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Variability and association analyses of powdery mildew disease scores, seed yield and component traits in blackgram [*Vigna mungo* (L.) Hepper]

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Abstract

The present study was focused on evaluating the F_3 population of VBN 11 x LBG 17 based on 10 yield components and the *per cent* disease index (PDI) for powdery mildew. Variability, correlation, and path analyses were performed to examine the data. The F_3 population exhibited a wide range of variation for both yield components and PDI. Notably, the number of branches per plant, PDI, and seed yield per plant (g) showed high phenotypic and genotypic coefficients of variation. Furthermore, PDI alone displayed high heritability along with a high genetic advance as a percentage of mean. Moderate heritability and high genetic advance as a percentage of mean were observed for plant height (cm), number of branches per plant, total number of pods per plant, and seed yield per plant (g). These findings suggest that these traits are influenced by additive gene action and are suitable for effective selection. Correlation analysis revealed that all traits, except PDI and 100-seed weight, were significantly associated with seed yield per plant (g). Path analysis indicated that the total number of pods per plant had a substantial direct effect. Consequently, the total number of pods per plant can serve as a selection index for yield improvement programs. Notably, PDI exhibited no association with seed yield per plant (g), suggesting that resistant genotypes can be developed without any adverse correlation among yield components.

Keywords: Blackgram, correlation, path analysis, powdery mildew, variability

INTRODUCTION

Blackgram [*Vigna mungo* (L.) Hepper] is a pulse crop of global importance, especially in South Asia. It is a major source of dietary protein, iron, calcium, and vitamin B_9. However, blackgram production is constrained by various biotic and abiotic stresses. Powdery mildew caused by *Erysiphe polygoni* DC is a serious fungal disease. Powdery mildew can cause up to 60% yield losses in blackgram, reduce the quality of the harvested produce and increase the production cost due to the use of fungicides to control the disease (Sharma *et al.*, 2016; Bandi *et al.*, 2018). Powdery mildew reduces photosynthesis, transpiration, and nitrogen fixation in blackgram plants, leading to stunted growth, premature defoliation, and forced maturity. One of the methods used to assess the severity of powdery mildew in blackgram is the *per cent* disease index (PDI), which is calculated based on the percentage of leaf area covered by the fungal growth (Sharma *et al.,* 2016). PDI can be used to compare the resistance levels of different genotypes and to estimate the yield losses due to the disease (Bandi *et al.*, 2018).

Powdery mildew resistance in blackgram can be attributed to genetic factors, environmental factors and their interactions. Various studies have been conducted to identify and characterize genes associated with powdery mildew resistance in blackgram. Additionally, studies have shown that environmental factors, such as temperature and humidity, can also influence the severity of powdery mildew infections.

Breeding for powdery mildew resistance is a sustainable solution to reduce the impact of the disease on blackgram production. The process of developing improved cultivars with enhanced resistance involves identifying and selecting genotypes with desirable traits and hybridizing them to produce new populations with improved genetic makeup (Sharma *et al.*, 2016). In this context, hybridization between a susceptible elite variety and a resistant variety is a common strategy used to develop improved cultivars with high resistance to powdery mildew. This study aimed to evaluate the variability and correlation of powdery mildew disease scores with yield and component traits in F_3 population of blackgram.

MATERIALS AND METHODS

Plant Material and Crosses: The research was conducted at the Department of Pulses, Tamil Nadu Agricultural University, Coimbatore, during the *Rabi* season of 2022-23. Two varieties, VBN 11 (susceptible to powdery mildew) and LBG 17 (resistant to powdery mildew) were selected for the study. Crosses were made using VBN 11 as the female parent and LBG 17 as the male parent. The resulting F_1 generation was selfed to obtain the F_2 generation. The F_2 plants were selfed, and the progeny from each individual plant were advanced to the F_3 generation through single seed descent.

Screening for Powdery Mildew Resistance: The $F_{2:3}$ population, along with the parental varieties, was screened for powdery mildew resistance under artificially created epiphytotic conditions. Disease symptoms were observed at the flowering stage. To enhance disease severity, the field was covered with a white net of 1 mm pore size. Optimum irrigation and shade were provided to increase spore load and disease severity. Additionally, a spore suspension in 1% sucrose solution was sprayed daily during the evening hours to intensify disease development.

