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SHORT RESEARCH ARTICLE

Unraveling the inheritance of powdery mildew disease resistance in blackgram [*Vigna mungo* L. Hepper]

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Abstract

The present investigation was carried out to unravel the inheritance of powdery mildew disease (PMD) resistance using two F_1 (LGB 752 × DBGV 5 and VBN 6 × LBG 17) and their corresponding F_2 segregating populations. Results showed that both the F_1 showed resistance and their F_2 populations segregated in to 9:3:3:1 ratio, and goodness of fit showed highly significant indicating PMD resistance is controlled by two major dominant genes, which are bi-allelic, non-epistatic, and di-genic in nature.

Keywords: Blackgram, inheritance, di-genic, dominance.

Powdery mildew disease (PMD) caused by the fungus *Erysiphe polygoni* D.C. is a significant threat to blackgram, leading to substantial yield losses. Host plant resistance is recognized as an effective and environmentally friendly strategy to combat this disease. The efficiency of disease resistance breeding depends on reliable information on the inheritance of the disease. In the present study we unraveled the inheritance pattern of PMD resistance under the genetic background of well-known PMD resistance sources (LBG752 and LBG17) of blackgram. The two F_1 (LGB 752 × DBGV 5 and VBN 6 × LBG 17), corresponding F_2 segregating populations and their parents were screened for PMD responses under natural conditions.

The PMD severity (Mayee and Datar 1986) of parents, F_1, and F_2 was recorded and converted into Per cent Disease Index (PDI) by using the following formula suggested by Wheeler (1969).

$$\text{Percent disease index (PDI)} = \frac{\text{Sum of the individual disease ratings}}{\text{No. of plants observed x maximum disease grade}} \times 100$$

The data on PMD severity wasused to classify the segregating population into distinct classes (r_0, r_1 and r_2 and s) and analyzed with the help of Chi-square (χ^2) test for a fixed ratio hypothesis. Heterogeneity/homogeneity among F_2 populations was evaluated using a contingency test.

Mode of inheritance

The analysis of results showed that all the F_1 plants of both the crosses showed highly resistant reactions to PMD (Table 1 and Fig. 1). The F_2 plants of LBG 752 × DBGV 5 and VBN 6 × LBG 17 were grouped into four distinct classes viz. r0: highly resistant/immune; r_1: resistant; r_2: moderately resistant; s: susceptible aligning with scale given by Mayee and Datar, 1986. Out of 200 F_2 plants derived from LBG 752 × DBGV 5, 131 F_2 plants showed no visible infections or less than 1% infection thus, classified as r_0 category under immune and

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Table 1. Mean disease severity, scoreand PDI of parents and F_1s of the two crosses and corresponding disease reaction in blackgram

Parent/F_1	Disease severity	Mean score	PDI	Reaction
LBG 752 (Female)	0.22	0.4	04.44	Highly Resistant
DBGV 5 (Male)	61.6	8.2	91.11	Highly Susceptible
LGB 752 × DBGV 5 (F_1)	0.26	0.6	06.67	Highly Resistant
VBN 6 (Female)	58.5	8.0	88.89	Highly Susceptible
LBG 17 (Male)	0.20	0.3	03.33	Highly Resistant
VBN 6 × LBG 17 (F_1)	0.24	0.5	05.56	Highly Resistant

Table 2. Inheritance of host plant resistance to powdery mildew disease in F₂ population derived from two crosses in blackgram

Cross	Parent/ generation	Observed number of F_2 plants					Expected ratio	Expected number of F_2 plants				$\chi2$ statistic	Pr> χ^2
		Total	r_0	r_1	r_2	s		r_0	r_1	r_2	s		
LBG 752 × DBGV 5	LBG 752	10	10	0	0	0	-	10	0	0	0	-	-
	DBGV 5	10	0	0	0	10	-	0	0	0	10	-	-
	F_1	10	10	0	0	0	-	10	0	0	0	-	-
	F_2	200	131	33	27	9	9:3:3:1	112.5	37.5	37.5	12.5	7.50	0.06
VBN 6 × LBG 17	VBN 6	10	0	0	0	10	-	0	0	0	10	-	-
	LBG 17	10	10	0	0	0	-	10	0	0	0	-	-
	F_1	10	10	0	0	0	-	10	0	0	0	-	-
	F_2	200	121	29	33	16	9:3:3:1	112.5	37.5	37.5	12.5	3.66	0.3
Heterogeneity c^2	F_2	-	-	-	-	-	-	-	-	-	-	4.66	0.19

r_0 = Highly resistant/immune; r_1 = Resistant; r_2 = Moderately resistant; s = Susceptible, $\chi2$ test @ 5 % level of significance.

