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Assessment of genetic variability and multi-trait selection in black gram (*Vigna mungo* L. Hepper) using the MGIDI index

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Abstract

Black gram (*Vigna mungo* L. Hepper) is an important pulse crop valued for its high protein content and adaptability to diverse agro-climatic conditions. The present investigation was undertaken to assess genetic variability, trait associations, and to identify superior genotypes through multivariate approaches. Fifteen early maturing black gram varieties were evaluated across two years (*Kharif* 2023 and *Kharif* 2024) and two locations in Tamil Nadu using randomized block design (RBD) with three replications. Significant variation among genotypes was observed for all the studied traits, indicating substantial genetic diversity in the experimental material. High heritability coupled with high genetic advance was recorded for most traits, suggesting the predominance of additive gene effects and the effectiveness of selection. Correlation analysis revealed a strong positive association of grain yield with number of branches per plant, number of pods per plant, and number of clusters per plant, indicating their importance as yield-contributing traits. Principal component analysis showed that the first four components explained 79.03% of the total variability, with yield and its component traits contributing largely to the variation among genotypes. The Multi-trait Genotype – Ideotype Distance Index (MGIDI) effectively integrated multiple traits and identified NUL 7 (Vishwas) and Vamban (VBN) 10 as superior genotypes based on their proximity to the ideotype. These genotypes exhibited favourable combinations of yield and yield-related traits and may serve as potential parental lines for future black gram improvement programs.

Keywords: Black gram, genetic variability, correlation, principal component analysis, MGIDI, yield improvement

Introduction

Pulses play an important role in the human diet as a major protein source, three times more than cereals and rich in sulphur, calories, and vitamins especially B-complex, as well as in the farm economy of our country. They are integral to sustainable crop production, especially in rainfed areas (Swaminathan *et al.*, 2020) [18]. Pulses are the major source of dietary protein in the vegetarian diet. Black gram [*Vigna mungo* (L.) Hepper] is an important short-duration and self-pollinated legume crop with a small genomic size of 0.56 g/PC (574 Mbp). It is a rich source of protein (25-28%), carbohydrates (62-65%), fiber (3.5-4.5%), ash (4.5-5.5%), oil (0.51.5%), amino acids like lysine, vitamins similarly thiamine, niacin, riboflavin, iron and phosphorus (Sobel *et al.*, 2016). Within this vast category, black gram, along with other pulses such as pigeon peas and green gram, play a crucial role in overall pulse production. During 2024-25, black gram is being cultivated in 3023.26 thousand hectares of land with production of 2106.18 thousand tonnes and productivity of 697 kg/ha. The urad dhal cultivation in terms of area is dominated by Madhya Pradesh (17.17%), Uttar Pradesh (14.22%), Maharashtra (12.97%), and Tamil Nadu (11.78%), while in terms of production, the states – Madhya Pradesh (17.2%), Andhra Pradesh (17.20%), Maharashtra (15.53%), Uttar Pradesh (13.68), and Tamil Nadu (7.89%). But in terms of productivity, Tamil Nadu stands in the 17th position with just 466 kg/ha (Ministry of Agriculture and Farmers Welfare). These regions provide varying agro-climatic conditions that influence the growth and yield of black gram. The yield of black gram seeds is shaped by a multitude of factors, including genetic, environmental, and agronomic practices (Priya *et al.*, 2019; Veeramani *et al.*, 2005) [13, 19]. Grain yield in black gram is a complex quantitative trait governed by multiple interrelated yield component traits. Direct selection for yield only may not always lead to consistent improvement due to the influence of correlated traits by environment. Therefore, simultaneous consideration of multiple yield related attributes is essential for achieving sustainable genetic gain (Gopinath *et al.*, 2018) [2]. A key factor in enhancing crop yield is the level of genetic variation present within the species and the efficacy with which desirable traits are passed down through generations. Understanding crucial parameters such as variability, heritability, genetic advancement, and diversity - specifically concerning yield and yield components—can provide significant insights into the potential for improvement through selective breeding techniques (Priya *et al.*, 2019; Veeramani *et al.*, 2005) [13, 19]. Heritability, an important metric in plant breeding, alongside genetic advancement, serves as a foundation for selection strategies. These estimates are indispensable for predicting expected gains when exerting selection pressure on specific traits (Johnson *et al.*, 1955) [3]. Although heritability and genetic advance provide valuable insights, selection based solely on individual traits may overlook the complex relationships among the traits. Classical selection indices such as the Smith – Hazel index, require predefine economic weights and may be affected by multicollinearity among traits, thereby limiting selection efficiency (Vieira *et al*., 2025).

In recent years, multivariate approaches integrating principal component and factor analysis have been increasingly employed to enhance multi-trait selection efficiency. The Multi-trait Genotype – Ideotype Distance Index (MGIDI) has emerged as a robust and efficient tool for identifying superior genotypes based on their proximity to an ideal ideotype. Unlike conventional indices, MGIDI eliminates the need for arbitrary economic weights and effectively addresses multicollinearity by grouping correlated traits into independent factors, thereby enabling balanced genetic improvement across multiple traits (Olivoto *et al*., 2022) [10].

