guntur, Andhra Pradesh, India

Bindhumadhavi G
Agricultural College, Bapatla, Acharya N.G. Ranga Agricultural University, Lam, Guntur, Andhra Pradesh, India

Ramana MV
Regional Agricultural Research Station, Acharya N.G. Ranga Agricultural University, Lam, Guntur, Andhra Pradesh, India

Corresponding Author:
Pushpa Reni Y
Regional Agricultural Research Station, Acharya N.G. Ranga Agricultural University, Lam, Guntur, Andhra Pradesh, India

Magnitude of genetic variability and genetic parameters for yield and quality traits in blackgram (*Vigna mungo* (L.) Hepper)

Pushpa Reni Y, Bindhumadhavi G and Ramana MV

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Abstract

The success of any crop improvement programme depends on the magnitude of genetic variability present in the breeding material. The present investigation was carried out to estimate the extent of genetic variability, heritability and genetic advance for fourteen morpho-physiological, yield and quality traits in blackgram (*Vigna mungo* (L.) Hepper). Fifty-nine genotypes, including checks, were evaluated in a randomized block design with three replications during kharif season. Analysis of variance revealed highly significant differences among genotypes for all the characters studied, indicating the presence of substantial variability. Phenotypic coefficient of variation (PCV) was slightly higher than genotypic coefficient of variation (GCV) for all traits, suggesting limited environmental influence. High heritability coupled with high genetic advance as per cent of mean was observed for seed yield per plant, plant height, number of clusters per plant, number of branches per plant, iron content and zinc content, indicating the predominance of additive gene action. These traits can be effectively exploited through direct selection for yield and nutritional improvement in blackgram. The present investigation was carried out to assess genetic variability, heritability and genetic advance for fourteen morpho-physiological, yield and nutritional characters in blackgram. Fifty-nine genotypes, including checks, were evaluated in a randomized block design with three replications during the kharif season. Analysis of variance revealed highly significant differences among genotypes for all the characters studied, indicating the presence of ample variability. Phenotypic coefficient of variation (PCV) was marginally higher than genotypic coefficient of variation (GCV) for all traits, suggesting limited environmental influence. High heritability coupled with high genetic advance as per cent of mean was observed for seed yield per plant, plant height, number of clusters per plant, number of branches per plant, iron content and zinc content, indicating the predominance of additive gene action. Hence, these traits can be effectively improved through direct selection in blackgram breeding programmes.

Keywords: Blackgram, genetic variability, heritability, genetic advance, yield, nutritional quality

Introduction

Blackgram (*Vigna mungo* (L.) Hepper) is an important pulse crop cultivated extensively in India owing to its high protein content, nutritional value and ability to improve soil fertility through symbiotic nitrogen fixation. It plays a significant role in ensuring nutritional security, particularly in vegetarian diets. Despite its importance, the productivity of blackgram remains low due to narrow genetic base, susceptibility to biotic and abiotic stresses and limited scope for genetic improvement.

Genetic variability is the basic requirement for crop improvement, as it provides the raw material for selection. Estimates of phenotypic and genotypic coefficients of variation, heritability and genetic advance help in understanding the nature and magnitude of variability and the effectiveness of selection for different traits. High heritability coupled with high genetic advance indicates the predominance of additive gene action and greater scope for improvement through selection. Hence, the present study was undertaken to assess genetic variability and genetic parameters for yield and quality traits in blackgram genotypes.

Blackgram (*Vigna mungo* (L.) Hepper) is one of the most important pulse crops cultivated in India due to its high protein content, nutritional value and ability to improve soil fertility through biological nitrogen fixation. It is an integral component of rainfed farming systems and contributes significantly to dietary protein security. Despite its importance, the productivity of blackgram remains low, mainly due to narrow genetic base, susceptibility to biotic stresses and limited scope of selection for yield and quality traits.

Assessment of genetic variability present in the germplasm is a prerequisite for any crop improvement programme. Parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance provide valuable information on the relative contribution of genetic and environmental factors in the expression of traits. High heritability coupled with high genetic advance indicates the predominance of additive gene action and effectiveness of selection. Therefore, the present study was undertaken to estimate the extent of genetic variability and genetic parameters for yield and quality traits in blackgram genotypes.

