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Genetics of mungbean yellow mosaic virus in Vigna crosses

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Abstract : Greengram and blackgram are most important species of *Vigna* group of grain legumes. Among these species mungbean [*Vigna radiata* (L.) Wilczek] and urdbean [*Vigna mungo* (L.) Heppar] are the major pulse crops of Indian subcontinents. One of the very significant problem with pulse crops is Mungbean Yellow Mosaic Virus. Therefore, inheritance of resistance to mungbean yellow mosaic virus was studied in six intraspecific and four interspecific crosses of *Vigna* involving three resistant varieties of mungbean namely HUM16, Samrat, TMV37 and three resistant varieties of urdbean namely PU31, Uttara and Sekhar. One susceptible genotype of each was LGG450 and Barabanki of mungbean and urdbean respectively. The parents F_1 , F_2 , BC₁ & BC₂ generation were grown with their respective susceptible genotype. Susceptibility of MYMV was dominant over resistance in the F_1 generation of all the crosses. Observations on disease incidence of F_2 , BC₁ and BC₂ generation indicated that pair of recessive genes showed resistance against MYMV in each of the crosses.

Key Words: Mungbean, Yellow Mosaic Virus, Resistance, Susceptible and Gene.

INTRODUCTION

Globally, grain legumes are the second most important group of crops. In legumes, green gram and black gram are important pulse crops. They are significant sources of dietary protein as well as mineral such as calcium and sodium. Dried mungbean seeds are high in vitamins A and B, while the sprouted mungbean are rich in vitamins B and C. The Mungbean yellow mosaic virus (MYMV) is a major cause of low productivity of green gram and black gram in India. It is a devastating pathogen is transmitted through *Bemisia tabaci* Genn. which can make yield penalty reach up to cent percent (Basak *et.al.* 2004) depending upon the severity of the disease. Thus, it is essential to understand the inheritance of resistance in mungbean and urdbean cultivar. Different scientists have

*Correspondent author : Phone : 09431426540 E-mail : simasinha11@gmail.com worked on this very subject and reached some contrasting conclusions. Dahia et al (1977), Reddy and Singh (1993) reported that resistance is governed by a single dominant gene, whereas Saleem et al. (1998) and khattak et al. (1999) reported that resistance to MYMV is governed by a single recessive gene. In contrast Solanki et al. (1982), Singh (2006), Verma & Singh (1989), Sirohi et al. (2000) and Ammavasi et al. (2004) have reported that resistance is governed by two recessive genes. In this view, the present day study was undertaken to understand the inheritance of MYMV in intra and interspecific crosses of vigna. To achieve the resistance among mungbean and urdbean, it is important to study the inheritance pattern of MYMV. It is a major biotic stress for mungbean and urdbean cultivar which causes significant yield loss. Genetic control of resistance to MYMV in mungbean and urdbean has been investigated using different methods for developing high yielding MYMV resistant varieties of Vigna.

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MATERIALS AND METHODS

The experimental material consisted of three resistant mungbean donar viz., HUM-16, TMB-37 and Samrat with a susceptible donor LGG 450 and other set for resistant donors of urdbean like PantU- 31, Uttara and Sekhar with their susceptible donor Barabanki local. Three genotypes of each mungbean and Urdbean planted in a crossing block with their susceptible parent as LGG450 and Barabanki respectively. Six intraspecific crosses were made namely HUM 16 x LGG450, TMB-37 x LGG450 and Samrat x LGG 450 of Mungbean as well as Urdbean crosses were PantU31x Barabanki, Samrat x Barabanki and TMB37x Barabanki.

Four interspecific crosses were made of mungbean x urdbean. In two crosses, resistant donors of mungbean were crossed with susceptible urdbean parent Barabanki namely Samrat x Barabanki and TMB-37 x Barabanki. In another two crosses, resistant donors of Urdbean were crossed with susceptible mungbean parent LGG 450 viz. Pant U 31 x LGG 450 and Uttara x LGG 450.

Six F₁ hybrid of intra specific and four inter specific hybrid F_1 were selfed to obtain F_2 seed as well as backcrossed to both the parent to obtain BC_1 and BC_2 . The F_1 , F_2 , BC_1 and BC_2 population were derived from three intraspecific crosses of each mung and urdbean as well as four interspecific crosses. The parents F1, F2, BC1 and BC2 were grown in a randomized block design with three replications at Tirhut College of Agriculture, Dholi under Rajendra Agricultural University, Pusa during 2009-2011. Each plot size of 2.4 m² with row to row spacing at 30 cm and Plant to plant 10 cm, while F, populations of each cross was grown in 4.8 m² plots having the 10 rows with 4 m length. SML 668 was used as a check. One row of LGG 450 was planted as infector row for MYMV after every two rows of the test entries to intensity MYMV inoculums in natural condition. In order to maintain a good natural population of white flies, no pesticide was sprayed. Dholi is the hot spot for MYMV of mungbean. Scoring of disease was done for every individual plant using 1-9 scale where 1 and 3 scale was treated as resistant and 5 to 9 scale was treated as susceptible as per the method suggested by Shukla (1977) and Shukla et al. (1978) in mungbean. The segregation in F2, BC1 and BC2 generation was tested for goodness of fit by using chi square test.

