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Genetic analysis of yield and yield components and powdery mildew resistance in F_4 and F_5 populations of blackgram

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Abstract

The present investigation aimed to evaluate 96 F_4 and F_5 genotypes, including two parental lines (*VBN11 and LBG17*) of blackgram, across two locations for yield, yield components and resistance to powdery mildew. Pooled analysis, genetic variability assessment, correlation studies, parent-regression coefficient analysis and the Multi-trait Genotype Ideotype Distance Index (MGIDI) were performed. Combined ANOVA (analysis of variance) revealed significant differences for all the traits studied. In the combined analysis, genotypes G3 and G1 exhibited desirable yields along with powdery mildew resistance. High heritability and genetic advance as a percentage of the mean (GAM) were observed for the traits such as single plant yield, the number of pods per plant and percent disease index (PDI). Seed yield per plant recorded significant and positive correlations with the number of clusters per plant, number of pods per plant, number of seeds per pod and 100-seed weight in both generations. Among the traits, PDI showed the highest regression coefficient. Principal component analysis exhibited four principal components (PCs) explaining the total variance in the F_4 and F_5 generations. The MGIDI index analysis revealed a total genetic gain for specific traits, including the number of pods per plant, single plant yield and the number of capsules per plant in the F_5 generation. Genotypes G18, G19, G4 and G38 were identified as valuable genetic resource through MGIDI, contributing significantly to blackgram improvement for high yield and powdery mildew resistance.

Keywords

blackgram; Multi-trait Genotype Ideotype Distance Index (MGIDI); parent- progeny regression; powdery mildew resistance

Introduction

Blackgram (*Vigna mungo* L. Hepper), also known as urdbean, is a vital short-duration legume crop primarily cultivated in tropical and subtropical regions (1). It contains approximately 24% protein and is a rich source of phosphoric acid, carbohydrates (67%), fibre (3.5%), fat (1.74%) and essential nutrients like calcium, potassium, niacin and vitamin B-rich protein (2). Blackgram contributes 10% of India's total pulse production, accounting for 3.06 million tonnes annually (3). It occupies 13% of the total area under pulse cultivation, covering 5.60 million ha (3), with a productivity of 546 kg/ha (4). Additionally, it is valued for its ability to fix atmospheric nitrogen, thereby enhancing soil fertility and serving as an effective green manure crop (5).

Despite its agronomic and nutritional significance, blackgram cultivation faces several constraints viz., biotic and abiotic stresses that significantly affect its productivity. Among biotic stresses, powdery mildew, caused by the fungus *Erysiphe* *polygoni*, is one of the most destructive diseases, causing yield losses ranging from 20% to 60%, (6) depending on disease severity and environmental conditions. Changing climatic patterns have further exacerbated the susceptibility of blackgram varieties to major biotic and abiotic stresses. Consequently, the development of climate-resilient blackgram varieties has become a prerequisite for enhancing productivity. Advanced populations need to be evaluated for yield, yield-related attributes and powdery mildew resistance under diverse environmental conditions to identify stable genotypes (7).

Genetic variation among plant traits is important for breeding programs, as it facilitates the selection of desirable genotypes. Crop improvement depends on the magnitude of genetic variability for economically important traits. Correlations between seed yield and its contributing components are essential for establishing selection criteria. Such analysis provides information into the interrelationships between traits, thereby enabling the formulation of directional models for yield improvement. Blackgram breeding populations exhibit wide genetic variability, which allows the expression of various traits (8) . In blackgram, the traits namely plant height, number of branches per plant, total number of pods per plant, single plant yield and per cent disease index have shown high genetic variability in breeding programme (7, 8). Parent-offspring's regression analysis further elucidates the heritability and trait associations to yield and disease resistance in blackgram populations.

Crop improvement programs must consider multiple traits rather than focusing on a single attribute, necessitating modifications in selection methodologies. Greater emphasis should be placed on selecting genotypes based on a comprehensive analysis of multiple traits. A novel method, the MGIDI, has been introduced to identify superior genotypes for multiple traits, enhancing blackgram breeding efforts.

Against this backdrop, 96 F_4 and F_5 genotypes derived from the cross *VBN 11* × *LBG 17* were evaluated across two locations to assess their mean performance, variability, correlation, parent-offspring regression and MGIDI for yield components and powdery mildew resistance. This study aims to identify promising genotypes that exhibit a desirable combination of high yield and resistance to powdery mildew, thereby contributing to the blackgram improvement program.

Materials and Methods

The experimental material consisted of 96 genotypes, including two parental lines. The F_1 generation was derived by crossing the parental lines *VBN 11* and *LBG 17*. *VBN 11* is a short-duration genotype resistance to mungbean yellow mosaic virus and urdbean leaf crinkle virus but susceptible to powdery mildew disease. In contrast, *LBG 17* is a long-duration genotype well-suited for the post-rainy season and exhibits resistance to powdery mildew disease. F_1 plants were selfed to produce the F_2 generation and all F_2 progeny were advanced to the F_3-F_4 generations using the single seed descent method.

The 96 F_4 genotypes, along with the two parental lines, were grown at the Glass House Farm, Tamil Nadu Agricultural University, Coimbatore (11° 10'N latitude and 76° 55' E longitude) during October-December 2023, a season conducive to powdery mildew incidence. Subsequently, the 96 F_5 genotypes were raised at the Hybrid Rice Evaluation Centre, Gudalur (11° 30'N latitude and 76° 30' E longitude), The Nilgiris, Tamil Nadu, during Feb-March 2024 for yield evaluation and powdery mildew screening. The experiment was conducted using an alpha lattice design with two replications. Recommended agronomic practices were followed throughout the cropping period.

Observations were recorded for ten biometrical traits, randomly selected from each plant; days to 50% flowering (DFF), plant height (PH), number of branches per plant (NOB), number of clusters per plant (NOC), number of pods per cluster (NOP), number of seeds per pod (NOS), number of pods per plant (NOPP), pod length (PODL), 100-seed weight (HSW) and single plant yield (SPY), in addition to PDI across both locations. Powdery mildew disease symptoms were observed at the flowering stage. To enhance disease severity, a 1% sucrose solution containing an aqueous conidial suspension (about 1 x 10^7 spores mL^{-1}) was sprayed on plants every alternate evening to intensify disease development. In addition, the field was covered with a white net of 1 mm pore size to create favorable conditions for the disease. No fungicides were used during the cropping season. Powdery mildew severity was assessed using the 0-9 scale (9). The recorded grade values were converted into the PDI as per the formula of Wheeler (10).

Statistical analysis

The statistical analyses were carried out using various R packages within R Studio 4.4.1. Specifically, ANOVA and genetic variability parameters were statistically analysed using the 'variability' packages. The MGIDI was computed using the 'metan' R package (11).