In light of these considerations, a comprehensive investigation was undertaken to assess the genetic variability associated with important agronomic traits of black gram. The present study was therefore undertaken to evaluate the performance of different black gram varieties across environments, estimate genetic variability parameters for yield and its component traits, assess the genetic diversity among the genotypes, and identify superior genotypes through Multi-trait Genotype – Ideotype Distance Index (MGIDI) for balanced genetic improvement in black gram.

Materials and Methods

Location and season

The current study aimed to evaluate the performance of black gram over 2 years (*Kharif* 2023 and *Kharif* 2024) and 2 locations (Jaya Agricultural College (Affiliated to Tamil Nadu Agricultural University), Tiruvallur, Tamil Nadu and Nalanda College of Agriculture (Affiliated to Tamil Nadu Agricultural University), Trichy, Tamil Nadu).

Material

Fifteen early maturing (60 – 75 days) black gram genotypes were acquired from National Pulses Research Center (Vamban), Tamil Nadu Rice Research Institute (Aduthurai) and Tamil Nadu Agricultural University (Coimbatore). The genotypes were Vamban (VBN)-2, VBN-3, VBN(Bg)-5, VBN-6, VBN(Bg)-7, VBN-8, VBN-9, VBN-10, VBN-11, Aduthurai(ADT)-3, ADT-6, Coimbatore(CO)-7, KM-2, NUL-7 (Viswas) and T-912 The material was evaluated in Randomised Block Design (RBD) in each location in each year with three replications. Observations for ten characteristics (Table 1) were recorded on five randomly selected plants for each genotype in each replication.

Table 1: Traits recorded in black gram and their description.

S. No.	Trait	Description
1.	Days to Flowering (DF)	This is the number of days it takes from sowing to the flowering of the first emerged pod in the selected plant
2.	Plant height (PH)	The height of the selected plant measured from ground level to the tip at harvest and expressed in centimetres.
3.	Number of Branches per plant (NB):	The total number of branches present in the selected plant was counted and considered as the number of branches.
4.	Number of Clusters per plant (NC):	This refers to the total number of clusters present in the selected plant was counted and considered as the number of clusters.
5.	Number of pods per cluster (NPC)	The total number of pods present in the selected cluster was counted and considered as the number of pods per cluster.
6.	Number of pods per plant (NP)	The total number of pods present in the selected plants was counted and considered as the number of pods.
7.	Number of Seeds per pod (SP)	The total number of seeds present in the selected pod was counted and considered as the number of seeds per pod.
8.	Pod length (PL)	The maximum length of the pod of the selected plant measured at harvest from the neck of the pod to its tip and expressed in centimetres.
9.	Test weight (TW)	One hundred filled grains were randomly handpicked from the selected plant and the weight was recorded and expressed in grams.
10.	Grain yield (GY)	After harvest, all the filled grains collected from all the pods of the selected plant were shade-dried to the moisture content of 8 percent, and the weight of these grains was recorded and expressed in grams.

Statistical Analysis

The pooled Analysis of Variance (ANOVA) was determined using agricolae package (de Mendiburu, 2023) in R-studio v4.3.2 (R Core Team, 2023) [1, 14]. Descriptive statistics including mean, minimum, maximum and standard deviation were computed using fBasics package (Wuertz *et al*., 2024) in R-studio v4.3.2 (R Core Team, 2023) [14, 22] for all traits using pooled genotype means. This analysis provided an overview of the distribution and extent of variation among the studied genotypes. The results helped in understanding the range and central tendency of the measured traits prior to multivariate analyses.

The trait means for all the genotypes across 2 years and 2 locations and Mean Sum of Squares (MSS) from ANOVA were used to calculate the genetic variability parameters *viz*., Genotypic variance (GV), Phenotypic Variance (PV), Genotypic Coefficient of Variation (GCV), Phenotypic Coefficient of Variation (PCV), Heritability – Broad Sense (h_{BS}), Genetic Advance (GA) and Genetic Advance over Mean (GAM) using variability package (Popat *et al*., 2020) in R-studio v4.3.2 (R Core Team, 2023) [14]. The Coefficients of Variation (GCV and PCV) were classified according to Sivasubramaniam and Menon (1973) [16], Heritability in broad sense (h^2_{BS}) is classified according to Robinson *et al*., (1949) [15], and the Genetic Advance over Mean (GAM) is classified as given by Johnson *et al*., (1955) [3]. To understand the association among difference quantitative traits, Pearson's correlation coefficients (Pearson, 1895) were computed using the pooled genotype means across environments and additionally, correlation heat map was generated using metan package (Olivoto and Lúcio, 2020) in R-studio v4.3.2 (R Core Team, 2023) [8, 14]. Principal Component Analysis (PCA) was performed to identify the major sources of variation among the genotypes and to determine the contribution of different traits to total variability. The analysis was conducted using standardized trait values to remove scale differences among variables (Olivoto *et al*., 2022) [10]. Eigenvalues and eigenvectors were obtained from the correlation matrix, and principal components with eigenvalues greater than one were retained following the Kaiser criterion (Kaiser, 1960) [4]. The percentage of variance explained by each component was estimated. PCA also facilitated grouping of correlated traits into underlying factors, thereby simplifying interpretation and reducing multicollinearity among traits. The PCA, and the biplot was computed R-studio v4.3.2 (R Core Team, 2023) [14], using FactoMineR (Le *et al*., 2008), factoextra (Kassambara and Mundt, 2020), ggplot2 (Wickham, 2016) and ggrepel (Slowikowski, 2024) [5, 17, 21] packages. The Multi-trait Genotype – Ideotype Distance Index (MGIDI), proposed by Olivoto and Nardino (2021) [9] was used to identify superior varieties based on multiple traits. The analysis was performed using metan package (Olivoto and Lúcio, 2020) in R-studio v4.3.2 (R Core Team, 2023) [8, 14]. All the traits were initially rescaled to a 0-100 range, where 100 represented the desired ideotype value. Factor analysis with varimax rotation was then conducted to group correlated traits in to independent factors and reduce multicollinearity. The MGIDI value was calculated as the Euclidean distance between each genotype and ideotype across the retained factors. Genotypes with lower MGIDI values were considered closer to the ideotype and selected as superior genotypes. The contribution of each factor to the MGIDI value was used to determine the strengths and weakness of genotypes. Traits belonging to factors with lower contributions represent weakness of the genotype.