Quantitative Traits and Data Collection: In this study, ten quantitative traits were recorded for all individual plants. These traits included plant height (cm), number of branches per plant, number of clusters per plant, number of pods per cluster, total number of pods per plant, pod length (cm), number of seeds per pod, 100-seed weight (g), seed yield per plant (g), and the *per cent* disease index (PDI) was calculated based on Mayee and Datar (1986) which is presented in **Table 1**. These traits were carefully measured and recorded to provide a comprehensive understanding of the relationship between powdery mildew and seed yield in blackgram.

Statistical Analysis: The average of parental variance was used to estimate environmental variation. Variability parameters were calculated using standard methods. Simple correlation analysis was performed according to the method suggested by (Johnson *et al.*, 1955). Path analysis was conducted using the TNAUSTAT statistical package (Manivannan, 2014), following the standard procedure.

RESULTS AND DISCUSSION

Genetic variability plays a crucial role in any specific trait for the development, further advancement and improvement. The analysis of various parameters including mean, range, phenotypic coefficient of variance (PCV), genotypic coefficient of variance (GCV), heritability (h^2), and genetic advance over the mean (GAM) for different traits were presented in **Table 2**.

The phenotypic coefficient of variance (PCV) reflects the variation in a trait due to both genetic and environmental factors. A higher PCV suggests greater variability, indicating the potential for selection and improvement of the trait. The genotypic coefficient of variance (GCV) estimates the genetic variation component, providing insights into the inherent genetic potential for the trait. Heritability (h^2) measures the proportion of phenotypic

Table 1. Powdery mildew disease scoring scale (0-9)

Rating	Reaction	Leaf area covered
0	Immune	No symptoms on the leaf
1	Highly resistant (HR)	Powdery mildew specks covering 1% or less leaf area
3	Resistant (R)	Powdery lesions covering 1-10% of leaf area
5	Moderate resistant/ moderate susceptible (MR/MS)	Enlarged powdery lesions covering 11-25% leaf area
7	Susceptible (S)	Powdery lesions coalesce to form big patches covering 26-50%
9	Highly susceptible (HS)	Powdery patches covering: 52% or more of leaf area and defoliation occur

Source: Mayee and Datar (1986)

Table 2. Mean, range and variability of VBN 11 x LBG 17 in F_3 population for various characters

Character	Mean	Range	PCV (%)	GCV (%)	h^2 (%)	GAM (%)
Plant height (cm)	29.96	14.00-46.00	20.66	15.66	57.49	24.47
No. of branches per plant	2.97	2.00-8.00	37.34	23.78	40.53	31.18
Number of clusters per plant	7.54	3.00-14.00	29.48	13.45	20.83	12.65
Number of pods per cluster	3.30	2.00-5.00	20.13	11.43	32.22	13.36
Total number of pods per plant	19.19	6.00-45.00	37.70	19.61	27.06	21.01
Pod length (cm)	4.24	3.00-5.50	11.13	3.86	12.06	2.76
Number of seeds per pod	6.36	4.00-8.00	11.81	6.87	33.82	8.23
100-seed weight (g)	4.10	2.70-6.30	14.30	5.76	16.24	4.78
Per cent disease index (%)	48.27	8.53-90.00	34.04	31.92	87.91	61.65
Seed yield per plant (g)	3.29	0.30-9.99	54.48	33.46	37.72	42.33

variation that can be attributed to genetic factors. High heritability indicates that the trait is primarily controlled by genetic factors and is likely to respond well to selection. On the other hand, low heritability suggests a significant influence of environmental factors on the trait's expression. Genetic advance over the mean (GAM) represents the expected gain through selection for a particular trait. It indicates the magnitude of improvement that can be achieved by selecting the best-performing individuals.