Results and Discussion

The analysis of variance for the F_4 genotype at Coimbatore and F_5 genotype at Gudalur revealed significant differences among the genotypes for all traits studied. This indicates the presence of sufficient genetic variability and the potential for effective selection of these traits across generations. After confirming the homogeneity of error variances, pooled data from the two locations were analysed. The pooled analysis of variance showed statistically significant genotypic differences for plant height, number of branches per plant, number of clusters per plant, number of pods per cluster, number of seeds per pod, number of pods per plant, pod length, 100-seed weight, single plant yield, days to 50% flowering and PDI (Table 1). These findings highlight considerable variation among the genotypes, providing a solid foundation for selection.

Furthermore, significant genotype-by-location interaction effects were observed for all the traits studied. Coimbatore is situated at an altitude of 452 m above mean sea level, with an average minimum temperature ranging from 16.23°C to 22.60°C and a maximum temperature ranging from 27.80°C to 30.70°C. The relative humidity during the cropping period ranged from 87.43% to 89.43% in the morning and 37.29% to 67.57% in the evening. Gudalur, on the other hand, is a hilly region in the Nilgiris district, located at an altitude of 1,100 m above mean sea level. The average minimum and maximum temperatures ranged from 15.39°C to 24.34°C, with relative humidity ranging from 84.20% to 88.91% in the morning and 51.90% to 65.41% in the evening

Table 1. Combined estimates of variance components for 11 traits in 96 blackgram genotypes

Traits	Source of variations			
	Genotype	**Environment**	**G x E**	**Residual error**
Plant height	52.80*	12300.10*	46.20**	19.10
Number of branches/plant	1.51*	348.65*	1.52*	0.23
Number of clusters/plant	1.76*	88.26*	1.22*	0.37
Number of pods/cluster	0.24*	26.73*	0.28*	0.09
Number of seeds/pod	0.56*	269.50*	0.53*	0.11
Number of pods/plant	100.1*	30199.9*	79.40*	11.2
Pod length	0.21*	22.86*	0.22*	0.05
100 seed weight	0.49*	24.55*	0.14**	0.08
Single plant yield	4.02*	956.66*	2.38*	0.38
Days to 50% flowering	17.11*	994.59*	4.19*	0.84
Percent disease index	960.30*	253.99*	29.38*	0.88

**, *=Significant at 1% and 5% probability levels, respectively

during the cropping period.

These results suggest that the performance of the genotypes varied significantly between the two locations due to environmental differences, underscoring the influence of environmental factors on trait expression.

Mean performance of genotypes

Coimbatore

The single plant yield at Coimbatore ranged from 3.45g and 10.40g. Higher single plant yields (Table 2) were recorded by genotypes G22 (10.30g), G59 (10.30g), G3 (10.30g), G56 (10.20g), G54 (10.20g), G75 (10.20g), G57 (10.15g), G71 (10.15g), G68 (10.00g) and G8 (10.00g). Conversely, genotypes G53 (3.45g), G52 (4.4g) and G74 (4.95g) exhibited the lowest yields at this location. Notably, genotypes G3 (10.30g & 18.05%) and G8 (10.00g & 23.68%) registered desirable yields alongside resistance to powdery mildew, surpassing their parental lines. It infers that the disease resistance traits of the parents were successfully inherited by certain progeny genotypes. These findings align with previous studies that screened F_2 and F_3 blackgram populations for powdery mildew resistance under field conditions, reporting higher seed yields in select genotypes (12).

Genotypes G2 (32 days), G74 (33 days) and G20 (34 days) demonstrated early flowering, which facilitates early pod formation and maturity, thereby potentially mitigating the risk of pathogen infestation. Additionally, some genotypes required fewer days to reach 50% flowering compared to their parents, highlighting the potential to identify progenies with early flowering traits. These early flowering genotypes could serve as valuable donors in future hybridization programs, consistent with earlier findings (13).

Gudalur

At Gudalur, the highest single plant yields were observed in genotypes G37 (9.9g), G32 (8.8g), G2 (8.4g), G39 (8.3g) and G1 (7.95 g), all of which outperformed their parental lines. In

Table 2. Best linear unbiased estimates (BLUE) of individual locations for the top and bottom 10 genotypes among 96 F_4 and F_5 blackgram genotypes raised at Coimbatore and Gudalur

Coimbatore										Gudalur									
Gen	**DFF**	**Gen**	**PH**	**Gen**	**NOPP**	**Gen**	**SPY**	**Gen**	**PDI**	**Gen**	**DFF**	**Gen**	**PH**	**Gen**	**NOPP**	**Gen**	**SPY**	**Gen**	**PDI**
G77	42.00	G88	34.55	G77	46.80	G22	10.30	G3	15.93	G54	46.00	G58	78.30	G2	38.56	G37	9.90	G3	18.05
G69	42.00	G76	33.20	G60	46.10	G59	10.30	G4	18.54	G27	45.00	G36	56.80	G37	35.82	G32	8.80	G1	18.25
G32	42.00	G71	32.95	G64	46.00	G3	10.30	G1	19.41	G13	45.00	G88	48.15	G32	35.42	G2	8.40	G4	21.15
G54	42.00	G73	32.95	G88	46.00	G56	10.20	G8	23.68	G32	45.00	G93	46.50	G39	33.95	G39	8.30	G33	25.05
G53	41.00	G78	32.60	G70	45.90	G54	10.20	G5	23.80	G18	45.00	G76	46.05	G1	31.84	G1	7.95	G13	25.30
G48	41.00	G74	32.45	G69	45.20	G75	10.20	G2	24.83	G42	45.00	G32	45.50	G10	31.52	G19	7.60	G5	28.00
G68	41.00	G54	32.00	G58	45.10	G57	10.15	G12	25.46	G68	44.00	G27	45.15	G27	29.85	G10	7.40	G12	28.30
G76	41.00	G70	31.85	G44	45.00	G71	10.15	G17	26.04	G83	44.00	G86	44.70	G8	29.62	G8	7.25	G2	28.75
G59	41.00	G77	31.75	G22	44.70	G68	10.00	G14	26.93	G48	44.00	G18	44.60	G7	28.10	G3	7.25	G14	28.85
G1	41.00	G83	31.75	G3	44.70	G8	10.00	G6	27.20	G38	44.00	G39	44.35	G45	28.04	G38	7.25	G8	29.00
G5	35.00	G58	27.65	G91	33.60	G93	8.05	G69	64.86	G9	38.00	G51	35.90	G84	13.80	G87	4.60	G89	67.90
G75	35.00	G82	27.60	G86	32.80	G86	7.90	G70	64.87	G5	38.00	G68	35.45	G83	13.73	G54	4.55	G93	68.00
G9	35.00	G45	27.20	G36	29.40	G82	7.85	G63	67.86	G35	38.00	G53	35.45	G52	13.66	G23	4.55	G60	69.35
G73	35.00	G29	26.90	G17	29.40	G91	7.50	G92	69.89	G45	38.00	G23	35.30	G85	13.50	G90	4.45	G91	69.45
G52	35.00	G72	25.60	G5	27.40	G4	7.10	G89	74.74	G74	38.00	G52	35.25	G23	13.42	G92	4.45	G69	70.65
G30	35.00	G61	25.55	G51	25.00	G51	5.80	G93	76.27	G63	38.00	G1	34.55	G86	13.01	G74	4.35	G92	72.20
G3	34.00	G51	23.50	G4	23.50	G29	5.25	G91	79.48	G81	37.00	G54	33.90	G54	13.00	G80	4.30	G87	72.95
G20	34.00	G53	22.05	G29	20.70	G74	4.95	G88	84.50	G30	37.00	G6	33.30	G57	12.96	G28	4.30	G63	75.60
G74	33.00	G52	21.65	G53	13.80	G52	4.40	G87	88.20	G82	37.00	G35	33.10	G82	12.87	G94	4.10	G88	76.10
G2	32.00	G4	19.35	G52	8.30	G53	3.45	G94	89.84	G44	36.00	G50	32.35	G43	12.87	G30	4.05	G94	80.75
95	46.00	95	32.95	95	3.80	95	3.25	95	4.88	95	54.00	95	79.80	95	12.76	95	2.80	95	6.30
96	36.10	96	26.20	96	39.60	96	7.15	96	88.20	96	40.00	96	40.30	96	30.30	96	6.35	96	95.9
Mean	38.12	Mean	29.53	Mean	38.23	Mean	8.96	Mean	45.48	Mean	41.35	Mean	40.85	Mean	20.49	Mean	5.80	Mean	47.10