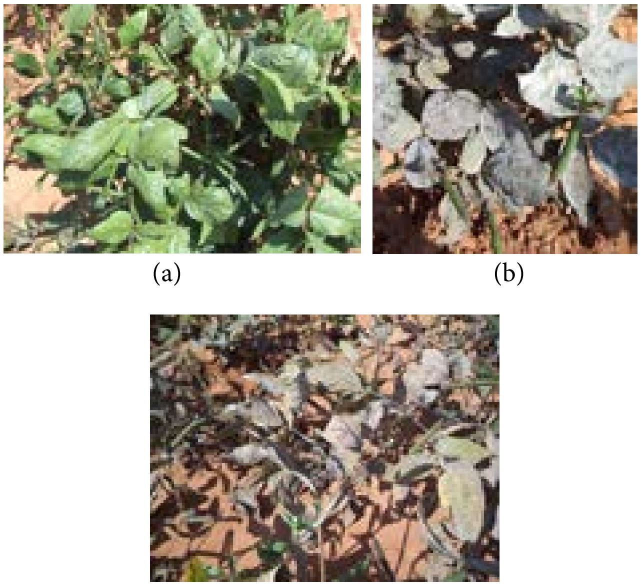
(a) (b) (c)

Fig. 1. Depiction of powdery mildew symptoms, (a) resistant parent; (b) susceptible parent and (c) F1 hybrid

highly resistant group (Table 2). While 33 plants had shown up to 10% leaf coverage by mycelial growth spots and hence, it was grouped under resistant and classified as r_1 category. Twenty seven F_2 plants showed infection covering approximately 11% to 25% of leaf area and slight infection on stems and thus grouped into moderately resistant and classified as r_2. The remaining9 plants were grouped into susceptible reactions (MS-medium susceptible and HS-highly susceptible) since they showed dense powdery coating covering more than 25% of leaf area, and stems including pods and hence classified as 's' category. The significance of the average PMD severity of F_2 individuals classified into these four classes as indicated by the 'F' test justified the classification. The visual examination of the data in r_0, r_1, r_2, and s classes intuitively suggested that resistance to PMD could be controlled by two independent non-epistatic genes with an expected 9:3:3:1 segregation in F_2 generation. Further, these observations were confirmed by Chi-square test with a χ^2 value of 7.50 (P= 0.06) when tested against the expected ratio of 9 highly resistant/immune (r_0): 3 resistant (r_1): 3 moderately resistant (r_2): 1 susceptible (s). Similarly, 121 of 200F_2 plants of VBN 6 × LBG 17 cross exhibited highly resistant/immune, 29 plants showeda resistant reaction, 33 plants displayed moderately resistant, and 16 plants were found susceptible to PM disease (MS and HS) with a c^2 value of 3.66 (P= 0.30) upon testing against the expected ratio 9 r_0:3 r_1:3 r_2:1 s (Table 2).

Bi-allelic non-epistatic di-genic inheritance of PMD resistance was evident from the segregation of F_2 plants (Fig. 1) derived from two crosses in 9:3:3:1 ratio. The F_1 and F_2 data confirmed the dominance of resistance to PMD. The non-significant heterogeneity c^2 statistic indicated consistent bi-allelic non-epistatic di-genic inheritance of PMD resistance across two crosses. The presence of dominant alleles at the two loci is necessary for plants to exhibit highly resistant or immune reaction and the presence of any single dominant allele at either of the loci exhibit resistant or moderately resistant reaction. While the presence of recessive alleles at both loci results in plants displaying susceptible reactions. The similar pattern ofinheritance of PMD resistance reported in our investigation and by Basamma (2011) may due to use of common parent i.e., LBG-17, which was confirmed as PMD resistant source at physio-biochemical level (Tirupathiswamy et al. 2017). Based on the findings our study, it was concluded that the two dominant genes involved in PMD resistance and thus the selection for PMD resistance can be initiated at early segregating generations and further which may be intermated to accumulate resistance genes and to fix resistance at the desired level. Further, the breeding potential and transgressive segregants of these crosses (Boraiah et al. 2022) justifying the concluding assumptions of our study. Hence, information on the inheritance of PMD from the present study can be useful for plant breeders involved in developing PMD resistant varieties of blackgram.

Authors' contribution

Conceptualization of research (KMB, MB); Designing of the experiments (KMB, CMK); Contribution of experimental materials (MB); Execution of field/lab experiments and data collection (KMB, CMK, PSB); Analysis of data and interpretation (KMB, CMK, C, CBH); Preparation of the manuscript (KMB, KBN).

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