RESULTS AND DISCUSSIONS

Three genotypes of mungbean namely HUM16, SAMART and TMB37 as well as three genotypes of urdbean vise PU31, Sekhar and Uttara showed resistant against MYMV. On other hand LGG450 and Barabanki of mungbean and urdbean respectively showed susceptible reaction to MYMV, The F_1 generation of all crosses exhibited susceptible reaction to MYMV. This indicates dominance of susceptibility over resistance which was in conformity with earlier report of Patel *et al* (2009), Singh (1980), Solanki *et al.* (1982), Verma and Singh (1989), Reddy and Singh (1993), Singh *et al.* (2002) and Ammavasai *et al.* (2004). In contrast, Dahiya *et al.* (1977) reported that resistance was dominant over susceptibility.

The segregation for resistance in the F_2 generation showed digenic inheritance with 15 (susceptible): 1 (resistant) ratio, which was further confirmed by BC, and BC₂ segregating progenies. It clearly indicates that resistance to MYMV is under control of digenic recessive genes in table: 2 and 3. Two recessive genes for resistance to MYMV have also been reported by Singh, (1980); Solanki et al. (1982); Verma and Singh (1992); Singh et al. (2002); Sirohi et al. (2000); Ammavasi et al. (2004). However, a single recessive gene for MYMV resistance has also been reported by Saleem et al. (1998), Khattak et al. (1999) and Khattak et al. (2000). The BC, population was observed in three classes (susceptible, resistant and segregating) and showed 3:1 (susceptible: resistant) ratio while BC, had 100 per cent susceptible population. In Contrast, Reddy and Singh (1993) suggested one dominant and one recessive gene for resistance to MYMV. Since two recessive genes for MYMV resistance are involved in the resistance donors genotypes of mungbean, it will be desirable to grow large segregating populations to recover a number of resistant plants coupled with other desirable traits to have a successful breeding programme. \

Three genotypes of each mungbean and Urdbean namely HUM 16, SAMRAT, TMB 37 and PU31, Uttara, Sekhar showed resistant whereas LGG450 and Barabanki showed susceptible reaction to MYMV presented in Table: 1. Number of plants in HUM-16 was 118 which showed only 1 and 3 score that indicates resistance. In a similar way TNB 37, Samrat, PantU 31, Uttara and Shekhar had

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depicted 1 and 3 score whereas, LGG 450 and Barabanki MYMV. Local check SML 668 also showed resistance to showed 7 and 9 score which was highly susceptible to MYMV.

SI.	Crosses	Total no.			Dise	eases sc	ore		Disease
No.		of plant	1	3	5	7	9	Weighted	Reaction
								mean	
1.	HUM-16	118	47	71	-	1	-	2.20	Resistant
2.	TMB 37	110	56	54	-	I	1	1.98	Resistant
3.	SAMRAT	121	85	36	-	-	-	1.59	Resistant
4.	Pant U 31	119	96	23	-	-	-	1.38	Resistant
5.	UTTARA	116	77	39	-	-	-	1.67	Resistant
6.	SEKHAR	112	92	20	-	1	-	1.35	Resistant
7.	LGG 450	108	-	-	-	10	98	8.35	Susceptible
8.	BARABANKI	114	-	-	-	26	89	8.62	Susceptible
9.	SML 668	117	35	82	-	-	-	2.40	Resistant

Table 1: Reaction of Mungbean Yellow Mosaic Virus in parents of Vigna

The disease reaction was scored in 1-9 scale as quantitative trait based on the frequencies of the plants towards both the extreme (resistance/susceptible) scores of 1 and 3 as resistant and 5, 7 and 9 as susceptible. Based on the same frequency scale of the plant the score of 5 worked as threshold level consequently and it was grouped into two discrete classes as susceptible which is shown in Table: 2

The segregating pattern for resistance to MYMV in F2, BC1 and BC2 was presented in Table: 3. F2 population

in all the crosses showed digenic inheritance with 15 (susceptible): 1 (resistant) ratio. The BC1 population was observed in three classes (susceptible, resistant and segregating) and showed 3 (susceptible): 1 (resistant) ratio while BC2 had 100% susceptible population. It clearly indicated that resistance to MYMV was due to dominance of two recessive genes which is in agreement with earlier report of Saleem et al. (1998), Singh et al. (2006) and Verma et al. (1989).