Materials and Methods

Experimental material and design

The experimental material consisted of fifty-nine blackgram genotypes, including standard checks. The experiment was conducted during the *kharif* 2019 season at Regional Agricultural Research station, Lam, Guntur situated at 16.10°N latitude, 28.29°E longitude and 31.5m altitude, is noted for its mean rainfall 905 mm, as well as its deep black soil with a pH 7.4, E.C 0.16 m.mhos / cm.under recommended agronomic practices. The trial was laid out in a Augmented Completely Randomized Block Design-II with four checks in 5 blocks. Standard agricultural practices of the region were adhered to in order to cultivate a healthy crop, free from insect pests and diseases. Each genotype was planted in two rows, each measuring 4 meters in length, with a spacing of 30 cm between rows and 10 cm between plants within each row.

About 59 varieties such as IPU 17-02, TBG 129, LBG 904, KU 96-7, MBG 1070, LBG 918, IPU 17-1, DBGV 16, OBG 103, DKU 90, Uttara, KPU 52-87, PU 31, KU 17-04, LBG 854, VBG 17-026, IPU 2-43, TU 94-2, LBG 972, LBG 885, LBG 883, VBG 17-029, OBG 101, IPU 11-6, WBU 108, KPU 1720-140, LBG 709, TU 50, LBG 868, TU 40, MU 52, RU 03-22-4, KUG 818, VBG 12-110, NUL 242, TJU-134, PU 1541, PU 1501, OBG 102, AKU 1608, IPU 12-5, VBG 13-003, IPU 12-5, VBG 13-003, TU 44, ADBG 13023, VBG-12-062, OBG 41, VBG 09-005, VBN -5, LBG 752, LBG 880, LBG 776, SBC 50, VBN -5, LBG 787, ADT 5, ADT 6, AKU 1608, CO 5, DKU 11, GJU 1509 and LBG 623 were obtained from Indian Institute of Pulses Research, Kanpur along with released varieties and advanced cultures of Regional Agricultural Research Station (RARS), Lam, Guntur.

Observations Recorded

Observations were recorded on fourteen characters, viz., days to 50 per cent flowering, days to maturity, plant height (cm), number of branches per plant, number of clusters per plant, number of pods per plant, pod length (cm), number of seeds per pod, 100-seed weight (g), seed yield per plant (g), harvest index (%), protein content (%), iron content (mg/100 g) and zinc content (mg/100 g).

Statistical Analysis

Analysis of variance was performed to test the significance of differences among genotypes. Phenotypic and genotypic coefficients of variation were estimated following Burton (1952) [2]. Broad sense heritability and genetic advance were computed as per Johnson *et al.* (1955) [5]. Genetic advance was expressed as percentage of mean to assess the expected response to selection.

Experimental Material and Design

The experimental material comprised fifty-nine blackgram genotypes, including released varieties and advanced breeding lines. The experiment was conducted during the kharif season at the experimental farm under recommended agronomic practices. The trial was laid out in a randomized block design (RBD) with three replications.

Observations Recorded

Data were recorded on fourteen characters, namely days to 50 per cent flowering, days to maturity, plant height (cm), number of branches per plant, number of clusters per plant, number of pods per plant, pod length (cm), number of seeds per pod, 100-seed weight (g), seed yield per plant (g), harvest index (%), protein content (%), iron content (mg/100 g) and zinc content (mg/100 g).

Statistical Analysis

Analysis of variance was carried out to test the significance of differences among genotypes. Phenotypic and genotypic coefficients of variation were calculated according to Burton (1952) [2]. Broad sense heritability was estimated as suggested by Johnson *et al.* (1955) [5]. Genetic advance and genetic advance as per cent of mean were computed to assess the expected response to selection.