DFF= days to 50% flowering, PH=plant height, NOPP= number of pods per plant, SPY= single plant yield, PDI= percent disease index contrast, the lowest yields was recorded in genotypes G30 (4.05g), G94 (4.10g), G28 (4.30g), G80 (4.30g) and G74 (4.35g). Genotypes G77, G69 and G32 required the longest duration (42 days) to reach 50% flowering, exceeding both parental lines in this traits. Conversely, genotypes G2 (32 days), G74 (33 days), G20 (34 days) and G3 (34 days) demonstrated the shortest flowering periods. The genotypes G3 (7.95g & 18.25%) and G1 (7.25g & 18.05%) showed higher yields along with powdery mildew resistance (Table 2).

The highest overall mean yield was recorded at Coimbatore (8.96g), representing a 54.48% increase compared to Gudalur. Genotypes such as G22, G59, G3, G56, G54, G75, G57 and G71 at Coimbatore, as well as G37, G32, G2 and G39 at Gudalur, demonstrated superior yield performances in their respective environments. These genotypes could serve as valuable candidates for location-specific cultivation based on their relative yield performance (Table 2).

Pooled locations

The combined analysis revealed a wide range of variations for traits including days to 50% flowering, plant height, number of pods per cluster, number of seeds per pod, number of pods per plant, pod length, 100-seed weight, single plant yield and percent disease index. The highest seed yield per plant was recorded in genotype G37 (9.65 g), followed by G39 (9.02 g), G32 (8.87 g), G1 (8.85) and G3 (8.77). These genotypes demonstrated relatively better yields than their parental lines, indicating their potential to perform well across diverse environmental conditions (Table 3).

The lowest single plant yield was recorded in genotypes G53 (4.12 g), G74 (4.65 g) and G52 (4.7g). With respect to flowering, the shortest days for 50% flowering was observed in genotypes G74 (35.5 days), G30 (35.99 days) and G82 (36.49), which were earlier than their parental genotypes. The selection of early-maturing genotypes is advantageous, as they can sometimes escape severe disease incidence when environmental conditions are unfavorable for pathogen infection. Early-seeded crops and early-maturing cultivars are often less affected by powdery mildew because the fungus has less time to spread and impact yield (14).

Genotypes with a low PDI indicate resistance to powdery mildew disease. Notably, genotypes G3 (17.00% disease index, 7.25 g yield) and G1 (18.79% disease index, 8.85 g yield) exhibited resistance to powdery mildew along with desirable yield levels. These genotypes can serve as donors for developing powdery mildew-resistant varieties.

A wide range of variation was also observed for traits such as the number of clusters per plant (4.25-7.9), number of pods per cluster (2.3-3.6), number of seeds per pod (3.77-5.10) and number of pods per plant (4.25-7.90). These traits are important selection criteria for improving blackgram for high yield combined with powdery mildew resistance (Table 3).

Genetic parameters

Genetic variability is a cornerstone for the development, evolution and enhancement of specific traits. The combined estimates of genetic variability parameters for 11 traits are presented in Table 4. The estimates of GCV (genotypic coefficient of variation) and PCV (phenotypic coefficient of variation) provide a comprehensive understanding of the variability present among the genotypes.

In all traits studied, PCV was higher than GCV, indicating the influence of environmental factors on these traits. The extent of environmental impact on the expression of any trait is assessed by the magnitude of the difference between GCV and PCV. A large difference suggests a strong environmental influence, whereas a smaller difference reflects minimal environmental effects and a high genetic contribution to the expression of the traits (15). Similar findings have been reported in previous studies (16-19).

Table 3. Best linear unbiased estimates (BLUE) of combined locations for the top and bottom 10 genotypes among 96 F_4 and F_5 blackgram genotypes raised at Coimbatore and Gudalur for important traits

Gen	DFF	Gen	PH	Gen	NOP	Gen	NOS	Gen	NOPP	Gen	PODL	Gen	HSW	Gen	SPY	Gen	PDI
G54	43.99	G58	52.97	G4	7.90	G5	3.60	G37	38.30	G39	5.15	G48	4.97	G37	9.65	G3	17.00
G32	43.50	G36	43.07	G37	7.50	G34	3.60	G2	36.90	G86	5.15	G47	4.80	G39	9.02	G1	18.79
G69	42.99	G88	41.35	G51	7.30	G14	3.50	G27	36.80	G88	5.15	G4	4.70	G32	8.87	G4	19.86
G48	42.50	G76	39.62	G69	7.00	G89	3.40	G39	36.65	G87	5.12	G45	4.65	G1	8.85	G5	25.91
G68	42.50	G27	38.27	G73	7.00	G12	3.40	G8	36.55	G90	5.07	G57	4.62	G3	8.77	G33	26.00
G76	42.49	G93	37.90	G75	7.00	G35	3.40	G3	36.10	G61	5.05	G68	4.60	G2	8.65	G8	26.33
G53	42.49	G18	37.67	G48	6.90	G15	3.40	G45	36.00	G22	5.04	G9	4.50	G8	8.65	G13	26.14
G27	42.49	G32	37.67	G76	6.90	G3	3.35	G32	35.50	G85	5.02	G35	4.50	G19	8.42	G2	26.78
G83	42.00	G39	37.40	G27	6.85	G70	3.35	G1	35.30	G91	4.99	G19	4.50	G40	8.37	G12	26.84
G77	41.99	G83	37.32	G39	6.80	G7	3.30	G44	35.25	G73	4.95	G35	4.50	G45	8.25	G17	27.62
G15	37.49	G61	32.57	G30	5.20	G84	2.80	G5	24.90	G12	4.35	G77	3.75	G94	6.35	G70	66.09
G2	37.00	G23	32.50	G13	5.10	G92	2.75	G84	24.10	G69	4.34	G91	3.75	G92	6.30	G69	67.73
G52	37.00	G1	32.50	G82	5.10	G32	2.70	G85	23.90	G64	4.32	G32	3.72	G82	6.27	G92	71.04
G81	36.99	G6	31.90	G17	5.07	G24	2.65	G82	23.20	G11	4.30	G6	3.70	G90	6.25	G89	71.19
G9	36.50	G35	31.47	G86	5.00	G60	2.60	G86	22.95	G72	4.29	G93	3.70	G29	6.10	G93	71.37
G5	36.49	G4	31.40	G43	4.90	G47	2.60	G36	22.45	G48	4.27	G94	3.70	G91	6.10	G63	71.73
G44	36.49	G50	31.27	G23	4.85	G19	2.55	G29	22.10	G49	4.25	G90	3.60	G51	5.57	G91	72.85
G82	36.49	G51	29.70	G36	4.75	G13	2.55	G51	20.50	G74	4.20	G53	3.55	G52	4.70	G88	77.78
G30	35.99	G53	28.75	G52	4.40	G38	2.40	G53	14.24	G75	4.17	G14	3.37	G74	4.65	G87	78.74
G74	35.50	G52	28.45	G53	4.25	G52	2.35	G52	10.80	G60	4.17	G80	3.22	G53	4.12	G94	85.30
95	49.99	95	56.37	95	4.90	95	2.30	95	8.15	95	4.07	95	2.62	95	3.02	95	5.58
96	38.00	96		96	7.20	96	2.60	96	35.05	96	4.84	96	3.75	96	6.75	96	92.03
Mean	39.73	Mean	35.19	Mean	5.98	Mean	3.01	Mean	29.36	Mean	4.63	Mean	4.17	Mean	7.38	Mean	46.29

