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SCREENING OF BLACKGRAM GENOTYPES AGAINST MUNGBEAN YELLOW MOSAIC VIRUS (MYMV) DISEASE

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ABSTRACT

Blackgram is an important *kharif* pulse crop in Karnataka and popularization of its cultivation during summer in command areas is very crucial for horizontal expansion of the crop for increasing production. For popularizing blackgram cultivation during summer after harvesting paddy, pigeonpea and Bt cotton in command areas, the blackgram varieties need to possess resistance to MYMV disease, which is rampant during summer. Therefore, it necessitates the identification/development of blackgram varieties resistant to MYMV and suitable for summer season. Therefore, study was undertaken with an objective to identify urdbean genotypes resistant against MYMV based on the phenotypic reaction. The screening of 100 blackgram genotypes for Mungbean Yellow Mosaic Virus (MYMV) disease under natural epiphytotic condition during summer-2018 season revealed that 33 genotypes were resistant to MYMV disease. The genotype TRCRU-22 recorded minimum per cent disease incidence (1.70) whereas, susceptible genotype, TAU-1 (67.01) recorded maximum per cent disease incidence.

Key words: Blackgram, summer season, genotype, MYMV, disease

Introduction

Blackgram [*Vigna mungo* (L.) Hepper] is an important pulse crop in India popularly known as urdbean. It is an important short duration, self-pollinated, diploid grain legume (2n=2x=22) crop belonging to the family Leguminaceae with a genome size of 574 Mbp (Gupta and Gopalakrishna, 2008). It is highly prized pulse, rich in phosphoric acid. Blackgram grain contains about 25% protein, 56% carbohydrate, 2% fat, 4% minerals and 0.4% vitamins. The productivity of blackgram 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 blackgram. The main factors responsible for low productivity in blackgram include-susceptibility to number of abiotic stresses and also suffers from several serious diseases like Mungbean yellow mosaic virus (MYMV), powdery mildew and *Cercospora* leaf spot. Among these, Mungbean yellow mosaic virus (MYMV) disease caused by gemini virus and transmitted by whitefly is a major disease in India and South East Asia. The most seriously affected leguminous crops by this disease are mungbean, blackgram, and soybean. Mungbean yellow mosaic disease causes 10–100% yield losses depending on the crop stage at which the plants are infected. An annual loss of over US$300 million is incurred due to MYMV infection in these crops (Gupta *et al.*, 2015). Therefore, study was undertaken with an objective to identify urdbean genotypes resistant against MYMV based on the phenotypic reaction.

Material and Methods

The experiment material for the present investigation consisted of 100 blackgram genotypes collected from

Table 1: MYMV disease severity rating scale 0-5 scale (Bashir, 2005).

Scale (0-5)	Per cent infection	Reaction group
0	All plants free of disease symptoms	Highly resistant (HR)
1	1 - 10% infection	Resistant (R)
2	11 -20% infection	Moderately resistant (MR)
3	21-30% infection	Moderately susceptible (MS)
4	30-50 % infection	Susceptible (S)
5	More than 50%	Highly susceptible (HS)

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. The entries were screened for their reaction to the Mungbean Yellow Mosaic Virus disease under natural epiphytotic condition during summer-2018 season. The screening experiment was conducted at Agricultural Research Station, Bidar under irrigated conditions and all the genotypes were sown in two rows of 4 meter length along with susceptible and resistant checks. Disease severity was recorded by using 0-5 scale given by Bashir, (2005) (Table 1) and per cent disease incidence (PDI) was calculated based on the following formula:

$$\text{Percent Disease Incidence} = \frac{\text{No. of Plants infected}}{\text{Total no. of plants observed}} \times 100$$

Results and Discussion

Yellow Mosaic Disease (YMD) is formidable threat to the flourishing urdbean production in India. Mungbean Yellow Mosaic Virus (MYMV) is main viral pathogen causing YMD predominantly in southern and western region of India (Girish and Usha, 2005). The virus is transmitted by the whitefly and infected plants produce very few flowers and pods, the pods are curled and reduced in size resulting in yield losses ranging from 85–100% (Karthikeyan *et al*., 2014). In this context, breeding blackgram cultivars with broad-spectrum and durable resistance is the most cost-effective and eco-friendly approaches for MYMV management in urdbean production. Thus, researchers are putting massive efforts in identifying MYMV resistance cultivars.