Results and Discussion

Analysis of Variance (Table 4.1)

The analysis of variance for fourteen morpho-physiological, yield and biochemical traits is presented in Table 4.1. Mean sum of squares due to genotypes (entries) were highly significant for all the characters studied, indicating the existence of substantial genetic variability among the 59 blackgram genotypes. Significant differences among genotypes for yield and its component traits have also been reported earlier in blackgram by Panigrahi *et al.* (2014) [9], Patidar and Sharma (2017) [11] and Hemalatha *et al.* (2018) [4].

The significance of genotypic effects for days to 50 per cent flowering, days to maturity, plant height, number of branches per plant, number of clusters per plant, number of pods per plant, pod length, seeds per pod, 100-seed weight, seed yield per plant, harvest index, protein content, iron content and zinc content clearly demonstrated wide variability in the experimental material, which can be effectively exploited for genetic improvement in blackgram, as suggested by earlier workers (Makeen *et al.*, 2007; Priyanka *et al.*, 2019) [7, 12].

Mean Performance of Genotypes (Table 4.2)

The mean performance of 59 blackgram genotypes for fourteen characters is presented in Table 4.2. Days to 50 per cent flowering and days to maturity showed relatively narrow ranges, indicating limited variability for phenological traits, which is in agreement with the findings of Gowsalya *et al.* (2016) [3] and Reddy *et al.* (2020) [15]. Plant height exhibited wide variation among genotypes, suggesting the presence of diverse plant types, as also reported by Kumar *et al.* (2014) [6].

The number of branches per plant, clusters per plant and pods per plant showed wide variability, which directly influenced seed yield per plant. Similar associations between these yield components and seed yield have been reported earlier in blackgram by Sushmitharaj *et al.* (2018) [14] and Meena *et al.* (2021) [8]. Higher seed yield per plant recorded in genotypes such as LBG 904 and LBG 752 may be attributed to their higher number of pods and better harvest index.

Moderate variability was observed for pod length, seeds per pod and 100-seed weight, which is consistent with earlier reports in blackgram and related pulse crops (Patel *et al.*, 2015) [10]. Considerable variation was also observed for protein, iron and zinc contents, indicating the scope for improvement of nutritional quality along with yield, as reported by Singh *et al.* (2019) [13] and Anusha *et al.* (2022) [1].

Genetic Variability, Heritability and Genetic Advance (Table 4.3)

Estimates of genetic parameters for yield and quality traits are presented in Table 4.3. In general, phenotypic coefficient of variation (PCV) was marginally higher than genotypic coefficient of variation (GCV) for all the characters, indicating the influence of environment on trait expression. However, the close correspondence between PCV and GCV values for most traits suggested that the variability was largely genetic in nature. Similar trends have been reported earlier by Johnson *et al.* (1955) [5] and Panigrahi *et al.* (2014) [9].

High PCV and GCV were recorded for seed yield per plant, plant height, number of clusters per plant, iron content and zinc content, indicating greater scope for selection. These findings are in conformity with the results reported by Hemalatha *et al.* (2018) [4], Sushmitharaj *et al.* (2018) [14] and Meena *et al.* (2021) [8] in blackgram.

High heritability estimates coupled with high genetic advance as per cent of mean were observed for seed yield per plant, plant height, clusters per plant, iron content and zinc content, suggesting the predominance of additive gene action. This indicates that direct selection would be effective for improvement of these traits, as reported earlier by Burton (1952) [2] and Patidar and Sharma (2017) [11]. Traits such as days to flowering and days to maturity exhibited high heritability but low genetic advance, indicating the involvement of non-additive gene action and limited response to direct selection, which is in agreement with the findings of Makeen *et al.* (2007) [7] and Gowsalya *et al.* (2016) [3].

High heritability estimates were recorded for most of the characters, particularly days to maturity (97.50%), plant height (96.00%), clusters per plant (95.70%), pods per plant (92.00%), harvest index (96.90%), iron content (98.66%) and zinc content (95.30%). High heritability coupled with high genetic advance as per cent of mean was observed for seed yield per plant (26.80%), zinc content (28.21%), iron content (25.58%), plant height (26.30%) and clusters per plant (26.67%), indicating the predominance of additive gene action and effectiveness of selection for these traits.

