

# Inheritance of Mungbean Yellow Mosaic Virus (MYMV) Resistance in Interspecific Crosses of Mungbean (*Vigna radiata* (L.) Wilczek) and Rice Bean (*Vigna umbellata* Thunb.)

Prithviraj\*, Niranj Murthy, Anand, Nagaraju N, Sriniva Redy, Ashwin KMJ, Ananya and Sowmya H

All India Co-ordinated Research Network on Potential Crops, Punjab Agricultural University (PAU), Ludhiana, India

## Abstract

Understanding of Mungbean Yellow Mosaic Virus resistance is crucial to develop resistant varieties to combat worldwide threat of the disease epidemics. Since there is no stable source of resistance in mungbean it's essential to take up interspecific hybridization with ricebean in order to introgress resistant genes from ricebean which is highly resistant to MYMV. Green gram variety KKM-3 which is susceptible to MYMV was used as a female parent and two rice bean lines KBR-1 and RBL-6 which are highly resistant to MYMV were used as male parents in generating interspecific hybrids. The inheritance of resistance to Mungbean Yellow Mosaic Virus (MYMV) in interspecific crosses of mungbean and ricebean was studied. F1 interspecific hybrids of the cross KKM-3 × KBR-1 were resistant and the cross KKM-3 × RBL-6 were found to be highly resistant. The F2 generations of the two crosses were screened for MYMV and Chi-square test confirmed the segregation ratio of 3:1 resistant: susceptible plants in the F2 generation of both the interspecific crosses indicating that the MYMV resistance in interspecific crosses of mungbean and ricebean is controlled by monogenic dominant gene.

**Keywords:** Inheritance; Interspecific; MYMV; Resistance; Susceptible; Segregation

## Introduction

Mungbean is one of the important minor pulse crops with an excellent source of easily digestible protein (24%) with low flatulence which complements the staple rice diet in Asia. Greengram is also one of the pulses being imported in India to meet domestic requirement of pulses. Just like other minor pulses mungbean is cultivated mostly in marginal land under rainfed situation and also because of biotic and abiotic stress factors productivity of green gram in India is very less. Amongst these factors Mungbean Yellow Mosaic Virus (MYMV) which is the most devastating one and accounts for yield losses up to 85% [1]. This MYMV which is transmitted in a circulative tenacious way by whitefly *Bemisia tabaci* has no stable resistance source among mungbean cultivars whereas ricebean (*Vigna umbellata* Thunb.) has been reported with high resistance to MYMV disease and is also cross compatible. Hence, transfer of resistant genes for MYMV from rice bean to mungbean may be a possible means to develop MYMV resistant mungbean varieties. In this context study was conducted with the objective to understand the inheritance of MYMV resistance in the interspecific crosses of mungbean and ricebean which may aid the breeders in effective selection of target genotype which ultimately leads to the development of MYMV resistant cultivars.

## Experimental Section

Interspecific hybridization was carried out between two *Vigna* species viz., *Vigna radiata* (mungbean) and *Vigna umbellata* (rice bean) during summer-2017 at field unit of AICRN on Potential Crops Scheme, Main Research Station, University of Agricultural Sciences, Hebbal, Bengaluru. Green gram variety KKM-3 which is agronomically superior and well adopted variety but susceptible to MYMV was used as a female parent. Two rice bean lines KBR-1 and RBL-6 which are highly resistant to MYMV were used as male parents. The F1 hybrids produced were raised during Kharif 2017 along with parents under natural field condition. The mungbean variety, yellowmung which is highly susceptible to MYMV was used as disease spreader and two rows of this variety were planted all around the experimental plot in

order to attract whitefly and enhance spread of MYMV. On individual plant basis, the per cent infection by MYMV in parents and F1 hybrids were recorded at 50 days after sowing, when 100 per cent disease was visible on the susceptible check. F2 seeds harvested from individual F1 plants of respective inter specific crosses were collected separately and evaluated during summer (February-April) 2018 under natural field condition and infector row technique was used. Each F2 was raised with minimum of 250-300 plant population. Yellowmung, a highly susceptible mungbean cultivar for MYMV, was used as spreader and was sown along with all the F2 populations of inter specific hybrids of mungbean and rice bean to create disease epidemic in the test plants. F2 populations (KKM-3 × KBR-1 and KKM-3 × RBL-6) were screened for yellow mosaic reaction using the disease incidence scale given by AVRDC (1-6). The susceptible check had 100 per cent disease incident at the time of scoring and Per cent Disease Index was calculated by,

$$\text{Per cent disease index} = \frac{\text{Sum of numerical observations}}{\text{Maximum disease scale} \times \text{Number of observations}} \times 100$$

Plants with MYMV score  $\leq 3$  were classified as resistant and those with MYMV score  $> 3$  were classified as susceptible. The recorded observations were subjected to Chi-square test based on expected ratios. The goodness of fit between expected and observed Mendelian segregation ratios were worked out in order to infer on the inheritance pattern of the resistant genes. The Chi-square was calculated by using the following formula.