One such effort was made in present study, where a total of 100 blackgram entries were evaluated for their reaction to the mungbean yellow mosaic virus disease under natural epiphytotic condition during summer-2018 season to identify resistant genotypes. Disease severity was recorded by using 0-5 scale given by Bashir (2005)

Table 2: Reaction of genotypes to the MYMV disease under natural epiphytotic condition during Summer- 2018.

S. No.	Genotype	PDI	Score (0-5)	Reaction
1	BDU-68	28.57	3	MS
2	TU-98-1-18	31.94	4	S
3	KML-8	18.37	2	MR
4	BDU-3-22	16.96	2	MR
5	2KU-64	26.51	3	MS
6	T-200-6	42.70	4	S
7	BDU-1	22.99	3	MS
8	GP-728	26.60	3	MS
9	TAU-1-12	42.39	4	S
10	KU-537	39.33	4	S
11	BDU-3-20	16.19	2	MR
12	COBG-647	5.88	1	R
13	BDU-3-23	36.27	4	S
14	GP-553	34.26	4	S
15	KU-5-527	16.09	2	MR
16	IC-436516	2.20	1	R
17	IC-436778	14.56	2	MR
18	TU-98-10-5	17.65	2	MR
19	BDU-3-21	16.67	2	MR
20	TRCRU-262	1.82	1	R
21	TU-99-852	36.59	4	S
22	LBG-623	16.67	2	MR
23	GPS-53-1	10.71	2	MR
24	VBN-4	8.85	1	R
25	2KU-63	8.25	1	R
26	BDU-3-3	34.31	3	MS
27	BDU-5	18.18	2	MR
28	BDU-6	17.35	2	MR
29	TRCRU-26	16.67	2	MR
30	BDU-58	12.90	2	MR
31	BDU-9	16.96	2	MR
32	BDU-10	14.29	2	MR
33	BDU-11	16.83	2	MR
34	BDU-12	16.00	2	MR
35	TAU-1	67.01	5	HS
36	DU-1	43.64	4	S
37	T-9	43.36	4	S
38	LBG-752	7.87	1	R
39	LBG-17	33.33	4	S
40	DU-2	42.16	4	S
41	DU-3-2	40.20	4	S
42	OBG-33	9.52	1	R
43	LBG-645	27.03	3	MS
44	LBG-465	14.95	2	MR
45	LBG-20	7.77	1	R
46	DBGV-5	17.24	2	MR
47	TU-94-2	3.53	1	R
48	I-447-2	39.60	4	S

Continue 2...