Traits such as days to 50 per cent flowering and days to maturity, despite exhibiting high heritability, recorded low genetic advance as per cent of mean, suggesting the involvement of non-additive gene action and limited response to direct selection. Similar observations have been reported earlier in blackgram and other pulse crops.

Implications for Breeding

The results obtained from Tables 4.1 to 4.3 clearly indicate the presence of substantial genetic variability for yield and nutritional traits in blackgram. Traits exhibiting high heritability along with high genetic advance can be effectively used as selection criteria in breeding programmes aimed at improving seed yield and micronutrient content.

Genotypes with superior performance for seed yield per plant and nutritional quality can be utilized as promising parents in hybridization programmes for the development of high-yielding and nutrient-rich blackgram varieties.

Table 1: Mean Performance for 14 characters under study in 59 genotypes of blackgram (*Vigna mungo* (L.) Hepper)

S.No	Genotype	DF	DM	PH (cm)	NBP	NCP	NPP	PL (cm)	NSP	100-SW (g)	HI (%)	Protein (%)	Iron (mg/ 100g)	Zn (mg/ 100g)	SYPP (g)
1	KU 96-7	35.0	73.0	41.3	3.0	7.4	28.0	5.3	6.4	4.6	31.8	23.4	8.2	3.1	7.8
2	MBG 1070	36.0	75.0	38.7	3.0	8.2	26.2	5.4	6.6	4.7	30.2	20.8	6.8	4.0	8.4
3	LBG 918	41.0	80.0	42.2	3.6	10.2	36.0	5.2	5.8	5.0	38.7	22.8	8.8	3.4	10.6
4	IPU 17-1	35.0	73.0	40.2	2.6	7.2	33.2	5.4	6.4	4.8	28.3	22.4	7.0	2.8	7.9
5	DBGV 16	35.0	75.0	35.5	2.7	9.8	32.4	5.5	6.2	5.0	30.1	22.0	5.8	3.2	10.9
6	OBG 103	36.0	74.0	38.2	3.3	7.6	25.2	4.6	5.8	4.8	29.0	20.2	7.9	2.4	7.7
7	DKU 90	35.0	74.0	33.4	2.6	8.0	30.6	4.5	5.2	4.9	28.0	23.0	7.1	2.9	8.6
8	Uttara	40.0	82.0	37.2	3.0	8.1	26.8	4.8	6.2	4.3	34.8	22.4	6.2	3.5	8.8
9	VBG 09-005	35.0	74.0	32.6	3.0	6.6	31.0	4.6	6.0	4.8	28.8	21.4	7.3	2.4	8.0
10	KPU 52-87	37.0	74.0	40.0	2.6	7.0	30.0	4.9	5.8	4.8	29.0	18.8	8.3	3.0	7.0
11	PU 31	37.0	73.0	35.8	3.0	11.0	35.2	5.0	6.4	5.0	41.2	20.3	6.8	3.1	12.8
12	KU 17-04	35.0	76.0	33.8	2.8	7.6	24.2	5.0	6.2	4.8	29.8	20.8	6.8	4.0	8.2
13	DKU 116	36.0	75.0	34.2	2.0	7.9	25.0	5.5	6.6	5.0	30.4	22.8	8.8	3.4	7.0
14	CO 5	36.0	75.0	36.0	2.8	7.0	28.8	4.8	6.0	4.6	29.8	22.4	7.0	2.8	7.4
15	GJU 1509	35.0	74.0	39.2	3.0	8.2	28.6	4.7	5.8	4.9	33.8	20.4	6.8	3.3	8.5
16	LBG 854	41.0	82.0	42.2	3.2	8.9	34.6	5.5	6.2	5.0	38.3	20.0	7.0	3.4	11.2
17	VBG 17-026	36.0	75.0	39.2	3.0	7.2	28.0	5.3	5.8	5.0	29.2	18.0	7.8	3.6	7.4
18	VBN -5	35.0	73.0	35.6	3.0	9.2	30.4	5.2	5.8	4.9	35.3	21.4	8.3	3.0	9.2
19	OBG 41	38.0	73.0	40.2	2.4	8.8	29.4	4.4	5.0	4.7	31.2	18.8	6.8	2.9	7.4
20	VBG 12-062	35.0	74.0	38.8	2.0	7.4	31.0	3.7	4.8	5.0	28.8	20.2	6.5	3.0	9.0
21	LBG 623	38.0	80.0	36.8	3.0	7.2	30.6	4.0	6.2	5.3	28.9	23.8	6.0	2.4	8.8