Results and Discussions

Descriptive statistics revealed substantial variation among the genotypes for all the traits under study (Table 2). The pooled ANOVA revealed significant differences among genotypes for all the studied traits, indicating the presence of substantial genetic variability among the genotypes (Table 3 and Table 4). The environment effect was only significant for days to 50% flowering ($p < 0.1$), number of seeds per pod ($p < 0.1$), and pod length ($p < 0.01$), whereas the interaction term between genotype and environment was non-significant for all the traits, suggesting that the genotypes performed consistently across environments. This may be attributed to the fact that the evaluated material are state-released varieties, which are generally well adapted and stable across a range of agro-climatic conditions. Therefore, the absence of significant G x E suggested stable expression of traits and allowed the use of pooled mean valued for further analyses. To further understand the distribution and extent of variation among the genotypes, descriptive statistical parameters were estimated. The phenotypic distribution of traits under study illustrated substantial variability among the genotypes, as evident from the wide range and dispersion of values observed across traits (Figure 1) Days to 50% flowering ranged from 26.18 to 41.3 days, with a mean of 33.87 days, while plant height ranged from 18.38 to 67 cm, with a mean of 43.27 cm. Grain yield per plant ranged from 0.97 to 8.85 g. with a mean value of 5.29 g. To quantify the magnitude and nature of this variability, the genetic variability parameters were estimated. They provide insights into the relative contribution of genetic and environmental factors to trait expression and help identify traits amenable for effective selection.

Table 2: Descriptive statistics for the traits under study in black gram.

S. No.	Trait	Range (Minimum to maximum)	Mean ± Standard error of mean	Standard Deviation
1.	Days to 50% flowering	26.18 – 41.3	33.87 ± 0.25	3.36
2.	Plant height (cm)	18.38 – 67	43.27 ± 0.75	10.08
3.	Number of branches	0.7 – 11.4	6.42 ± 0.14	1.87
4.	Number of clusters per plant	2.06 – 23.67	12.7 ± 0.35	4.65
5.	Number of pods per cluster	1.62 – 18.75	9.45 ± 0.24	3.16
6.	Number of pods per plant	1.87 – 8.34	4.57 ± 0.1	1.46
7.	Number of seed per pod	3.4 – 10.75	5.6 ± 0.11	1.41
8.	Pod length (cm)	0.36 – 7.29	5.58 ± 0.45	1.56
9.	Test weight (g)	0.9 – 19.12	8.42 ± 0.21	2.79
10.	Grain yield per plant (g/plant)	0.97 – 8.84	5.29 ± 0.11	1.43

Table 3: Mean Sum of Squares (MSS) from pooled Analysis of Variance (ANOVA) of the traits under study in black gram.

