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Genetic Diversity for Grain Yield and Its Attributed Traits in Blackgram [*Vigna mungo* (L.) Hepper]

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

Grain legumes are a wonderful gift from nature and serve as a significant complement to a diet primarily along with cereals. In India, blackgram [*Vigna mungo* (L.) Hepper] is a significant legume crop that is widely cultivated. It is one of the most abundant sources of protein, minerals and vitamins. An essential aspect for this crop's genetic improvement is the study of genetic diversity. The present study explores about genetic diversity for grain Yield and its attributed Traits in Blackgram [*Vigna mungo* (L.) Hepper]. The investigation was conducted during kharif-2024 in the Field Experimentation Centre of the Department of Genetics and Plant Breeding to examine 21 blackgram genotypes. The objective was to assess the direct and indirect contributions of different variables on blackgram seed yield, as well as genetic variability and character associations. The experiment was laid out in an randomised complete block design (RCBD) with three replications. High genetic diversity was demonstrated by the significant differences found between genotypes

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for every variable. High genetic progress and high heritability were seen in biological yield, harvest index, seed yield per plant, and number of major branches, suggesting that direct selection may improve these traits and that additive gene action largely controls them. At both the genotypic and phenotypic levels, correlation analysis showed a strong positive relationship between seed yield per plant and harvest index, seed index, pod length, number of major branches, and number of pods per plant. Seed index and harvest index had the most positive direct influence on seed yield, followed by pod length and number of primary branches, according to path coefficient analysis. According to the study, these characteristics are essential selection criteria for enhancing blackgram breeding programs' seed yield. Top-performing genotypes were identified as IC-330861, IC-330885, IC-426495, IC-385718, and SHEKAR-2, which had a high potential for seed yield with desired yield-contributing features. These genotypes are recommended for future hybridization projects that aim to combine advantageous traits to produce stable and high-yielding blackgram cultivars. All things considered, the study provides a precise genetic basis for wise parent choice and effective selection strategies in programs aimed at improving blackgram.

Keywords: Genetic variability; correlation; path analysis; urdbean; seed yield.

1. INTRODUCTION

“The availability of genetically diverse germplasm is the basic need for the progress in plant breeding. Choice of parents for hybridization is one of the important considerations for creating new variability. Several biometrical approaches have been shown to be useful in selecting parents for successful hybridization programme. Yield is an important quantitative trait for any crop improvement programme. To increase production of blackgram there is need of developing high yielding varieties which requires a systematic breeding approach to be adopted. Assessment of variability is a first step in any breeding programme” (Pallavi et al., 2021). “Pulses are considered poor man’s meat and a nutritional powerhouse as one of the best complementary to animal protein. They are high in fiber, low in methionine and cysteine, and high in protein (mostly globulins). But compared to grains, they have a higher lysine content. For vegans in particular, pulses are a vital source of protein. They become essential components of our regular diet. They fix nitrogen in the soil, which enriches it and also serves as food and fodder” (Yergude et al., 2021). “Blackgram botanically known as *Vigna mungo* (L.) Hepper, popularly known as Urdbean or mash, is a grain legume domesticated from *Vigna mungo var. silvestris*. It is also a good source of phosphoric acid and calcium. It contains a wide variety of nutrients and is popular for its fermenting action and thus it is largely used in making fermented foods. Its chromosomal number is 2n=2x=22, which places it in the *Leguminosae* family. It is thought that blackgram originated in India” (Vavilov, 1936). It is an important short-duration and self-pollinated legume crop. Since it is a leguminous crop, it improves the soil Fertility status by fixing atmospheric nitrogen and thus stops Soil erosion. One important pulse crop that is widely grown in India is blackgram, which makes up 24% of the country's protein intake and is reasonably priced. In vegetarian diets, it also contributes significantly to fat content (1.74%), dietary fiber (3-5%), and carbohydrates (76%). Additionally, when compared to other crops, blackgram contains 5–10 times higher amounts of phosphoric acid, establishing it as a distinctive source of phosphoric acid and lysine (Bressani and Elias, 1980). “The availability of genetically diverse germplasm is the basic need for the progress in plant breeding. Choice of parents for hybridization is one of the important considerations for creating new variability. Several biometrical approaches have been shown to be useful in selecting parents for successful hybridization programme” (Kumawat et al., 2024).