Variability parameters in F_3 population: In the present study, a wide range of variability was observed for various traits in the F_3 population. The mean plant height was 29.96 cm, with a range from 14.00 cm to 46.00 cm. This indicates that there is considerable diversity in the plant height among the individuals in the population. Similarly, the number of branches per plant showed a mean value of 2.97, ranging from 2.00 to 8.00 branches. The number of clusters per plant exhibited a mean of 7.54, varying from 3.00 clusters to 14.00 clusters. Furthermore, the total number of pods per plant had a mean value of 19.19, with a range of 6.00 to 45.00 pods per plant. The average pod length was recorded as 4.24 cm, with values ranging from 3.00 cm to 5.50 cm. The number of seeds per pod showed a mean value of 6.36, varying from 4.00 seeds to 8.00 seeds per pod. Additionally, the mean 100-seed weight was 4.10 g, with a range of 2.70 g to 6.30 g. The *per cent* disease index (PDI), a measure of disease severity, had an average value of 48.27%, ranging from 8.53% to 90.00%. This wide range suggests considerable variation in disease susceptibility among the individuals in the population. Finally, the mean seed yield per plant was determined to be 3.29 g, with values ranging from 0.30 g to 9.99 g. These results indicate significant variability in seed yield potential. Overall, the mean values provide a summary of the average trait performance within the population, while the range illustrates the extent of variability present for each trait. These findings highlight the potential for selection and breeding strategies to effectively improve these traits by targeting individuals with desirable trait combinations within the observed ranges.

The difference between the phenotypic coefficient of variation (PCV) and the genotypic coefficient of variation (GCV) values was found to be higher for all the traits, indicating a significant influence of environmental factors on trait expression. Higher PCV and GCV values generally indicate greater variability within the population, making them valuable for breeding programs aimed at selecting desirable traits. Notably, plant height (20.66%), number of branches per plant (37.34%), number of clusters per plant (29.48%), number of pods per cluster (20.13%), total number of pods per plant (37.70%), *per cent* disease index (34.04%) and seed yield per plant (54.48%) exhibited high PCV values. High GCV was recorded for number of branches per plant (23.78%), *per cent* disease index (31.92%) and seed yield per plant (33.46%). These results align with previous studies conducted by Sathya *et al.* (2018), Punithavathy *et al.* (2020) and Kuralarasan and Jayamani (2021).

However, it should be noted that the observed phenotype may not be entirely transmitted to the next generation, indicating the necessity of studying the heritable portion of variability. Heritability serves as a useful indicator to assess the extent to which traits are inherited from parents to offspring. It provides a precise estimate of the heritable variability within a population. In the current study, high heritability (87.91%) was observed for the *per cent* disease index, while plant height (57.49%), number of branches per plant (40.53%), number of pods per cluster (32.22%), number of seeds per pod (33.82%), and seed yield per plant (37.72%) exhibited moderate heritability. These findings are consistent with the results reported by Sagar *et al.* (2021) and Saran *et al.* (2021).

To predict the genetic gain under selection, genetic advance is an important parameter that is estimated based on heritability, phenotypic standard deviation, and intensity of selection. Genetic advance as a percentage of mean (GAM) provides a reliable measure for evaluating the efficiency of selection in improving traits. In this study, plant height (24.47%), number of branches per plant (31.18%), total number of pods per plant (21.01%), *per cent* disease index (61.65%), and seed yield per plant (42.33%) exhibited high genetic advance. Similar outcomes were reported by Khan *et al.* (2020) and Kundagar *et al.* (2021) in blackgram. Moderate GAM was observed for the number of clusters per plant (12.65%) and number of pods per cluster (13.36%).

Considering the heritability and GAM values, the trait with the highest heritability and genetic advance was the *per cent* disease index. Plant height (cm), number of branches per plant, and seed yield per plant (g) exhibited moderate heritability and high genetic advance. These results suggest that the inheritance of these traits is primarily influenced by additive gene effects, indicating that selection could be effective in improving these traits. The simple pedigree method of selection can be employed to enhance these traits.