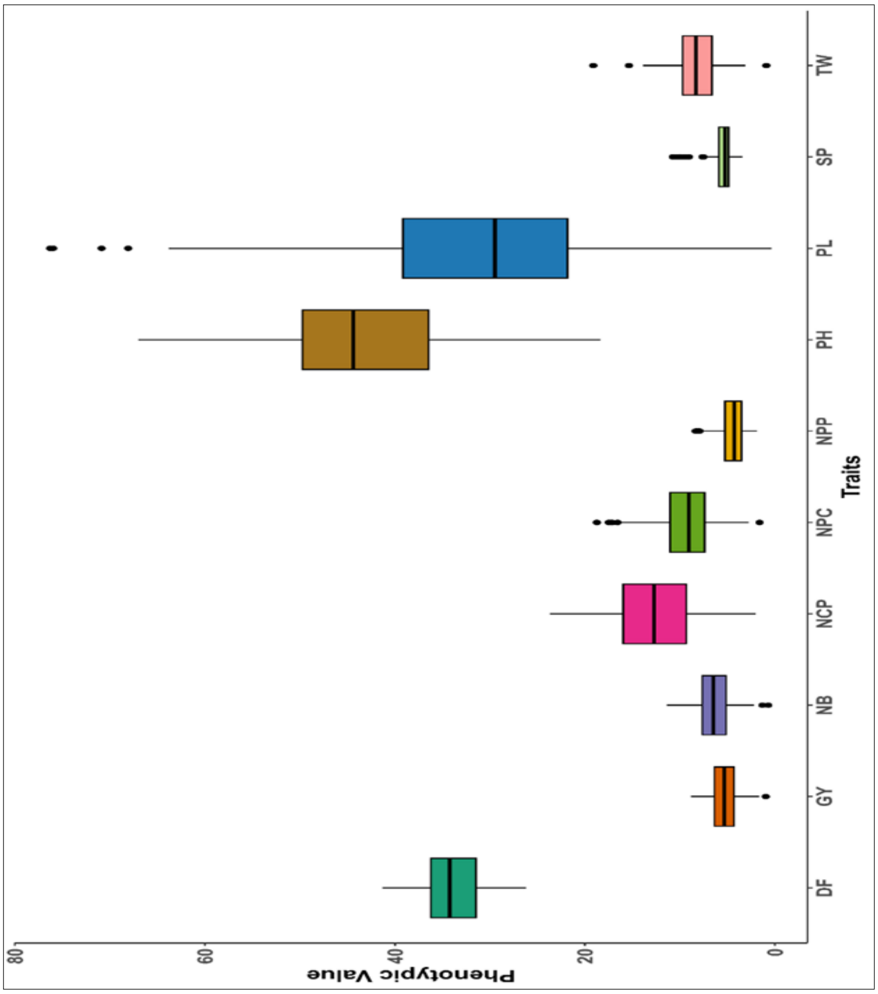
Source of Variation	Degrees of freedom	DF	PH	NB	NCP	NPC
Replication	2	3.84	9.1	1.73	9.12	2.37
Genotype	14	94.23***	799.7***	29.2***	174.61***	80.12***
Environment	3	10.51	17.5	0.39	10.17	4.21
Genotype X Environment	42	3.9	33	1.30	9.64	3.74
Residuals	118	4.25	47	1.34	8.17	4.13
Least Significant Difference at 5%		1.67	5.54	0.94	2.31	1.64

'***' – Significant at 0.1%, '**' – Significant at 1%, and '*' – Significant at 5%. DF – days to 50% flowering, PH – plant height (cm), NB – number of branches per plant, NCP – number of clusters per plant, and NPC – number of pods per cluster.

Table 4: Mean Sum of Squares (MSS) from pooled Analysis of Variance (ANOVA) of the traits under study in black gram.

Source of Variation	Degrees of freedom	NPP	SP	PL	TW	GYP
Replication	2	0.53	0.007	105.2	0.17	0.137
Genotype	14	15.65***	22.98***	1448***	60.35***	15.94***
Environment	3	1.72	0.18	416.4**	6.74	1.75
Genotype X Environment	42	0.79	0.65	92.5	2.95	0.79
Residuals	118	1.03	0.067	82.4	3.4	0.89
Least Significant Difference at 5%		0.82	0.21	7.34	1.49	0.76

‘***’ – Significant at 0.1%, ‘**’ – Significant at 1%, and ‘*’ – Significant at 5%. NPP – Number of pods per plant, NC – Number of clusters per plant, SP – Number of seeds per pod, PL – Pod length (cm), TW – Test weight (g), and GY – Grain yield per plant (g).



DF – days to 50% flowering, PH – plant height (cm), NB – number of branches per plant, NCP – number of clusters per plant, NPC – number of pods per cluster, NPP – Number of pods per plant, NC – Number of clusters per plant, SP – Number of seeds per pod, PL – Pod length (cm), TW – Test weight (g), and GY – Grain yield per plant (g).

Fig 1: Boxplot showing phenotypic variation of the traits under study in black gram.

The estimates of genetic variability parameters including environmental variance (EV), genotypic variance (GV), phenotypic variance (PV), coefficients of variation (ECV, GCV, PCV), heritability (h^2_{BS}), and genetic advance for the studied traits are presented in Table 5 and Table 6. For all the traits, phenotypic variance was higher than the corresponding genotypic variance, indicating the influence of environmental factors on trait expression, although the differences between PV and GV were relatively small for all the traits, suggesting that the environmental effect was limited. All the traits, except days to 50% flowering, exhibited high GCV and PCV, while the former exhibited moderate GCV and PCV (Figure 2). The variation coefficients ranged from 16.17 to 67.35% and 17.28 to 73.83 %, respectively. The heritability in broad-sense (h^2_{BS}) was high for all the traits, ranging from 0.83 to 0.97, indicating a large proportion of the phenotypic variation was attributable to genetic factors. High heritability coupled with high genetic advance as percent of mean (GAM) was observed for all the traits under study, suggesting the predominance of additive gene action in the inheritance of those characters. The GAM value ranged from 31.16 to 126.57 %, indicating a high potential for improvement through selection. Following the assessment of genetic variability parameters, correlation analysis was performed to understand he relationships among grain yield and its associated characters. While genetic variability parameters indicate the extent of genetic variation, correlation analysis helps identify the direction and strength of association among the traits.

