

Genetic Diversity, Trait Associations and Selection Indices in Blackgram (*Vigna mungo* L. Hepper) Across Multi- Environment Trials

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Abstract

The present study was carried out across four *Kharif* (monsoon) environments to assess the genetic diversity and trait associations of 105 blackgram (*Vigna mungo* L. Hepper) genotypes using multivariate statistical approaches. Significant variation among genotypes for 18 agro-morphogenic traits confirmed a broad genetic base. Traits such as thousand seed weight (TSW), single pod weight (SPW), number of seeds per pod (NSPP), biological yield per plant (BYPP), % of first harvest over total harvest, and greenness exhibited high heritability and selection accuracy indicating their potential for direct selection. Seed yield per plant (SYPP) showed moderate heritability but strong associations with highly heritable traits like BYPP, TSW, and SPW indicating value for indirect selection. BYPP was identified by path analysis as the most influential trait directly affecting SYPP while others influencing indirectly through it. Hierarchical clustering grouped the genotypes into five distinct clusters. Genotypes in cluster IV showed superior performance for yield related traits. Yield related traits such as SYPP, BYPP, and NCP were found to be the major contributors to the total genetic variation. In the PCA-biplot, phenological and vegetative traits aligned along distinct and opposing axes of diversity. Altogether, the findings reveal significant genetic diversity and identify key selection indices (TSW, SPW, NSPP, and BYPP). Hybridization between early-maturing and bold-seeded genotypes from cluster V and high-yielding genotypes from cluster IV is recommended to combine earliness, productivity, and broad adaptability for developing superior blackgram varieties suited to diverse environments.

Introduction

Blackgram (*Vigna mungo* L. Hepper), known locally as mashkalai, is a self-pollinated annual diploid species ($2n = 22$). Its genome size is approximately 574 Mbp (Raizada & Souframanien 2019). It is widely grown pulse crop across South and Southeast Asia (Kanth et al. 2021). Blackgram is a good source of protein and micronutrients. It also contributes to soil improvement by symbiotic nitrogen fixation with rhizobia (Jangir et al. 2017; Swaminathan et al. 2021; Marimuthu et al. 2024). It fits well into diverse production systems because of its short duration, adaptability to diverse environments and usefulness as both food and forage crop (Dey et al. 2017; Kanth et al. 2021). Yet, blackgram has historically received less research attention compared to other pulses (Dipti & Khaleque 2019; Dhasarathan et al. 2021; Nair et al. 2024). This limitation has slowed genetic improvement of blackgram resulting in relatively narrow genetic base and modest productivity levels. Genetic diversity forms the basis for crop improvement. A broad genetic base ensures enough variability for selection, supporting long term progress in both yield and adaptability (Gomathi et al. 2021; Jawad et al. 2024). Choice of genetically distinct and agronomically promising parents play critical role in exploiting heterosis and development of desirable recombinants (Priya et al. 2019; Narendrabhai & Bala 2020; Reddy et al. 2021). Knowledge of trait association is equally crucial for designing breeding strategies. As yield is a complex, polygenic trait with strong environmental influence, direct selection is often inefficient (Rajalakshmi et al. 2024a). Indirect selection can be rewarding when traits that are heritable, stable, and strongly correlated with yield are available (Gomathi et al. 2021; Kuralarasan & Jayamani 2021). Character association and path coefficient analyses are valuable tools to support this. Character association clarifies how traits are related. Path analysis partition correlations into direct and indirect effects helping identification of the most effective selection indices (Sood et al. 2023).

Multivariate approaches provide complementary insights (Mohanlal et al. 2018). Cluster analysis groups similar genotypes and helps identify those that are genetically divergent (Gayacharan et al. 2022). Principal component analysis (PCA) reduces complex trait data into few major components. It reveals the traits that contribute most to overall variability. PCA also estimates trait's contribution to genetic divergence identifying the most contributing traits (Ajaykumar et al. 2022). These approaches collectively provide an integrated framework to classify genotypes and assess relationships among traits guiding targeted breeding decisions. Previous research has emphasized the need to combine multi-environment evaluation with comprehensive genetic analyses to identify stable and high-yielding blackgram genotypes (Vadivel et al. 2020; Dhasarathan et al. 2021; Gomathi et al. 2021; Rajalakshmi et al. 2024). However, most studies have focused on limited environments or single trait analyses providing an incomplete picture of genetic structure and adaptability. Therefore, this study evaluated 105 blackgram genotypes across four *Kharif* environments to quantify genetic diversity and trait associations aiming to identify the most reliable direct and indirect selection criteria for yield improvement and to classify genotypes based on multivariate analyses.

Materials and Methods

Plant Material and Experimental Design

A total of 105 blackgram genotypes (Supplementary Table 1) were evaluated in a randomized complete block design (RCBD) with three replications. Each experimental unit consisted of a plot measuring 2.0×0.5 m, with plants spaced 10 cm apart within rows.

Study Sites and Environmental Conditions

The experiments were conducted over four *Kharif* environments spanning from 2023 to 2025. The four seasons were Gazipur *Kharif* 1 (April to July 2023), Gazipur *Kharif* 2 (August to November 2023), Dhaka *Kharif* 2 (August to November 2024) and Dhaka *Kharif* 1 (April to July 2025). The first two trials were conducted at the field of Biotechnology Division, Bangladesh Agricultural Research Institute (BARI), Gazipur. The subsequent two trials were conducted at the central field of Sher-e-Bangla Agricultural University (SAU), Dhaka. The average temperature and rainfall during the experimental period are shown in Fig. 1.

Crop Management

Each site was fertilized with well decomposed cow dung at 5 t ha^{-1} during final land preparation. Inorganic fertilizers were applied at the rates of 45 kg N, 90 kg P_2O_5 , 45 kg K_2O , 55 kg S, and 10 kg B per hectare as a basal dose. Standard agronomic practices were followed throughout the growing period. Manual weeding, light irrigation, and other intercultural operations were carried out as required to maintain uniform crop growth. Harvesting was done in three successive pickings to ensure complete yield recovery.

Data Collection

Data were recorded on 18 agro-morphogenic traits from five randomly selected plants per plot to ensure representative sampling. These traits were: days to first flowering (DFrF), days to 50% flowering (DFF), days to first pod maturity (DFrPM), plant height (PH, cm), petiole length (PL, cm), terminal leaf length (TLL, cm), terminal leaf width (TLW, cm), greenness (GN, SPAD value), number of branches per plant (NBP), number of clusters per plant (NCP), number of pods per cluster (NCP), pod length (PodL, cm), number of seeds per pod (NSPP), single pod weight (SPW, g), biological yield per plant (BYPP, g), seed yield per plant (SYPP, g), % of first harvest over total harvest (FH/TH, %) and thousand seed weight (TSW, g). Data collection followed standard descriptors and procedures recommended for blackgram phenotypic evaluation.

Statistical Analysis

All recorded data were analyzed using R (version 4.3.1) statistical software. A joint ANOVA (analysis of variance) across environments was performed to assess the significance of genotype, environment, and genotype by environment effects. Genetic parameters such as heritability, genotypic and phenotypic coefficients of variation and genetic advance were estimated using the "metan" package. Trait associatinss were determined by calculating Pearson's correlation coefficients. Path coefficient analysis was employed to partition these correlations into direct and indirect effects on SYPP utilizing the "agricolae" package. For multivariate analyses, hierarchical cluster analysis was performed to group genotypes into clusters and estimate genetic divergence among them based on Ward's method and Euclidean distance. Principal Component Analysis was also applied to identify the most important traits contributing to overall variation and PCA-biplot was generated to visualize them. These analyses were carried out using the "cluster", "factoextra", and "ggplot2" packages respectively.

Results

Genetic Variability and Descriptive Statistics

The variance for 18 agro-morphogenic traits among 105 blackgram genotypes was analyzed combinedly across four *Kharif* environments. There was significant genetic variation for all traits. The mean performance of the genotypes across environments showed wide range for most of the traits (Supplementary Table 2). The descriptive statistics for the traits studied further supported these observations (Table 1). High coefficients of variation (CV%) were recorded for biological yield per plant (41.28%), seed yield per plant (44.45%), and number of branches per plant (30.56%). Days to first flowering (DFrF) varied from 27 to 55.5 days, indicating the presence of both early and late flowering genotypes. For instance, G33 flowered the earliest in Gazipur *Kharif* 1 (E-1) and G7 flowered later in Gazipur *Kharif* 2 (E-2). Plant height (PH) varied from 15.81 cm (G8, E-1) to 158 cm (G17, E-4) indicating a strong genotype by environment interaction for vegetative growth. Yield-related traits also showed wide variation. Seed yield per plant (SYPP) ranged from 0.62 g (G17 in E-3) to 32.09 g (G63 in E-2) representing more than a fifteen-fold difference among the genotypes. Thousand seed weight (TSW) varied from 22.47 g to 59.01 g, with G57 scoring the highest value in E-4. Pod related traits such as single pod weight (SPW) and pod length (PodL) also varied widely. The environments E-2 and E-4 were the most favorable for trait expression supporting superior genotypic performance and E-1 showed less variation among genotypes. The genotypes G63, G57, G99, and G17 consistently performed well across environment for yield and related traits highlighting their potential use in breeding programs and yield stability studies.