22	TU 44	36.0	74.0	30.2	3.0	9.0	32.2	3.9	6.4	4.9	37.2	21.0	7.0	3.8	10.7
23	ADBG 13023	35.0	73.0	38.2	2.8	8.8	33.4	5.4	6.6	5.0	39.1	23.0	8.2	2.9	11.4
24	AKU 1608	36.0	74.0	36.6	2.0	10.2	36.6	4.9	6.4	4.9	39.8	23.4	8.3	3.1	11.7
25	IPU 12-5	37.0	75.0	40.2	2.8	8.4	28.8	5.4	6.4	4.3	32.0	18.8	6.2	2.7	8.1
26	VBG 13-003	35.0	74.0	42.1	2.4	7.4	29.0	3.9	5.8	4.1	32.2	20.2	5.8	1.9	8.0
27	LBG 904	41.0	80.0	40.8	3.4	14.2	45.2	5.2	6.8	5.1	44.3	20.8	8.0	3.2	14.4
28	SBC 50	35.0	74.0	38.0	3.0	8.0	28.0	4.1	5.6	5.0	32.0	22.2	5.8	3.0	8.0
29	TJU 134	38.0	75.0	25.2	2.4	7.2	30.0	4.0	4.8	5.1	31.8	21.8	6.6	2.4	7.8
30	PU 1541	36.0	73.0	33.4	2.4	9.2	28.4	4.8	5.8	4.9	34.2	22.2	5.4	1.9	8.2
31	PU 1501	35.0	74.0	30.8	2.4	9.8	32.2	4.8	5.9	4.8	36.3	22.8	6.5	3.0	9.4
32	OBG 102	35.0	75.0	27.6	1.8	8.6	26.8	5.1	6.0	4.4	31.2	19.0	7.2	2.7	8.0
33	TBG 129	39.0	78.0	39.8	3.4	11.8	38.8	4.9	6.2	5.0	41.2	20.8	7.2	2.9	12.2
34	LBG 776	40.0	79.0	35.6	3.0	9.8	32.2	5.2	6.2	4.7	36.6	21.2	6.6	3.0	9.5
35	WBU 108	36.0	74.0	27.8	2.0	8.0	27.8	4.8	5.9	4.3	32.2	19.8	5.4	2.3	8.0
36	KPU1720-140	37.0	75.0	19.2	2.2	9.2	29.8	5.0	6.0	4.4	33.5	22.8	6.0	2.5	9.0
37	LBG 709	38.0	80.0	40.2	2.8	9.2	28.4	5.4	6.4	5.1	35.8	22.6	6.2	2.4	9.4
38	TU 50	35.0	75.0	35.2	2.4	8.4	31.0	5.3	6.4	4.9	33.8	22.0	7.0	2.8	8.4
39	LBG 868	39.0	80.0	36.2	3.2	8.8	28.8	5.6	6.6	4.8	37.4	22.8	8.2	3.4	9.5
40	TU 40	38.0	73.0	30.8	3.2	9.0	33.0	5.2	6.0	4.7	35.4	19.2	5.8	3.4	9.8
41	MU 52	38.0	74.0	28.4	2.4	8.6	34.2	5.0	5.8	4.5	30.1	18.8	6.0	2.9	9.1