In India, 20.55 lakh tons of blackgram are produced on 33.08 lakh hectares of land. With 6.45 lakh hectares and 4.42 lakh tons produced, Madhya Pradesh leads the field in both area and output. Uttar Pradesh is the second-largest producer of this crop, with 3.91 lakh hectares and 1.87 lakh tons produced (Directorate of Agriculture, 2023-24). India is the largest producer as well as the consumer of pulses, accounting for more than 70 percent of global production. Blackgram ranks fourth in position after Bengal gram, red gram, and green gram and is cultivated in India. Though India ranks first globally in terms of area and production of pulses, having superior nutritional quality over cereals and being well adapted under local conditions. Low output may be caused by a number of issues, including the poor harvest index, the lack of location-specific cultivars that can be grown year-round, and the susceptibility to biotic and abiotic (heat, drought, and pre-harvest sprouting) factors.

Among the several illnesses that restrict the formation of blackgrams. “One of the factors responsible for the poor productivity of Blackgram is the lack of stable cultivars. Hence, improvement of blackgram is an important task for pulse breeders” (Bharathi et al., 2022). “The improvement of crop mainly depends in the degree of genetic variability and the degree to which the deciding characteristics are passed down from one generation to the next generation. The strength and direction of the relationship between yield components are shown by correlation coefficients” (Johnson et al., 1955). In order to create productive genotypes, character association aids in the formulation of an efficient breeding strategy. The yield components that both directly and indirectly affect the yield are identified using path analysis (Divyansukumar et al., 2024). In order to discover important features and promising genotypes for increasing blackgram seed yield, the current study was conducted to assess genetic variability, correlation, and path coefficient analysis.

2. MATERIALS AND METHODS

The current study was conducted at the Department of Genetics and Plant Breeding's Field Experimentation Center at the Naini Agricultural Institute. Sam Higginbottom University of Agriculture. Technology and Sciences. Allahabad. UP during Kharif 2024. A randomised block design was adopted with three replications and row to row spacing is 30cm and plant to plant spacing is 10cm, with plot size of 1mx1m. Twenty genotypes and one control were cultivated during Kharif 2024 in order to investigate the effects of different variables for heritability and genetic divergence on seed yield over time. Replication-specific data were gathered for the following thirteen (13) quantitative attributes based on five competitive plants chosen at random from each replication: Days until 50% of the flowers bloom, 50% of the pods set, and the maturity date, height of plant, number of main branches, number of clusters, number of pods, number of seeds per plant, length of pod (cm), biological yield per plant, harvest index, and seed yield per plant. The genotypes utilized in the experiment are listed in Table 1.

All of the recorded data for the characters under consideration were analyzed for variance using the formula. Additionally, the genetic parameters as Genotypic coefficient of variance (GCV) and Phenotypic coefficient of variance (PCV) were calculated using Johnson, Burton and Devane's formula included heritability (in the broadest sense), genetic advance as percent of the mean, and correlation analysis was carried out by using the appropriate statistical procedure (Burton and Devane, 1953). Al-Jibouri recommended methods were used to calculate correlation. while the analysis was carried out as per the procedures suggested by Al-Jibouri et al. (1958), Wright, (1921), and Dewey & Lu, (1959).

Table 1. List of 20 genotype of blackgram used in the present experiment

S no.	Genotypes	S no.	Genotypes
1	IC-330885	11	IC- 321704
2	IC-321654	12	IC-47443
3	IC-305255	13	IC- 343812
4	IC-334268	14	IC- 330906
5	IC-38971	15	IC- 25025
6	IC-395519	16	IC-385718
7	IC-251913	17	IC-426495
8	IC-328971	18	IC-410049
9	IC-261175	19	IC-250256
10	IC-328904	20	IC-330861
		21	SHEKHAR-2

3. RESULTS AND DISCUSSION

Any crop must have genetic variability in order to pick a superior genotype over the current cultivars (Burt and Austin, 2000). Significant differences between the genotypes under study were found by analysis for every attribute. The analysis of variance showed significant differences among 21 blackgram genotypes for all the characters under study (Table 2), indicating that there is ample scope for selection of promising genotypes from present germplasm for yield improvement. All investigated features showed a wide range of variance, as seen by the mean values, coefficient of variation (C.V.), standard error of the mean (Sem+), critical difference (C.D.) at 5% and 1%, and range of 21 genotypes.

