

## MODE OF INHERITANCE OF RESISTANCE TO MUNGBEAN YELLOW MOSAIC VIRUS (MYMV) IN MUNGBEAN (*Vigna radiata* (L.) Wilczek)

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### ABSTRACT

The mode of inheritance of resistance to Mungbean Yellow Mosaic Virus (MYMV) in mungbean has been studied in the present investigation at Nuclear Institute for Food and Agriculture Tarnab Peshawar during Kharif 2002. The MYMV resistance was inherited through a major recessive gene. No maternal effect was found for the inheritance of MYMV resistance in mungbean. According to the mean disease (MYMV) score, genotypes VC1560D, VC3902A and Berken were found susceptible (S), VC2272, Emerald, Pusa Baisaki were moderately susceptible (MS) and 6601, NM92 were highly resistant (HR). Among 22F<sub>1</sub> hybrid combinations, 12 were detected susceptible and 10 moderately susceptible towards MYMV reaction.

**Keywords:** Mung bean, MYMV, Resistance, *Vigna radiata* L.

### INTRODUCTION

In Indian sub-continent Mungbean Yellow Mosaic Virus (MYMV) is one of the serious diseases common to many leguminous crops and causes tremendous losses in production of mungbean crop (Chenulu and Verma, 1988). First of all this disease was reported in 1955 on mungbean crop growing at the Indian Agricultural Research Institute (IARI), Delhi (Nariani, 1960). This disease has been reported to be transmitted by an insect vector white fly (*Bemisia tabaci*) and not by seed, soil or mechanical inoculation (Ahmad & Harwood, 1973; Nair & Nene, 1973).

Knowledge of the mode of inheritance to MYMV in mungbean is useful for incorporation of resistance into agronomically poor, but desirable genetic resources. There are only a few contrasting published reports on the inheritance of resistance to MYMV in mungbean. The monogenic recessive inheritance for MYMV has been reported by Singh and Patel (1977), Malik *et al.* (1986 & 1988), Malik (1992), Saleem *et al.* (1998) and Khattak *et al.* (2000). The present investigation was carried out to understand the mode of inheritance of resistance to MYMV in mungbean.

### MATERIALS AND METHODS

Ten mungbean genotypes viz; 3902A, NM92, VC2272, 6601, Pusa Baisaki, ML-5, Berken, Emerald, VC1560D and NM98 were used in the present study. They were crossed to each other in 22 different combinations. The parents, 22 F<sub>1</sub> (Table I and II) and 8 F<sub>2</sub> hybrid families (Table III) of different cross combinations were planted in a single replicated experiment for studies regarding inheritance of resistance to MYMV during Kharif 2002. The experiment (parents, F<sub>1</sub> and F<sub>2</sub>) was conducted during Kharif (July-October) 2002 at

Nuclear Institute for Food and Agriculture (NIFA), Tarnab, Peshawar. The plot size of 2.4m<sup>2</sup> (2 rows each 4 meter long) was assigned for parents, F<sub>1</sub> and 48m<sup>2</sup> (40 rows each 4 meter long) for F<sub>2</sub> populations. Plant to plant and row to row spacing was maintained 10cm and 30cm, respectively. Mungkabuli a highly susceptible check to MYMV was used as disease spreader and was planted after each five rows to intensify MYMV inoculums from natural resources. On individual plant basis, the percent infection by MYMV in parents, F<sub>1</sub> and F<sub>2</sub> generations were recorded 4 weeks after sowing when 100% plants of the susceptible check were completely infected with MYMV. The mean disease score for parents, F<sub>1</sub> and F<sub>2</sub> generations was calculated as (infection rate x frequency/ total number of plants). All the plants of a cross having disease reaction of highly resistant (HR) to moderately resistant (MR) and from moderately susceptible (MS) to highly susceptible (HS) were grouped as resistant and susceptible, respectively (Table Ia). The F<sub>2</sub> was statistically analyzed using chi-square test ( $\chi^2$ ) for determining inheritance of MYMV.