42	RU 03-22-4	34.0	71.0	32.2	2.2	9.8	32.0	4.8	5.4	4.9	34.4	22.1	5.8	2.8	9.1
43	KUG 818	36.0	73.0	30.8	2.0	10.8	35.6	5.2	6.2	4.9	38.4	20.3	6.0	2.4	9.8
44	VBG 12-110	36.0	74.0	32.8	2.0	9.0	30.0	5.4	6.0	4.8	31.0	22.2	6.0	2.0	9.0
45	NUL 242	36.0	74.0	25.8	2.0	8.2	31.8	4.5	4.8	4.5	32.2	19.0	6.2	2.9	9.0
46	ADT 5	35.0	74.0	22.0	2.8	9.2	29.8	4.6	5.4	3.7	30.0	17.3	7.1	2.8	10.0
47	ADT6	38.0	75.0	38.2	3.0	8.8	27.8	4.7	5.8	3.8	28.9	22.6	8.1	2.8	8.4
48	VBG 17-029	37.0	78.0	40.0	3.2	10.2	32.0	5.2	5.6	4.9	32.6	21.8	6.2	2.5	9.6
49	OBG 101	42.0	76.0	38.2	2.8	8.2	30.2	5.0	5.6	4.8	36.0	22.0	7.5	2.7	8.4
50	IPU 11-6	36.0	76.0	32.4	2.4	7.2	26.8	5.3	5.8	4.9	31.2	21.2	9.2	3.4	8.0
51	IPU 1702	36.0	77.0	29.3	2.6	7.9	28.8	5.0	6.1	4.8	32.2	22.8	8.6	3.6	8.4
52	LBG 972	39.0	80.0	38.8	3.2	9.0	29.4	5.1	6.2	4.2	33.0	23.0	8.0	3.8	9.7
53	LBG 885	38.0	80.0	40.0	3.0	8.8	37.8	5.0	6.0	5.0	37.1	18.3	8.9	3.0	11.4
54	LBG 883	38.0	80.0	42.8	3.0	9.2	30.4	4.9	5.9	4.8	33.1	21.2	7.2	3.0	8.7
55	LBG 880	38.0	79.0	40.2	2.8	9.0	34.8	5.4	6.1	5.1	35.9	22.0	6.0	3.2	10.8
	Checks														
56	LBG 787	38.3	82.0	42.3	3.1	10.7	32.2	4.3	6.0	4.8	35.3	22.1	7.0	1.9	10.8
57	IPU 2-43	37.5	81.8	37.1	3.0	7.2	34.0	5.1	6.3	4.7	35.1	20.9	6.8	3.0	10.1
58	LBG 752	38.0	80.5	42.2	3.3	12.6	47.4	4.8	6.7	5.2	41.0	22.2	6.9	2.9	14.1
59	TU 94-2	41.0	78.0	38.0	3.0	3.8	13.8	4.4	5.8	5.0	30.0	19.0	6.6	2.8	6.2
	Overall mean	37.0	76.0	35.8	2.8	8.8	31.2	4.9	6.0	4.8	33.5	21.2	7.0	2.9	9.3
	CV%	3.8	5.2	12.4	12.2	12.0	13.5	9.4	7.9	6.7	12.1	7.4	13.6	14.9	13.4