DFF= days to 50% flowering, PH=plant height, NOP= number of pods per cluster, NOS= number of seeds per pod, NOPP= number of pods per plant, PODL= pod length, HSW 100 seed weight, SPY= single plant yield, PDI= percent disease index

Table 4. Combined estimates of genetic parameters for 11 traits in 96 blackgram genotypes

Character	Mean	Range	σ_p	σ_g	PCV (%)	GCV (%)	h^2 (%)	GAM (%)
Plant height	35.19	18.10-79.80	28.23	8.28	15.09	8.18	29.31	9.12
Number of branches/ plant	5.19	3.00-9.00	0.50	0.26	13.68	9.83	52.00	14.53
Number of clusters/ plant	5.98	3.00-10.00	0.69	0.35	14.05	9.87	50.90	14.46
Number of pods/ cluster	3.01	2.00-5.00	0.15	0.06	12.29	7.31	40.00	11.10
Number of seeds/ pod	4.47	2.00-8.00	0.22	0.10	10.74	7.38	44.19	9.12
Number of pods/ plant	29.36	3.00-52.00	34.73	23.53	20.06	16.52	67.75	28.02
Pod length	4.63	3.50-5.70	0.10	0.04	6.91	4.32	40.00	5.56
100 seed weight	4.17	2.50-5.50	0.18	0.10	10.07	7.67	55.56	11.76
Single plant yield	7.38	2.80-11.00	1.31	1.00	15.45	13.55	76.29	24.32
Days to 50% flowering	39.73	32.00-54.00	49.40	4.10	5.59	5.08	82.99	9.57
Percent disease index	46.29	5.00-95.00	240.74	239.86	33.61	33.46	98.63	68.60

A higher magnitude of GCV was recorded for the PDI (32.80%), aligning with earlier reports (20). Moderate GCV values were observed for the number of pods per plant (16.52%) and single plant yield (13.55%). The remaining traits exhibited a low magnitude of GCV, ranging from 4.32% to 9.87%, indicating a significant environmental influence on the expression of these traits. These findings are consistent with earlier studies (21, 22).

However, it is important to note that the observed phenotype may not be fully transmitted to the next generation, highlighting the necessity of examining the heritable portion of variability. Heritability serves as a critical parameter, indicating the extent to which traits are inherited from parents to offspring and providing an estimate of heritable variation within the population. In the current study, high heritability was observed for PDI (98.63%), followed by days to 50% flowering (82.99%), single plant yield (76.29%) and the number of pods per plant (67.75%). All other traits exhibited moderate heritability, except for plant height (29.31%). These high heritability traits could serve as effective selection criteria for further breeding advancements.

GAM offers a reliable metric for evaluating the efficiency of selection in trait improvement. The traits PDI (68.60%), number of pods per plant (28.02%) and single plant yield (24.72%) recorded higher GAM values. Similar findings have been previously reported for the number of pods and single plant yield (22). Moderate GAM values were observed for traits such as the number of branches per plant (%), number of clusters per plant (%), 100-seed weight (11.76%) and number of pods per cluster (11.10%).

Heritability alone does not fully reflect the genetic potential of a genotype. When combined with high GAM, it provides a more comprehensive understanding of genetic gain. The traits single plant yield, number of pods per plant and PDI demonstrated high heritability along with high GAM. This observation aligns with earlier reports (23). It can be inferred that these traits are primarily influenced by additive gene effects, making selection highly effective for their improvement. Simple selection methods, such as the pedigree method, can be employed for further enhancement of these traits.

Association studies

The correlation coefficients, computed to evaluate the relationship between seed yield and its component traits in the F_4 and F_5 generations, are presented in Fig. 1 and Fig. 2. Seed yield per plant exhibited a significantly positive correlation with the number of pods per plant (0.84 and 0.88), the number of seeds per pod (0.47 and 0.41) and 100-seed weight (0.46 and 0.35) in both generations. These results are consistent with previous studies (22, 24-28). These findings highlight that the primary pod characteristics of genotypes play a crucial role in enhancing the seed yield of blackgram across both generations. Consequently, selecting these traits during the breeding process would contribute to yield improvement in blackgram.

The traits "days to 50% flowering" and "PDI" showed a weak association with seed yield in the F_4 generation due to their positive but non-significant correlation values. However, the PDI in the F_5 generation demonstrated a significantly negative correlation with seed yield. This observation suggests that the severity of powdery mildew disease adversely impacts seed yield.

Intercorrelation studies

In the F_4 and F_5 generations, the number of branches per plant showed a significantly positive correlation with the number of capsules per plant (0.17 and 0.21) and days to 50% flowering (0.28 and 0.21). The number of clusters per plant was positively correlated with the number of pods per plant (0.47 and 0.61), while the number of seeds per pod was positively correlated with the number of pods per plant (0.53 and 0.38) and 100-seed weight (0.46 and 0.19). Additionally, the number of pods per plant showed a positive correlation with 100-seed weight (0.48 and 0.26) in both generations. These findings align with previous studies (17, 28-31). The traits "number of seeds per pod," "number of pods per plant," and "days to 50% flowering" recorded significant negative correlations with PDI in the F_5 generation. This is likely due to the mycelium of *Erysiphe polygoni* covering the upper surface of the leaves, which affects photosynthetic efficiency, leading to ovule abortion, senescence and a reduction in pods (32).

It can be concluded that the traits-number of pods per plant, number of clusters per plant, number of pods per cluster and 100-seed weight-showed significant and positive associations with single plant yield.