\*Corresponding author: Prithviraj, Dept. of Genetics and Plant Breeding, Punjab Agricultural University, Ludhiana, India, E-mail: prithvi.gkvk@gmail.com

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**Table 1:** Screening of F1 interspecific hybrids of rice bean and mungbean for MYMV.

Sl. No.	Parents/ crosses	Total No. of plants screened	No. of infected plants	Per cent Disease incidence (%)	Per cent Disease Index (%)	Disease score	Disease Reaction (as per AVRDC scale)
1.	KKM-3	22	12	54.55	76.67	5	S
	KBR-1	20	0	0.0	0.0	1	HR
	F <sub>1</sub> 'S	23	3	13.04	16.67	2	R
2.	KKM-3	20	14	70.00	80.00	5	S
	RBL-6	20	0	0.0	0.0	1	HR
	F <sub>1</sub> 'S	11	1	9.09	3.33	1	HR

**Table 2:** Inheritance of MYMV resistance in F2 populations of interspecific crosses as per Chi-Square test.

Parentage of Interspecific Crosses	Total Plants	Number of plants in F <sub>2</sub>		Expected Ratio	χ <sup>2</sup> calculated value (3: 1)	χ <sup>2</sup> Table value
		Resistant	Susceptible			
KKM-3 × KBR-1	248	177	71	3: 1	1.74	3.84
KKM-3 × RBL-6	257	182	75	3: 1	2.40	3.84

$$\chi^2 = \sum \frac{(O - E)^2}{E}$$

Where,

O = Observed frequency

E = Expected frequency

The significance of Chi-square value was tested by comparing the calculated Chi-square value with table value at 5 % and 1 % level of significance at appropriate degrees of freedom (n-1), where, n = number of classes of trait under consideration.

## Discussion

### Screening of interspecific F1 hybrids for MYMV resistance

The two male parents used in interspecific hybridization recorded highly resistant (HR) disease reaction taking a disease score of 1. Female parent KKM-3 used in the study were found to be susceptible with the disease score of 5. F1 interspecific hybrids of the cross KKM-3 × KBR-1 were found to be resistant taking a disease score of 2 where as F<sub>1</sub>'s of the cross KKM-3 × RBL-6 were highly resistant with the AVRDC score of 1 suggesting that there may be a successful introgression of MYMV resistance from ricebean to mungbean (Table 1).

### The genetics of MYMV resistance in the interspecific crosses

Further to find out the inheritance pattern of MYMV resistance in interspecific crosses of mungbean and ricebean, the F2 generation of the crosses, KKM-3 × KBR-1 and KKM-3 × RBL-6 were screened for resistance against Mungbean Yellow Mosaic Virus. The Chi-square test was done to confirm goodness of fit of Mendelian F2 segregating ratios in these populations (Table 2). The results of calculated Chi-square values were compared with table Chi-square values. The calculated χ<sup>2</sup> values were non-significant at both 5% and 1% level of significance at one degree of freedom in both the crosses. This indicates non-significant deviation of observed F2 segregation ratios from Mendelian monogenic cross ratio of 3:1 (Resistance: Susceptible). These results suggests that in both the F2 populations of interspecific crosses of mungbean × rice bean, the observed segregation ratio of 3:1 (Resistance: Susceptible) was on par with the expected ratio of 3:1 (Resistance: Susceptible). A good fit of 3:1 (Resistant: Susceptible) ratio was observed which suggested that a single dominant gene controls the resistance to MYMV disease in interspecific crosses of mungbean and ricebean. These results are in accordance with the findings of Gupta SK

[2], Singh SK and Singh MN [3], Rashmi J [4], Sudha M [5], Basavaraja T [6] and Mohan HN [7]. On the other hand, the digenic recessive nature of resistance [8] and monogenic recessive control of MYMV resistance has also been reported [9-13].

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