### RESULTS AND DISCUSSION

The mean disease score, disease reaction and distribution of plants of 10 diverse mungbean genotypes in their respective MYMV disease rating are presented in Table I. The mean disease score and disease rating of MYMV ranged from 1.45 (HR) to 7.1 (S) for NM92 and VC1560D, respectively. Plants of disease score 8 (HS) were found in susceptible and moderately susceptible parents (Table I) as well as in F<sub>1</sub> and F<sub>2</sub> progenies (Tables II & III). Plants of immune score rating to MYMV were not observed in any of the parents and their cross combinations of F<sub>1</sub> and F<sub>2</sub>

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progenies. Mishra and Asthana (1996) have reported the absence of immunity for MYMV in world mungbean germplasm.

The F<sub>1</sub> of all combinations clearly indicated that susceptibility to MYMV was dominant over resistance (Table II) because the crosses developed from such parents, having HR/T and MS/S behavior to MYMV. The same behavior of F<sub>1</sub> and the reciprocals in crosses NM92 x VC 1560D, 6601 x VC 1560D, and VC 3902A x 6601 and VC 2272 x VC 1560D towards MYMV susceptibility also indicated that there was no maternal effect on the inheritance of MYMV in mungbean. Similar results regarding dominant behavior of MYMV susceptibility and the absence of maternal effect in F<sub>1</sub> have already been reported in mungbean by Shukla *et al.* (1978), Mishra (1989) and Khattak *et al.* (2000).

The F<sub>2</sub> segregation of 8 different crosses for MYMV resistance (HR-MT) and susceptibility (MS-HS) are presented in the Tables III and IV. The segregation ratio of 3 (MS-HS) : 1 (HR-MT) was observed in progenies of all F<sub>2</sub> populations of 8 different combinations. The F<sub>2</sub> segregation ratio of these crosses indicated that it is a single gene inherited character with dominance effect of susceptibility over resistance to MYMV. Such monogenic recessive inheritance of MYMV resistance in mungbean has also been reported by previous researchers like (Singh and Patel, 1977; Malik *et al.* 1986 & 1988; Malik, 1992; Saleem *et al.* 1998 and Khattak *et al.* 2000). Mishra and Asthana (1996) have reported that the variation in degree of MYMV resistance/ susceptibility among genotypes is based on genetic back ground, while the variation in incidence of MYMV among the plants of a parent and F<sub>1</sub> (Tables I & II) may have been due to vector population and the visits performed by the vector White fly on each plant.

**Table I** Origin, total number of plants observed, mean disease (MYMV) score and disease reaction of parent genotypes accessions.

Genotypes	Origin	Total No. of plants Observed	No of plants in disease score								Mean disease score	Disease reaction
			1	2	3	4	5	6	7	8		
VC 1560D	Taiwan	200	-	-	1	2	3	4	138	52	7.1	S
VC 2272	do	200	-	-	-	1	2	14	170	13	6.2	MS
VC 3902A	do	200	-	1	-	3	11	20	159	6	6.7	S
Berken	Australia	200	-	2	6	5	4	17	145	21	6.7	S
Emerald	do	200	-	2	5	14	20	24	128	7	6.3	MS
ML-5	India	200	30	143	27	-	-	-	-	-	1.9	HR
Pusa	do	200	4	6	7	3	17	27	135	1	6.1	MS
Baisaki												
NM-92	Pakistan	200	128	54	18	-	-	-	-	-	1.45	HR
6601	do	200	7	23	11	104	55	-	-	-	3.8	T
NM98	do	200	94	72	34	-	-	-	-	-	3.8	T

**Table Ia. MYMV Disease Score**

Plant parts infected/disease (%)	Score	Disease reaction
No infection	0	Immune (I)
1 – 5	1	Highly resistant (HR)
6 – 10	2	Resistant ( R)
11 – 20	3	Moderately resistant (MR)
21 – 30	4	Tolerant (T)
31 – 40	5	Moderately tolerant (MT)
41 – 50	6	Moderately susceptible (MS)
51 – 80	7	Susceptible (S)
81 – 100	8	Highly susceptible (HS)

Table II. Division of Mungbean F1 hybrid plants in their respective MYMV disease rating.

