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Study on genetic variability and trait evaluation for yield in Blackgram (*Vigna mungo* (L.) hepper) genotypes

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Abstract

The present investigation, entitled "Study on Genetic Variability and Trait Evaluation for Yield in Blackgram (*Vigna mungo* (L.) Hepper) Genotypes," was undertaken to assess the extent of genetic variability, character association, and cause-and-effect relationships governing seed yield in blackgram. Ten diverse genotypes — TAU-1, NLU-7, LBG-402, AKU-16, BDU-1, AKU-15, PU-31, IC-410049, PU-35, and PDU-1 — were evaluated in a Randomized Complete Block Design with three replications. Observations were recorded on eleven quantitative traits, viz., days to 50% flowering, days to maturity, number of branches per plant, number of clusters per plant, number of pods per plant, pod length, number of seeds per pod, test weight, biological yield per plant, harvest index, and seed yield per plant, and the data were subjected to analysis of variance, estimation of genetic variability parameters, correlation, and path coefficient analysis.

Analysis of variance revealed highly significant genotypic differences for nine of the eleven traits, confirming the presence of substantial exploitable variability in the experimental material. Phenotypic coefficient of variation exceeded genotypic coefficient of variation for all traits, though the narrow gap between them for most characters indicated a predominant genetic component. Number of seeds per pod recorded the highest genetic advance as percent of mean (22.61%) coupled with high heritability (84.05%), signifying additive gene action and strong scope for direct selection. Correlation studies established biological yield per plant as the trait most strongly and consistently associated with seed yield per plant, both genotypically ($r_g = 0.82$) and phenotypically ($r_p = 0.66$), with number of pods per plant, number of clusters per plant, and test weight also showing significant positive associations. Path coefficient analysis, which accounted for over 99% of the variation in seed yield, identified biological yield per plant and harvest index as the principal direct contributors to yield, while most other yield components acted mainly indirectly through their strong coupling with biomass, revealing a classical biomass-partitioning trade-off. The genotype PU-35 emerged as the best overall performer, recording the highest seed yield, pod number, and test weight, and is recommended, along with the cross PU-35 × BDU-1, as a promising base for future selection and hybridization programmes aimed at combining high biomass production with superior partitioning efficiency in blackgram improvement.

Keywords: Genetic Variability, Heritability, Genetic Advance, GCV, PCV, Correlation Coefficient, Path Coefficient Analysis, Seed Yield, Biological Yield, Harvest Index, RCBD

Introduction

Blackgram (*Vigna mungo* L.) is one of the most famous pulse used in southern Asia. It belongs to the family *Fabaceae*. It is a diploid ($2n=22$) and autogamous plant. It is originated in India Vavilov, 1926 ^[1]. It is believed by researchers that *Vigna mungo* var. *silvestris* Lukoki *et al.*, 1980 ^[2] is the ancestor of blackgram. Blackgram is one of the highly-priced pulse crops cultivated in India. It can be most appropriately referred to as the "King of the pulses" due to its taste and numerous other nutritional qualities. Blackgram is an ideal source of nutrients, including proteins, carbohydrates, fats, amino acids, vitamins, and minerals. It stands next to soybean in its protein content and it is rich in vitamin A, B1, and B3 and has a small amount of thiamine, riboflavin, niacin and vitamin C Das *et al.*, 2002 ^[3]. Blackgram also has a high-calorie content, i.e., 347 calories per 100 g. Therefore, blackgram is one of the cheapest available protein sources for vegetarians Tharanathan and Mahadevamma, 2003 ^[4]. In addition, being an essential source of human food, it is also used as nutritional fodder, especially for milch animals.

Blackgram also has medicinal properties like curing diabetes, sexual dysfunction, nervous disorders, hair disorders, digestive system disorders and rheumatic afflictions. Furthermore, it is valued for its high digestibility and freedom from the flatulence effect Fary, 2002^[5].