Association studies: The results of the correlation analysis for seed yield (g) and its component traits are presented in **Table 3**. Seed yield per plant (g) exhibited a significantly positive correlation with plant height (cm) (r = 0.391**), number of branches per plant (r = 0.340**), number of clusters per plant (r = 0.538**), number of pods per cluster (r = 0.497**), total number of pods (r = 0.750**), pod length (cm) (r = 0.358**), and number of seeds per pod (r = 0.322**) in the cross combination of VBN 11 x LBG 17. These findings are consistent with previous studies conducted by Umadevi and Ganesan (2005), Chauhan *et al.* (2007), Reddy *et al.* (2011), and Anuradha *et al.* (2020).

In terms of inter correlation studies, plant height (cm) exhibited a significantly positive association with traits such as the number of branches per plant (r = 0.407**), number of clusters per plant (r = 0.400**), number of pods per cluster (r = 0.322**), total number of pods per plant (r = 0.477**), pod length (cm) (r = 0.410**), number of seeds per pod (r = 0.390**), and 100-seed weight (g) (r = 0.405**). These results align with the reports of Panigrahi and Baisakh (2014), Patel *et al.* (2014), and Mathivathana *et al.* (2015).

The number of branches per plant showed a positive and significant correlation with the number of clusters per plant (r = 0.224**), total number of pods per plant (r = 0.227**), pod length (cm) (r = 0.449**), number of seeds per pod (r = 0.213**), and 100-seed weight (g) (r =0.274**). Similar outcomes were reported by Gowsalya *et al.* (2016), and Suguna *et al.* (2017).

The number of clusters per plant exhibited a significant and positive association with the number of pods per cluster (r = 0.406**), total number of pods per plant (r = 0.790**), pod length (cm) (r = 0.241**), and number of seeds per pod (r = 0.355**). Patel *et al.* (2014), and Bandi *et al.* (2018) also reported similar findings. The number of pods per cluster displayed a significant and positive correlation with the total number of pods per plant (r = 0.550**), pod length (cm) (r = 0.346**), and number of seeds per pod (r = 0.365**). The total number of pods per plant demonstrated a significant positive correlation with pod length (cm) (r = 0.350**) and the number of seeds per pod (r = 0.405**). Prasad and Murugan (2015) also reported the same results.

Pod length (cm) exhibited a significantly positive association with the number of seeds per pod (r = 0.527**) and 100-seed weight (g) (r = 0.221**). These findings are in line with those reported by Miah *et al.* (2016), Hemalatha *et al.* (2017), and Shalini and Lal (2019). The number of seeds per pod displayed a significant and positive correlation with 100-seed weight (g) (r = 0.187*). Similar results were reported by Kumar *et al.* (2014) and Sohel *et al.* (2016).

Table 3. Correlation analysis for seed yield and its yield component traits in VBN 11 x LBG 17

Characters	PH (cm)	NBP	NCP	NPC	TNP	PL (cm)	NSP	HSW (g)	PDI (%)
NBP	0.407**								
NCP	0.400**	0.224**							
NPC	0.322**	0.110	0.406**						
TNP	0.477**	0.227**	0.790**	0.550**					
PL (cm)	0.410**	0.449**	0.241**	0.346**	0.350**				
NSP	0.390**	0.213*	0.355**	0.365**	0.405**	0.527**			
HSW (g)	0.405**	0.274**	0.116	-0.021	0.056	0.221**	0.187*		
PDI (%)	-0.072	-0.110	0.070	-0.039	0.095	-0.039	-0.061	-0.062	
SYP (g)	0.391**	0.340**	0.538**	0.497**	0.750**	0.358**	0.322**	0.134	0.112

*, ** Significant at 5 and 1 *per cent* level

(PH- Plant height, NBP- Number of branches per plant, NCP- Number of clusters per plant, NPC- Number of pods per cluster, TNP- Total number of pods per plant, PL – Pod length, NSP- Number of seeds per pod, HSW- 100-seed weight, PDI- *Per cent* disease index, SYP- Seed yield per plant)

Table 4. Path analysis for seed yield and its yield component traits in VBN 11 x LBG 17