Table 5: Estimates of genetic variability parameters for the trait under study in black gram.

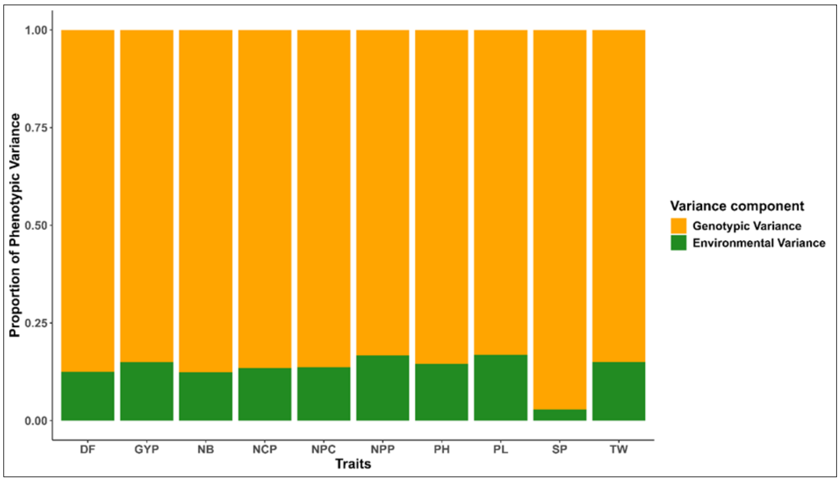
Trait	DF	PH	NB	NCP	NPC
Environmental Variance (EV)	4.2705	42.8365	1.313	8.5865	4.0289
Genotypic Variance (GV)	29.9863	252.2776	9.2955	55.3401	25.365
Phenotypic Variance (PV)	34.2568	295.1141	10.6085	63.9266	29.3939
Environmental Coefficient of Variation (ECV)	6.1019	15.1266	17.855	23.067	21.2375
Genotypic Coefficient of Variation (GCV)	16.1692	36.7091	47.5083	58.5602	53.2878
GCV classification	Moderate	High	High	High	High
Phenotypic Coefficient of Variation (PCV)	17.2823	39.7035	50.7528	62.9395	57.3639
PCV classification	Moderate	High	High	High	High
Heritability (h^2_{BS})	0.8753	0.8548	0.8762	0.8657	0.8629
h^2_{BS} classification	High	High	High	High	High
Genetic Advance	10.554	30.2518	5.8791	14.2583	9.6377
Genetic Advance over Mean	31.1633	69.9174	91.6102	112.241	101.973
GAM classification	High	High	High	High	High

DF – days to 50% flowering, PH – plant height (cm), NB – number of branches per plant, NCP – number of clusters per plant, and NPC – number of pods per cluster.

Table 6: Estimates of genetic variability parameters for the trait under study in black gram.

Trait	NPP	SP	PL	TW	GYP
Environmental Variance (EV)	0.9779	0.2186	91.1802	3.3453	0.8809
Genotypic Variance (GV)	4.89	7.5871	452.2712	19.002	5.0196
Phenotypic Variance (PV)	5.8679	7.8057	543.4514	22.3473	5.9005
Environmental Coefficient of Variation (ECV)	21.6474	8.3534	30.2411	21.7169	17.76
Genotypic Coefficient of Variation (GCV)	48.4065	49.2109	67.3515	51.758	42.3962
GCV classification	High	High	High	High	High
Phenotypic Coefficient of Variation (PCV)	53.0262	49.9148	73.8292	56.1294	45.966
PCV classification	High	High	High	High	High
Heritability (h^2_{BS})	0.8333	0.972	0.8322	0.8503	0.8507
h^2_{BS} classification	High	High	High	High	High
Genetic Advance	4.1585	5.5942	39.9656	8.2805	4.2569
Genetic Advance over Mean	91.0303	99.945	126.571	98.3183	80.5537
GAM classification	High	High	High	High	High

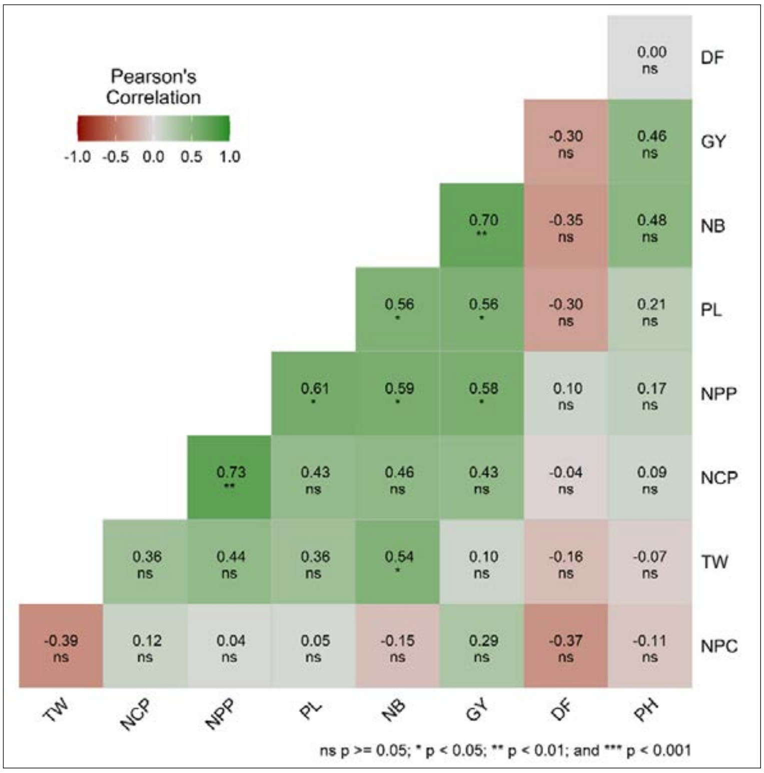
NPP – Number of pods per plant, NC – Number of clusters per plant, SP – Number of seeds per pod, PL – Pod length (cm), TW – Test weight (g), and GY – Grain yield per plant (g).