Genetic Parameters and Selection Criteria

The analysis of genetic parameters revealed a clear distinction among the traits studied (Table 2). High heritability on a mean basis ($h^2_{gm} > 0.70$) and high accuracy of selection ($Ac > 0.85$) were observed for several key yield components. TSW emerged as the most consistent and dependable target for selection. It exhibited highest broad sense heritability ($h^2_b = 0.5$), h^2_{gm} (0.84), and Ac (0.92), along with a favorable coefficient of variation ratio (1.62). TSW also showed a substantial genetic advance (GA, 5.23) and a moderate genetic advance as percent of mean (GAM, 12.92%) indicating the presence of additive genetic variability and a strong response to selection. The trait % of first harvest over total harvest (FH/TH) also displayed genetic control. Its value of h^2_b , h^2_{gm} , and Ac were 0.45, 0.83, and 0.91, respectively. The trait also recorded high GA (17.64) and a very high GAM (35.86%). Similarly, h^2_b , h^2_{gm} , and Ac value of number of seeds per pod (NSPP) were 0.37, 0.88, and 0.94, respectively. In case of single-pod weight, h^2_b , h^2_{gm} , and Ac value were 0.37, 0.76, and 0.87, respectively and for greenness (GN) were 0.38, 0.75, and 0.87, respectively. These results also revealed high heritability and selection accuracy for those traits. In contrast, SYPP showed moderate h^2_b (0.24), h^2_{gm} (0.63) and moderate GAM (19.47%) indicating stronger environmental influence. Several morphological traits, *Viz.*, terminal leaf length, terminal leaf width, and number of pods per cluster showed low heritability (both h^2_b and h^2_{gm}) and poor coefficient of variation ratios (0.22, 0.26, and 0.32, respectively). Their GA and GAM values were also small, suggesting a limited scope for genetic improvement through phenotypic selection. Furthermore, traits such as PH and NCP exhibited considerable genotype by environment interaction (0.58 AND 0.60, respectively).

Table 1. Descriptive statistics of 18 agro-morphogenic characters for 105 blackgram genotypes across four *Kharif* environments

Traits	Mean	SE	CV%	Min.	Max.	Min.ENV	Max.ENV	Min.GEN	Max.GEN
DfrF	34.99	0.1	10.39	27 (G ₃₃ , E-1)	55.5 (G ₇ , E-2)	E-1 (33.39)	E-3 (36.74)	G ₃₇ (31.04)	G ₇ (42.46)
DFF	38.77	0.12	11.06	29 (G ₅₂ , E-1)	58 (G ₇ , E-2)	E-1 (36.49)	E-3 (41.71)	G ₃₁ (34.67)	G ₇ (48.75)
DfrPM	56.45	0.15	9.49	41 (G ₅ , E-1)	82 (G ₉₇ , E-3)	E-1 (52.41)	E-2 (59.48)	G ₆ (50.08)	G ₉₇ (65.67)
PH	53.56	0.6	39.71	15.81 (G ₈ , E-1)	158 (G ₁₇ , E-4)	E-1 (37.02)	E-4 (62.31)	G ₃₁ (38.4)	G ₁₇ (97.76)
PL	9.82	0.08	29.78	2.5 (G ₄₅ , E-1)	24.27 (G ₄₈ , E-3)	E-1 (7.09)	E-3 (12.75)	G ₈₈ (7.62)	G ₁ (13.71)
TLL	7.76	0.07	32.76	1.5 (G ₉₇ , E-1)	75 (G ₁₀₄ , E-2)	E-1 (6.12)	E-2 (8.49)	G ₇₃ (6.15)	G ₁₀₄ (13.15)
TLW	4.85	0.05	38.28	1.9 (G ₃ , E-1)	55.5 (G ₂ , E-2)	E-1 (3.88)	E-2 (5.26)	G ₆₅ (3.69)	G ₂ (8.74)
GN	59	0.14	8.14	43.5 (G ₆ , E-1)	77.1 (G ₄₆ , E-2)	E-1 (56.8)	E-2 (60.73)	G ₈₇ (53.13)	G ₇₅ (67.63)
NBP	5.6	0.05	30.56	1.0 (G ₆₇ , E-2)	12.25 (G ₄ , E-3)	E-4 (4.7)	E-3 (6.82)	G ₉₁ (3.6)	G ₆₈ (7.27)
NCP	19.2	0.22	40.8	2.5 (G ₁₇ , E-3)	43 (G ₂₄ , E-2)	E-1 (12.41)	E-2 (25.64)	G ₁₀₀ (11.15)	G ₇₆ (25.18)
NPPC	2.96	0.02	23.4	0.59 (G ₈₆ , E-4)	5.25 (G ₄₈ , E-4)	E-1 (2.74)	E-2 (3.15)	G ₉₄ (2.24)	G ₄₆ (3.71)
PodL	4.31	0.04	30.7	2.08 (G ₁₀₀ , E-3)	44 (G ₆₃ , E-1)	E-4 (4.07)	E-3 (4.56)	G ₁₀₀ (3.61)	G ₆₃ (9.21)
NSPP	6.12	0.02	11.04	3.0 (G ₅₂ , E-1)	9.0 (G ₄₂ , E-3)	E-1 (5.96)	E-3 (6.23)	G ₇₀ (4.98)	G ₈₈ (6.98)
SPW	0.33	0.01	18.68	0.14 (G ₁₇ , E-1)	0.53 (G ₈₈ , E1)	E-4 (0.33)	E-1 (0.35)	G ₉₉ (0.21)	G ₅₇ (0.42)
BYPP	18.32	0.26	41.28	1.2 (G ₁₇ , E-3)	53.46 (G ₂₈ , E-2)	E-1 (10.89)	E-2 (25.84)	G ₁₀₀ (7.06)	G ₆₃ (27.35)
SYPP	10.51	0.16	44.45	0.62 (G ₁₇ , E-3)	32.09 (G ₆₃ , E-2)	E-1 (6.42)	E-2 (14.92)	G ₁₀₀ (4.14)	G ₆₃ (16.91)
FH/TH	49.19	0.56	40.46	2.01 (G ₃₂ , E-3)	100 (G ₉₁ , E-2)	E-3 (39.52)	E-4 (55.29)	G ₂₄ (18.15)	G ₉₂ (84.14)
TSW	40.51	0.16	14.16	22.47 (G ₁₀₀ , E-3)	59.01 (G ₅₇ , E-4)	E-3 (36.74)	E-4 (43.35)	G ₁₀₀ (27.25)	G ₉₉ (48.9)
Here, DfrF = days to first flowering, DFF = days to 50% flowering, DfrPM = days to first pod maturity, PH = plant height (cm), PL = petiole length (cm), TLL = terminal leaf length (cm), TLW = terminal leaf width (cm), GN = greenness (SPAD), NBP = number of branch per plant, NCP = number of cluster per plant, NPCP = number of pods per cluster, PodL= pod length (cm), NSPP = number of seeds per pod, SPW = single pod weight (g), BYPP = biological yield per plant (g), SYPP = seed yield per plant (g), FH/TH = % of first harvest over total harvest, TSW = thousand seed weight (g), G _i = i th genotype, E-1 = Gazipur <i>Kharif</i> 1, E-2 = Gazipur <i>Kharif</i> 2, E-3 = Dhaka <i>Kharif</i> 1, E-4 = Dhaka <i>Kharif</i> 2									

Table 2: Genetic parameters for the 18 agro-morphogenic characters of 105 blackgram genotypes as per mean performance across four environments