Parent progeny regression

Parent-progeny regression analysis was employed to estimate the heritability of traits by examining the relationship between parental and progeny values across different traits. In parent-offspring regression, the slope of the regression line represents the heritability, while R^2 indicates the proportion of variation in the offspring's trait (F_5) that can be explained by the variation in

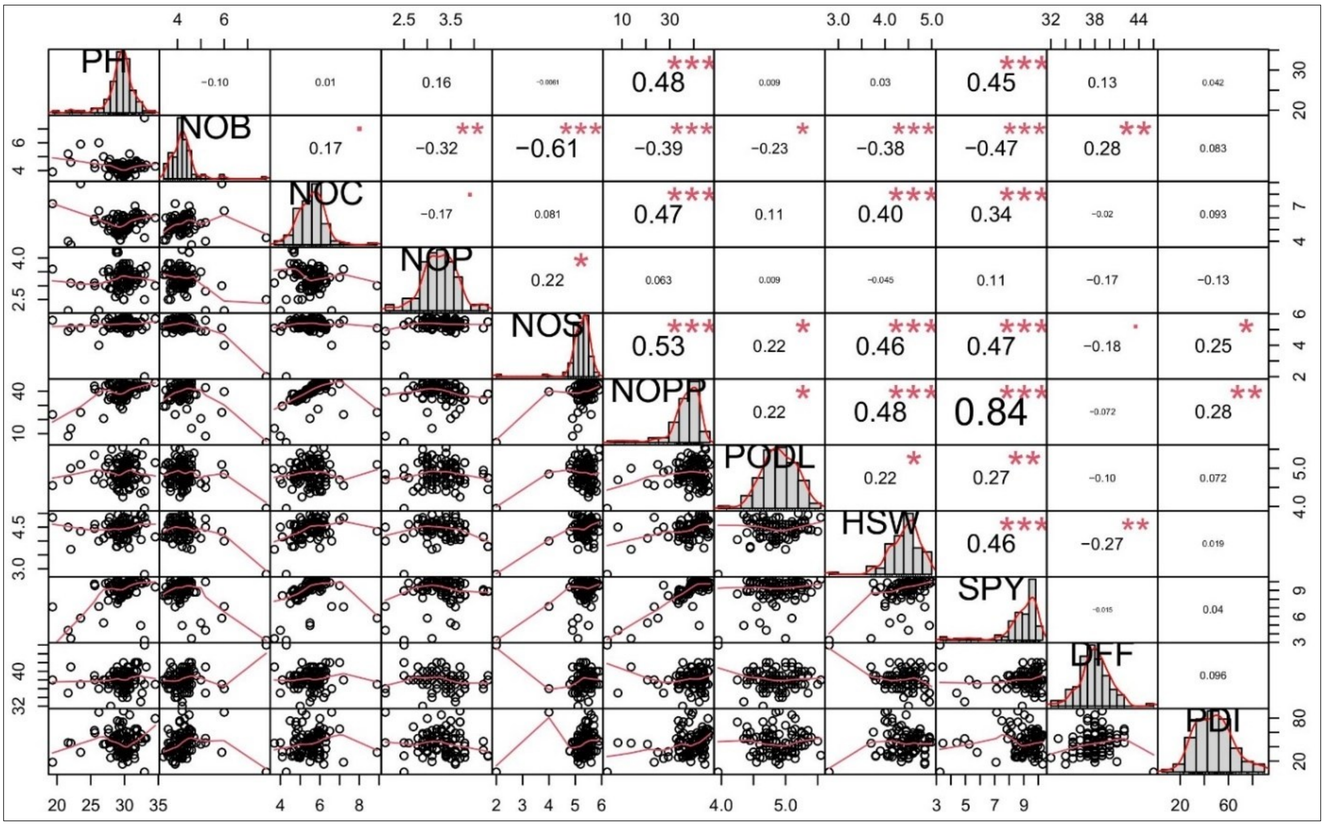

Fig. 1. Correlation analysis for seed yield and its component traits in 96 F_4 blackgram genotypes.

PH=plant height, NOB=number of branches per plant, NOC=number of clusters per plant, NOP= number of pods per cluster, NOS= number of seeds per pod, NOPP= number of pods per plant, PODL= pod length, HSW =100 seed weight, SPY= single plant yield, DFF=days to 50% percent flowering, PDI= percent disease index

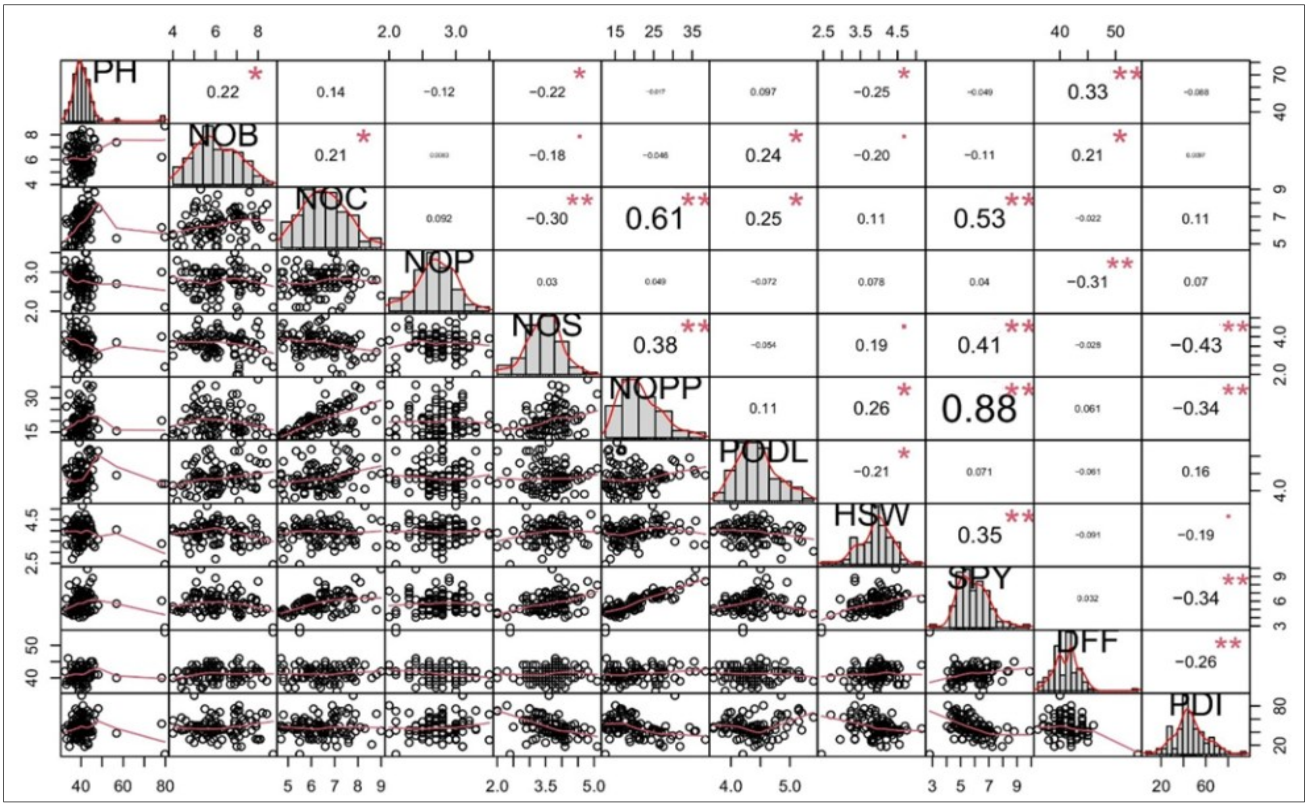

Fig. 2. Correlation analysis for seed yield and its component traits in 96 F_5 blackgram genotypes.

