



## Genetic Study for Inheritance of Powdery Mildew Disease Resistance in Blackgram [*Vigna mungo* (L.) Hepper]

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**ABSTRACT:** In this study, powdery mildew susceptible parent TBU-43-1 and resistant parent PU-609-43 were crossed. Parents, F<sub>1</sub>, F<sub>2</sub>, B<sub>1</sub> and B<sub>2</sub> of cross TBU-43-1 × PU-609-43 were screened for powdery mildew disease incidence and PDI was worked out. On the basis of PDI, plants were classified into two classes *i.e.*, susceptible and resistant. The F<sub>1</sub> showed susceptible reaction to powdery mildew. The segregating F<sub>2</sub> population displayed the segregation in 3:1 ratio for susceptible and resistant reaction to powdery mildew disease. The segregation of F<sub>2</sub> generation for powdery mildew disease reaction was confirmed in backcross generation. Also the Chi-square test indicated that the 3:1 ratio was perfectly fit for the susceptible and resistant reaction for powdery mildew disease. Thus, the current investigation revealed that a monogenic recessive gene controls powdery mildew resistance.

**Keywords:** Blackgram, inheritance, resistance, powdery mildew, monogenic, recessive gene.

### INTRODUCTION

Black gram, scientifically known as *Vigna mungo* (L.) Hepper, is a one of the important short-duration crop which belongs to family Fabaceae. It is important legume crop which is widely grown around the world, especially in Asia (Sharma *et al.*, 2019; Khan *et al.*, 2020). It is also known as urdbean, urd, mash and black lentil. India is primary centre of origin of blackgram. It is mainly grown in Asian nations such as Pakistan, Myanmar, and various regions of southern Asia (Basamma, 2011). World's largest producer as well as consumer of blackgram is India. It is cultivated on over 3.56 lakh hectares in Maharashtra, where it produces 2.27 lakh tons and has a productivity of 638 kg ha<sup>-1</sup> (Ministry of Agriculture, Govt. of India, 2022). Blackgram is nutritious crop which is rich in protein (20-26%) with high lysine content. But since last few years, there is decrease in yield due to biotic and abiotic stresses. Among the biotic stresses, powdery mildew is an important disease on blackgram with an estimated yield loss of 20-40% (Singh, 1980). To tackle powdery mildew in blackgram, breeding for resistance has been acknowledged as a sustainable and effective strategy (Manivannan *et al.*, 2021). To minimize the further epidemic losses, it is important to identify and utilize the resistant sources or cultivars for development of disease resistant varieties. Significant knowledge about the genetic mechanism behind the resistance may be

obtained by examining the genetic basis of resistance to powdery mildew in black gram. By using marker-assisted selection or other breeding approaches, this knowledge may helps in the identification of superior parental lines for breeding programs and serve as a guide for the development of resistant cultivars. In regard to this, the current investigation uses six generations of a cross to investigate the inheritance of powdery mildew resistance in blackgram.

### MATERIAL AND METHODS

The current study was carried out at Botany farm, PGI, Mahatma Phule Krishi Vidyapeeth, Rahuri during Kharif, 2021. It includes six generations of cross *i.e.*, parents, F<sub>1</sub>, F<sub>2</sub>, B<sub>1</sub> and B<sub>2</sub>. The experimental material consist of two genotypes *viz.*, TBU-43-1 (susceptible parent) and PU-609-43 (resistant parent) obtained from Oilseed Research Station, Jalgaon (Plate 1). F<sub>1</sub>'s were made during Rabi, 2020. During Kharif, 2020, F<sub>2</sub> population was raised from these F<sub>1</sub> and new F<sub>1</sub>'s were developed for final evaluation trial. B<sub>1</sub> and B<sub>2</sub> were made during Rabi, 2021. For screening powdery mildew disease use of spreader row technique was done. In this experiment, susceptible powdery mildew variety TBU-43-1 was sown as a border row on 24 June, 2021. Susceptible variety was sown after every four test entries to ensure high disease pressure at the time of normal sowing *i.e.*, on 8 July, 2021. Furthermore, infection spreads at vulnerable times,

which are 20 and 40 days after sowing, increasing the pressure for spreading the disease. To establish the crop, recommended agronomic techniques were followed. To sustain the conidial spore population in the field during the cropping season, fungicides were not used.

When 100% disease was detected on infector rows (TBU-43-1), percent disease intensity (PDI) observations were recorded. The incidence of powdery mildew disease was noted on selected leaves of each plant in the parent, F<sub>1</sub>, F<sub>2</sub>, B<sub>1</sub>, and B<sub>2</sub> generations. The leaves were graded using a progressive scale ranging from 0 to 5 (Table 1). The PDI was calculated using the formula given by Wheeler (1969). The data was analyzed using the Chi-square test to confirm the goodness of fit (Fisher, 1930).

