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## Research Article

### Genetics of powdery mildew disease resistance in blackgram [*Vigna mungo* (L.) Hepper]

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#### Abstract

Powdery mildew susceptible (VBN 11) and resistant (LBG 17) blackgram genotypes were crossed. Parents, F<sub>1</sub>, F<sub>2</sub>, F<sub>3</sub>, F<sub>4</sub> and BC<sub>1</sub>F<sub>2</sub> of cross VBN 11 X LBG 17 were screened against powdery mildew disease. Based on the *per cent* disease index (PDI), two phenotypic classes were formed as resistant and susceptible. The F<sub>1</sub> showed susceptible reaction to powdery mildew disease. The segregating population in F<sub>2</sub>, F<sub>3</sub>, F<sub>4</sub> and BC<sub>1</sub>F<sub>2</sub> segregated in 3:1 ratio for susceptible and resistant reaction to powdery mildew disease. The *Chi-square* test indicated that the 3:1 ratio was perfectly fit for the susceptible and resistant reaction for powdery mildew disease in all segregating populations. Hence, the present study confirmed that the resistance of powdery mildew resistance is governed by a monogenic recessive gene.

**Keywords:** Blackgram, genetics, powdery mildew, resistance, monogenic.

#### INTRODUCTION

Blackgram [*Vigna mungo* (L.) Hepper], also known as urad bean or black lentil, is an important legume crop widely cultivated in many parts of the world, particularly in Asia (Sharma *et al.*, 2019; Khan *et al.*, 2020). It is valued for its high protein content (20-25 %) and nutritional benefits, making it an essential food source for millions of people. However, blackgram production is often hampered by various biotic and abiotic stresses, among which powdery mildew (*Erysiphe polygoni*) stands out as a significant threat. Powdery mildew is a fungal disease that affects a wide range of plants, including most legumes. In Tamil Nadu, blackgram occupies in an area of 4.05lakh ha with production of 3.17lakh tones with productivity of

783 kg/ha during the year 2019-20 (TN Statistics, 2021) and 75% of the area being cultivated during *Rabi* and rice fallow conditions. In Tamil Nadu, powdery mildew incidence when the crop is grown particularly during *Rabi* season as well as rice fallow and cause yield losses up to 20-40% (Soria and Quebral 1973; Legaspi *et al.*, 1978). It manifests as a white powdery growth on the leaves, stems and pods of infected plants, leading to reduced photosynthetic efficiency, stunted growth, and yield losses (Chauhan *et al.*, 2018; Singh *et al.*, 2021). The disease can spread rapidly under favorable environmental conditions, causing devastating economic consequences for blackgram farmers.

To combat powdery mildew in blackgram, breeding for resistance has been recognized as a sustainable and effective strategy (Manivannan *et al.*, 2021). Identifying and utilizing resistant cultivars is a crucial step to develop disease-resistant varieties, which helps to reduce the reliance on chemical fungicides and mitigate the negative impact of the disease on blackgram production. Understanding the inheritance of resistance for particular disease is essential for breeders to develop improved blackgram varieties with durable resistance to powdery mildew.

By studying the genetics of powdery mildew resistance in blackgram, valuable insights can be gained into the genetic mechanisms underlying resistance. This knowledge can aid in the selection of superior parental lines for breeding programs and guide the development of resistant varieties through marker-assisted selection or other breeding strategies. With this background, the present investigation was carried out with various segregating generations of a cross to study the genetics of powdery mildew resistance in blackgram.

## MATERIALS AND METHODS

This investigation was carried out at Department of Pulses, Tamil Nadu Agricultural University, Coimbatore. Crosses were made between the blackgram genotypes VBN 11 (susceptible to powdery mildew) and LBG 17 (resistant to powdery mildew) during *Rabi* 2021-22 season. The  $F_1$  and their parents were raised together. True  $F_1$  plants were identified to raise the  $F_2$  population during *Summer* season 2022.  $F_2$  population was raised during *Kharif* 2022. True  $F_1$  was backcrossed with a susceptible parent (VBN 11) during *Kharif* 2022. The  $F_3$  population was raised in *Rabi* 2022. Part of seeds of all generations were kept as reserve for simultaneous evaluation for powdery mildew disease reaction. All generations  $F_1$ ,  $F_2$ ,  $F_3$ ,  $F_4$  and  $BC_1F_2$  populations including the parents VBN 11 and LBG 17 were raised under shade nets to induce conducive environments for screening of powdery mildew disease at Hybrid Rice Evaluation Centre, Tamil Nadu Agricultural University, Gudalur, The Nilgiris district during February 2023. The weather parameters like minimum (18.5 °C) and maximum temperature

(29.8 °C), the relative humidity in the morning (87%) and in the evening (59.0%) were observed during the cropping period. Recommended agronomic practices were used to establish the crop. Fungicides were not used during the cropping season to maintain the conidial spore population in the field. Additionally, plants were sprayed with an aqueous conidial suspension of the fungus *Erysiphe polygoni* (approximately  $1 \times 10^7$  spores  $ml^{-1}$ ) to ensure uniform infection and to increase disease pressure. The resistance of individual plants from different populations to powdery mildew was measured based on *per cent* disease index (PDI) observations. The blackgram plants were divided into six categories (**Table 1**) based on the *per cent* disease index (PDI) score (Mayee and Datar, 1986): Immune (0), Highly Resistant (1), Resistant (3), Moderately Resistant / Susceptible (5), Susceptible (7) and Highly Susceptible (9). Plants that are immune, resistant, highly resistant and moderately resistant were grouped as resistant group, whereas plants that are susceptible and highly susceptible were grouped as susceptible. In order to verify the goodness of fit, the data was examined using the *Chi-square* test.