SI.	Crosses	Genera	Total		Di	seases s	core		Disease	Reaction	
No.		tions	no. of	1	3	5	7	9	Suscept	Resista	
			plant						ible	nt	
1.	HUM-16 x LGG 450	F ₂	147	3	8	13	58	65	136	11	
		BC ₁	63	5	9	3	26	20	49	14	
		BC ₂	69	-	-	5	29	35	69	-	
2.	SAMRAT x LGG 450	F ₂	149	5	7	9	59	69	137	12	
		BC ₁	66	6	9	2	27	22	51	15	
		BC ₂	74	-	-	8	29	37	74	0	
3.	TMB 37 x LGG 450	F ₂	127	2	4	7	60	54	121	6	
		BC ₁	59	5	8	4	19	23	46	13	
		BC ₂	71	-	-	5	37	32	74	0	
4.	SEKHAR x BARABANKI	F ₂	159	7	6	11	66	69	146	13	
		BC_1	72	7	10	3	22	30	55	17	
		BC ₂	61	-	-	6	19	26	61	0	
5.	PU 31 x BARABANKI	F ₂	127	2	4	13	49	59	121	6	
		BC ₁	65	5	8	4	21	27	52	13	
		BC ₂	56	-	-	6	22	28	56	0	Co

Table 2: Reaction of Mungbean Yellow Mosaic Virus in intra and interspecific crosses of Vigna

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Table 2 Contd..

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6.	UTTARA x BARABANKI	F ₂	154	4	7	14	62	67	143	11
		BC ₁	67	5	10	7	21	24	52	15
		BC ₂	74	-	-	9	29	36	74	0
7.	SAMRAT x BARABANKI	F ₂	114	2	9	17	47	39	103	11
		BC ₁	67	3	12	3	23	26	52	15
		BC ₂	66	-	-	6	28	32	66	0
8.	TMB 37 x BARABANKI	F ₂	132	2	9	11	59	51	121	11
		BC ₁	71	3	11	6	28	23	57	14
		BC ₂	76	-	-	13	24	29	76	0
9.	PU 31 x LGG 450	F ₂	100	2	6	9	46	37	92	8
		BC ₁	59	4	8	2	26	19	47	12
		BC ₂	47	-	-	6	25	16	47	0
10.	UTTARA x LGG 450	F ₂	126	2	5	17	53	49	119	7
		BC ₁	68	5	11	2	22	28	52	16
		BC ₂	53	-	-	5	20	28	53	0

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SI.	Crosses	Generations	Total no. of	No. of plants by	ants by	Observed	Expected	Calculated	Tabulated
No.			plant	segregating population	population	Ratio	ratio	x2 value	x2 value
		-		Susceptible	Resistant				
	HUM-16 x LGG 450	F ₂	147	136	11	12.4:1	15:1	0.4733	3.84
		BC1	63	49	14	3.5:1	3:1	1.085	3.84
		BC_2	69	69		1			
2.	SAMRAT x LGG 450	\mathbf{F}_2	149	137	12	11.4:1	15:1	1.064	3.84
		BC ₁	99	51	15	3.4:1	3:1	0.083	3.84
		BC_2	74	74	0	I	I	1	I
<i>т</i> .	TMB 37 x LGG 450	F ₂	127	121	6	20.2:1	15:1	0.534	3.84
		BC1	59	46	13	3.5:1	3:1	0.358	3.84
		BC_2	71	74	00	-	1	-	1
4.	Sekhar x Barabanki	F ₂	159	146	13	11:2	15:1	0.069	3.84
		BC ₁	72	55	17	3:2	3:1	0.074	3.84
		BC_2	61	61	00		-	-	I
5.	PU 31 x BARABANKI	\mathbf{F}_2	127	121	6	20.2:1	15:1	0.534	3.84
		BC	65	52	13	4:1	3:1	0.747	3.84
9.	UTTARA x BARABANKI	F2	154	143	11	13:1	15:1	0.107	3.84
		BC_1	67	52	15	3.5:1	3:1	0.315	3.84
		BC_2	74	00	00	-	-	-	1
7.	SAMRAT x BARABANKI	\mathbf{F}_2	114	103	11	9.4:1	15:1	2.435	3.84
		BC1	67	52	15	3.5:1	3:1	0.315	3.84
		BC_2	66	00	00	I	I	1	I
%	TMB 37 x BARABANKI	F ₂	132	121	11	1:11	15:1	1.198	3.84
		BC_1	71	57	14	4.1:1	3:1	1.191	3.84
		BC_2	26	00	00	1	1	1	1
9.	PU 31 x LGG 450	\mathbf{F}_2	100	92	8	11.5:1	15:1	0.709	3.84
		BC_1	59	47	12	3.9:1	3:1	0.805	3.84
		BC_2	47	00	00	1	1	1	1
10	UTTARA x LGG 450	F_2	126	119	7	17:1	15:1	0.1335	3.84
		BC_1	68	52	16	3.3;1	3.1	0.178	3.84
		BC_2	53	00	00	-		-	1

Table 3: Inheritance Pattern of MYMV in Intra and Inter specific crosses of vigna

*Signific ant at P=0.05

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