Genetic parameters Traits	σ_p^2	h_b^2	GA	GAM (%)	GEI r^2	h_{gm}^2	Ac	rge	CVg	CVr	CV ratio
Days to first flowering	11.33	0.19	1.32	3.77	0.52	0.55	0.74	0.64	4.16	5.24	0.79
Days to 50% flowering	14.62	0.25	1.97	5.08	0.47	0.64	0.80	0.62	4.90	5.26	0.93
Days to first pod maturity	20.63	0.32	2.99	5.30	0.38	0.73	0.85	0.56	4.54	4.40	1.03
Plant height (cm)	387.76	0.25	10.14	18.93	0.58	0.61	0.78	0.77	18.23	15.15	1.20
Petiole length (cm)	4.41	0.21	0.91	9.25	0.19	0.68	0.82	0.24	9.70	16.66	0.58
Terminal leaf length (cm)	5.53	0.04	0.19	2.50	0.08	0.30	0.55	0.08	6.13	28.39	0.22
Terminal leaf width (cm)	3.09	0.06	0.22	4.48	0.06	0.40	0.63	0.07	8.76	34.00	0.26
Greenness (SPAD)	18.36	0.38	3.35	5.69	0.45	0.75	0.87	0.73	4.50	2.93	1.53
Number of branches per plant	1.89	0.16	0.45	8.09	0.19	0.61	0.78	0.23	9.81	19.88	0.49
Number of clusters per plant	24.77	0.11	1.13	5.87	0.60	0.39	0.63	0.68	8.67	13.91	0.62
Number of pods per cluster	0.44	0.05	0.07	2.31	0.41	0.27	0.52	0.43	5.21	16.47	0.32
Pod length (cm)	1.72	0.09	0.24	5.64	0.00	0.54	0.74	0.00	9.14	29.04	0.31
Number of seeds per pod	0.44	0.37	0.51	8.26	0.00	0.88	0.94	0.00	6.60	8.54	0.77
Single pod weight (g)	0.00	0.37	0.00	0.00	0.39	0.76	0.87	0.62	11.15	8.94	1.25
Biological yield per plant (g)	44.52	0.21	2.89	15.76	0.50	0.59	0.77	0.63	16.83	19.55	0.86
Seed yield per plant (g)	17.13	0.24	2.05	19.47	0.46	0.63	0.79	0.60	19.16	21.75	0.88
% of first harvest over total harvest	362.02	0.45	17.64	35.86	0.29	0.83	0.91	0.53	26.03	19.52	1.33
Thousand seed weight (g)	25.81	0.50	5.23	12.92	0.31	0.84	0.92	0.62	8.88	5.48	1.62

Here, σ_p^2 = phenotypic variance, h_b^2 = broad-sense heritability, GA = genetic advance, GAM = genetic advance as percent of mean, GEI r^2 = coefficient of determination of the interaction effects, h_{gm}^2 = heritability on the mean basis, Ac = accuracy of selection, rge = genotype-environment correlation, CVg = genotypic coefficient of variation, CVr = the residual coefficient of variation

Correlation analysis was employed to dissect the character association among the traits studied (Fig. 2). Path coefficient analysis partitioned the correlations into their direct and indirect effect on SYPP (Table 3). The correlation matrix exhibited a strong positive correlation between SYPP and BYPP (0.97), indicating that increased BYPP directly contributed to higher seed yield. The trait SYPP was also positively correlated with TSW (0.48) and SPW (0.48). Significant correlation (0.41) between SPW and TSW further suggested that genotypes with heavier pods tend to produce larger seeds. BYPP also maintained positive associations with NCP (0.20) and NPPC (0.18) significantly, emphasizing their contribution on enhancing yield components. Traits associated with leaf morphology *Viz.* TLL and TLW were positively correlated with each other and plant height which reflects that taller genotypes tend to have vigorous vegetative growth. In contrast, early phenological traits such as DFrF and DFF were strongly correlated (0.76) with each other but weakly or negatively correlated with yield components suggesting that early flowering may compromise yield potential.

Path analysis provided deeper insights, confirming BYPP as the trait with the strongest positive direct effect (1.0446) on SYPP. Other traits such as NSPP (0.0209) and DFrPM (0.0081) exhibited positive direct effects. Several traits including SPW (-0.0394), DFF (-0.0439), and NCP (-0.0692) exerted negative direct effects on yield. The strong positive correlation (0.84) of NCP and SYPP was largely mediated by its high positive indirect effect via BYPP (0.9088). Similarly, TSW also contributed indirectly to SYPP through its association with BYPP (0.5014). On the other hand, phenological traits like DFrF and DFF showed weak or negative direct effects (-0.0031 and -0.0439, respectively) underscoring the trade-offs between earliness and yield potential. These analyses established BYPP as the principal determinant of seed yield. Traits like TSW, SPW, and NCP contributed indirectly by enhancing BYPP.

Cluster Analysis

The 105 blackgram genotypes were grouped into five distinct clusters according to their mean performance across four *Kharif* environments. The dendrogram generated through hierarchical clustering clarified clear genetic relationships and grouping among the genotypes (Fig. 3). Quantitative measures of genetic divergence, including intra-cluster and inter-cluster distances were presented in Fig. 4. The intra-cluster distances for cluster

Table 3 Direct and indirect effects of different traits on seed yield per plant in 105 blackgram genotypes evaluated across four *Kharif* environments

	DFF	DFF	DFFPM	PH	PL	TLL	TLW	GN	NBP	NCP	NPPC	PodL	NSPP	SPW
DFF	-0.0031	-0.0334	0.0049	-0.0027	-0.0058	-0.0012	0.0007	0.0000	-0.0030	-0.0028	-0.0006	0.0000	0.0010	0.0
DFF	-0.0024	-0.0439	0.0042	-0.0032	-0.0071	-0.0016	0.0009	0.0000	-0.0038	0.0000	0.0006	0.0000	0.0015	0.0
DFFPM	-0.0019	-0.0224	0.0081	-0.0024	-0.0058	-0.0021	0.0010	-0.0001	-0.0006	-0.0138	-0.0035	0.0000	0.0031	0.0
PH	-0.0013	-0.0211	0.0029	-0.0067	-0.0083	-0.0024	0.0014	0.0000	-0.0023	-0.0138	-0.0029	0.0000	0.0019	0.0
PL	-0.0011	-0.0189	0.0028	-0.0033	-0.0166	-0.0037	0.0019	-0.0001	-0.0042	-0.0021	-0.0016	0.0000	0.0021	0.0
TLL	-0.0004	-0.0070	0.0017	-0.0016	-0.0061	-0.0101	0.0016	-0.0001	0.0005	-0.0138	-0.0025	0.0000	0.0002	-0.0
TLW	-0.0004	-0.0079	0.0016	-0.0017	-0.0060	-0.0031	0.0052	0.0000	0.0000	-0.0132	-0.0019	0.0000	0.0002	0.0
GN	-0.0001	-0.0031	0.0013	-0.0005	-0.0030	-0.0012	0.0004	-0.0006	-0.0006	-0.0104	-0.0010	0.0000	0.0017	0.0
NBP	-0.0006	-0.0110	0.0003	-0.0010	-0.0046	0.0003	0.0000	0.0000	-0.0150	0.0222	0.0019	0.0000	-0.0002	-0.0
NCP	-0.0001	0.0000	0.0016	-0.0013	-0.0005	-0.0020	0.0010	-0.0001	0.0048	-0.0692	-0.0057	0.0000	0.0002	0.0
NPPC	-0.0001	0.0009	0.0009	-0.0006	-0.0008	-0.0008	0.0003	0.0000	0.0009	-0.0125	-0.0318	0.0000	0.0010	0.0
PodL	0.0000	0.0009	0.0002	0.0001	-0.0007	-0.0002	0.0000	0.0000	-0.0009	0.0035	0.0000	0.0001	0.0015	-0.0
NSPP	-0.0002	-0.0031	0.0012	-0.0006	-0.0017	-0.0001	0.0001	0.0000	0.0002	-0.0007	-0.0016	0.0000	0.0209	-0.0
SPW	0.0004	0.0070	-0.0005	0.0012	0.0013	-0.0004	0.0000	0.0000	-0.0003	0.0055	0.0029	0.0000	0.0035	-0.0
BYPP	0.0000	0.0026	0.0015	-0.0007	-0.0002	-0.0021	0.0008	-0.0001	0.0044	-0.0602	-0.0134	0.0000	0.0013	-0.0
FH/TH	0.0003	0.0066	0.0002	0.0005	0.0028	-0.0001	-0.0005	0.0000	0.0030	-0.0007	0.0029	0.0000	0.0013	0.0
TSW	0.0007	0.0136	-0.0002	0.0009	0.0030	-0.0006	0.0000	0.0000	0.0051	-0.0284	-0.0054	0.0000	0.0000	-0.0

DFF = days to first flowering, DFF = days to 50% flowering, DFFPM = days to first pod maturity, PH = plant height (cm), PL = petiole length (cm), TLL = terminal leaf width (cm), GN = greenness (SPAD), NBP = number of branch per plant, NCP = number of cluster per plant, NPPC = number of pods per cluster, PodL = seeds per pod, SPW = single pod weight (g), BYPP = biological yield per plant (g), FH/TH = % of first harvest over total harvest, TSW = thousand seed weight

I, cluster II, cluster III, cluster IV and cluster V were 5.63, 4.61, 4.26, 4.70 and 5.42, respectively revealing the degree of genetic dissimilarity within each group. Cluster III showed the smallest intra-cluster distance (4.26), suggesting high genetic homogeneity within the group. However, cluster IV demonstrated the largest intra-cluster distance (4.70) reflecting greater internal diversity and potential for selection within this group. The inter-cluster distances revealed the highest genetic variation between cluster I and cluster IV (9.09), followed by cluster I and cluster III (7.31). The lowest inter-cluster distance was recorded between cluster II and cluster IV (4.51), followed by cluster III and cluster V (4.60) and cluster II and cluster V (4.79), suggesting these groups share relatively narrow genetic base.