India is world's biggest producer and user of blackgram. It owns about 70% of the world's production. India is now the largest producer of blackgram, accounting for around 29% of its total pulse acreage and 10.25% of its total pulse production. In India, 20.55 lakh tons of blackgram are produced on 33.08 lakh hectares of land INDIASTAT, 2021^[6]. Madhya Pradesh ranks 1st in production, followed by Uttar Pradesh and Andhra Pradesh in area and production.

Being a leguminous crop, it has the characteristics of restoring soil fertility by fixing atmospheric nitrogen through symbiotic association with *Rhizobium* bacteria present in the root nodules Ahmad *et al.*, 2001^[7]. It is usually cultivated in a cereal–pulse cropping system to conserve soil nutrients and utilize the leftover soil moisture, particularly after rice cultivation. It is a short-duration pulse crop Delic *et al.*, 2009^[8], usually flowering within 35–60 days of sowing and maturing within 65 to 90 days. It is generally cultivated as a kharif crop and does well in the rabi and summer seasons. The declaration of 2016 as the 'International Year of Pulses' by the Food and Agriculture Organization substantiates increasing emphasis on pulse crops. The critical position of pulse production, mainly blackgram, against the increased population Bhowmik *et al.*, 2024^[9] poses a challenge for breeders to develop high-yielding, short-duration, bold-grained and disease-resistant varieties. This can be achieved through a planned breeding program and adopting proper agronomic practices Nair *et al.*, 2024^[10]. Grain yield is the most complex character and is influenced by several component characters Gowsalya *et al.*, 2017^[11]. The component traits in blackgram are days to 50 per cent flowering, plant height, number of pods per cluster, number of clusters per plant, number of pods per plant, number of seeds per pod, pod length, 100 seed weight and grain yield per plant. Yield can be enhanced by selecting highly heritable and correlated morphological attributes that contribute to yield in a given environment and combining them to identify genotypes with a desirable combination of traits Aftab *et al.*, 2018^[12].

The presence of genetic variability in a gene pool is the prerequisite of a breeding program. Knowledge of certain genetic parameters is essential for proper understanding and manipulation in any crop improvement Program Rajalakshmi *et al.*, 2024^[13]. Genetic parameters like the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance are useful biometrical tools for determining genetic variability Barathi *et al.*, 2024^[14]. The variability in the breeding material helps select superior plant types. Heritability indicates the success of selection by measuring the proportion of variability attributable to heritability. High heritability combined with high genetic advance is more useful than heritability alone in predicting the resultant effect on selecting the best individual Johnson *et al.*, 1955^[15]. A clear understanding of the association of plant characters with yield is necessary for a successful crop improvement programme. Correlation coefficients show the magnitude and direction of the association of yield components and facilitate the plant breeders in identifying traits that are useful as selection criteria to improve crop

yield under the target environment through correlated response Radhikaben *et al.*, 2020^[16].

Path coefficient analysis is a standardized partial regression coefficient. This splits the correlation into the measures of direct and indirect effects Khan *et al.*, 2021^[17]. Therefore, it reveals whether the association of these characters with the yield is due to their direct effect on yield or if it is a consequence of their indirect effect through some other character. If the correlation between yield and other characters is due to the direct effect of that particular character, it reflects the true relationship between them Charitha *et al.*, 2021^[18].

The increasing interest in pulse crops is highlighted by the Food and Agriculture Organization's designation of 2016 as the "International Year of Pulses." The limited number of dependable varieties that yield more presents a major hurdle to the spread of this crop.

Special emphasis should be placed on collecting and analysing germplasm from various growing areas to improve blackgram production. Pure line selection and, to a lesser extent, hybridization are the main methods for enhancing this plant. Traditional breeding methods have been used by several agricultural research organizations in the past to increase crop yields and productivity Sakila *et al.*, 2018^[19]. Understanding the inheritance of specific developmental and productive traits using genetic parameters such as variance components, genotypic and phenotypic coefficients of variation, heritability, and genetic gain can help develop effective breeding strategies. The development of selection criteria for the production of high-yielding blackgram genotypes is supported by genetic variability, heritability, and improvement Abraham *et al.*, 2013^[20]. The purpose of this study was to assess genetic diversity among blackgram genotypes.