Table 2: Analysis of variance for 14 morpho-physiological and biochemical characters studied in blackgram (*Vigna mungo* (L.) Hepper)

	DF	DM	DFF	PH	NBP	NCP	NPP	PL
Block	4	0.178	0.500	1.721	0.013	0.190	1.487	0.011
Entries	58	13.663***	4.392 ***	33.509***	0.206 ***	3.375***	33.293***	0.248***
Checks	3	16.183***	8.600 ***	37.869***	0.114 **	27.618***	230.007***	0.616***
Varieties	54	7.267***	3.521 ***	28.559***	0.183 ***	1.785***	14.047***	0.210***
Checks vs. Varieties	1	351.494***	38.838 ***	287.714***	1.723 ***	16.484***	482.466***	1.167***
Error	12	0.141	0.433	0.876	0.016	0.060	0.879	0.006

* Significant at 5% level ** Significant at 1% level

Table 3: Analysis of variance for 14 morpho-physiological and biochemical characters studied in blackgram (*Vigna mungo* (L.) Hepper)

	DF	NSP	100-SW	HI	Protein	Iron	Zinc	SYPP
Block	4	0.058**	0.020	2.998**	0.055	0.021	0.007	0.325
Entries	58	0.247***	0.116***	19.104***	2.933***	0.962 ***	0.302***	4.089***
Checks	3	0.813***	0.254***	86.157***	10.651***	0.194 ***	1.159***	21.847***
Varieties	54	0.209***	0.105***	14.688***	2.549***	1.009 ***	0.231***	2.302***
Checks vs. Varieties	1	0.561***	0.279***	56.417***	0.465	0.739 ***	1.532***	47.299***
Error	12	0.008	0.007	0.350	0.154	0.010	0.008	0.216

* Significant at 5% level ** Significant at 1% level

Table 4: Estimates of genetic parameters for grain yield and quality components in blackgram (*Vigna mungo* (L.) Hepper)

S. No	Character	Range		Mean	Coefficient of variation		Heritability (Broad sense) (%)	Genetic advance	Genetic advance as% of mean
		Minimum	Maximum		PCV (%)	GCV (%)			
1	Days to 50% flowering	34.0	42.0	37.0	4.55	4.18	84.61	2.92	7.93
2	Days to maturity	71.0	82.0	76.0	3.13	3.09	97.50	4.76	6.30
3	Plant height (cm)	19.2	42.8	35.8	13.29	13.02	96.00	9.33	26.30
4	Branches / plant	1.8	3.6	2.8	13.95	13.17	89.18	0.69	25.60
5	Clusters / plant	6.6	14.2	8.8	13.53	13.23	95.70	2.32	26.67
6	Pods / plant	24.2	47.4	31.2	10.76	10.33	92.00	6.29	20.41
7	Pod length (cm)	3.6	5.6	4.9	8.20	8.05	96.40	0.80	16.29
8	Seeds / pod	4.8	6.8	6.0	6.77	6.60	95.00	0.79	13.27
9	100 seed weight (g)	3.7	5.3	4.8	6.03	5.78	91.80	0.54	11.43
10	Seed yield per plant	7.0	14.4	9.3	14.75	13.85	88.18	2.45	26.80
11	Harvest Index (%)	28.0	44.3	33.5	10.11	9.95	96.90	6.70	20.18
12	Protein content (%)	17.3	23.8	21.2	6.66	6.40	92.30	2.69	12.67
13	Iron content (mg/100g)	5.4	9.2	7.0	12.58	12.50	98.66	1.79	25.58
14	Zinc content (mg/100g)	1.9	4.0	2.9	14.35	14.02	95.3	0.83	28.21

Conclusion

The present study revealed the existence of considerable genetic variability among blackgram genotypes for yield and quality traits. High heritability coupled with high genetic advance for seed yield per plant, plant height, number of clusters per plant, iron content and zinc content suggests that these traits are predominantly governed by additive gene action and can be effectively improved through direct selection. The results provide valuable information for formulating efficient breeding strategies for yield and nutritional improvement in blackgram.

The per se performance of the blackgram genotypes revealed that RU 03-22-4 was identified to have a shorter duration in days to 50% flowering and maturity than 248 other genotypes. When compared to other genotypes, the entry LBG 904 has the highest harvest index, number of clusters per plant, number of seeds per pod, and seed yield per plant. The entry LBG 752 has the maximum number of pods per plant. The genotype LBG 623 was reported to contain more protein and 100 seed weight. IPU 11-6 had the highest iron content, whereas MBG 1070 had the highest zinc content. These two entries (IPU 11-6 & MBG 1070) could be used in biofortification research projects as sources of micronutrients.

PCV values are higher than GCV values, indicating the role of the environment in the expression of these traits. All of the evaluated traits had high heritability overall, with the exception of days to 50% flowering and days to maturity, which has high heritability but poor genetic advancement. For plant height, number of branches per plant, number of clusters per plant, number of pods per plant, harvest index, iron content, and zinc content, high heritability along with high genetic advance as percent mean was perceived, specifying the prevalence of additive gene action in the expression of the traits.

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