3.1 Variability

"In the current study, it was observed that in general, estimates of phenotypic coefficient of variation (PCV) were found higher than their corresponding genotypic coefficient of variation (GCV), indicating the influence of environment on the expression of these characters" (Burt and Austin., 2000, Priyanka et al., 2016, Hemalatha et al., 2017, Gomathi et al., 2021). "The genotypic and phenotypic variations were obtained for different characters, and they are presented in Table 3. Phenotypic coefficient of variation (PCV) ranged from 1.93% (days to maturity) to 13.91% (number of primary branches per plant). Genotypic coefficient of variation (GCV) ranged from 1.48% (days to maturity) to 11.27% (Harvest index). Both high GCV and PCV were recorded for none of the characters. Moderate GCV and PCV (10- 20%) were recorded for harvest index (11.27%) and number of primary branches per plant (11.07%) only. In comparison to other characters, this indicates the presence of a high amount of genetic variability for these characters. This also suggests that improvement in these characters might be gained to a reasonable extent; therefore, selection for these characters would be effective because the response to selection is directly proportional to the variability present in the experimental material." (Sarma et al., 2025).

3.2 Heritability and Genetic Advance

In present study, heritability (broad sense) ranged from ranged from 56.424% to 74.59% for days to 50% Pod setting and biological yield per plant respectively. High heritability (broad sense) estimates (60% and above) had been observed for biological yield (74.59%), seed yield per plant (71.43%), harvest index (69.70%), number of clusters per plant (69.4%), pod length (66.63%), number of seeds per pod (65.93%), number of pods per plant (65.73%), seed index (64.42%), number of primary branches per plant (63.37%) and plant height (62%). Because of their high heritability values, these traits are mostly controlled by additive gene action and may be enhanced by individual plant selection. Understanding the sort of gene activity involved in the development of different features is made easier with the use of genetic advanced estimation. The estimation of genetic advance helps to understand the type of gene action involved in the expression of various characters. The Genetic advance ranged from 0.17 to 6.43. High (>20) and moderate (10-20) genetic advance was observed for none of the characters. Almost all the characters had low Genetic advance (<10). The high or moderate value of genetic advance indicates additive gene action, whereas a low genetic advance value indicates non-additive gene action. Genetic advance as percent of mean varied from 2.34% to 19.4%. High genetic advance as percent of mean (>20%) was observed for none of the characters. Moderate Genetic advance as percent of mean (10-20%) was recorded for plant height (11.79%), number of primary branches per plant (18.16%), number of clusters per plant (11.14%), number of pods per plant (10.67%), biological yield per plant (16.43%), harvest index (19,4%) and seed yield per plant (12.40%).

"In the present study, High heritability coupled with high genetic advance as percent of mean was observed for biological yield, harvest index and number of primary branches per plant, indicating the predominance of additive gene action and high potential for improvement through simple selection. Traits like days to maturity, days to 50% flowering, and days to 50% pod setting showed moderate heritability and low genetic advance, implying slower progress through direct selection, similar to other researchers findings" (Kamannavar et al., 2016, Sanjeev et al., 2014).

3.3 Correlation Analysis

The pleotropic influence of various genes and the existence of linkage are the usual causes of correlation between various phenotypes. A key factor in the formation of phenotypic correlation is the environment. Genomic correlations were generally larger than their phenotypic correlations in every instance, indicating a substantial genetically based underlying link between different features. Table 4&5 show the intercharacter association between the 13 traits that were examined at the phenotypic and genotypic levels.

At both the genotypic and phenotypic levels, the harvest index (0.642**), pod length (0.368**) and number of primary branches per plant (0.282*) showed a strong positive association with grain production in the current study, indicating that higher yields of blackgram could result from an increase in growth-related features. This meant that the above traits, with their rising magnitude, had to be taken into consideration in order to select high-yielding genotypes of blackgram. It assisted in improving all of the positively associated qualities at the same time.

