



## INHERITANCE AND SEGREGATION PATTERN OF MUNGBEAN YELLOW MOSAIC VIRUS RESISTANCE IN BLACKGRAM (*VIGNA MUNGO* (L). HEPPER)

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### Abstract

In the present investigation, seven crosses of black gram (*Vigna mungo* L.) were evaluated in F<sub>3</sub> generations for study the pattern of inheritance and segregation of disease resistant in Blackgram. The segregating generation of the crosses included Viz., VBN8 x LBG652; Vamban3 x VNB8; Vamban3 x VBN6; MDU1 x VBN6; CO5 x Mash 1008; CO5 x Mash114; and CO5x VBN6. Observations were recorded on number of plants infected and not infected with yellow mosaic symptoms at flowering and maturity stage. Based on these data, ratio of resistance and susceptible to YMV and percentage of infestation were calculated. Inheritance and segregating pattern showed the resistance crosses Vamban3 x VNB8 (51.5:1) and VBN8 x LBG652 (46.8:1) and susceptible crosses (CO5x VBN6). These two resistant crosses were shortlisted as the ones amenable for selection.

**Keywords:** Mung bean yellow mosaic virus, blackgram, resistance

### Introduction

Yellow mosaic virus, YMV, causes one of the most severe of biotic stresses in *Vignas*, an important group of pulse crops. The viral disease is transmitted through the white fly, *Bemisia tabaci*, and the yield of the plants is affected drastically. Lack of sufficient genetic variability for economically important characters is one of the reasons attributed for insignificant progress in crop improvement. Hence, it is advocated that, extensive hybridization involving larger number of parents of diverse origin be adopted to synthesize broad based gene pool. Knowledge of the inheritance and segregation pattern of the resistance would provide the opportunity to develop resistant cultivars, strategies to maximize the efficiency of developing improved Germplasm. Hence the present study was undertaken with hybridization programme to explore the segregation pattern of YMV resistance lines from the segregating materials.

### Materials and Methods

The material for the present study was generated at National Pulse Research Centre, Vamban. Following seven crosses such as VBN8 x LBG652, Vamban3 x VNB8, Vamban3 x VBN6, MDU1 x VBN6, CO5 x Mash 1008, CO5 x Mash114, CO5x VBN6 were made and F<sub>1</sub>

and F<sub>2</sub> generation were evaluated at NPRC, Vamban for MYMV resistance. In F<sub>2</sub> generation the resistance lines seeds were pooled and advanced to next generation. The F<sub>3</sub> generation seeds were raised at Agricultural Research station, Pattukkottai at Rabi 2018 season along with the yield checks VBN6, VBN8, ADT5 and ADT6. The spacing between the rows was 30 cm and spacing between the individual plants was 10 cm. Recommended agronomic practices were followed to raise the crop. Observations were recorded on number of plants infected and not infected with yellow

mosaic symptoms at flowering and maturity stage. . Based on these data, ratio of resistance and susceptible to YMV and percentage of infestation were calculated. The MYMV occurrence was recorded on all the plants of F<sub>3</sub> population of the cross based on the visual scores on 50th day while the susceptible check CO5 recorded scale 9 (Shad,*et al.*, 2006) . To confirm goodness of fit of the performed cross Mendelian segregation ratio for MYMV (resistance: susceptible) in the segregating population was tested through Chi-square test.

### Results and Discussion

This study was undertaken to determine the inheritance and segregation pattern of Mungbean yellow Mosaic virus resistance in Blackgram. Wide segregation for resistance and susceptible was observed in F<sub>3</sub> populations of crosses of Vamban3 x VNB8 (51.5:1) and VBN8 x LBG652 (46.8:1). The phenotypic segregation ratios (resistant: susceptible) were in the range 2.13 ±3.34. The results indicate that segregation in the F<sub>3</sub> populations generally fit the Mendelian monogenic ratio based on chi-square test. Similar inheritance studies of MYMV have been carried out earlier in which resistance is reported to be governed by one or two genes (monogenic or digenic inheritance) with different type of gene interaction. Inheritance of MYMIV resistance gene was studied in black gram using F<sub>1</sub>, F<sub>2</sub> and F<sub>2</sub>:3 produced from cross DPU 88-31 (resistant) × AKU 9904 (susceptible). The results of genetic analysis depicted that a dominant gene controls the MYMIV resistance in black gram genotype DPU 88-31 (Gupta *et al.*, 2013). Similarly, Kumari *et al.* (2015) studied genetics of resistance to MYMV in black gram by using F<sub>2</sub> and F<sub>3</sub> populations produced from a cross between the susceptible parent TAU-1 and the resistant parent BDU-4 under artificial conditions. The results depicted that the yellow mosaic disease resistance in black gram is controlled by a dominant gene.

**Table 1 :** MYMV disease reaction of F<sub>3</sub> generation of blackgram under natural field conditions

S. No	Name of the Crosses	No of rows evaluated in F <sub>3</sub> generation	No of plants evaluated in F <sub>3</sub> generation	No of plants not infested in F <sub>3</sub> generation	No of plants infested in F <sub>3</sub> generation	Ratio of Resistance and susceptible	Percentage of incidence	
1.	VBN8 x LBG652	8	765	749	16	46.8:1	2.09	
2.	Vamban3 x VNB8	14	1260	1236	24	51.5:1	1.90	
3.	Vamban3 x VBN6	10	827	808	19	42.5:1	2.29	
4.	MDU1 x VBN6	8	715	700	15	46.7:1	2.09	
5.	CO5 x Mash 1008	11	903	880	23	38.2:1	2.55	
6.	CO5 x Mash114	10	805	743	62	12.0:1	7.70	
7.	CO5x VBN6	10	655	586	69	8.49:1	8.12	
8.	ADT5	10	855	812	43	18.9:1	5.09	
9.	VBN6	Resistant Checks	10	855	846	9	94:1	1.37
10.	ADT6		10	855	837	18	46.5:1	2.10
11.	VBN8		10	859	855	4	213.7:1	0.46

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