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EVALUATION OF BLACK GRAM GENOTYPES FOR POWDERY MILDEW DISEASE RESISTANCE UNDER NATURAL EPIPHYTOTIC CONDITION

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ABSTRACT

Among pulses, black gram [*Vigna mungo* (L.)] is an important short duration crop widely cultivated in India. The main factors responsible for low productivity in black gram include-susceptibility to several serious diseases like powdery mildew, Mungbean yellow mosaic virus (MYMV) and *Cercospora* leaf spot. Among these, powdery mildew caused by the fungus *Erysiphe polygoni* D.C. is a common foliar disease of urdbean causing yield losses upto 40%. The study was undertaken with an objective to identify urdbean genotypes resistant against powdery mildew disease based on the phenotypic reaction. The screening of 100 black gram genotypes for powdery mildew disease under natural epiphytotic condition during *kharif*-2018 season revealed that, nine genotypes *viz*., LBG-17, LBG-645, LBG-20, KU-5-527, LBG-752, COBG-647, LBG-623, LBG-465 and LBG 685 registered resistant reaction to powdery mildew disease. The genotype, LBG-17 (0.49) recorded minimum whereas, susceptible check, TAU-1 (69.92) recorded maximum per cent disease severity.

Key words : Black gram, Genotype, Powdery mildew, Per cent disease severity, Disease.

Introduction

Among pulses, black gram [*Vigna mungo* (L.)] is an important short duration crop widely cultivated in India. It is an excellent source of easily digestible good quality protein and also has ability to restore the soil fertility through symbiotic nitrogen fixation like any other leguminous crop. It is cultivated in almost all parts of India and is third most important pulse crop both in acreage and production. The productivity of black gram in India is very low and is plagued with a number of biotic and abiotic stresses, which reduce the yields considerably. Improvement of yield forms the prime objective of breeding in any crop species including black gram. The main factors responsible for low productivity in black gram include-susceptibility to several serious diseases like powdery mildew, Mungbean yellow mosaic virus (MYMV) and *Cercospora* leaf spot. Among these, powdery mildew caused by the fungus *Erysiphe polygoni* D.C. is a common foliar disease of urdbean, particularly in the cool dry season. The disease epidemic covers the upper side of leaves with white floury patches and parts of the leaves and later changes into brown. Yield losses due to the disease were reported to be 20-40% at the reproductive stages (Fernandez and Shanmuga sundaram, 1988), but the damage can be more serious when the epidemic starts at the seedling stage (Reddy *et al.* 1994). Therefore, identification of potential resistance source becomes very important for the development of resistant varieties of black gram for the disease.

Materials and Methods

The experiment material for the present investigation consisted of 100 black gram genotypes collected from different sources *viz*., Agricultural Research Station, Bidar; Nuclear Agriculture and Biotechnology Division, Bhabha Atomic Research Centre, Trombay, Mumbai; Indian Institute of Pulse research, regional station, Dharwad and Regional Agricultural Research Station, LAM, Guntur. All the 100 black gram entries were

Table 1 : Powdery mildew severity rating scale (0-9 scale) (Mayee and Datar, 1986).

Scale	Description	Category
0	No symptoms on leaf	Immune
1	Small white specks on the leaf covering 1 percent or less of the area	Resistant (R)
3	Small powdery patches covering 1-10 percent of leaf area	Moderately Resistance (MR)
5	Powdery lesions enlarged covering 11-25 percent of leaf area	Moderately susceptible (MS)
7	Powdery patches irregular in size covering 26-50 percent of leaf area	Susceptible (S)
9	White powdery growth covering more than 50 percent of the leaf area	Highly susceptible (HS)

screened for their reaction to the powdery mildew disease under natural epiphytotic condition during *kharif*-2018 at Agricultural Research Station, Bidar. The screening was done during *kharif*-2018 because disease incidence will be high during the *kharif* season. All the genotypes were sown in two rows of 3 meter length and per cent disease severity was recorded and based on their reaction, genotypes categorised into immune, resistant, moderately resistant, susceptible and highly susceptible, using 0 to 9 scale (Mayee and Datar, 1986) (Table 1).

Further, Per cent Disease Index (PDI) can be calculated by using following formula given by Wheeler (1969).

$$\text{Per cent Disease Index (PDI)} = \frac{\text{Sum of the individual disease ratings}}{\text{Total number of ratings} \times \text{Maximum disease grade}} \times 100$$

Results and Discussion

Powdery mildew has long been known as important disease of plants in all parts of world. The disease noticed generally on all aerial parts of the plants. Powdery mildew caused by *Erysiphe polygoni* D.C. is one of the major constraints in the production of black gram, which cause both qualitative and quantitative loss of grains. Cultivation of resistant genotypes is an effective and cheaper method to manage the disease by the farmers.