DF – days to 50% flowering, PH – plant height (cm), NB – number of branches per plant, NCP – number of clusters per plant, NPC – number of pods per cluster, NPP – Number of pods per plant, NC – Number of clusters per plant, SP – Number of seeds per pod, PL – Pod length (cm), TW – Test weight (g), and GY – Grain yield per plant (g).

Fig 2: Partitioning of phenotypic variance into genotypic and environmental variance of the traits under study in black gram.

The Pearson's correlation heatmap (Figure 3) revealed several important associations among grain yield and its component traits. Grain yield exhibited a strong positive and significant correlation with number of branches per plant ($r = 0.7$, $p < 0.01$), indicating that increased branching contributes positively to yield. Significant positive correlations were also observed among yield component traits such as number of pods per plant ($r = 0.58$, $p < 0.05$), and pod length ($r = 0.56$, $p < 0.05$). In contrast, days to 50% flowering showed negative associations with most yield-related traits. Suggesting that relatively early flowering genotypes may favour improved yield performance. Overall, the correlation heat map revealed that traits such as number of branches, clusters, and pods per plant could serve as important selection criteria for yield improvement in black gram. To further understand the multivariate relationship among the traits and to identify the major sources of variation, Principal Component Analysis (PCA) was performed. It helps in reducing data dimensionality and summarizing the variability present among traits in to a few principal components.



DF – days to 50% flowering, PH – plant height (cm), NB – number of branches per plant, NCP – number of clusters per plant, NPC – number of pods per cluster, NPP – Number of pods per plant, NC – Number of clusters per plant, SP – Number of seeds per pod, PL – Pod length (cm), TW – Test weight (g), and GY – Grain yield per plant (g).

Fig 3: Pearson's correlation heat map between the traits under study in black gram.

PCA revealed that the first four PCs had eigenvalues greater than one and together explained 79.03% of the total variance (Table 7). Among them, PC1 accounted for 37.53% of the total variance, followed by PC2 (17.35%), PC3 (12.24%), PC4 (11.92%). The relatively high contribution of the first two components suggests that these axes sufficiently represent the overall variability present in the genotypes. The contribution of individual traits to each PC was presented in Table 8. The PC1 was mainly influenced by number of branches per plant, grain yield per plant, number of pods per plant, and number of clusters per plant, indicating that these yield-contributing traits largely determined the primary axis of variation. The PC2 was predominantly explained by number of pods per cluster, test weight, and days to 50% flowering, suggesting that these traits contributed substantially to the secondary axis of variation. In PC3, number of seeds per pod, and number of clusters per plant showed the highest contributions, whereas plant height and test weight were the major contributors to PC4.

Table 7: Eigenvalues and percentage contribution of principal components for the traits under study in black gram.

Principal Component	Eigenvalue	Percentage of Variance	Cumulative %
PC1	3.75	37.53	37.53
PC2	1.73	17.35	54.87
PC3	1.22	12.24	67.12
PC4	1.19	11.92	79.03
PC5	0.97	9.73	88.77
PC6	0.48	4.77	93.54
PC7	0.26	2.64	96.18
PC8	0.22	2.21	98.4
PC9	0.1	0.98	99.38
PC10	0.06	0.62	100

Table 8: Trait contribution to the four significant principal components (PCs) in black gram.

Trait	PC1	PC2	PC3	PC4
Days to 50% flowering	3.7	17.25	7.07	5.19
Plant height (cm)	2.89	2.06	8.31	56.24
Number of branches	19.95	1.69	4.31	0.97
Number of clusters per plant	13.67	0.27	20.29	1.03
Number of pods per cluster	0.88	45.19	5.11	0.1
Number of pods per plant	17.8	2.71	9.56	0.3
Number of seed per pod	1.36	1.83	36.53	11.19
Pod length (cm)	16.23	0.11	2.4	0.04
Test weight (g)	4.53	23.39	3.05	21.46
Grain yield per plant (g/plant)	18.99	5.51	3.38	3.48

The PCA biplot based on the PC1 and PC2 (Figure 4) further illustrates the relationship among traits. Traits such as number of pods per plant, number of branches per plant, number of clusters per plant, and pod length were oriented in a similar direction, indicating a positive association among these characters and their collective contribution to yield improvement. Grain yield per plant aligned with several yield components traits, suggesting their potential importance in determining productivity. In contrast, traits such as days to 50% flowering and seeds per pod were positioned in a different direction, reflecting their relatively independent contribution to the overall variation. To conclude, the PCA results highlighted the traits that contributed most to the observed variability among genotypes and helped in identifying the major yield-contributing characters. The information derived from PC was subsequently utilized in the Multi-trait Genotype – Ideotype Distance Index (MGIDI) to integrate multiple traits simultaneously and to facilitate the identification of superior genotypes based on their overall performance across the studied characters.