**Table 1: Rating scale for powdery mildew reaction.**

| Scale | PDI        | Reaction               |
|-------|------------|------------------------|
| 0     | 0          | Immune                 |
| 1     | 0.1-10     | Resistant              |
| 2     | 10.1-25    | Moderately resistant   |
| 3     | 25.1-50    | Moderately susceptible |
| 4     | 50.1-75    | Susceptible            |
| 5     | Above 75.1 | Highly susceptible     |

$$PDI = \frac{\text{Sum of all numerical ratings}}{\text{Number of leaves observed} \times \text{Maximum rating}} \times 100$$

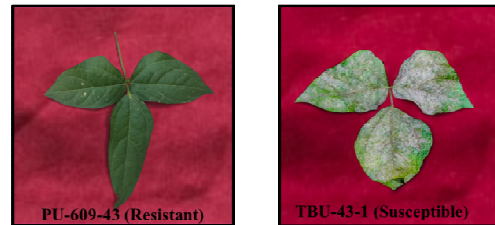
## RESULTS AND DISCUSSION

The result of present study revealed the resistance of powdery mildew in blackgram for cross TBU-43-1 × PU-609-43. In parent PU-609-43, the PDI ranged from 2.22 to 8.89 with mean of 6.67. Hence was classified as resistant to powdery mildew disease. The PDI value in parent TBU-43-1 ranged from 26.67 to 48.89 with a mean value of 38.32 and classified as moderately susceptible for powdery mildew.

PDI values in the F<sub>1</sub> of cross (TBU-43-1 × PU-609-43) was ranged from 24.44-48.89 with mean value of 33.73. The susceptible reaction in F<sub>1</sub> generation of cross (S × R) was indicating that is recessive gene controls the resistance (Table 2).

Out of total 275 F<sub>2</sub> population of cross (TBU-43-1 × PU-609-43), 196 plants were found to be susceptible with PDI value between 25.1- 50 hence grouped as moderately susceptible. Apart from this, 79 plants were found to be resistant. From these 79 plants, 13 plants

showed PDI values between 0.1-10 which were grouped as resistant. Remaining 66 plants showed PDI values between 10.1 – 25 which were grouped as moderately resistant. Thus according to disease rating scale F<sub>2</sub> population of cross (TBU-43-1 × PU-609-43) was grouped into two main classes viz., resistant and susceptible (Table 3). The ratio of resistant : susceptible was good fit into monogenic ratio *i.e.*, 1 resistant : 3 susceptible with  $\chi^2$  value of 2.03 which was non-significant for observed and expected frequency with 'p' value 0.15 (Table 4).



**Plate 1.** Parents reaction to powdery mildew.

**Table 2: The reaction of parents and their F<sub>1</sub> of cross TBU-43-1 × PU-609-43 against powdery mildew disease in black gram.**

|                      | Percent disease intensity (PDI) |             | Reaction         |
|----------------------|---------------------------------|-------------|------------------|
|                      | Mean                            | Range       |                  |
| <b>Parents</b>       |                                 |             |                  |
| TBU-43-1             | 38.32                           | 26.67-48.89 | Mod. Susceptible |
| PU-609-43            | 6.67                            | 2.22-8.89   | Resistant        |
| <b>F<sub>1</sub></b> |                                 |             |                  |
| TBU-43-1 × PU-609-43 | 33.73                           | 24.44-48.89 | Mod. Susceptible |

**Table 3: Segregation of powdery mildew resistance in F<sub>2</sub>, B<sub>1</sub> and B<sub>2</sub> generations of cross (TBU-43-1 × PU-609-43) in black gram.**

| Generations                            | Number of plants observed |             |       |
|--|---------------------------|-------------|-------|
|  | Resistant                 | Susceptible | Total |
| <b>Cross</b><br>(TBU-43-1 × PU-609-43) |                           |             |       |
| P <sub>1</sub>                         | 0                         | 30          | 30    |
| P <sub>2</sub>                         | 30                        | 0           | 30    |
| F <sub>1</sub>                         | 0                         | 28          | 28    |
| F <sub>2</sub>                         | 79                        | 196         | 275   |
| B <sub>1</sub>                         | 0                         | 29          | 29    |
| B <sub>2</sub>                         | 11                        | 17          | 28    |