Cluster mean values for 18 agro-morphogenic traits are presented in Table 4. Cluster I recorded the highest means for DFF (39.70 days), DFF (45.71 days), DFFPM (58.79 days), PH (79.96 cm), and PL (12.05 cm), but the lowest value for SYPP (7.33 g). Cluster II had relatively high means for NCP (21.06) and SYPP (11.08 g), along with moderate flowering duration. Cluster III demonstrated the lowest means for flowering traits, but favorable values found for NPPC (3.09), BYPP (17.69 g), and SYPP (10.19 g). Cluster IV demonstrated superior performance for most yield contributing traits including GN (61.95), NCP (21.25), NPPC (3.17), PodL (4.61 cm), NSPP (6.38), SPW (0.36 g), BYPP (23.31 g), and SYPP (13.79 g). Cluster V had the highest FH/TH (66.60%) suggesting early maturing and bold-seeded genotypes with improved harvest efficiency.

Table 4 Cluster wise mean values for 18 agro-morphogenic traits among clusters based on mean performance of 105 blackgram genotypes across four Kharif environments

Traits	Cluster means					Population means
	I	II	III	IV	V	
Days to first flowering	39.70	35.70	34.39	34.12	34.61	34.99
Days to 50% flowering	45.71	39.04	38.13	37.58	38.48	38.77
Days to first pod maturity	58.79	56.66	55.28	55.83	57.90	56.45
Plant height (cm)	79.96	60.85	47.50	48.02	53.27	53.56
Petiole length (cm)	12.05	10.36	9.38	9.60	9.52	9.82
Terminal leaf length (cm)	7.86	8.09	7.42	7.82	7.95	7.76
Terminal leaf width (cm)	5.34	5.34	4.49	4.87	4.81	4.85
Greenness (SPAD)	59.00	59.20	58.28	61.95	58.30	59
Number of branches per plant	6.56	6.07	5.41	5.36	5.23	5.6
Number of clusters per plant	17.60	21.06	18.56	21.25	17.44	19.2
Number of pods per cluster	2.71	2.87	3.09	3.17	2.74	2.96
Pod length (cm)	3.97	4.34	4.16	4.61	4.38	4.31
Number of seeds per pod	5.99	6.02	5.95	6.38	6.31	6.12
Single pod weight (g)	0.27	0.34	0.32	0.36	0.34	0.33
Biological yield per plant (g)	13.59	19.90	17.69	23.31	15.24	18.32
Seed yield per plant (g)	7.33	11.08	10.19	13.79	8.77	10.51
% of first harvest over total harvest	49.93	37.37	45.07	48.07	66.60	49.19
Thousand seed weight (g)	32.64	41.46	40.10	42.35	41.18	40.51

Genotype × Trait Interaction Analysis Using PCA

Principal Component Analysis (PCA) was employed to assess the contribution of agro-morphogenic traits to genetic divergence among the genotypes and the interrelationships. The first two principal components (PC1 and PC2) together explained 42.08% of the total variation. PC1 accounted for 24.12% and PC2 for 17.95% with eigenvalue of 4.342 and 3.232, respectively (Table 5). PC1 was primarily associated with yield-related traits including SYPP, BYPP, NCP, and SPW showing high positive loadings. Conversely, DFrF, DFF, and PH contributed negatively to PC1 indicating a strategic choice between earliness and yield potential. PC2 was greatly influenced by FH/TH and vegetative traits such as PL, TLL, and NBP.

Table 5. Eigen values, percent variation and cumulative percentage of variation explained by the six PCs and PCA trait contributions for 18 agro-morphogenic traits of 105 blackgram genotypes

Principal components	PC1	PC2	PC3	PC4	PC5	PC6
Eigen values	4.342	3.232	1.715	1.451	1.046	1.010
Percent variation	24.121	17.954	9.531	8.062	5.809	5.611
Cumulative % of Percent variation	24.121	42.075	51.605	59.667	65.476	71.087
Traits	PCA Trait contributions					
Days to first flowering	12.46	5.23	0.69	8.85	1.4	0.000003
Days to 50% flowering	13.93	4.06	0.06	6.59	2.21	0.01
Days to first pod maturity	3.37	1.11	13.23	13.24	0.0005	5.1
Plant height (cm)	11.83	3.38	0.91	0.06	4.17	0.37
Petiole length (cm)	5.88	10.8	0.21	3.87	3.5	1.12
Terminal leaf length (cm)	0.14	5.35	9	27.07	1.48	0.6
Terminal leaf width (cm)	1.87	7.04	1.28	20.62	0.18	0.22
Greenness (SPAD)	0.7	1.31	0.18	1.3	53.22	13.37
Number of branches per plant	3.25	8.36	3.39	0.46	3.3	8.48
Number of clusters per plant	3.04	14.7	1.45	0.16	1.74	9.62
Number of pods per cluster	4.05	3.59	5.33	2.87	3.94	0.45
Pod length (cm)	1.53	2.5	5.08	0.31	4.58	30.49
Number of seeds per pod	0.81	0.1	19.26	9.55	0.68	8.07
Single pod weight (g)	7.3	0.23	12.76	0.01	3.64	7.41
Biological yield per plant (g)	10.34	14.42	0.002	1.18	1.07	0.48
Seed yield per plant (g)	12	11.14	0.01	2.96	0.28	0.22
% of first harvest over total harvest	0.29	6.12	21.16	0.01	3.73	7.17
Thousand seed weight (g)	7.21	0.55	6.01	0.9	10.9	6.81

The PCA biplot grouped the genotypes into five clusters aligning with the hierarchical clustering pattern (Fig. 5). Cluster I was on the negative side of PC1 which represented late-flowering, tall genotypes with lower yield potential. Cluster III and IV were on the positive side of PC1 associated with high-yielding genotypes. Cluster IV exhibited strongest interrelationships with yield-related traits such as NCP, NPPC, PL, NSPP, SPW, BYPP, and SYPP. Cluster V aligned with the positive side of PC2 and was distinguished by early maturity. Traits with vectors oriented in similar directions, such as SYPP, BYPP, and NCP were positively correlated, highlighting their combined influence on yield performance. Conversely, flowering traits (DFF and DFrF) pointed in the opposite direction, confirming their negative relationship with yield traits. These results collectively highlighted that yield-related traits were the main contributor of genetic variation, whereas flowering and vegetative characters showed opposing dimension of diversity in the evaluated blackgram germplasm.

Discussion

The analysis of variance revealed significant genetic variability among blackgram genotypes across multiple environments establishing a robust foundation for crop improvement (Gomathi et al. 2021; Reddy et al. 2023). This variation indicates wide genetic base that can be exploited to improve specific traits (Jawad et al. 2024; Sagar et al. 2021). High coefficients of variation for BYPP, SYPP, and NBP suggest better responsiveness to selection. These findings were supported by earlier researchers (Appa et al. 2020; Gomathi et al. 2021; Kuralarasan & Jayamani 2021; Sathees et al. 2019). The broad phenotypic range for traits like DFrF, DFF, PH, and SYPP also highlighted the presence of considerable genetic diversity in the germplasm. This diversity can be exploited to develop suitable varieties for diverse environments (Verma et al. 2024). Early flowering genotypes may fit as short-duration varieties into the cropping system while late-maturing ones may serve to maximize the yield potential under favorable environments. The significant genotype by environment interactions for several traits emphasize the need for multi-environment testing in selection programs (Appa et al. 2020). Genotypes that demonstrate stability and adaptability across environments represent promising parents for hybridization or candidates for release after further evaluation. Several researchers such as Gomathi et al. (2021) and Reddy et al. (2023) also reported similar findings and emphasized the importance of exploiting genetic diversity in blackgram for yield enhancement.

The high heritability estimates and selection accuracy for specific yield components like TSW, FH/TH, NSPP, SPW, and GN indicate strong genetic control making them highly amenable to selection. These traits can be improved through direct selection. Strong genetic control of these characters and their importance in yield enhancement were also reported by others (Appa et al. 2020; Kuralarasan & Jayamani 2021; Sagar et al. 2021). Among these, TSW emerged as a particularly dependable and stable selection criterion for improving blackgram productivity (Gomathi et al. 2021; Rajalakshmi et al. 2024a). Although SYPP is the prime target for the breeders, it exhibited moderate heritability suggesting significant environmental influence. However, strong associations of SYPP with highly heritable traits like BYPP, TSW, and SPW indicated value for indirect selection (Sagar et al. 2021). Indirect selection supports

genetic gain for a complex trait like yield by targeting its highly heritable, genetically correlated components (Gomathi et al. 2021; Kuralarasan & Jayamani 2021). The substantial GA and GAM values for TSW and FH/TH further indicate the presence of additive genetic variability and a strong potential for response to selection for these traits in blackgram (Appa et al. 2020; Kamble et al. 2024). Traits such as TLL, TLW, and NPPC with low heritability and weak genetic control has limited their value as direct selection criteria. Selection based on these traits would likely result in inconsistent genetic gains across different environments (Reddy et al. 2023).