Characters	PH (cm)	NBP	NCP	NPC	TNP	PL (cm)	NSP	HSW (g)	PDI (%)	Correlation with SYP (g)
PH (cm)	**-0.069**	0.079	-0.067	0.047	0.374	0.003	-0.008	0.038	-0.006	0.391**
NBP	-0.028	**0.195**	-0.038	0.016	0.178	0.003	-0.004	0.026	-0.008	0.340**
NCP	-0.028	0.044	**-0.168**	0.059	0.620	0.002	-0.007	0.011	0.005	0.538**
NPC	-0.022	0.022	-0.068	**0.145**	0.431	0.002	-0.007	-0.002	-0.003	0.497**
TNP	-0.033	0.044	-0.133	0.080	**0.785**	0.002	-0.008	0.005	0.007	0.750**
PL (cm)	-0.028	0.088	-0.040	0.050	0.274	**0.007**	-0.010	0.021	-0.003	0.358**
NSP	-0.027	0.041	-0.060	0.053	0.318	0.004	**-0.020**	0.018	-0.005	0.322
HSW (g)	-0.028	0.054	-0.020	-0.003	0.044	0.002	-0.004	**0.094**	-0.005	0.134
PDI (%)	0.005	-0.022	-0.012	-0.006	0.075	0.000	0.001	-0.006	**0.076**	0.112

Residual effect = 0.31; (PH- Plant height, NBP- Number of branches per plant, NCP- Number of clusters per plant, NPC- Number of pods per cluster, TNP- Total number of pods per plant, PL – Pod length, NSP- Number of seeds per pod, HSW- 100-seed weight, PDI- *Per cent* disease index, SYP- Seed yield per plant)

Therefore, to improve seed yield in blackgram, it is advisable to focus on traits such as plant height (cm), number of branches per plant, number of clusters per plant, number of pods per cluster, total number of pods, pod length (cm), and number of seeds per pod. Hence, simultaneous selection for the aforementioned traits would be more effective in enhancing blackgram. However, no association was found between the *per cent* disease index (PDI) and yield or any of the yield components. Hence, the association studies revealed significant positive correlations between seed yield and various component traits. These findings provide valuable insights for breeders and researchers aiming to enhance seed yield in blackgram through targeted trait selection.

Path coefficient analysis :The estimation of correlation coefficients alone does not provide a comprehensive understanding of the direct and indirect effects of different traits on seed yield. To obtain a more detailed understanding, a path analysis was conducted on seed yield, allowing for the partitioning of the correlation coefficient into direct and indirect effects of yield components. **Table 4** presents the results of the path analysis, specifically focusing on the direct and indirect effects on seed yield per plant (g). The residual effect of 0.31 indicates the adequacy of the selected traits for the path analysis on seed yield per plant (g).

Among the various traits examined, the total number of pods per plant exhibited a highly positive direct effect (0.785) on seed yield per plant (g). Additionally, the number of branches per plant (0.195) and the number of pods per cluster (0.145) had low positive direct effects on seed yield per plant (g), while the number of clusters per plant (-0.168) had a low negative direct effect on seed yield per plant (g). These findings indicate that an increase in the total number of pods per plant has the most significant direct impact on enhancing seed yield per plant (g). Furthermore, the indirect effects of various yield components revealed that many traits had moderate to high indirect effects via the total number of pods per plant. These results align with the findings reported by Miah *et al.* (2016).

In conclusion, the improvement of seed yield per plant (g) can be achieved primarily through an increase in the total number of pods per plant. Furthermore, the association analysis demonstrated that the powdery mildew disease's *per cent* disease index (PDI) displayed no significant association with seed yield or any of the yield components. Therefore, the development of disease-resistant genotypes can be pursued without adversely affecting seed yield and its related components.

In summary, based on the findings of variability, association, and path analysis, it is recommended to focus on improving traits such as plant height, number of branches per plant, number of clusters per plant, number of pods per cluster, total number of pods per plant, pod length, and number of seeds per pod to enhance seed yield in blackgram. The study also emphasizes the possibility of developing disease-resistant genotypes without compromising seed yield. These findings provide valuable insights for breeders and researchers aiming to improve seed yield and disease resistance in blackgram through targeted trait selection and breeding strategies.

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