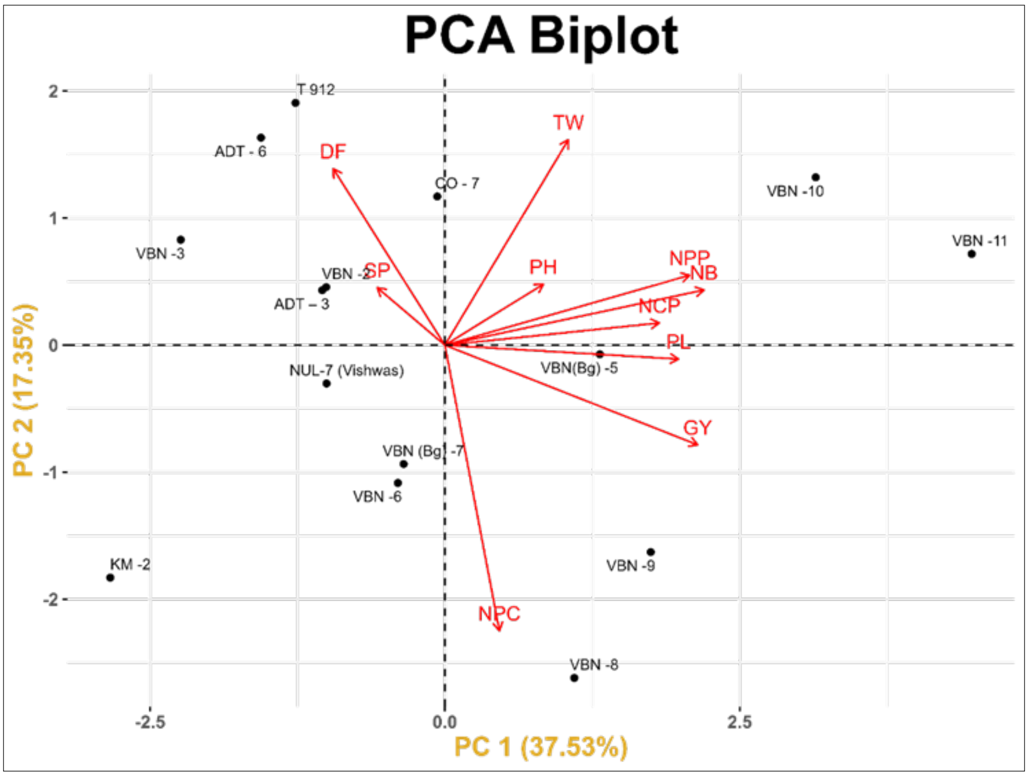


Fig 4: PCA biplot showing the relationship among the traits under study based on the PC1 and PC2.

Factor analysis grouped the studied traits into four factors explaining the major variation among the traits (Table 9). Factor 1 showed high loadings for number of branches (-0.667), number of clusters per plant (-0.873), number of pods per plant (-0.901), and pod length (-0.765), indicating that these traits collectively represent an important yield component complex. Factor 2 was mainly associated with number of pods per cluster (-0.862) and test weight (0.797), whereas Factor 3 was dominated by days to 50% flowering (0.674), and number of seeds per pod (-0.794). Factor 4 showed a strong loading for plant height (0.05). The high communalities observed for most traits suggest that the extracted factors effectively explained the variability present. Based on the MGIDI analysis, two genotypes were selected as superior genotypes as indicated by their lower MGIDI values (Table 10) and their position within the selection boundary in the MGIDI radial plot (Figure 5). Among the genotypes evaluated, NUL 7 (Vishwas) recorded the lowest MGIDI value (2.54), followed by VBN 10 (3.16), indicating that these genotypes are closer to the ideotype and possess desirable combinations of traits (Table 9). Genotypes such as Km 2, VBN 3, and VBN 2 also showed relatively lower MGIDI values, suggesting moderate suitability for selection.

Table 9: Factor Loadings of different factors and communalities after varimax rotation.

Trait	Factor 1	Factor 2	Factor 3	Factor 4	Communality	Uniquenesses
Days to 50% flowering	-0.176	-0.314	0.674	0.046	0.586	0.414
Plant height (cm)	0.08	-0.045	0.069	0.95	0.916	0.084
Number of branches	-0.667	0.226	0.363	-0.463	0.842	0.158
Number of clusters per plant	-0.873	-0.039	-0.089	0.079	0.778	0.222
Number of pods per cluster	-0.197	-0.862	0.257	0.184	0.881	0.119
Number of pods per plant	-0.901	0.132	-0.02	-0.077	0.836	0.164
Number of seed per pod	-0.075	-0.166	-0.794	0.009	0.663	0.337
Pod length (cm)	-0.765	-0.06	0.181	-0.138	0.641	0.359
Test weight (g)	-0.389	0.797	0.241	0.154	0.869	0.131
Grain yield per plant (g/plant)	-0.608	-0.244	0.49	-0.471	0.891	0.109

Table 10: Ranking of black gram genotypes based on MGIDI value.