Table 2. Analysis of variance (ANOVA) for 13 different quantitative characters in Blackgram genotypes

S. No.	Traits	Mean sum of squares		
		Replication (df = 2)	Treatment (df = 20)	Error (df = 40)
1.	Days to 50% flowering	0.254	4.43**	0.867
2.	Days to 50% Pod setting	0.429	5.919**	1.212
3.	Days to Maturity	2.945	5.221**	0.982
4.	Plant height(cm)	28.93	56.794**	9.639
5.	Number of Primary Branches per Plant	0.029	0.115**	0.019
6.	Number of clusters per plant	0.975	2.536**	0.325
7.	Number of pods per plant	4.614	10.404**	1.540
8.	Pod length (cm)	0.029	0.068**	0.010
9.	Number of seeds per pod	0.032	0.189**	0.028
10.	Biological yield per Plant	2.117	7.18**	0.732
11.	Harvest index	9.019	23.694**	2.998
12.	Seed Index	0.018	0.039**	0.006
13.	Seed yield per plant(g)	0.08	0.229**	0.027

*** Significant at 1% level of probability*

Table 3. Genetic Parameters for 13 quantitative characters in Blackgram genotypes

S. No.	Traits	GCV (%)	PCV (%)	h^2b (%)	GA @5%	GAM (%)
1.	Days to 50% flowering	2.513	3.306	57.788	1.707	3.935
2.	Days to 50% Pod setting	2.357	3.138	56.424	1.938	3.647
3.	Days to Maturity	1.485	1.933	59.003	1.881	2.349
4.	Plant height(cm)	7.263	9.225	61.989	6.430	11.780
5.	Number of Primary Branches per Plant	11.077	13.914	63.372	0.295	18.165
6.	Number of clusters per plant	6.494	7.795	69.391	1.473	11.143
7.	Number of pods per plant	6.391	7.882	65.739	2.871	10.674
8.	Pod length (cm)	3.309	4.053	66.638	0.235	5.564
9.	Number of seeds per pod	5.298	6.525	65.933	0.388	8.862
10.	Biological yield per Plant	9.237	10.694	74.596	2.609	16.434
11.	Harvest index	11.274	13.504	69.703	4.517	19.390
12.	Seed Index	2.821	3.515	64.427	0.174	4.665
13.	Seed yield per plant(g)	7.123	8.428	71.436	0.452	12.402

[Abbreviations: PCV: Phenotypic Coefficient of Variation, GCV: Genotypic Coefficient of Variation, h^2 heritability (Broad sense), GA: Genetic advancement, GAM: Genetic Advance as percent of Mean]

The genetic correlation coefficient was higher than their corresponding phenotypic correlation coefficient for many characters was similarly reported earlier by (Kumar et al., 2015, Sridhar et al., 2020, Yadav et al., 2024).

Other characteristics of the study, including the number of primary branches per plant, the number of clusters per plant, the number of days until 50% flowering, the number of days until 50% pod setting, the number of days until maturity, and the height of the plant, all showed a weak but positive correlation with yield. Other characteristics, such as the number of seeds per pod, biological yield per plant, and seed index, on the other hand, exhibited a negative and non-significant relationship with yield. There was a modest correlation between yield and the features' negative and non-significant connection, as well as a complex linkage relation between the two combinations (Deshmukh et al., 2024).

Table 4. Correlation coefficient between yield and its attributing traits in 21 blackgram genotypes at phenotypic level