PH=plant height, NOB=number of branches per plant, NOC=number of clusters per plant, NOP= number of pods per cluster, NOS= number of seeds per pod, NOPP= number of pods per plant, PODL= pod length, HSW = 100 seed weight, SPY= single plant yield, DFF= days to 50% percent flowering, PDI = percent disease index the parent's trait (F_4). Essentially, it reflects how well the parent's trait predicts the offspring's trait in the regression model, thereby indicating the strength of the relationship between generations. Fig. 3a and 3b, present the regression analysis of offspring (O) relative to the parent (P) for the 11 traits.

Among the traits, the highest regression coefficient (R^2 = 0.89) was observed for the powdery mildew disease index. This suggests that 89% of the variance in the offspring's trait can be accounted for by the parent's trait. An intermediate regression coefficient was observed for days to 50% flowering (R^2 = 0.38), followed by 100-seed weight (R^2 = 0.33), indicating that 38% and 33% of the variation in the offspring's traits can be attributed to the parental traits, respectively. Selecting these traits in early generations can significantly help in obtaining plants with higher yields and resistance to powdery mildew disease. A higher regression coefficient suggests greater genetic inheritance and limited environmental influence (33). Parent regression coefficient analysis is used to determine the narrow-sense heritability of traits, which results from additive genetic variance (33). For the remaining traits, very low regression coefficients (R^2) were observed, indicating that little to no variation in the offspring's traits can be explained by the parent's traits. This suggests either no genetic inheritance or that the traits are predominantly influenced by environmental factors or random variation.

Multi-trait genotype ideotype distance index (MGIDI)

MGIDI defines the ideotype by rescaling the original means between values of 0 and 100. Traits that need improvement are assigned a maximum value of 100 and a minimum value of 0. Conversely, traits such as days to 50% flowering and PDI, which require negative gains, are assigned a maximum value of 0 and a minimum value of 100. PCA is a dimensionality reduction technique that converts the corrected variables into uncorrelated PCs. Four PCs were found to have eigenvalues greater than 1, collectively explaining 69.65% and 67.92% of the total variance in F_4 and F_5 generations, respectively (Table 5).

PC1, with eigenvalues of 3.49 and 2.78, accounted for 31.8% and 25.2% of the total variability, respectively. PC2, with eigenvalues of 1.69 and 1.99, explained 15.3% and 18.1% of the variability; PC3, with eigenvalues of 1.38 and 1.67, contributed 12.6% and 15.2%; and PC4, with eigenvalues of 1.09 and 1.04, accounted for 9.95% and 9.42% of the variability in F_4 and F_5 generations, respectively. The remaining PCs exhibited a declining trend in variability. The variability captured by PC1 (31.8% and 25.2%) highlights its importance in guiding the selection of lines and making them desirable for further improvement.

FA1 included the following traits: NOB, NOS, PODL, HSW and DFF. Similarly, the traits NOC and NOP were grouped under FA2. The traits PH, NOPP and SPY were classified under FA3. The PDI was placed under FA4 in the F_4 generation.

In the F_5 generation, traits of economic importance, NOC, NOPP and SPY, were grouped in FA1. Similarly, NOS and PDI were assigned to FA2. The traits PH, NOP and DFF were placed under FA3. Finally, the traits NOB, PODL and HSW were grouped in FA4 (Table 6). The rescaled values were used to calculate the MGIDI score.

The MGIDI index showed promising genetic gains, with a total genetic gain of 95.27% in the F_5 generation. The traits number of pods per plant, single plant yield and number of capsules per plant exhibited substantial genetic gains of 44.6%, 26.0% and 11.6%, respectively. The F_4 generation exhibited lower genetic gains. In the present study, 11 traits were used to assess variations among 96 blackgram genotypes, as depicted in Fig. 4. Promising genotypes in the F_4 generation included G27, G24, G47, G20, G67, G8, G75, G22, G73 and G3, while in the F5 generation, G19, G33, G8, G7, G1, G3, G27, G10, G2, G37, G39 and G32 were identified.

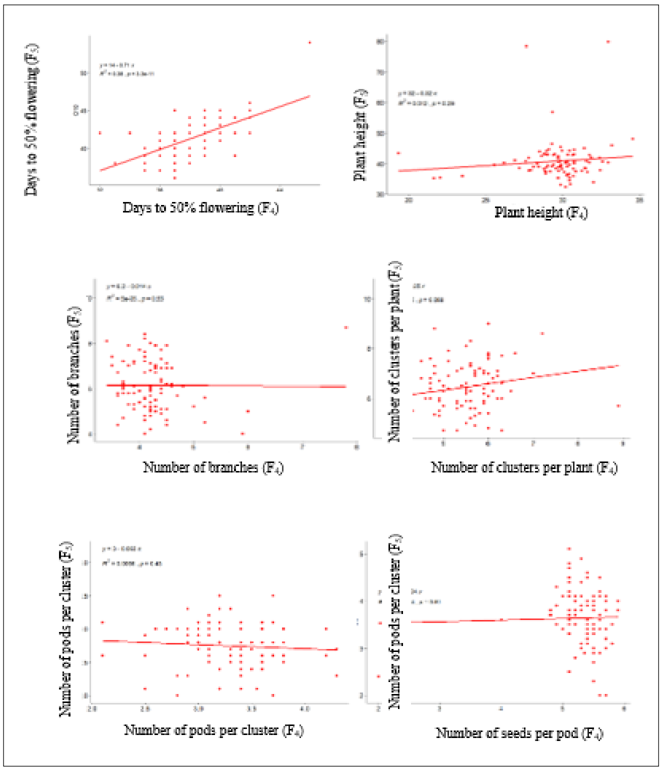

Fig. 3a. Regression graph showing the inheritance pattern between parent and progeny under study for important traits.