In the present investigation, 100 genotypes were screened for their reaction to the powdery mildew disease under natural epiphytotic condition during *kharif* -2018 to identify resistant genotypes. Powdery mildew disease severity was recorded at pod formation stage of the crop using 0-9 scale (Mayee and Datar, 1986) and results are presented in Table 2. The results revealed that, the per cent disease severity varied from 0.49 to 69.92 and the resistant genotype, LBG-17 recorded minimum per cent disease severity (0.49) whereas, susceptible check TAU-1 recorded maximum per cent disease severity of 69.92 per cent. It indicates that the disease pressure was high during the screening of genotypes and which in-turn helped in proper screening and classification of genotypes into different disease reaction groups.

Out of 100 entries, a total of 9, 28, 20, 37 and 6 genotypes exhibited different levels of resistance reaction and are classified into resistant (R), moderately resistant (MR), moderately susceptible (MS), susceptible (S) and highly susceptible (HS), respectively, as indicated in the Table 3. None of them exhibited immune reaction, however, nine genotypes *viz.*, LBG-17, LBG-645, LBG-20, KU-5-527, LBG-752, COBG-647, LBG-623, LBG-465 and LBG-685 recorded resistant reaction.

The per cent disease severity varied from 0.49 to 69.92.The genotype LBG-17 recorded minimum per cent disease severity (0.49), whereas, susceptible check TAU-1 (69.92) recorded maximum per cent disease severity. In Resistant disease reaction category, the per cent disease severity ranged from 0.49 (LBG-17) to 0.97 (LBG-685); in moderately resistant disease reaction category, ranged from 6.85 (BDU-5) to 9.83 (TRCRU-18); in moderately susceptible disease reaction category, ranged from 13.20 (TRCRU-262) to 24.63 (RU-16-14); in susceptible disease reaction category ranged from 26.36 (2KU-15) to 43.50 (TU-98-10-5) and in highly susceptible disease reaction category ranged from 58.27 (RU-16-15) to 69.92 (TAU-1).

Among the genotypes screened none of the genotypes found to have exhibited immune disease reaction. However, nine genotypes *viz.*, LBG-17, LBG-645, LBG-20, KU-5-527, LBG-752, COBG-647, LBG-623, LBG-465 and LBG 685 recorded resistant disease reaction, 28 genotypes recorded moderately resistant disease reaction, while, remaining genotypes recorded varied range of susceptible disease reaction. Similar studies were carried out by many researchers and to mention few of them are; Channaveeresh *et al*. (2014), who reported three black gram genotypes *viz.*, LBG-17, LBG-685 and LBG-685×VT (F_2-F_3) as resistant; Nadarajan and Gupta (2010) reported LBG 17, LBG 402, CoBG 5, WBU 108, Vamban-4 black gram genotypes as powdery mildew disease resistant; Priyanka *et al*. (2018), reported genotype, LBG-645 as highly resistant and Akthar *et al*. (2014) recorded BS 2-3, IPU 02-43 and B 3-8-8 as resistant genotypes for powdery mildew disease. Shweta Deshmukh *et al*. (2022) recorded 3 genotypes Pusa B-43, RVSTU 21-1 and Pant U-30 as immune and two

Table 2 : Reaction of black gram genotypes to the powdery mildew disease under natural epiphytotic condition during *kharif*.

S. no.	Genotype	Per cent disease severity	Rating (0-9 scale)	Reaction	S. no.	Genotype	Per cent disease severity	Rating (0-9 scale)	Reaction
1	BDU-68	29.37	7	S	44	LBG-465	0.93	1	R
2	TU-98-1-18	13.56	5	MS	45	LBG-20	0.75	1	R
3	KML-8	31.20	7	S	46	DBGV-5	16.96	5	MS
4	BDU-3-22	9.37	3	MR	47	TU-94-2	9.52	3	MR
5	2KU-64	8.13	3	MR	48	I-447-2	29.21	7	S
6	T-200-6	35.20	7	S	49	DU-7-638	30.46	7	S
7	BDU-1	24.14	5	MS	50	Manikya	31.56	7	S
8	GP-728	33.27	7	S	51	VBN-3	29.81	7	S
9	TAU-1-12	33.91	7	S	52	RU-16-12	28.53	7	S
10	KU-537	23.24	5	MS	53	DBG-11	35.12	7	S
11	BDU-3-20	7.74	3	MR	54	2KU-15	26.36	7	S
12	COBG-647	0.82	1	R	55	PMS-2	35.26	7	S
13	BDU-3-23	23.67	5	MS	56	RU-16-15	58.27	9	HS
14	GP-553	41.62	7	S	57	TRCRU-111	13.52	5	MS
15	KU-5-527	0.76	1	R	58	TRCRU-24	14.12	5	MS
16	IC-436516	8.27	3	MR	59	TRCRU-134	9.20	3	MR
17	IC-436778	8.32	3	MR	60	TRCRU-43-1	29.42	7	S
18	TU-98-10-5	43.50	7	S	61	TRCRU-67	21.24	5	MS
19	BDU-3-21	9.15	3	MR	62	BDU-17	8.10	3	MR
20	TRCRU-262	13.20	5	MS	63	BDU-18	8.62	3	MR
21	TU-99-852	28.30	7	S	64	AKU-15	8.33	3	MR
22	LBG-623	0.86	1	R	65	TRCRU-136	24.30	5	MS
23	GPS-53-1	18.65	5	MS	66	TRCRU-339	9.15	3	MR
24	VBN-4	9.68	3	MR	67	TRCRU-22	8.60	3	MR
25	2KU-63	17.20	5	MS	68	BDU-20	9.21	3	MR
26	BDU-3-3	27.60	7	S	69	PU-31	29.53	7	S
27	BDU-5	6.85	3	MR	70	TRCRU-103	18.90	5	MS
28	BDU-6	31.15	7	S	71	TRCRU-18	9.83	3	MR
29	TRCRU-26	35.70	7	S	72	GP-BDU-3-01	31.60	7	S
30	BDU-58	9.23	3	MR	73	RU-16-14	24.63	5	MS
31	BDU-9	8.20	3	MR	74	RU-16-07	34.56	7	S
32	BDU-10	8.32	3	MR	75	COBG-657	7.62	3	MR
33	BDU-11	27.20	7	S	76	BG-17-06	65.66	9	HS
34	BDU-12	7.21	3	MR	77	BG-17-10	9.32	3	MR
35	TAU-1	69.92	9	HS	78	BG-17-03	30.84	7	S
36	DU-1	42.17	7	S	79	RU-16-8	60.33	9	HS
37	T-9	37.20	7	S	80	RU-16-10	9.33	3	MR
38	LBG-752	0.78	1	R	81	RU-16-02	36.22	7	S
39	LBG-17	0.49	1	R	82	RU-16-05	65.20	9	HS
40	DU-2	34.70	7	S	83	Uttara	28.00	7	S
41	DU-3-2	36.84	7	S	84	IPU-2-43	19.32	5	MS
42	OBG-33	9.80	3	MR	85	VBG-4	8.30	3	MR
43	LBG-645	0.63	1	R	86	TU-94-04	29.23	7	S