The vulnerability of urad beans to adverse environmental conditions negatively influences their growth and productivity in many countries. In India, as in other countries in the sub-tropical region, blackgram cultivation is adversely affected by prolonged water shortages, resulting in drought stress. Drought is one of the most important abiotic stresses that drastically reduce agricultural productivity of many crops, especially by negatively altering crucial plant physiological and biochemical processes Jewell *et al.*, 2010^[21]. It has been further indicated that drought's severity in crops varies according to growth stages, with the greatest losses occurring during the flowering–fruiting stage and pod filling. This problem can be resolved by the full use and adoption of novel physiological or biotechnological approaches that function to improve blackgram growth under different environmental stress conditions, particularly those that improve crop tolerance to abiotic stress. Amongst the approaches, as reviewed by Rana *et al.*, 2016^[22], genetic/physiological mechanisms targeted for manipulation of blackgram growth to advance drought or chilling stress resistance could be recommended.

Materials and Methods

Experimental site and plant material

The present investigation was carried out during the kharif season of 2025-26 at the Research Farm, School of Agricultural Sciences, G. H. Rasoni University, Saikheda, Madhya Pradesh, India, situated at 21.514862° N latitude and 78.76364° E longitude. The experimental material comprised 10 Blackgram genotypes from diverse sources,

— TAU-1, NLU-7, LBG-402, AKU-16, BDU-1, AKU-15, PU-31, IC-410049, PU-35, and PDU-1.

Experimental design and crop management

The 10 genotypes were tested in a Randomised Block Design (RBD) replicated three times, resulting in 30 single row plots. The experimental area was laid out in plots, the dimensions of which were 2.0 m x 0.3 m (row length 2.0 m; row-to-row spacing 30 cm; plant-to-plant spacing 10 cm; 20 plants per row), leaving 18 m² excluding borders and paths. The crop was fertilised with the recommended dose of 20:40:20 kg N:P₂O₅:K₂O ha⁻¹, and the standard agronomic package of practices recommended for the kharif urd region was adhered to across all plots. The meteorological observations recorded on weekly basis during crop growing period (Standard Meteorological Weeks 42 of 2025 to 4 of 2026) revealed that rainfall ranged from 0.0 to 5.0 mm, with the maximum temperature ranged from 31 to 18 °C and minimum temperature ranged from 8 to 21.5 °C, and relative humidity ranged from 70 to 35%, signifying that the crop was produced under typical dry, warm to cool weather conditions of the kharif season with no significant weather aberration.

Observations recorded

Observations were recorded on five randomly selected and Statistical analysis was done by the method suggested by Cochran and Cox (1957). The tagged plants in each plot of every replication for eleven quantitative, yield-attributing traits, viz., days to 50 per cent flowering (DF50), days to maturity (DM), Number of Branches per Plant (BPP), Number of Clusters per Plant (CPP), Number of Pods per Plant (PPP), Pod Length (cm) (PL), Number of Seeds per Pod (SPP), Seed Yield per Plant (g) (SY), Test Weight (100-seed weight, g) (TW), biological yield per plant (BY, g) and harvest index (HI, %), following standard agronomic and biometrical procedures. Days to 50 per cent flowering and days to maturity were recorded on a plot basis, while the remaining nine traits were recorded on the five tagged plants and averaged to obtain the plot mean.