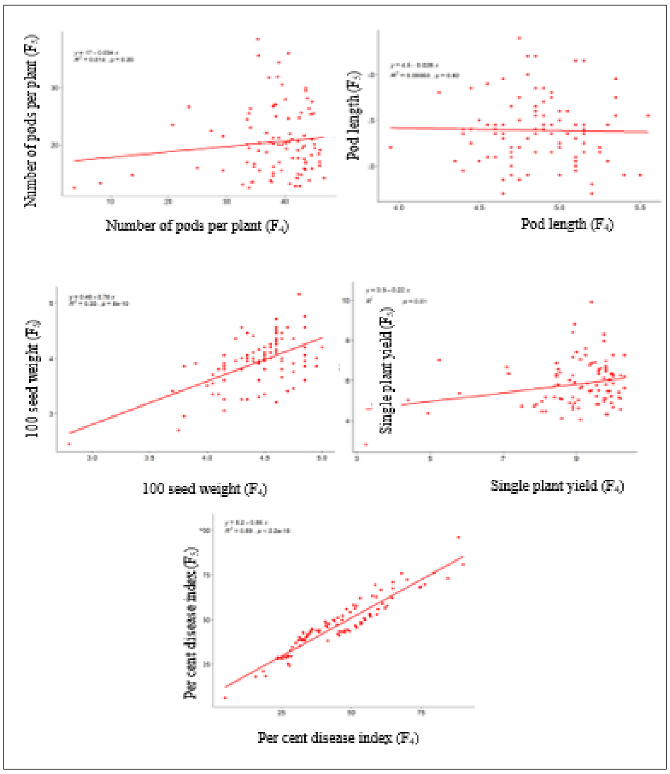

Fig. 3b. Regression graphs showing the inheritance pattern between parent and progeny under study for important traits.

Table 5. Principal component analysis in F_4 and F_5 genotypes of the cross *VBN11x LBG17*

PC	EV	V	CV	EV	V	CuV (%)
		F_5			F_5	
PC1	3.49	31.8	31.8	2.78	25.2	25.2
PC2	1.69	15.3	47.1	1.99	18.1	43.3
PC3	1.38	12.6	59.7	1.67	15.2	58.5
PC4	1.09	9.95	69.6	1.04	9.42	68
PC5	0.88	8.03	77.7	0.96	8.71	76.7
PC6	0.76	6.92	84.6	0.78	7.09	83.8
PC7	0.68	6.15	90.7	0.6	5.46	89.2
PC8	0.42	3.84	94.6	0.5	4.58	93.8
PC9	0.26	2.41	97	0.45	4.05	97.8
PC10	0.23	2.12	99.1	0.14	1.29	99.1
PC11	0.1	0.89	100	0.1	0.87	100

EV - Eigen value, V - variance, CuV - cumulative variance

Notably, genotypes G18 and G19 in F_4 and G4 and G38 in F_5 were located near the cut point indicated by the red line, suggesting interesting features that warrant further investigation. The MGIDI index identified G18, G19, G4 and G38 as promising genotypes for the improvement of blackgram, particularly for high yield and powdery mildew resistance. Previous studies have reported that the MGIDI is an efficient index for selecting genotypes with desired traits, further supporting its applicability and effectiveness in crop improvement strategies (10). The selected genotypes based on the MGIDI index will serve as a valuable resource for breeding programs.

Fig. 5 provides a comprehensive overview of the strengths and weaknesses demonstrated by various genotypes, as described by the contribution of each factor to the MGIDI in the F_4 and F_5 generations. In the F_4 generation, the genotypes associated with Factor 1 (FA 1), including G18, G8, G20, G37, G5 and G24, exhibited particular strength in traits such as number of branches per plant, number of seeds per pod, pod length, 100 seed weight and days to 50% flowering. The genotypes G75, G47 and G19, associated with Factor 2 (FA 2), showed notable strength in the traits number of clusters per plant and number of pods per cluster. The genotypes G27, G67, G18 and G8, associated with Factor 3 (FA 3), exhibited strength in traits like plant height, number of pods per plant and single plant yield. Lastly, Factor 4 (FA 4), represented by the genotypes G3, G20 and G5, demonstrated strength in the trait percent disease index.

In the F_5 generation, the genotypes G37 and G4, associated with FA1, exhibit strength in traits such as number of clusters per plant, number of pods per plant and single plant yield. The genotypes G3, G19 and G38 demonstrate particular strength in the traits NOS and PDI. The genotypes G10, G37, G32, G4, G3 and G33, associated with FA3, show strength in traits like plant height, number of pods per cluster and days to 50% flowering. The genotypes G2 and G1, associated with FA4, exhibit strength in traits such as number of branches per plant, pod length and 100 seed weight. These insights into the strengths and weaknesses of genotypes can serve as valuable guidance for selecting parents in future breeding programs. The genotypes G18, G19, G4 and G38, identified through MGIDI, highlight their potential as donors for hybridization or as key breeding material for the development of high-yield and powdery mildew-resistant varieties.

Conclusion

It is concluded that the genotypes G3 (8.77g & 17.00%) and G1 (8.85g & 18.79%) exhibited desirable yield with powdery mildew resistance in the pooled analysis. The traits of single plant yield, number of pods per plant and percent disease index demonstrated high heritability and GAM. These traits are influenced by additive gene effects and simple selection methods, such as the pedigree method, would be effective for their improvement. Seed yield per plant showed a significant positive correlation with the number of pods per plant (0.84 & 0.88), number of seeds per pod (0.47 & 0.41) and 100 seed weight (0.46 & 0.35) in both generations. The PDI exhibited the highest regression coefficient (R^2 = 0.89), indicating that 89% of the variance in the offspring's trait can be explained by the parental trait. The MGIDI index analysis demonstrated a total genetic gain of 95.27%, primarily from the traits number of pods per plant, single plant yield and number of capsules per plant in the F_5 generation. The genotypes G18, G19, G4 and G38, identified through the MGIDI index, serve as valuable resources and promising candidates for further breeding.

Table 6. Selection gain (%) derived in F_4 and F_5 derived through MGIDI based selection

VAR	Factor	SG	SG perc	sense	VAR	Factor	SG	SG perc	Sense
		F_4					F_5		
NOB	FA1	-0.05871	-1.384	increase	**NOC**	FA1	0.72	11.2	increase
NOS	FA1	-0.09193	-1.73	increase	**NOPP**	FA1	9.15	44.6	increase
PODL	FA1	0.02443	0.5009	increase	**SPY**	FA1	1.51	26	increase
HSW	FA1	0.04947	1.118	increase	**NOS**	FA2	0.207	5.69	increase
DFF	FA1	-1.035	-2.714	decrease	**PDI**	FA2	-14.2	-30.1	decrease
NOC	FA2	0.2238	4.067	increase	**PH**	FA3	0.08	0.20	increase
NOP	FA2	0.008762	0.2672	increase	**NOP**	FA3	-0.04	-1.76	increase
PH	FA3	0.4264	1.444	increase	**DFF**	FA3	1.03	2.49	increase
NOPP	FA3	2.359	6.17	increase	**NOB**	FA4	0.007	0.12	increase
SPY	FA3	0.653	7.283	increase	**PODL**	FA4	0.09	2.16	increase
PDI	FA4	-12.53	-27.56	decrease	**HSW**	FA4	0.11	2.81	increase

PH=plant height, NOB=number of branches per plant, NOC=number of clusters per plant, NOP= number of pods per cluster, NOS= number of seeds per pod, NOPP= number of pods per plant, PODL= pod length, HSW =100 seed weight, SPY= single plant yield, DFF=days to 50% percent flowering, PDI= percent disease index