## RESULTS AND DISCUSSION

The experiment aimed to study the segregation of the blackgram powdery mildew disease resistance in different generations of a cross between VBN 11 and LBG 17. **Table 2** shows that the parent VBN 11 is susceptible to powdery mildew disease, with a mean *per cent* disease index (PDI) of 81.00. In contrast, the parent LBG 17 is resistant to the disease, with a mean PDI of 4.05.

**Table 3** shows the segregation of powdery mildew resistance in parents along with different generations *viz.*,  $F_1$ ,  $F_2$ ,  $F_3$ ,  $F_4$ , and  $BC_1F_2$ . The  $\chi^2$  test was used to compare the observed values to the expected ratio and determine if there was a significant difference between them. The  $\chi^2$  values for all generations in **Table 3** were not significant (ns), indicating that the observed segregation of powdery mildew resistance in these generations was consistent with the expected ratio. This suggests that the genetic model used to explain the inheritance of powdery mildew disease resistance in this cross perfectly fits the observed data.

**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

**Table 2. Reaction of parents against powdery mildew disease resistance in blackgram**

Parents	Per cent disease index (PDI)		Reaction
	Mean	Range	
VBN 11	81	42-100	Susceptible
LBG 17	4.05	0-4	Resistant

**Table 3. Segregation for powdery mildew resistance in different generation of a cross between VBN 11 x LBG 17**

Generation	Number of plants	Number of plants		Expected ratio	$\chi^2$ values	$\chi^2$ table value (0.05)
		Susceptible	Resistant			
VBN 11	20	20	-	-	-	-
LBG 17	20	-	20	-	-	-
F <sub>1</sub>	10	10	-	-	-	-
F <sub>2</sub>	140	98	42	3:1	0.93 <sup>ns</sup>	3.84
F <sub>3</sub>	147	120	27	3:1	3.45 <sup>ns</sup>	3.84
F <sub>4</sub>	169	122	47	3:1	0.71 <sup>ns</sup>	3.84
BC <sub>1</sub> F <sub>2</sub>	100	74	26	3:1	0.05 <sup>ns</sup>	3.84

Note: "ns" indicates non-significant difference at the 0.05 significance level.

In the F<sub>2</sub> generation, out of 140 plants evaluated, 98 were classified as susceptible, and 42 were classified as resistant. The observed ratio of susceptible to resistant plants was 3:1, which did not deviate significantly from the expected ratio. The calculated  $\chi^2$  value of 0.93 was lower than the  $\chi^2$  table value of 3.84, indicating a non-significant difference between the observed and expected ratios. These results showed this character had a monogenic nature. Kaushal and Singh (1989) and Kanwade *et al.* (2019) reported similar findings. Additional genetic analyses and experiments, such as further crosses and molecular studies, may be necessary to confirm and understand the underlying genetic mechanisms responsible for the observed 3:1 inheritance ratio.

Similarly, in the F<sub>3</sub> generation, out of 147 plants evaluated, 120 were classified as susceptible, and 27 were classified as resistant. The observed ratio of susceptible to resistant plants was 3:1, which again did not deviate significantly from the expected ratio. The calculated  $\chi^2$  value of 3.45 was lower than the  $\chi^2$  table value of 3.84, indicating a non-significant difference. These results showed this trait was governed by monogenic gene action.

In the F<sub>4</sub> generation, out of 169 plants evaluated, 122 were classified as susceptible, and 47 were classified as resistant. The observed ratio of susceptible to resistant plants was 3:1, which showed no significant deviation from the expected ratio. The calculated  $\chi^2$  value of 0.71 was lower than the  $\chi^2$  table value of 3.84, indicating a non-significant difference. The F<sub>4</sub> population exhibited the

best goodness of fit and suggests that a single recessive gene was responsible for control of powdery mildew resistance in blackgram.

Finally, in the BC<sub>1</sub>F<sub>2</sub> generation, out of 100 plants evaluated, 74 were classified as susceptible, and 26 were classified as resistant. The observed ratio of susceptible to resistant plants was 3:1, which showed no significant deviation from the expected ratio. The calculated  $\chi^2$  value of 0.05 was lower than the  $\chi^2$  table value of 3.84, indicating a non-significant difference. Nisar and Ghafoor (2010) and Kute *et al.* (2003) have reported a single recessive gene control for powdery mildew resistance in blackgram.

To conclude, the present study provides evidence that the segregation of powdery mildew disease resistance in different generations of a cross between VBN 11 and LBG 17 blackgram follows the monogenic ratio. This information can be useful for understanding how powdery mildew disease resistance is inherited in blackgram for developing breeding strategies to improve disease resistance. According to the aforementioned findings, monogenic recessive genes control the expression of the resistance of powdery mildew disease in blackgram. Therefore, it might be appropriate to recommend that recombination breeding and immediate selection could be useful in improving resistance to the powdery mildew disease in blackgram. The obligate parasite nature of powdery mildew disease organism and difficulty in the creation of disease pressure creates hardship in the



VBN 11 (Susceptible)



LBG 17 (Resistant)

Fig. 1. Field photos for VBN 11 and LBG 17 with disease incidence

conventional breeding programme. Hence, identification of QTLs and marker assisted selection are more helpful for breeding powdery mildew disease resistance in blackgram.

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