**Table 4 : Inheritance of powdery mildew disease resistance in blackgram.**

| Parents /Crosses  | Generations                 | Number of observed plants |     |       | Number of expected plants |        | Expected Ratio (3:1) |   | $\chi^2$  | $\chi^2$ table value | 'P' Value |
|---|-----------------------------|---------------------------|-----|-------|---------------------------|--------|----------------------|---|-----------|----------------------|-----------|
|   |                             | R                         | S   | Total | R                         | S      | R                    | S |           |                      |           |
| <b>Parents</b>  | TBU-43-1 (P <sub>1</sub> )  | 0                         | 30  | 30    | -                         | -      | -                    | - | -         | -                    | -         |
|   | PU-609-43 (P <sub>2</sub> ) | 30                        | 0   | 30    | -                         | -      | -                    | - | -         | -                    | -         |
| <b>Cross (S×R)</b><br><b>TBU-43-1</b><br><b>×</b><br><b>PU-609-43</b> | F <sub>1</sub>              | 0                         | 28  | 28    | -                         | -      | -                    | - | -         | -                    | -         |
|   | F <sub>2</sub>              | 79                        | 196 | 275   | 68.75                     | 206.25 | 1                    | 3 | 2.03 (ns) | 3.84                 | 0.15      |
|   | B <sub>1</sub>              | 0                         | 29  | 29    | -                         | -      | -                    | - | -         | -                    | -         |
|   | B <sub>2</sub>              | 11                        | 17  | 28    | 14                        | 14     | 1                    | 1 | 1.28 (ns) | 3.84                 | 0.26      |

R: Resistant, S: Susceptible,  $\chi^2$ : Chi-square value, P: Probability, ns.: Non-significant

The segregation of F<sub>2</sub> generation for powdery mildew disease reaction was confirmed in backcross generation. In B<sub>1</sub> generation, all 29 plants were found to be susceptible. In contrast, from 28 plants examined in B<sub>2</sub>, 17 were categorized as susceptible, and 11 as resistant (Table 3). From these 11 plants, 3 were resistant and 8 were moderately resistant. The observed ratio of susceptible to resistant plants was 1:1, which again did not deviate significantly from the expected ratio. The segregation of resistant and susceptible plants good fit into ratio of 1 resistant : 1 susceptible. The calculated  $\chi^2$  value of 1.28 was lower than the  $\chi^2$  table value of 3.84, indicating a non-significant difference with 0.26 probability value (Table 4).

Similar outcomes were stated by Kaushal and Singh (1989), Nisar and Ghafoor (2009); Kanwade *et al.* (2019); Punithavathy *et al.* (2023). According to Kute *et al.* (2003), duplicate recessive genes control resistance. Nonetheless, Chaitieng *et al.* (2002); Khajudparn *et al.* (2007); Srivastava *et al.* (2013); Pulate (2016) ; Kohakade (2021) revealed the contradicting results. They reported that one dominant gene controlled the resistance to powdery mildew. Reddy (2009); Basamma (2011), however, showed that resistance was controlled by two dominant genes. Additive gene action was reported by Sorajjapinun *et al.* (2005); Waraluk *et al.* (2009) to influence mungbean resistance to powdery mildew.

## CONCLUSIONS

To summarize, the current research conclude that the segregation of resistance to powdery mildew disease of a blackgram cross TBU-43-1 × PU-609-43 follows the monogenic ratio. These results may be helpful in the development of breeding techniques to increase disease resistance as well as to understand the resistant of blackgram to the powdery mildew disease. The result above suggests that expression of blackgram's resistance to powdery mildew disease is controlled by a single recessive gene. Recombination breeding or immediate selection would be preferred to increase resistance in blackgram for powdery mildew.

## FUTURE SCOPE

For the development of a powdery mildew resistant variety in blackgram, the resistant plants recognized for powdery mildew in F<sub>2</sub> should be used. The causal organism is an obligate parasite and infected plants can serve as a means of artificial inoculation. However, environmental variables may mitigate the severity of the disease which makes conventional breeding quite challenging. In order to develop blackgram resistant to the powdery mildew disease, it is therefore more beneficial to identify QTLs and use marker assisted selection.

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**Conflict of Interest.** None.