Table 2 continued...

Table 2 continued...

S. no.	Genotype	Per cent disease severity	Rating (0-9 scale)	Reaction	S. no.	Genotype	Per cent disease severity	Rating (0-9 scale)	Reaction
87	LBG 685	0.97	1	R	94	MASH-1	64.00	9	HS
88	VBG-5	28.64	7	S	95	TU-91-2	29.84	7	S
89	PU-19	18.62	5	MS	96	WBU-1372	9.50	3	MR
90	PU-30	17.80	5	MS	97	LBG-3-4	8.12	3	MR
91	LBG-757	16.20	5	MS	98	RU-16-9	39.70	7	S
92	PANT-U-40	31.56	7	S	99	488-15-16	29.68	7	S
93	Shekhar	17.88	5	MS	100	K-3	21.20	5	MS

Table 3 : Categorization of black gram genotypes into different groups based on per cent disease severity.

S. no.	Grade (0-9)	Reaction	Name of the genotype	No. of genotypes
1	0	Immune	Nil	0
2	1	Resistant (R)	LBG-17, LBG-645, LBG-20, KU-5-527, LBG-752, COBG-647, LBG-623, LBG-465 and LBG 685	9
3	3	Moderately Resistance (MR)	BDU-5, BDU-12, COBG-657, BDU-3-20, BDU-17, LBG-3-4, 2KU-64, BDU-9, IC-436516, VBG-4, IC-436778, BDU-10, AKU-15, TRCRU-22, BDU-18, BDU-3-21, TRCRU-339, TRCRU-134, BDU-20, BDU-58, BG-17-10, RU-16-10, BDU-3-22, WBU-1372, TU-94-2, VBN-4, OBG-33 and TRCRU-18	28
4	5	Moderately susceptible (MS)	TRCRU-262, TRCRU-111, TU-98-1-18, TRCRU-24, LBG-757, DBGV-5, 2KU-63, PU-30, Shekhar, PU-19, GPS-53-1, TRCRU-103, IPU-2-43,K-3, TRCRU-67, KU-537, BDU-3-23, BDU-1, TRCRU-136 and RU-16-14	20
5	7	Susceptible (S)	2KU-15, BDU-11, BDU-3-3, Uttara, TU-99-852, RU-16-12, VBG-5, I-447-2, TU-94-04 ,BDU-68, TRCRU-43-1, PU-31, 488-15-16, VBN-3, TU-91-2, DU-7-638, BG-17-03, BDU-6, KML-8, Manikya, PANT-U-40, GP BDU-3-01, GP-728, TAU-1-12, RU-16-07, DU-2, BG-11, T-200-6, PMS-2, TRCRU-26, RU-16-02, DU-3-2, T-9, RU-16-9, GP-553, DU-1 and TU-98-10-5	37
6	9	Highly susceptible (HS)	RU-16-15, RU-16-8, MASH-1, RU-16-05, BG-17-06 and TAU-1	6

genotypes DKU 87 and PU 31 as resistant. Among nine resistant genotypes identified, five genotypes *viz.*, LBG-17, LBG-645, LBG-20, LBG-752 and LBG 685 were also found superior for seed yield and hence they could be used for disease management by direct cultivation and could also be utilized in hybridization programme as donors for disease resistance breeding.

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