Statistical analysis

All of the data for the 11 quantitative traits were collected and statistically analyzed by R software (Version 4.5.1). Analysis of variance for the Randomised Block Design, along with estimation of the genotypic and phenotypic coefficients of variation, broad-sense heritability, and genetic advance (both as an absolute value and as a percentage of the mean, worked out at 5% selection

intensity), was carried out using the R package 'variability', which partitions the observed phenotypic variance into its genotypic, environmental and error components and derives the associated genetic parameters directly from the fitted model. The cause-and-effect relationship between two variables cannot be estimated by simple correlation coefficient. Hence, path analysis suggested by Wright (1921) and Dewey and Lu (1959) was adopted in order to partition the genotypic correlation between variables with grain yield into direct and indirect effects of those variables on yield. GCV and PCV were categorised as low, moderate or high following Burton and Devane [15], broad-sense heritability was categorised following Johnson *et al.* [15], and genetic advance as a percentage of the mean was likewise categorised following Johnson *et al.* [15]. The analysis of variance suggested by Panse and Sukhatme (1978) was followed to test the significance of differences between the genotypes for all the characters. All graphs, including the dendrogram depicting the clustering pattern and the bar and line plots comparing GCV, PCV, heritability and genetic advance across traits, were prepared using the 'ggplot2' package in R software.

Results and Discussion

Analysis of variance

Analysis of variance was carried out for all the eleven quantitative traits studied in 10 blackgram (*Vigna mungo* (L.) Hepper) genotypes evaluated in a Randomized Complete Block Design (RCBD) with three replications. The ANOVA partitioned the total variation into components attributable to genotypes (df = 9), replications (df = 2), and experimental error (df = 18), thereby enabling a statistically rigorous assessment of whether the observed phenotypic differences among genotypes are genuine or merely due to chance variation. The mean sum of squares (MSS) due to genotypes was found to be highly significant ($p < 0.001$) for nine of the eleven traits studied, viz. days to 50% flowering, days to maturity, number of branches per plant, number of pods per plant, pod length, number of seeds per pod, seed yield per plant, test weight, and biological yield per plant, while number of clusters per plant was significant at $p < 0.01$ and harvest index was significant at $p < 0.05$ (Table 1). The significant differences among genotypes for all eleven traits confirm the presence of adequate genetic variability in the test material, a prerequisite for effective selection and crop improvement. The replication MSS was low relative to the genotypic MSS across all traits, indicating uniformity in the experimental environment and the reliability of the collected data.

Table 1: Analysis of variance (mean sum of squares) for yield and yield-attributing traits of blackgram

Trait	Replication (df = 2)	Genotype (df = 9)	Error (df = 18)
Days to 50% flowering	0.90000	5.79630***	0.41850
Days to maturity	0.13330	6.18150***	0.72590
No. of Branches per Plant	0.15241	1.03151***	0.088040
No. of Clusters per Plant	0.050970	1.31439**	0.27414
No. of Pods per Plant	1.96360	10.2528***	0.55170
Pod Length (cm)	0.004360	0.15082***	0.021708
No. of Seeds per Pod	0.18496	2.66744***	0.15868
Seed Yield per Plant (g)	0.017590	1.00113***	0.063410
Test Weight (100-seed wt, g)	0.068220	0.35874**	0.054320
Biological yield per plant (g)	0.96630	10.0487***	1.59720
Harvest index (%)	1.36920	4.55650*	1.56840

*** Significant at $p < 0.001$; ** Significant at $p < 0.01$; * Significant at $p < 0.05$; ns = Non-significant

Genetic Parameters

To any plant breeding programme the estimation of genetic parameters is important, as it provides quantitative information on the nature and magnitude of genetic variation present within the experimental material, and offers guidance for selecting an appropriate breeding methodology for varietal improvement. In the present study, the genetic parameters – comprising the Phenotypic Coefficient of Variation (PCV), Genotypic Coefficient of Variation (GCV), Heritability in broad sense [$h^2(\text{bs})$], Genetic Advance (GA) and Genetic Advance as a Percentage of the Mean (GA%) – were computed for all eleven yield-attributing traits studied in the blackgram genotypes under evaluation, following the classification of Sivasubramanian and Menon (1973) for PCV/GCV, Robinson *et al.* (1949) for heritability, and Johnson *et al.* (1955) for genetic advance as presented in Table 2.