Traits	DFF	DFPS	DM	PH	NPBP	NCPP	NPPP	PL	NSPP	BYPP	HI	SI	SYPP
DFF	1	0.795**	0.555**	-0.0715	0.1738	0.0801	0.0832	-0.063	0.284*	0.209	-0.147	-0.1611	0.086
DFPS		1	0.605**	-0.0261	0.1422	0.0963	0.0545	0.0055	0.281*	0.1537	-0.0571	-0.0929	0.1106
DM			1	0.0968	0.1202	0.292*	0.15	-0.0122	0.256*	0.248	-0.1757	-0.1	0.022
PH				1	0.1899	0.386**	0.093	0.1057	-0.1683	0.303*	-0.1077	-0.1802	0.2465
NPBP					1	0.520**	0.551**	-0.164	-0.076	0.655**	-0.439**	0.1488	0.0434
NCPP						1	0.613**	0.2415	0.0624	0.650**	-0.378**	0.301*	0.1109
NPPP							1	0.2416	-0.0128	0.561**	-0.1673	0.286*	0.282*
PL								1	0.1114	-0.1072	0.311*	-0.0228	0.368**
NSPP									1	0.0996	-0.083	0.365**	-0.0293
BYPP										1	-0.743**	0.1625	-0.0801
HI											1	-0.1912	0.642**
SI												1	-0.1619

[Abbreviations: DFF: Days to 50% flowering, DFPS: Days to 50% pod setting, DM: Days to maturity, PH: Plant height (cm), NPBP: Number of primary branches per plant, NCPP: Number of clusters per plant, NPPP: Number of pods per plant, PL: Pod length (cm), NSPP: Number of seeds per pod, BYPP: Biological Yield per plant (g), HI: Harvest index (%),SI: Seed index (g), SYPP: Seed yield per plant (g)]
, at 5% and 1% level of significance*

Table 5. Correlation coefficient between yield and its attributing traits in 21 blackgram genotypes at genotypic level

Traits	DFF	DFPS	DM	PH	NPBP	NCPP	NPPP	PL	NSPP	BYPP	HI	SI	SYPP
DFF	1	0.791**	0.531**	-0.0816	0.1777	0.069	0.0713	-0.0523	0.288*	0.1977	-0.1336	-0.169	0.094
DFPS		1	0.596**	-0.0299	0.1478	0.1004	0.0594	-0.0017	0.282*	0.1574	-0.0548	-0.0961	0.1032
DM			1	0.1242	0.105	0.315*	0.18	-0.0458	0.2322	0.270*	-0.2011	-0.0678	-0.0111
PH				1	0.1619	0.396**	0.1142	0.0811	-0.1858	0.313*	-0.1363	-0.1385	0.2166
NPBP					1	0.501**	0.530**	-0.1563	-0.0605	0.637**	-0.411**	0.1219	0.0479
NCPP						1	0.626**	0.2033	0.049	0.659**	-0.392**	0.312*	0.0791
NPPP							1	0.2013	-0.0254	0.573**	-0.1882	0.298*	0.2427
PL								1	0.1197	-0.1319	0.325**	-0.0404	0.387**
NSPP									1	0.0881	-0.0626	0.335**	-0.0171
BYPP										1	-0.744**	0.1741	-0.1037
HI											1	-0.2156	0.647**
SI												1	-0.1764

*[Abbreviations: DFF: Days to 50% flowering, DFPS: Days to 50% pod setting, DM: Days to maturity, PH: Plant height (cm), NPBP: Number of primary branches per plant, NCPP: Number of clusters per plant, NPPP: Number of pods per plant, PL: Pod length (cm), NSPP: Number of seeds per pod, BYPP: Biological Yield per plant (g), HI: Harvest index (%),SI: Seed index (g), SYPP: Seed yield per plant (g)] *,** at 5% and 1% level of significance*

Table 6. Direct and Indirect effects of yield attributing traits on seed yield at phenotypic level