S. No.	Genotype	MGIDI
1.	NUL-7 (Vishwas)	2.54
2.	VBN -10	3.16
3.	KM -2	3.848
4.	VBN -3	3.987
5.	VBN -2	4.125
6.	VBN -6	4.156
7.	C) - 7	4.348
8.	T 912	4.439
9.	ADT - 6	4.444
10.	VBN -9	4.586
11.	VBN -11	4.79
12.	VBN -8	4.844
13.	VBN(Bg) -5	4.99
14.	ADT – 3	5.659
15.	VBN (Bg) -7	5.803

G1 – ADT 3, G2 – ADT 6, G3 – CO 7, G4 – VBN 2, G5 – VBN 3, G6 – VBN(bg) 5, G7 – VBN 6, G8 – VBN(bg) 7, G9 – VBN 8, G10 – VBN 9, G11 – VBN 10, G12 – VBN 11, G13 – KM 2, G14 – NUL 7 (Vishwas) and G15 – T 912.

Fig 5: Genotype ranking based on the Multi-trait Genotype Ideotype Distance Index (MGIDI). Selected genotypes at 10% selection intensity were represented in red dots.

The selection differential analysis further revealed the expected genetic gains from selecting the superior genotypes (Table 11). Positive gains were observed for most traits, including plant height (38.08%), number of branches (31.51%), number of clusters per plant (39.19%), number of pods per plant (7.70%), and number of seeds per pod (26.74%). These results indicate that the selected genotypes possess improved yield component traits compared to the overall population mean. Conversely, slight negative gains were observed for pod length (-2.2%), test weight (-2.52%), and grain yield per plant (-18.61%), suggesting improvement in some component traits may not necessarily translate into immediate yield gains due to complex interactions among traits. Overall, the MGIDI approach effectively integrated multiple agronomic traits and facilitated the identification of promising genotypes with desirable trait combinations. The superior performance of NUL 7 (Vishwas) and VBN 10 indicates their potential as elite parental lines for future breeding programs aimed at improving yield and associated traits in black gram.

Table 8: Selection differential and predicted genetic gains for traits under study based on the MGIDI.

Traits	Factor	Observed mean	Selected genotype means	Selection Differential	Percentage Gain	Sense	Goal
Days to 50% flowering	FA1	6.418	6.326	-0.091	-1.425	increase	0
Plant height (cm)	FA1	12.703	17.541	4.837	38.079	increase	100
Number of branches	FA1	4.568	6.008	1.439	31.506	increase	100
Number of clusters per plant	FA1	31.576	43.951	12.376	39.193	increase	100
Number of pods per cluster	FA1	5.285	5.572	0.287	5.432	increase	100
Number of pods per plant	FA2	9.451	10.179	0.728	7.702	increase	100
Number of seed per pod	FA2	8.422	10.674	2.252	26.742	increase	100
Pod length (cm)	FA3	33.867	33.12	-0.747	-2.204	decrease	100
Test weight (g)	FA3	5.597	5.456	-0.141	-2.52	increase	0
Grain yield per plant (g/plant)	FA4	43.268	35.217	-8.05	-18.606	decrease	100

Conclusion

The present study revealed substantial genetic variability among the evaluated black gram genotypes for all the traits studied, indicating the availability of considerable genetic potential for yield improvement. High heritability coupled with high genetic advance observed for most traits suggests the predominance of additive gene action, implying that these characters can be effectively improved through direct selection. Correlation analysis indicated that grain yield was positively associated with important yield component traits such as number of branches per plant, number of clusters per plant, number of pods per plant, and pod length, highlighting their importance as reliable selection criteria in black gram breeding programs.

Principal Component Analysis further revealed that a major proportion of the total variability was explained by the first four principal components, with yield-related traits contributing significantly to the observed variation. The MGIDI approach effectively integrated multiple traits and enabled simultaneous selection of superior genotypes by minimizing multicollinearity among traits through factor analysis. Based on MGIDI values, NUL-7 (Vishwas) and VBN-10 were identified as superior genotypes with desirable combinations of agronomic and yield-related traits, indicating their close proximity to the ideotype.

Overall, the integration of genetic variability analysis, correlation studies, PCA, and MGIDI provided a comprehensive framework for multi-trait selection in black gram. The identified superior genotypes can serve as promising parental lines in future breeding programs aimed at developing high-yielding and well-balanced varieties for diverse agro-climatic conditions.

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Author Contributions: MV, and ALN conceptualized the study and collected the material, BG, and ASP laid out the experiment and collected the data. MR analyzed the data and prepared the first draft. All the authors commented on the previous versions, and approved the final manuscript.

Data Availability: The datasets generated and analyzed during the current study are available as supplementary material.

Ethics Approval: The study does not contain any studies involving human participants or animals performed by any of the authors.

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