49	DU-7-638	43.06	4	S
50	Manikya	42.70	4	S
51	VBN-3	8.91	1	R
52	RU-16-12	28.74	3	MS
53	DBG-11	24.72	3	MS
54	2KU-15	45.24	4	S
55	PMS-2	42.37	4	S
56	RU-16-15	16.85	2	MR
57	TRCRU-111	5.88	1	R
58	TRCRU-24	9.21	1	R
59	TRCRU-134	2.10	1	R
60	TRCRU-43-1	3.23	1	R
61	TRCRU-67	15.29	2	MR
62	BDU-17	15.31	2	MR
63	BDU-18	12.63	2	MR
64	AKU-15	16.67	2	MR
65	TRCRU-136	5.15	1	R
66	TRCRU-339	1.90	1	R
67	TRCRU-22	1.70	1	R
68	BDU-20	13.79	2	MR
69	PU-31	4.44	1	R
70	TRCRU-103	6.00	1	R
71	TRCRU-18	3.16	1	R
72	GP-BDU-3-01	15.45	2	MR
73	RU-16-14	17.89	2	MR
74	RU-16-07	17.86	2	MR
75	COBG-657	2.01	1	R
76	BG-17-06	40.82	4	S
77	BG-17-10	11.95	2	MR
78	BG-17-03	39.22	4	S
79	RU-16-8	59.18	5	HS
80	RU-16-10	7.06	1	R
81	RU-16-02	26.67	3	MS
82	RU-16-05	5.56	1	R
83	Uttara	15.74	2	MR
84	IPU-2-43	7.77	1	R
85	VBG-4	8.05	1	R
86	TU-94-04	17.86	2	MR
87	LBG 685	16.65	2	MR
88	VBG-5	16.47	2	MR
89	PU-19	3.16	1	R
90	PU-30	4.71	1	R
91	LBG-757	25.71	3	MS
92	PANT-U-40	6.80	1	R
93	Shekhar	8.05	1	R
94	MASH-1	8.70	1	R
95	TU-91-2	8.08	1	R
96	WBU-1372	7.62	1	R
97	LBG-3-4	38.37	4	S
98	RU-16-9	5.62	1	R
99	488-15-16	27.66	3	MS
100	K-3	42.11	4	S

Table 3: Categorization of genotypes into different groups based on per cent disease incidence.

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

HR: Highly Resistant; R: Resistant; MR: Moderately Resistance; MS: Moderately Susceptible; S: Susceptible; HS: Highly Susceptible and results are presented in Table 2. The per cent disease incidence (PDI) varied from 1.70 to 67.01. Among the genotypes screened none of them found to have highly resistant reaction and maximum numbers of entries were grouped under resistant and moderately resistant reaction categories. The genotypes showed different levels of resistance reaction and were grouped into five different categories as indicated in the Table 3. Out of 100 genotypes, total of 33 (R), 33 (MR), 10 (MS), 22 (S) and 2 (HS) genotypes are classified into resistant (R), moderately resistant (MR), moderately susceptible (MS), susceptible (S) and highly susceptible (HS), respectively.

The genotype TRCRU-22 recorded minimum per cent disease incidence (1.70) followed by TRCRU-339 (1.90), COBG-657 (2.01) and TRCRU-134 (2.10), whereas, genotypes, TAU-1 (67.01) and RU-16-8 (59.18) recorded maximum per cent disease incidence. In resistant category, the per cent disease incidence ranged from 1.70 (TRCRU-22) to 9.21 (OBG-33); in moderately resistant category, ranged from 10.71 (GPS-53-1) to 18.37(KML-8); in moderately susceptible category ranged from 22.99 (BDU-1) to 28.74 (RU-16-12); in susceptible category ranged from 31.94 (TU-98-1-18) to 43.64 (DU-1) and in highly susceptible category ranged from 59.18 (RU-16-8) to 67.01 (TAU-1) (Table-2).

The above presented results revealed that, the per cent disease incidence (PDI) varied from 1.70 to 67.01 indicating the prevalence of high disease pressure during the genotypes screening period and which was ideal for screening and categorization of genotypes into different reaction groups *viz.*, resistant (R), moderately resistant (MR), moderately susceptible (MS), susceptible (S) and highly susceptible (HS) based on per cent disease incidence. The genotype, TRCRU-22 recorded lowest PDI, whereas, highly susceptible variety TAU-1 recorded highest PDI. Many researchers have also undertaken study to identify resistant genotypes. Few of them to mention here are viz., Tamilzharasi *et al*., (2018) evaluated 48 genotypes and found 14 resistant types; Gopi *et al.*, (2016) identified two resistant genotypes out of 49 entries. Similarly, Devi *et al.*, (2019) and Kumari *et al.*, (2020) also reported MYMV resistant genotypes from their investigation.

The perusal of data reveals that none of the genotypes exhibited highly resistant disease reaction but two third of genotypes were found to be having either resistant or moderately resistant disease reaction. By this, one can say that genotypes under study were good source of resistance for MYMV disease and could be utilized in hybridization programme as donor parents for MYMV disease resistance.

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