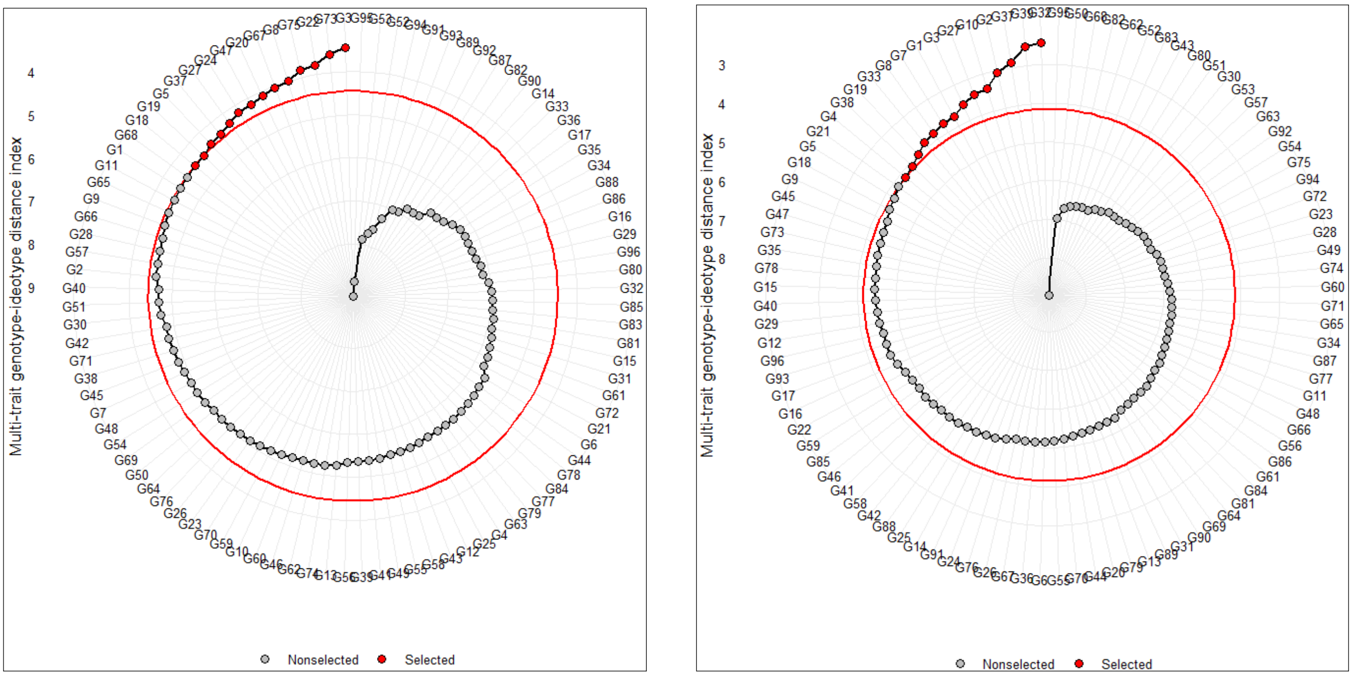

Fig. 4. Genotype ranking order for the MGIDI index in F_4 and F_5 blackgram genotypes.

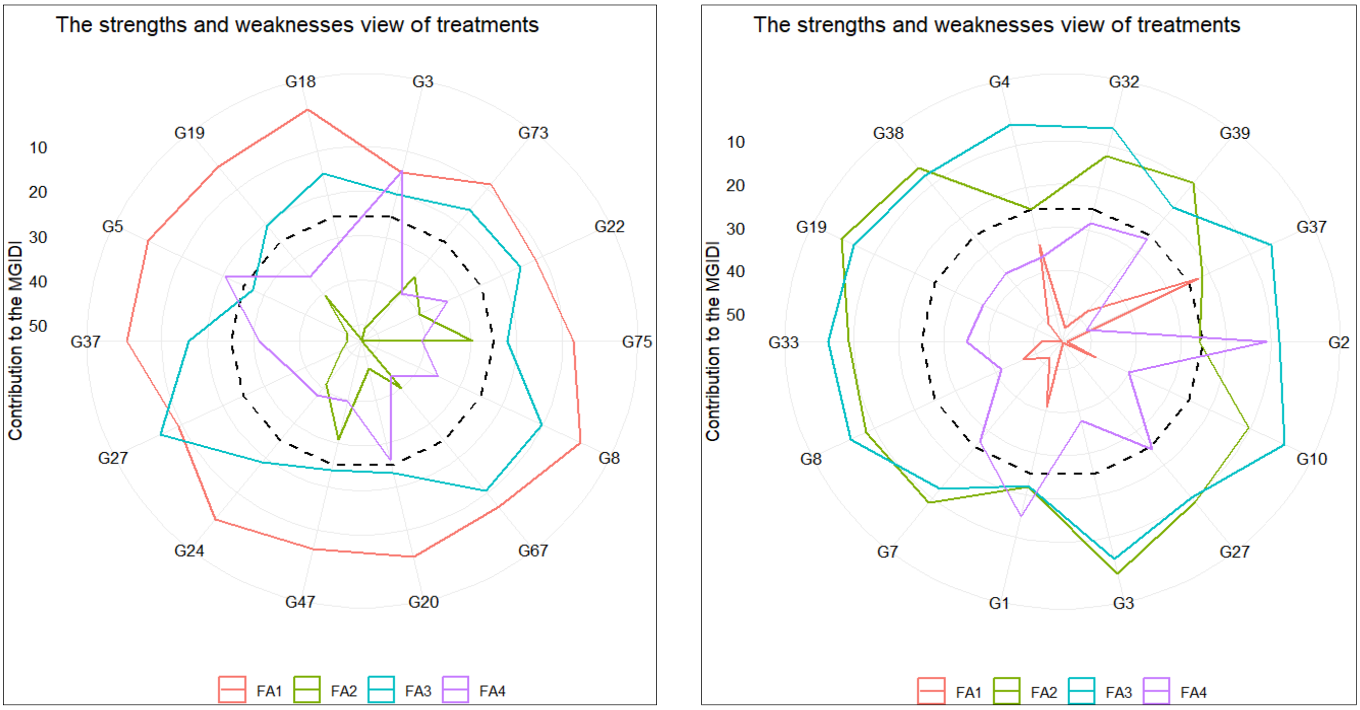

Fig. 5. Visualization of strengths and weaknesses of the selected F_4 and F_5 blackgram genotypes.

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Authors' contributions

NA carried out experimentation and drafted the manuscript. KD planned, supervised and edited the manuscript. MN participated in the study and performed the statistical analysis. SG carried out disease screening. MBN involved in planning and provided critical feedback on the manuscript. All authors read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interests to declare.

Ethical issues: None

Declaration of generative AI and AI-assisted technologies in the writing process

During the preparation of this work, Quillbot was used to improve language and readability. Authors reviewed and edited the content as needed and take full responsibility for the content of the publication.

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