Significant genotype by environment interactions (GEI) for PH and NCP highlights their varied performance under varying environmental conditions (Rajalakshmi et al. 2024). Their moderate GA values, low-moderate GAM, coupled with significant GEI also indicate that these traits are highly environment dependent (Vadivel et al. 2020; Kuralarasan & Jayamani 2021). Multi environment trials are essential to evaluate genotype stability and adaptability for those traits (Dhasarathan et al. 2021). Knowledge of GEI is crucial for identification of both broadly adapted genotypes suitable across regions and those that excel in specific areas (Nair et al. 2024). The use of heritability estimates on a mean basis helps breeders to predict selection response and potential genetic gain more accurately under variable environmental conditions (Reddy et al. 2023). Therefore, breeding should focus on traits with high heritability and selection accuracy. Our findings showed that TSW, SPW, and BYPP are reliable markers of yield potential. Traits that are sensitive to environmental variation should be carefully validated across different environments before final decision (Gomathi et al. 2021; Kuralarasan & Jayamani 2021).

Correlation and path analysis provided key insights into trait association and identification of the traits that contributed most to total divergence. These insights are essential for precise breeding strategies (Sagar et al. 2021). SYPP displayed strong positive correlation with BYPP, NCP, and TSW. This confirms these traits as the key yield determinants aligning with earlier findings in blackgram (Sood et al. 2023; Gomathi et al. 2021; Islam 2021). Path analysis further revealed that BYPP had an exceptionally high positive direct effect (1.0446) on SYPP. This indicates that increased biological yield is a direct driver of seed yield (Sood et al. 2023). However, when a path coefficient is greater than 1.0, it may indicate multicollinearity. So, the results should be interpreted carefully as negative indirect effects can confuse the true contribution of the trait (Deegan 1978; Sgarbossa et al. 2024). NCP positively correlated with SYPP but had a negative direct effect. This was explained by its strong positive indirect effect through BYPP (Islam 2021). TSW also contributed to SYPP primarily through BYPP, suggesting that heavier seeds are associated with overall plant productivity (Sood et al. 2023). Phenological traits like DFrF and DFF were highly correlated with each other but moderately associated with plant height. However, their minimal direct effect on SYPP indicates their relevance to adaptation and determining cropping duration than for direct selection for yield improvement (Sagar et al. 2021). The weak or non-significant correlations of NSPP, GN, and NBP with SYPP confirms their limited utility as selection criteria for yield improvement in the studied germplasm. Overall, BYPP, NCP, and TSW emerged as the most effective indirect selection criteria for yield improvement in blackgram. Prioritizing these traits may lead to more consistent genetic gains, particularly across varied environments where direct selection for yield is often compromised by significant GEI (Kuralarasan & Jayamani, 2021; Singh et al. 2023). This study reaffirms that integrating correlation and path analyses enables breeders to distinguish traits with a genuine causal effect on yield from those that operate indirectly.

Substantial genetic diversity was portrayed by the five distinct clusters by hierarchical clustering of the genotypes. This clustering offers a structured framework for identification of promising parental lines (Gayacharan et al. 2021; Das et al. 2024). The clusters exhibited varying levels of internal diversity. The smallest intra-cluster distance of cluster III indicates genetically uniform group suitable for developing stable varieties through direct or recurrent selection. The higher intra-cluster variability within cluster IV offers a broader genetic base for identification of novel recombinants (Narendrabhai & Bala 2020). The maximum inter-cluster distance between cluster I and cluster IV suggests that hybridization between genotypes from these groups is expected to produce maximum heterosis and generate wide variability in segregating generations. Such crosses are crucial for developing high yielding, diverse progenies (Sidramappa et al. 2021). On the contrary, hybrids between genetically closer clusters, such as cluster II and cluster IV, may offer less heterotic potential but could be valuable for introgression of specific traits (Partap et al. 2020). The distinct cluster means provide a practical basis for targeted breeding. Cluster III and cluster IV exhibited the lowest means for phenological traits. Early flowering genotypes are ideal for developing short-duration varieties and/or suitable for drought-prone environments (Gayacharan et al. 2021). Cluster IV showed the highest means for SYPP, BYPP, and most of the yield attributes positioning it as a valuable reservoir of direct yield enhancement (Narendrabhai & Bala, 2020). Premeditated selection of parents from genetically divergent but phenotypically complementary clusters can thus maximize the expression of heterosis. This will hasten the development of resilient, high-yielding blackgram varieties (Partap et al. 2020; Sood et al. 2023).

Principal component analysis offered a useful way to visualize and summarize the relationships among the traits and genotypes studied. The PCA-biplot reaffirms the presence of substantial genetic variability. This genetic variability is essential for effective crop improvement (Rajalakshmi et al. 2024). A notable outcome was the strong positive correlations between BYPP, SYPP, and NCP. Simultaneous improvement of these traits could significantly increase overall productivity (Ajaykumar et al. 2022). High yielding genotypes from clusters IV can be used as promising candidates for direct use or as donors in hybridization programs. The early-maturing genotypes grouped in cluster V represent valuable sources for developing short-duration varieties. The analysis also pointed to an expected trade-off with earliness often being inversely related to yield components. Shorter growing period helps escaping terminal stress, but it can also limit biomass accumulation and eventually restrict yield (Sagar et al. 2021). Therefore, breeding strategies should aim to balance earliness with yield potential (Reddy et al. 2021). Crossing early maturing genotypes from cluster V with high-yielding genotypes from cluster IV are expected to maximize heterosis. Such crosses may also generate transgressive segregants with favorable trait combinations (Narendrabhai & Bala, 2020; Sidramappa et al. 2021). Multivariate tools like cluster analysis and PCA allowed a broader view of the trait associations and helped identify promising groups of parents for hybridization (Gomathi et al. 2021). The observed genetic divergence offers a clear path for targeted hybridization. By crossing parents from complementary clusters, breeders can exploit genetic variation to develop productive and adaptable genotypes for diverse agro-ecological regions (Nair et al. 2024).

Conclusion

The present study evaluated 105 blackgram genotypes grown in four *Kharif* environments and revealed a wide range of genetic variation among them. Eighteen agro-morphogenic traits showed significant variation confirming a broad genetic base for future breeding work. Several traits including TSW, SPW,

NSPP, BYPP, FH/TH, and GN exhibited high heritability and selection accuracy suggesting that they can be effectively improved through direct selection. The substantial GA and GAM values for TSW and FH/TH also pointed toward the presence of additive gene action. SYPP displayed only moderate heritability and GAM. However, its strong positive associations with BYPP, TSW, and SPW make indirect selection a practical strategy for yield improvement. Path analysis also identified BYPP as the major direct contributor to SYPP with several traits acting through it. Cluster analysis grouped the genotypes into five distinct clusters. Cluster IV represented high yielding genotypes and cluster V accounted for early maturity and bold seed characteristics. PCA supported these observations emphasizing yield-related traits as the main contributors to total genetic variation. Based on these outcomes, crossing early maturing and bold-seeded genotypes from cluster V with high-yielding genotypes from cluster IV are recommended. Such combinations could help integrate earliness with productivity and ultimately facilitate the development of well-adapted, high yielding blackgram varieties.

Declarations

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Competing Interests

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Author Contributions

Kamrun Nahar¹ conducted the experiments, performed data analysis and prepared the draft manuscript. Naheed Zeba and Kamrun Nahar² contributed to experimental design and provided critical feedback and revisions. Syed Nazmul Alam and Md. Habib Hasan Himel helped in data collection, contributed to result interpretation and reference management. All authors reviewed and approved the final version of the manuscript.

Data Availability

The datasets generated during and/or analyzed during the current study are available from the corresponding author on reasonable request.