## REFERENCES

- Chaitieng, B., Kaga, A., Han, O. K., Wang, Y. W., Wongkaew, S., Laosuwan, P., Tomooka, N. and Vaughan, D. A. (2002). Mapping a new source of resistance to powdery mildew in mungbean. *Plant Breeding*, 121, 521-525.
- Fisher, R. A. (1930). The genetic theory of natural selection. In: Strickberger, M.W., Genetics. McMillan Co., New York. Pp 772.
- Kaushal, R. P. and Singh, B. M. (1989). Genetics of resistance in blackgram (*Phaseolus mungo*) to powdery mildew caused by *Erysiphe polygoni*. *Indian Journal of Agricultural Science*, 59(10), 684-685.
- Khajudparn, P., Wongkaew, S. and Thipyapong, P. (2007). Mungbean powdery mildew resistance identification of gene for resistance to powdery mildew in mungbean. *African Crop Science Conference Proceedings*, 8, 743-745.
- Khan, M. A., Awan, M. S. and Ahmad, S. (2020). Black gram (*Vigna mungo* L.): A review on morphology, cultivation, genetic diversity and breeding prospects. *Journal of Animal and Plant Sciences*, 30(3), 785-796.
- Kanwade, D. G., Kute, N. S., Bedis, M. R., Pawar, V. Y., Deshmukh, G. P., Jaybhaye, C. P. and Giri, M. D. (2019). Inheritance of powdery mildew resistance in mungbean [*Vigna radiata* (L.) R. Wilczek]. *Journal of Pharmacognosy and Phytochemistry*, 8(3), 3642-3644.
- Kohakade, S. N. (2021). Genetic studies for quantitative traits and inheritance of powdery mildew resistance in green gram [*Vigna radiata* (L.) Wilczek] Ph.D. Thesis, Mahatma Phule Krishi Vidyapeeth, Rahuri, Maharashtra, India.
- Kumari Basamma (2011). Conventional and molecular approaches in breeding for high yield and disease resistance in urdbean (*Vigna mungo* (L.) Hepper). Ph.D. Thesis, USA, Dharwad, India.
- Kute, N. S., Deshmukh, R. B. and Patil, J. V. (2003). Inheritance of resistance to powdery mildew (*Erysiphe polygoni* DC) in mungbean (*Vigna radiata* L. Wilczek). *Legume Research-An International Journal*, 26(1), 24-27.
- Manivannan, S., Subramanian, K., Jaganathan, D., Kumar, N., Manikandan, R. and Ulaganathan, V. (2021). Inheritance of powdery mildew (*Erysiphe polygoni* DC.) resistance in blackgram (*Vigna mungo* L. Hepper). *Journal of Pharmacognosy and Phytochemistry*, 10(6), 2713-2717.
- Ministry of Agriculture and FW (DAC&FW) Government of India (2022).
- Nisar, M. and Ghafoor, A. (2010). Inheritance studies of Pisum sativum F<sub>1</sub>, F<sub>2</sub> and F<sub>3</sub> generation based morphological traits and selection of high yielding powdery mildew resistant lines. *Molecular Plant Breeding*, 7(2), 335-340.
- Pulate, S.C. (2016). Inheritance of powdery mildew resistance, grain yield and yield components in black gram (*Vigna mungo* (L.) Hepper). Ph.D. Thesis, Mahatma Phule Krishi Vidyapeeth, Rahuri, Maharashtra, India.
- Punithavathy P., Kumaresan D., Manivannan N., Manikanda Boopathi N. and Senthilraja G. (2023). Genetics of powdery mildew disease resistance in blackgram [*Vigna mungo* (L.) Hepper]. *Electronic Journal of Plant Breeding*, 14(4), 1421-1424.

- Reddy, K. S. (2009). Identification and inheritance of a new gene for powdery mildew resistance in mungbean (*Vigna radiata* L. Wilczek). *Plant Breeding*, 128(5), 521-523.
- Singh, D. P. (1980). Inheritance of resistance to yellow mosaic virus in blackgram (*Vigna mungo* L.). *Theoretical and Applied Genetics*, 57, 233-235.
- Sharma, S. K., Saxena, D. R., Chaurasia, O. P. and Saxena, K. B. (2019). Breeding for powdery mildew resistance in urdbean (*Vigna mungo* L. Hepper). *The Bioscan*, 14(1), 365-369.
- Shrivastava P., Pandey A., and Singh M. (2013). Identification of the RAPD marker linked to powdery mildew resistant gene(s) in black gram by using Bulk Segregants Analysis. *Research Journal of Biotechnology*, 8(2), 9-15.
- Sorojjapinum, W., Rewthongchum, S., Koizumin, M., and Srinives, P. (2005). Quantitative inheritance of resistance to powdery mildew disease in mungbean (*Vigna radiata* L. Wilczek). *Sabrao Journal of Breeding and Genetics*, 37(2), 91-96.
- Waraluk, K., Prakit, S. and Peerasak, S. (2009). Genetics of the resistance to powdery mildew disease in mungbean (*Vigna radiata* (L.)Wilczek). *Journal of Crop Science and Biotechnology*, 121, 37-42.
- Wheeler, B. E. J. (1969). An introduction to plant diseases. John Wiley and Sons Ltd., London, Pp. 300-309.

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