Phenotypic Path Matrix													
	DFF	**DFPS**	**DM**	**PH**	**NPBP**	**NCPP**	**NPPP**	**PL**	**NSPP**	**BYPP**	**HI**	**SI**	**SYPP**
DFF	**0.1867**	0.1484	0.1037	-0.0133	0.0325	0.015	0.0155	-0.0118	0.0529	0.039	-0.0274	-0.0301	0.086
DFPS	-0.0563	**-0.0709**	-0.0429	0.0019	-0.0101	-0.0068	-0.0039	-0.0004	-0.0199	-0.0109	0.004	0.0066	0.1106
DM	-0.0119	-0.0129	**-0.0213**	-0.0021	-0.0026	-0.0062	-0.0032	0.0003	-0.0055	-0.0053	0.0038	0.0021	0.022
PH	-0.0114	-0.0042	0.0154	**0.1591**	0.0302	0.0614	0.0148	0.0168	-0.0268	0.0482	-0.0171	-0.0287	0.2465
NPBP	0.0129	0.0106	0.0089	0.0141	**0.0742**	0.0386	0.0409	-0.0122	-0.0056	0.0486	-0.0326	0.011	0.0434
NCPP	-0.0023	-0.0027	-0.0083	-0.0109	-0.0147	**-0.0283**	-0.0174	-0.0068	-0.0018	-0.0184	0.0107	-0.0085	0.1109
NPPP	0.0012	0.0008	0.0022	0.0014	0.0082	0.0092	**0.015**	0.0036	-0.0002	0.0084	-0.0025	0.0043	0.282*
PL	-0.005	0.0004	-0.001	0.0083	-0.0129	0.019	0.019	**0.0788**	0.0088	-0.0084	0.0245	-0.0018	0.368**
NSPP	-0.0005	-0.0005	-0.0004	0.0003	0.0001	-0.0001	0	-0.0002	**-0.0018**	-0.0002	0.0001	-0.0006	-0.0293
BYPP	0.1505	0.1107	0.1786	0.2182	0.4713	0.4682	0.4041	-0.0772	0.0717	**0.7201**	-0.5349	0.117	-0.0801
HI	-0.1783	-0.0692	-0.2131	-0.1307	-0.5327	-0.4586	-0.2029	0.3774	-0.1007	-0.901	**1.213**	-0.2319	0.642**
SI	0.0002	0.0001	0.0001	0.0002	-0.0002	-0.0004	-0.0004	0	-0.0005	-0.0002	0.0003	**-0.0013**	-0.1619

[Abbreviations: DFF: Days to 50% flowering, DFPS: Days to 50% pod setting, DM: Days to maturity, PH: Plant height (cm), NPBP: Number of primary branches per plant, NCPP: Number of clusters per plant, NPPP: Number of pods per plant, PL: Pod length (cm), NSPP: Number of seeds per pod, BYPP: Biological Yield per plant (g), HI: Harvest index (%),SI: Seed index (g), SYPP: Seed yield per plant (g)]

*Residual effect: 0.444 *,** at 5% and 1% Level of Significance*

Table 7. Direct and Indirect effects of yield attributing traits on seed yield at genotypic level

Genotypic Path Matrix													
	DFF	**DFPS**	**DM**	**PH**	**NPBP**	**NCPP**	**NPPP**	**PL**	**NSPP**	**BYPP**	**HI**	**SI**	**SYPP**
DFF	**0.2262**	0.1790	0.1201	-0.0185	0.0402	0.0156	0.0161	-0.0118	0.0651	0.0447	-0.0302	-0.0382	0.094
DFPS	-0.0801	**-0.1012**	-0.0603	0.0030	-0.0150	-0.0102	-0.0060	0.0002	-0.0285	-0.0159	0.0055	0.0097	0.1032
DM	-0.0107	-0.0120	**-0.0201**	-0.0025	-0.0021	-0.0063	-0.0036	0.0009	-0.0047	-0.0054	0.0040	0.0014	-0.0111
PH	-0.0146	-0.0053	0.0222	**0.1789**	0.0290	0.0709	0.0204	0.0145	-0.0332	0.0559	-0.0244	-0.0248	0.2166
NPBP	0.0146	0.0122	0.0086	0.0133	**0.0823**	0.0413	0.0436	-0.0129	-0.0050	0.0524	-0.0338	0.0100	0.0479
NCPP	-0.0042	-0.0062	-0.0194	-0.0244	-0.0309	**-0.0616**	-0.0385	-0.0125	-0.0030	-0.0406	0.0241	-0.0192	0.0791
NPPP	-0.0003	-0.0002	-0.0006	-0.0004	-0.0019	-0.0023	**-0.0036**	-0.0007	0.0001	-0.0021	0.0007	-0.0011	0.2427
PL	-0.0062	-0.0002	-0.0054	0.0096	-0.0184	0.0240	0.0237	**0.1179**	0.0141	-0.0156	0.0383	-0.0048	0.387**
NSPP	-0.0058	-0.0057	-0.0047	0.0037	0.0012	-0.0010	0.0005	-0.0024	**-0.0201**	-0.0018	0.0013	-0.0067	-0.0171
BYPP	0.1399	0.1114	0.1908	0.2210	0.4507	0.4664	0.4055	-0.0933	0.0624	**0.7074**	-0.5261	0.1232	-0.1037
HI	-0.1595	-0.0655	-0.2402	-0.1628	-0.4910	-0.4676	-0.2248	0.3884	-0.0748	-0.8884	**1.1946**	-0.2575	0.647**
SI	-0.0053	-0.0030	-0.0021	-0.0044	0.0038	0.0099	0.0094	-0.0013	0.0106	0.0055	-0.0068	**0.0316**	-0.1764