S. No.	F1 hybrid	Number of F1 plants according to disease score								Mean disease score	Mean disease reaction
		1	2	3	4	5	6	7	8		
1	VC3902A × NM92	-	-	-	-	4	23	31	2	7.2	S
2	VC 1560D × VC 3902A	-	-	-	1	1	2	41	5	6.9	MS
3	NM92 × VC2272	-	-	-	4	7	4	33	12	6.5	MS
4	VC3902A × NM98	-	-	-	1	8	15	34	2	6.4	MS
5	6601 × VC2272	-	-	-	1	5	11	31	12	6.7	S
6	VC3902A × 6601	-	-	-	3	5	10	41	1	6.5	MS
7	6601 × 3902A	-	-	-	5	5	15	34	1	6.2	MS
8	NM92 × Pusa Baisakhi	1	3	-	5	1	17	33	-	6.0	MS
9	VC 1560D × ML-5	-	-	-	-	6	6	45	3	6.7	S
10	6601 × Pusa Baisakhi	1	1	-	5	9	15	29	-	6.0	MS
11	VC 1560D × NM98	-	-	-	-	6	12	35	7	6.7	S
12	VC3902A × ML-5	-	1	2	1	1	11	43	1	6.5	MS
13	Emerald × NM92	-	-	-	5	9	12	27	7	6.3	MS
14	Berken × NM92	-	-	3	3	3	6	36	9	6.5	MS
15	NM92 × Berken	-	-	-	2	2	6	43	7	6.6	S
16	ML-5 × VC 1560D	-	-	-	-	7	9	38	6	6.6	S
17	NM92 × VC 1560D	-	-	-	-	2	6	52	-	6.8	S
18	VC 1560D × NM92	-	-	-	2	-	2	46	10	7.0	S
19	6601 × VC 1560D	-	-	-	-	2	4	51	3	6.9	S
20	VC 1560D × 6601	-	-	1	-	2	9	47	1	6.7	S
21	VC2272 × VC 1560D	-	-	-	2	10	20	28	-	6.3	MS
22	VC 1560D × VC2272	-	-	-	1	8	21	30	-	6.9	S

Table III. Distribution of Mungbean F<sub>2</sub> plants of different combination in term of MYMV disease rating.

S. No.	Cross combination	Number of F <sub>2</sub> plants according to disease score							
		(HR – MT)				(MS – HS)			
		1	2	3	4	5	6	7	8
1	NM92 × VC2272	11	13	17	19	23	17	178	22
2	6601 × VC2272	9	17	32	9	5	15	134	19
3	6601 × Pusa Baisaki	5	8	17	12	21	30	135	12
4	VC3902A × NM92	19	22	31	11	18	13	170	56
5	VC3902A × ML-5	23	29	8	22	15	17	212	34
6	NM92 × Pusa Baisaki	15	4	5	7	12	35	128	14
7	VC 1560D × 6601	15	22	34	17	15	8	251	38
8	VC 1560D × NM92	28	19	32	7	8	27	269	10

Table IV. Segregation for susceptibility (MS – HS) and resistance (HR – MT) to MYMV in F<sub>2</sub> generation under natural epiphytotic conditions.

S. NO.	Cross combination	Number of F <sub>2</sub> plants				Expected ratio	X <sup>2</sup>	P
		Total	Susceptible (MS – HS)	Resistant (HR – MT)				
1	NM92 × VC2272	300	217	83	3:1	1.07	0.300	
2	6601 × VC2272	240	168	72	3:1	3.07	0.0797	
3	6601 × Pusa Baisaki	240	177	63	3:1	0.17	0.680	
4	VC3902A × NM92	340	239	101	3:1	3.89	0.048	
5	VC3902A × ML-5	360	263	97	3:1	0.68	0.409	
6	NM92 × Pusa Baisaki	220	177	43	3:1	3.64	0.056	
7	VC 1560D × 6601	400	297	103	3:1	0.10	0.7518	
8	VC 1560D × NM92	400	306	94	3:1	0.52	0.4708	

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