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References

1. Ajaykumar R, Harishankar K, Chandrasekaran P, Navinkumar C, Sekar S, Sabarinathan C, Reddy BKK (2022) Principle component analysis (PCA) and character interrelationship of irrigated blackgram [*Vigna mungo* (L.) Hepper] influenced by liquid organic biostimulants in western zone of Tamil Nadu. *Legume Res Int J* 46(3):690-694. <https://doi.org/10.18805/lr-5038>
2. Appa S, Kuchanur PH, Shobharani M, Arunkumar B, Kulkarni S, Sowmya HC, Sheela D, Man L, Bharati S (2020) Genetic variability, heritability and genetic advance studies in blackgram [*Vigna mungo* (L.) Hepper] across seasons. *Int J Curr Microbiol Appl Sci* 9(10):879. <https://doi.org/10.20546/ijcmas.2020.910.105>
3. Deegan J (1978) On the Occurrence of Standardized Regression Coefficients Greater Than One. *Educational and Psychological Measurement* 38(4):873. <https://doi.org/10.1177/001316447803800404>
4. Dey A, De PS, Gangopadhyay PK (2017) Black gram (*Vigna mungo* L.) foliage supplementation to crossbred cows: effects on feed intake, nutrient digestibility and milk production. *Asian-Australas J Anim Sci* 30(2):187-191. <https://doi.org/10.5713/ajas.16.0286>
5. Dhasarathan M, Geetha S, Karthikeyan A, Sassikumar D, Meenakshiganesan N (2021) Development of novel blackgram (*Vigna mungo* (L.) Hepper) mutants and deciphering genotype × environment interaction for yield-related traits of mutants. *Agronomy* 11(7):1287. <https://doi.org/10.3390/agronomy11071287>
6. Dipti RJ, Khaleque MA (2019) Study of variability and genetic diversity of 50% heading date and seed yield in blackgram (*Vigna mungo* L.). *South Asian J Agric* 7(1-2):1-5. <https://doi.org/10.3329/saja.v7i1-2.56742>
7. Gayacharan C, Tripathi K, Aski MS, Singh N, Kumar A, Lal H (2022) Understanding genetic diversity in blackgram collections of Indian National Genebank. *Genet Resour Crop Evol* 69:1229-1245. <https://doi.org/10.1007/s10722-021-01301-6>
8. Gomathi D, Shoba D, Ramamoorthy V, Pillai MA (2021) Studies on variability, heritability, correlation and path analysis in segregating population of blackgram [*Vigna mungo* (L.) Hepper]. *Legume Res Int J* 46(6): 690-694. <https://doi.org/10.18805/lr-4411>
9. Islam MDH (2021) Character association and genetic diversity analysis in blackgram (*Vigna mungo* L.). Dissertation, Sher-e-Bangla Agricultural University, Dhaka-1207.

10. Jangir CK, Singh D, Meena R, Yadav MK (2017) Effect of fertility levels and biofertilizers on physical and chemical properties of soil under blackgram (*Vigna mungo* L.). *Int J Curr Microbiol Appl Sci* 6(3):223. <https://doi.org/10.20546/ijcmas.2017.603.023>
11. Jawad M, Malik SR, Samad RA, Asif T, Arshad M (2024) Genetic variability and multivariate analysis for plant architecture and yield components in blackgram (*Vigna mungo* L. Hepper) under rainfed conditions. *Int J Biosci* 24(1):39-46. <https://doi.org/10.12692/ijb/24.1.39-46>
12. Kamble, A. P., Chaudhari, Snehal. R., Kute, N. S., & Shinde, G. C. (2024). Generation mean analysis for grain yield and yield contributing traits in blackgram [*Vigna mungo* (L.) Hepper]. *Int J Adv Biochem Res* 8: 1294. <https://doi.org/10.33545/26174693.2024.v8.i12sp.3340>
13. Kanth A, Goswami K, Shukla P (2021) Product formulation from black gram and its evaluation for nutritional and sensory quality. *Int J Chem Stud* 9(1):308. <https://doi.org/10.22271/chemi.2021.v9.i1f.11748>
14. Kuralarasan V, Jayamani P (2021) Genetic analysis for seed yield and yield component traits in recombinant inbred lines (RIL) population of blackgram [*Vigna mungo* (L.) Hepper]. *J Pharmacogn Phytochem* 10(1):811. <https://doi.org/10.22271/phyto.2021.v10.i1f.13426>
15. Marimuthu S, Navamaniraj KN, Kathiravan M, Balasubramanian P, Surendran U, Mattar MA, Mattar MA (2024) Response of blackgram (*Vigna mungo* L.) cultivars for nipping and graded levels of nitrogen for higher productivity under irrigated conditions. *Agronomy* 14(7):1474. <https://doi.org/10.3390/agronomy14071474>
16. Mohanlal V, Kandasamy S, Sabesan T (2018) Multivariate analysis in blackgram (*Vigna mungo* (L.) hepper) genotypes. *Journal of Pharmacognosy and Phytochemistry* 7(6):860. <https://www.phytojournal.com/archives/2018/vol7issue6/PartO/7-6-27-620.pdf>
17. Nair RM, Chaudhari S, Devi N, Shivanna A, Gowda A, Boddepalli VN, Pradhan H, Schafleitner R, Souframanien J, Somta P (2024) Genetics, genomics, and breeding of black gram [*Vigna mungo* (L.) Hepper]. *Front Plant Sci* 14. <https://doi.org/10.3389/fpls.2023.1273363>
18. Narendrabhai PR, Bala M (2020) Genetic divergence studies in black gram [*Vigna mungo* (L.) Hepper]. *Int J Chem Stud* 8(4):2777. <https://doi.org/10.22271/chemi.2020.v8.i4ag.10063>
19. Partap B, Kumar M, Singh SK, Chand P, Singh PK (2020) Studies on genetic diversity analysis in black gram (*Vigna mungo* L. Hepper) genotypes under western U.P. conditions. *J Rural Agric Res* 20(1):56-60
20. Priya LS, Pillai MA, Shoba D (2019) Genetic divergence, variability and correlation studies in black gram [*Vigna mungo* (L.) Hepper]. *Legume Res Int J* 44(1):36-40. <https://doi.org/10.18805/lr-4065>
21. R Core Team (2023) R: A language and environment for statistical computing (Version 4.3.1). R Foundation for Statistical Computing, Vienna. <https://www.R-project.org/>
22. Raizada A, Souframanien J (2019) Transcriptome sequencing, de novo assembly, characterisation of wild accession of blackgram (*Vigna mungo* var. *silvestris*) as a rich resource for development of molecular markers and validation of SNPs by high resolution melting (HRM) analysis. *BMC Plant Biol* 19(1). <https://doi.org/10.1186/s12870-019-1954-0>
23. Rajalakshmi K, Manivannan N, Anand G, Vanniarajan C, Harish S (2024) AMMI and GGE biplot analysis of seed yield and batter quality traits in blackgram [*Vigna mungo* (L.) Hepper]. *Legume Res Int J* 47(5):810-816. <https://doi.org/10.18805/lr-4574>
24. Rajalakshmi K, Murugan E, Anand G, Renuka R, Ramamoorthy V (2024) Exploring the genetic variability of blackgram [*Vigna mungo* (L.) Hepper] genotypes over environments. *Agric Sci Dig* 44(6):1098-1101. <https://doi.org/10.18805/ag.d-5925>
25. Reddy AK, Reddy DM, Vemireddy LR, Sudhakar P, Reddy BVB (2021) Studies on heterotic trends in blackgram [*Vigna mungo* (L.) Hepper] for yield and earliness. *Legume Res Int J* 47(10):1680-1685. <https://doi.org/10.18805/lr-4764>
26. Reddy S, T S, Rao N, Madhavi B, Rao S (2023) Estimates of PCV, GCV and heritability studies for yield components and nutritional traits in blackgram [*Vigna mungo* (L.) Hepper]. *Biol Forum Int J* 15(10):1197-1201.
27. Sagar KP, Bg S, Lal G (2021) Correlation and path analysis for yield and yield contributing traits in black gram [*Vigna mungo* (L.) Hepper]. *J Pharmacogn Phytochem* 10(5):299. <https://doi.org/10.22271/phyto.2021.v10.i5d.14238>
28. Sathees N, Shoba D, Saravanan S, Kumari SMP, Pillai MA (2019) Studies on genetic variability, association and path coefficient analysis in black gram (*Vigna mungo* L. Hepper). *Int J Curr Microbiol Appl Sci* 8(6):1892. <https://doi.org/10.20546/ijcmas.2019.806.227>
29. Sgarbossa J, Lúcio AD, Silva JAG da, Caron BO, Diel MI, Olivoto T, Nardini C, Alessi O, Lambrecht DM (2024) Multivariate assumptions and effect of model parameters in path analysis in oat crop. *Crop and Pasture Science* 75(3). <https://doi.org/10.1071/cp23135>
30. Sidramappa S, Kuchanur PH, Shobharani M, Arunkumar B, Kulkarni SA, Sowmya HC (2021) Nature and magnitude of genetic divergence among blackgram [*Vigna mungo* (L.) Hepper] genotypes. *Agric Sci Dig* 42(1):63-67. <https://doi.org/10.18805/ag.d-5261>
31. Singh V, Singh M, Singh AK, Madankar K, Sinha B (2023) Identification of high yielding and yellow mosaic virus resistance blackgram (*Vigna mungo* L. Wilczek) genotypes using multivariate analysis. *Vegetos* 37:363-372. <https://doi.org/10.1007/s42535-023-00615-3>
32. Sood R, Mittal RK, Sood VK, Sharma S (2023) Correlation and path analysis studies for various yield and component traits in the segregating generations of blackgram [*Vigna mungo* (L.) Hepper]. *Legume Res* 46(9):1141-1147. <https://doi.org/10.18805/LR-4732>
33. Swaminathan C, Surya R, Subramanian E, Arunachalam P (2021) Challenges in pulses productivity and agronomic opportunities for enhancing growth and yield in blackgram [*Vigna mungo* (L.) Hepper]: a review. *Legume Res Int J* 46(1):1-9. <https://doi.org/10.18805/lr-4357>
34. Vadivel K, Manivannan N, Mahalingam A, Satya VK, Vanniarajan C (2020) Combining ability analysis for seed yield and component traits over season in blackgram [*Vigna mungo* (L.) Hepper]. *Legume Res Int J* 45(5):545-550. <https://doi.org/10.18805/lr-4225>
35. Verma J, Gore PG, Kumari J, Wankhede DP, Jacob SR, Kumar TVA, Nair RM, Tripathi K (2024) Exploring genetic diversity in black gram (*Vigna mungo* (L.) Hepper) for pre-harvest sprouting tolerance. *Agronomy* 14(1):197. <https://doi.org/10.3390/agronomy14010197>