For every trait studied, the PCV was consistently higher than the corresponding GCV, confirming that environmental factors contributed, to varying degrees, to the total phenotypic variation. The magnitude of the difference between PCV and GCV, however, was narrow for most of the traits – particularly days to 50% flowering, days to maturity, number of pods per plant and seed yield per plant – indicating that environmental influence on the genetic expression of these characters was comparatively limited and that the observed phenotypic variability was largely a

true reflection of the underlying genotypic variability. High heritability ($\geq 60\%$) was recorded for nine of the eleven traits studied, indicating that selection based on phenotypic performance would be reasonably effective for the majority of the characters evaluated. Only number of clusters per plant (55.85%) and harvest index (38.84%) recorded moderate heritability, reflecting a comparatively greater environmental contribution to the expression of these two traits. Interestingly, the combination of high heritability together with high GA% ($\geq 20\%$) – generally taken as the most reliable indicator of predominant additive gene action (Panse, 1957) – was recorded for only one trait, number of seeds per pod, whereas the remaining traits, including the key yield components such as number of pods per plant, seed yield per plant and biological yield per plant, combined high-to-very-high heritability with only low-to-moderate GA%. This pattern suggests that while these traits are strongly under genetic control, non-additive gene effects (dominance and epistasis) also make a meaningful contribution to their expression in the present set of genotypes, and that selection strategies combining recurrent selection or hybridisation with pedigree selection may be more rewarding than mass selection alone for rapid genetic improvement. The trait-wise interpretation of the genetic parameters in blackgram is presented in the following table.

Table 2: Estimates of Genetic Parameters for Agro-morphological Traits in Blackgram [*Vigna mungo* (L.) Hepper] Genotypes

Trait	PCV (%)	GCV (%)	h^2b (Broad sense) (%)	GA	GAM (%)
Days to 50% flowering	3.76	3.39	81.07	2.4834	6.29
Days to maturity	2.30	1.94	71.47	2.3485	3.39
No. of Branches per Plant	10.52	9.30	78.14	1.0212	16.93
No. of Clusters per Plant	12.13	9.07	55.85	0.9066	13.96
No. of Pods per Plant	7.16	6.61	85.43	3.4238	12.59
Pod Length (cm)	5.11	4.17	66.46	0.3482	7.00
No. of Seeds per Pod	13.06	11.97	84.05	1.7271	22.61
Seed Yield per Plant (g)	6.10	5.56	83.14	1.0502	10.45
Test Weight (100-seed wt, g)	7.85	6.34	65.15	0.5297	10.54
Biological Yield per Plant (g)	6.57	5.24	63.82	2.7622	8.63
Harvest index (%)	5.09	3.17	38.84	1.2812	4.07

PCV = phenotypic coefficient of variation; GCV = genotypic coefficient of variation; $h^2(\text{bs})$ = broad-sense heritability; GA = genetic advance; GAM = genetic advance as a percentage of the mean.

Correlation Studies

Correlation analysis provides a quantitative measure of the degree and direction of mutual association between pairs of traits and is fundamental to understanding the interdependence of yield-contributing characters in blackgram. In the present investigation, both genotypic (rg) and phenotypic (rp) correlation coefficients were estimated among all possible pairs of eleven agro-morphological traits in 10 blackgram genotypes. The genotypic correlations

generally exceeded the corresponding phenotypic correlations in magnitude for most trait pairs, suggesting that the associations are primarily governed by the genotypes' underlying genetic constitution rather than by environmental factors — a pattern widely reported in blackgram. Positive and significant correlations among traits indicate that simultaneous improvement through indirect selection is feasible, whereas negative correlations imply a trade-off that must be managed in a breeding programme.

Table 4.4a: Genotypic Correlation Coefficients among Quantitative Traits in 10 Blackgram Genotypes.