[Abbreviations: DFF: Days to 50% flowering, DFPS: Days to 50% pod setting, DM: Days to maturity, PH: Plant height (cm), NPBP: Number of primary branches per plant, NCPP: Number of clusters per plant, NPPP: Number of pods per plant, PL: Pod length (cm), NSPP: Number of seeds per pod, BYPP: Biological Yield per plant (g), HI: Harvest index (%),SI: Seed index (g), SYPP: Seed yield per plant (g)]

*Residual effect: 0.460 *,** at 5% and 1% Level of Significance*

3.4 Path Analysis

The estimations of correlation coefficients did not demonstrate the direct and indirect effects of various features on yield; instead, they merely showed the relationship between yield components. This is due to the fact that the properties that are associated with other components do not exist independently. However, genotypic correlations to direct and indirect impacts can be described by the results of route coefficient analysis for grain yield and yield components.

The harvest index (1.1946), seed index (0.0316), biological yield (0.7074), Pod length (0.1179), number of primary branches per plant (0.0823), plant height (0.1789),days to 50% flowering (0.2262) showed the maximum positive direct effects on seed yield at the genotypic level, while days to 50% pod setting (-0.1012), days to maturity (-0.0201), number of clusters per plant (-0.0616), number of pods per plant (-0.0036), number of seeds per pod (-0.02010) showed the maximum negative direct effects.

The harvest index (1.213), biological yield (0.7201), pod length (0.0788), number of pods per plant (0.015), number of primary branches per plant (0.0742), plant height (0.1591),days to 50% flowering (0.1867) showed the maximum positive direct effects on seed yield at the phenotypic level, while days to 50% pod setting (-0.0709), days to maturity (-0.0213), number of clusters per plant (-0.0283), number of seeds per plant (-0.0018) seed index (-0.0013) showed the maximum negative direct effects. According to the data, the number of primary branches per plant, days to 50% pod setting, harvest index, seed index, pod length, and plant height all had a positive direct impact on the number of seeds produced per plant, which were found to be similar to the findings of other researchers (Sohel et al., 2016, Suryawanshi et al., 2018, Charitha and Lal., 2021) Traits including the number of clusters per plant, the number of seeds per pod, and the number of days to maturity, on the other hand, had detrimental direct effects on seed output; however, these direct negative effects were occasionally offset by their indirect effects through other features that contributed positively (Gowsalya et al., 2016).

4. CONCLUSION

There was significant genetic variation in seed production and its constituent characteristics across blackgram genotypes in the current study, indicating plenty of potential for improvement via selection. Seed index, harvest index, pod length, number of primary branches per plant, number of pods per plant, and biological yield are all characteristics that showed strong heritability along with great genetic progress, substantial positive correlations with seed yield, and positive direct impacts in path coefficient analysis. These characteristics were found to be trustworthy indicators for improving yield in blackgram. Top-performing genotypes were identified as IC-330861, IC-330885, IC-426495, IC-385718, and SHEKAR-2, which had a high potential for seed yield with desired yield-contributing features. These genotypes are recommended for future hybridisation projects that aim to combine advantageous traits to produce stable and high-yielding blackgram cultivars. All things considered, the study provides a precise genetic basis for wise parent choice and effective selection strategies in programs aimed at improving blackgram.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

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COMPETING INTERESTS

Authors have declared that they have no known competing financial interests OR non-financial interests OR personal relationships that could have appeared to influence the work reported in this paper.

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