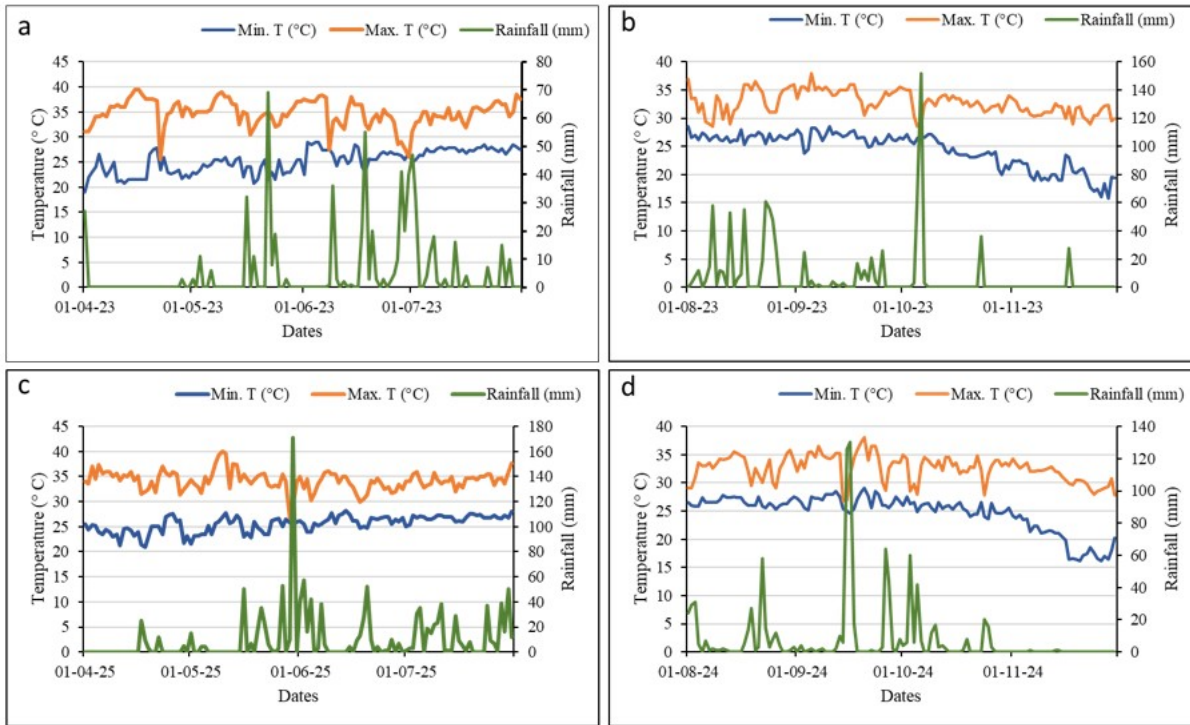


Figure 1

Climatographic prepared from weather report showing maximum and minimum temperature and rainfall across the four *Kharif* environments. Here a = Gazipur *Kharif*1 (E-1), b = Gazipur *Kharif*2 (E-2), c = Dhaka *Kharif*1 (E-3), d = Dhaka *Kharif*2 (E-4)

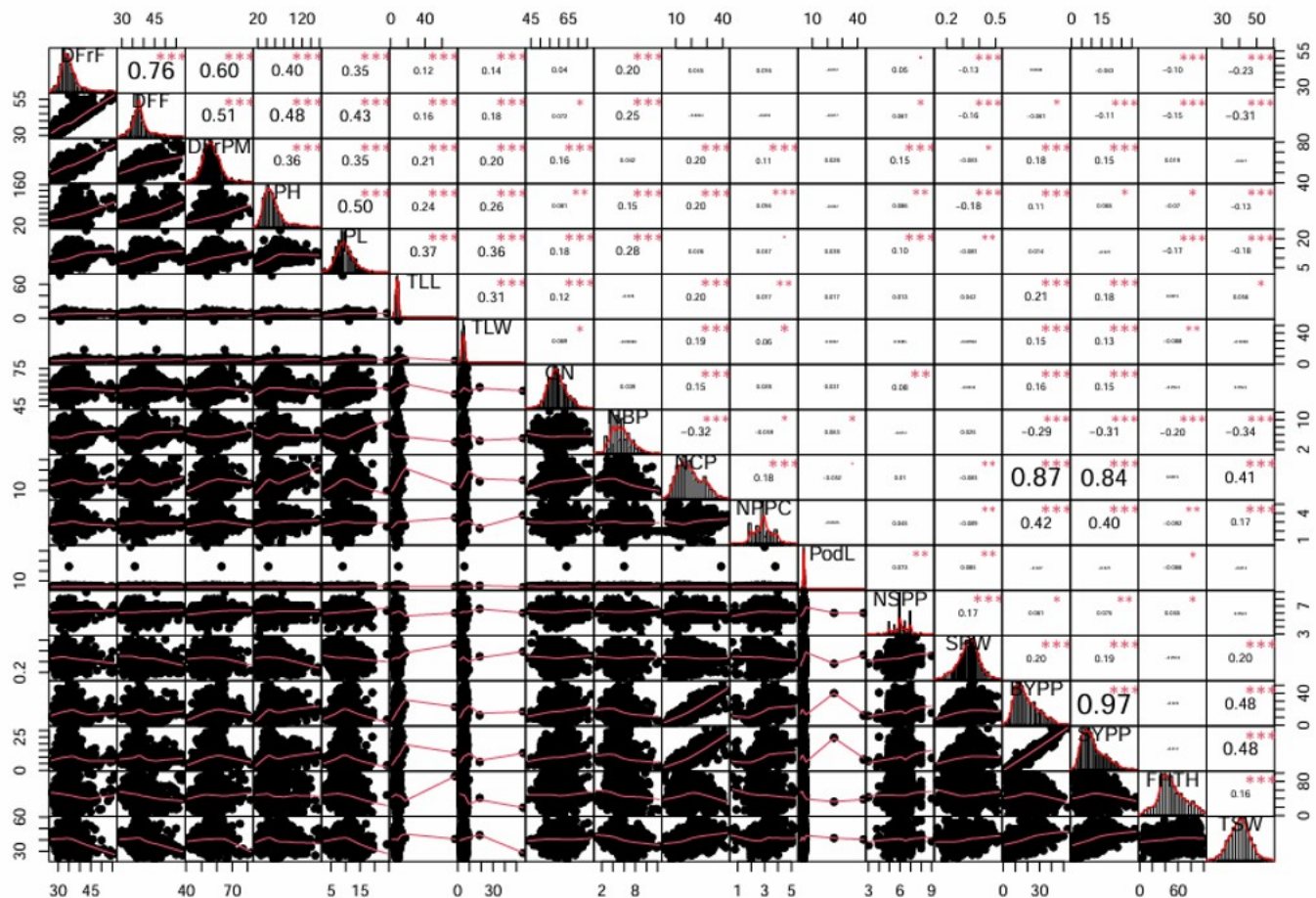


Figure 2

Plot showing pearson's correlation coefficients among different pairs of yield and yield contributing characters for different genotypes of blackgram as per mean performance across four environments. Note. DFrF = days to first flowering, DFF = days to 50% flowering, DFrPM = days to first pod maturity, PH = plant height (cm), PL = petiole length (cm), TLL = terminal leaf length (cm), TLW = terminal leaf width (cm), GN = greenness (SPAD), NBP = number of branch per plant, NCP = number of cluster per plant, NPPC = number of pods per cluster, PodL= pod length (cm), NSPP = number of seeds per pod, SPW = single pod weight (g), BYPP = biological yield per plant (g), SYPP = seed yield per plant (g), FH/TH = % of first harvest over total harvest, TSW = thousand seed weight (g)