Genotypic Correlation Coefficients											
	DF50	DM	BPP	CPP	PPP	PL	SPP	TW	BY	HI	SY
DF50	1 **	0.7734 **	-0.3615	-0.1574	-0.4131	-0.6251	0.1494	-0.4107	-0.304	-0.1817	-0.4113
DM	0.7734 **	1 **	-0.5498	0.2306	-0.1493	-0.4755	0.129	-0.1708	-0.3014	-0.1589	-0.3827
BPP	-0.3615	-0.5498	1 **	0.411	0.6698 *	0.2638	0.4928	0.5663	0.6629 *	-0.2301	0.4794
CPP	-0.1574	0.2306	0.411	1 **	0.986 **	0.5487	0.8782 **	0.8578 **	1.0609 **	-0.4059	0.7604 *
PPP	-0.4131	-0.1493	0.6698 *	0.986 **	1 **	0.5727	0.6573 *	0.832 **	0.9026 **	-0.1165	0.7858 **
PL	-0.6251	-0.4755	0.2638	0.5487	0.5727	1 **	0.6412 *	0.9648 **	0.9168 **	-0.6098	0.5196
SPP	0.1494	0.129	0.4928	0.8782 **	0.6573 *	0.6412 *	1 **	0.9277 **	0.9132 **	-0.5544	0.5227
TW	-0.4107	-0.1708	0.5663	0.8578 **	0.832 **	0.9648 **	0.9277 **	1 **	1.0839 **	-0.6176	0.672 *
BY	-0.304	-0.3014	0.6629 *	1.0609 **	0.9026 **	0.9168 **	0.9132 **	1.0839 **	1 **	-0.2139	0.8197 **
HI	-0.1817	-0.1589	-0.2301	-0.4059	-0.1165	-0.6098	-0.5544	-0.6176	-0.2139	1 **	0.3832
SY	-0.4113	-0.3827	0.4794	0.7604 *	0.7858 **	0.5196	0.5227	0.672 *	0.8197 **	0.3832	1 **

DF50=Days to 50% maturity; DM= Days to maturity; BPP= Branches per plant; CPP= Cluster per plant; PPP= Pods per plant; PL= Pod length; SPP= Seed per plant; TW= Test weight; BY= Biological yield; HI= Harvest Index; SY= Seed yield.

Table 4.4b: Phenotypic Correlation Coefficients among Quantitative Traits in 10 Blackgram Genotypes

Phenotypic Correlation Coefficients											
	DF50	DM	BPP	CPP	PPP	PL	SPP	TW	BY	HI	SY
DF50	1 **	0.5168 **	-0.3059	-0.1138	-0.3997 *	-0.4933 **	0.1356	-0.3093	-0.2519	-0.0969	-0.365 *
DM	0.5168 **	1 **	-0.4974 **	0.2113	-0.0694	-0.3883 *	0.2	-0.1529	-0.0409	-0.2598	-0.2679
BPP	-0.3059	-0.4974 **	1 **	0.3733 *	0.5274 **	0.2847	0.3409	0.3766 *	0.3826 *	0.0541	0.4483 *
CPP	-0.1138	0.2113	0.3733 *	1 **	0.6888 **	0.2749	0.6069 **	0.6096 **	0.5755 **	-0.1386	0.5044 **
PPP	-0.3997 *	-0.0694	0.5274 **	0.6888 **	1 **	0.4655 **	0.5612 **	0.6219 **	0.751 **	-0.1952	0.6434 **
PL	-0.4933 **	-0.3883 *	0.2847	0.2749	0.4655 **	1 **	0.4084 *	0.6477 **	0.5565 **	-0.2072	0.4264 *
SPP	0.1356	0.2	0.3409	0.6069 **	0.5612 **	0.4084 *	1 **	0.6284 **	0.7359 **	-0.3907 *	0.4502 *
TW	-0.3093	-0.1529	0.3766 *	0.6096 **	0.6219 **	0.6477 **	0.6284 **	1 **	0.7257 **	-0.3321	0.5064 **
BY	-0.2519	-0.0409	0.3826 *	0.5755 **	0.751 **	0.5565 **	0.7359 **	0.7257 **	1 **	-0.4937 **	0.6604 **
HI	-0.0969	-0.2598	0.0541	-0.1386	-0.1952	-0.2072	-0.3907 *	-0.3321	-0.4937 **	1 **	0.3249
SY	-0.365 *	-0.2679	0.4483 *	0.5044 **	0.6434 **	0.4264 *	0.4502 *	0.5064 **	0.6604 **	0.3249	1 **