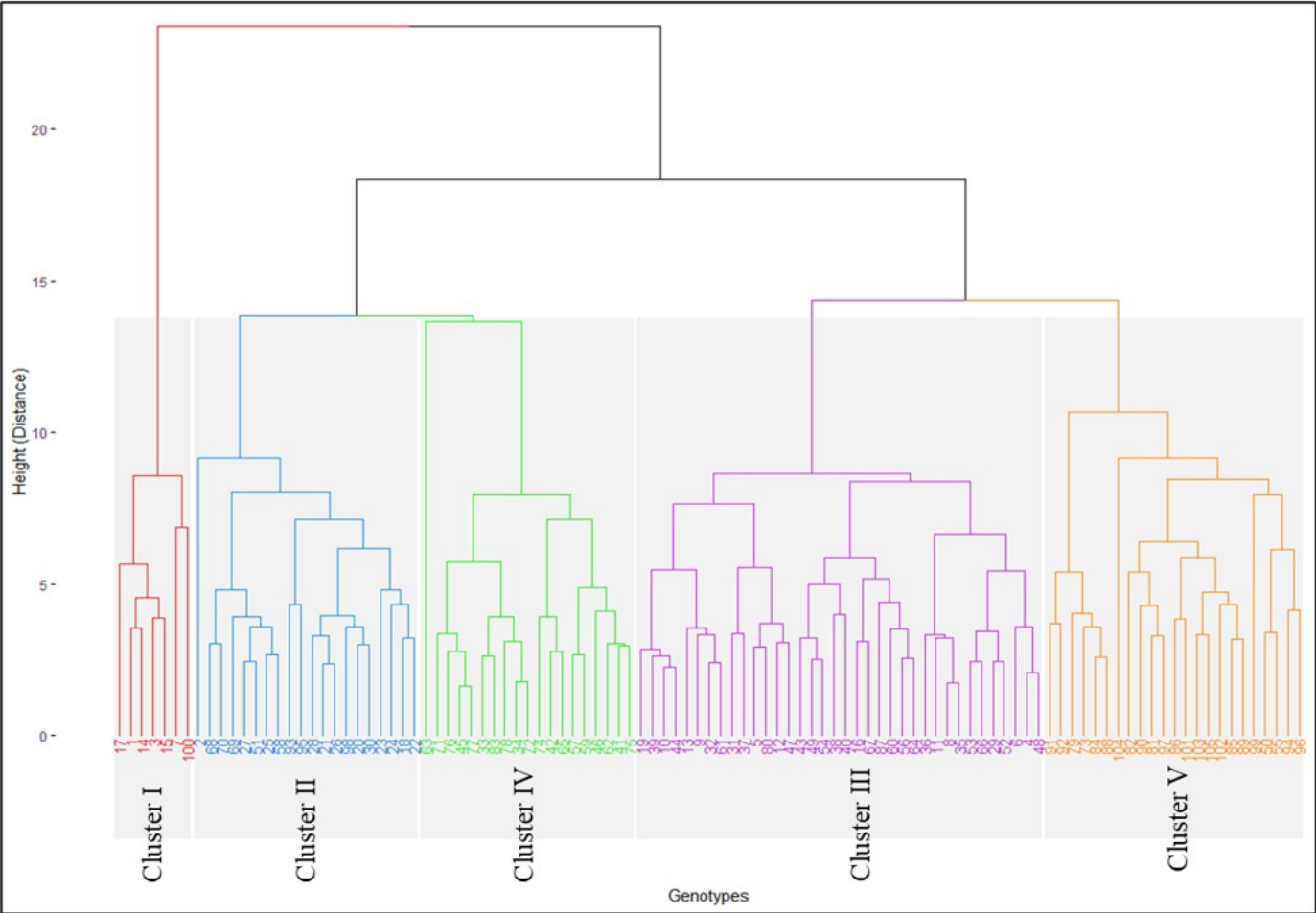


Figure 3

Dendrogram showing distribution of genotypes into different clusters based on mean performance of 105 blackgram genotypes across four *Kharif* environments

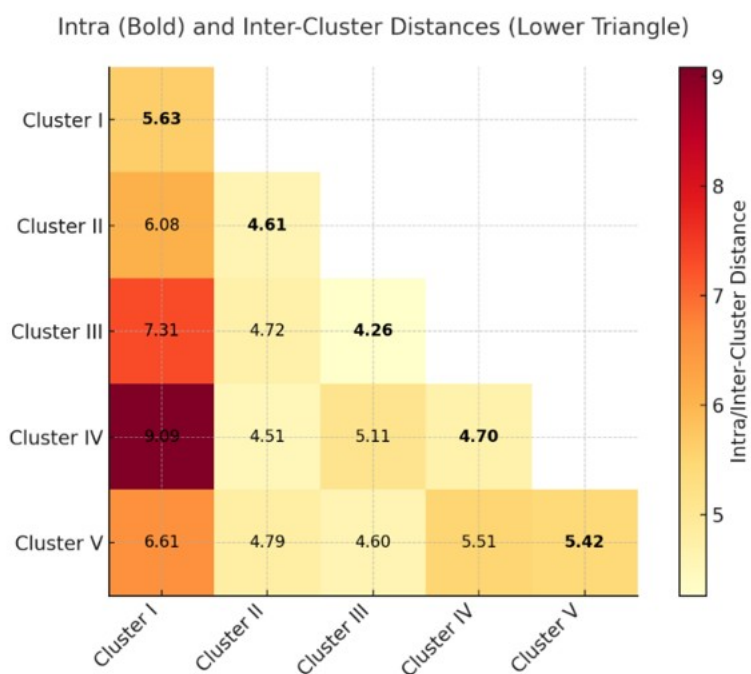


Figure 4

Intra (Bold) and inter cluster distances of five clusters based on mean performance of 105 blackgram genotypes across four *Kharif* environments

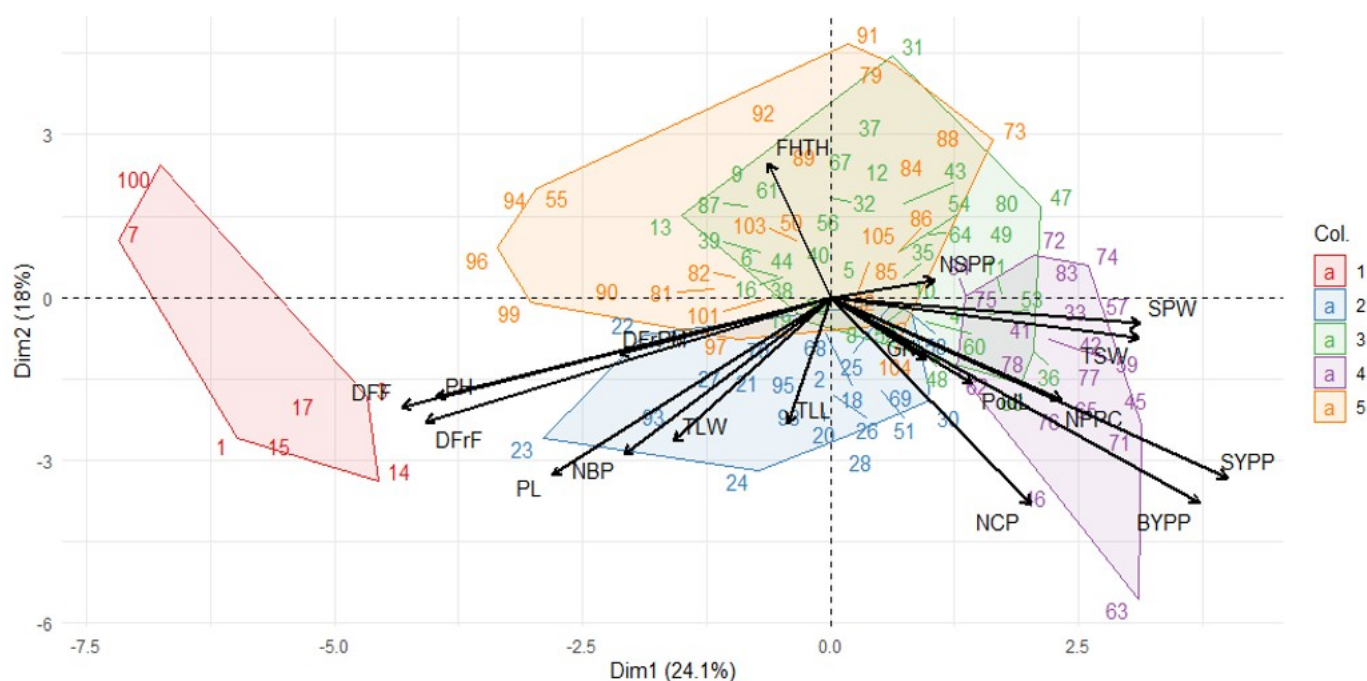


Figure 5

PCA-Biplot showing genotype $\times$ trait interaction for the 105 blackgram genotypes and 18 agro-morphogenic characters. Here, DFrF = days to first flowering, DFF = days to 50% flowering, DFrPM = days to first pod maturity, PH = plant height (cm), PL = petiole length (cm), TLL = terminal leaf length (cm), TLW = terminal leaf width (cm), GN = greenness (SPAD), NBP = number of branch per plant, NCP = number of cluster per plant, NPPC = number of pods per cluster, PodL = pod length (cm), NSPP = number of seeds per pod, SPW = single pod weight (g), BYPP = biological yield per plant (g), SYPP = seed yield per plant (g), FH/TH = % of first harvest over total harvest, TSW = thousand seed weight (g)

Supplementary Files

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- [Supplementarymaterial.pdf](#)