DF50=Days to 50% maturity; DM= Days to maturity; BPP= Branches per plant; CPP= Cluster per plant; PPP= Pods per plant; PL= Pod length; SPP= Seed per plant; TW= Test weight; BY= Biological yield; HI= Harvest Index; SY= Seed yield.

Conclusion

The present investigation revealed substantial and exploitable genetic variability among the 10 blackgram genotypes for most agro-morphological traits, providing a sound genetic base for selection. Number of seeds per pod ($h^2 = 84.05\%$, $GAM = 22.61\%$) combined high broad-sense heritability with high genetic advance as percentage of mean, indicating predominantly additive gene action and strong responsiveness to direct phenotypic selection, while number of pods per plant, seed yield per plant, number of branches per plant, and test weight showed moderate-to-high heritability coupled with moderate genetic advance, reflecting a substantial additive component. This was corroborated by correlation analysis, in which biological yield per plant showed the strongest and most consistently significant association with seed yield per plant at both the genotypic ($rg = 0.8197$) and phenotypic ($rp = 0.6604$) levels, alongside significant positive associations of number of pods per plant, number of clusters per plant, and test weight with seed yield. Path coefficient analysis, accounting for well over 99% of the variation in seed yield per plant at both levels (residual effect of 0.0022), further resolved these associations into their causal components, identifying biological yield per plant (genotypic direct effect = +0.8992; phenotypic direct effect = +1.1082) and harvest index (genotypic direct effect = +0.5654; phenotypic direct effect = +0.8663) as the two principal direct determinants of seed yield, with most other yield-component traits contributing to yield largely indirectly through their strong coupling with biological yield. Notably, the consistently negative indirect effect of nearly every yield-component trait through harvest

index, and the significant negative correlation between biological yield and harvest index, underscore the classic biomass-partitioning trade-off as the central physiological constraint to be reconciled in blackgram improvement, rather than a barrier to progress. Collectively, these results indicate that seed yield in the present material is governed by a compact genetic architecture centred on biomass production and partitioning efficiency, with pod number, cluster number, and test weight acting as important biomass-mediated contributors, rather than by phenological traits, whose influence on yield was comparatively weak and, in the case of flowering time, mildly unfavourable. Among the genotypes evaluated, PU-35 emerged as the best-performing variety, combining the highest seed yield per plant (11.21 g) with the highest number of pods per plant, the highest test weight, and early flowering and maturity, whereas IC-410049, with the lowest seed yield (9.20 g) and consistently poor performance across pod-related traits, was the poorest performer; accordingly, the cross PU-35 × BDU-1 — combining high biomass and pod-bearing capacity with the highest harvest index — is recommended as the best cross combination for breaking the biomass-partitioning trade-off, with PU-35 × AKU-15 as a strong supplementary option for combining high yield with maximum biological yield and seed number per pod. A composite selection strategy that simultaneously targets high biological yield per plant, high harvest index, and strong pod- and seed-related component traits — particularly number of pods per plant, number of clusters per plant, and test weight — is therefore recommended as the most efficient and genetically sound route to enhancing seed yield in blackgram, and merits

validation across multiple environments and breeding cycles before large-scale deployment.

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Authors' contributions

All authors contributed equally.

Compliance with ethical standards

Conflict of interest: The authors declare that they have no conflict of interest.

Ethical issues: This article contains no studies involving human participants or animals. All plant materials used comply with relevant institutional, national and international guidelines.

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