



Genetic Study of Inheritance of Mungbean Yellow Mosaic Virus (MYMV) Resistance in Blackgram (*Vigna Mungo* (L.) Hepper)

KEYWORDS

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ABSTRACT *Blackgram is one of the most highly valuable pulse crop, cultivated in almost all parts of India. Beside different constraints, viral diseases mostly yellow mosaic disease is the prime threat for massive economic losses in blackgram especially in the Indian subcontinent. The Yellow Mosaic disease (YMD) caused by Mungbean Yellow Mosaic Virus (MYMV) is one of the most downfall diseases of blackgram. In the present study the inheritance of resistance to YMV was checked out in F₂ population of a cross LBG 759 (susceptible parent) × T9 (resistant parent). Resistance nature of F₁ of the crosses proves clearly the resistance was dominant over susceptibility. Goodness of fit test (chi square test) relevant to test the deviation of observed ratio to Mendelian segregation ratio for MYMV (resistance: susceptible) in the segregating population suited well with 1:3 (resistance: susceptible).*

INTRODUCTION

Blackgram (*Vigna mungo* (L.) Hepper) also known as Uradbean, is one of the important pulse crops of India. India is the largest producer and also consumer of blackgram. It has surely marked itself as the most popular pulse and can be most consequently referred to as the "king of the pulses" due to its delicious taste and numerous other nutritional qualities. Blackgram is superb combination of all nutrients, which contains proteins (25-26%), carbohydrates (60%), fat (1.5%), minerals, amino acids and vitamins (Karamany, 2006). Being a good leguminous crop, it is itself a mini-fertilizer depository, as it has special characteristics of maintaining and restoring soil fertility through fixing atmospheric nitrogen in symbiotic association with Rhizobium bacteria, present in the root nodules (Ahmad et al., 2001). It is short duration pulse crop (Delic et al., 2009), usually flowering within 30-60 days of sowing and maturing within 60-90 days.

Among various biotic and abiotic yield limiting factors, mungbean yellow mosaic disease (MYD) caused by mungbean yellow mosaic virus (MYMV) is the most destructive limiting factor in blackgram. Infection of MYMV may cause up to 85-100% yield loss in uradbean (Singh et al., 2011).

The virus is transmitted by white flies (*Bemisia tabaci*). The awareness on mode of inheritance of YMV resistance is crucial to develop relevant breeding strategy targeted to incorporation useful gene contributing resistance to MYMV. There are only few divergent reports were published on mode of inheritance and gene governing the resistance. In blackgram, monogenic dominant nature of resistance was reported by Dahiya et al. (1977), Kaushal and Singh (1988) and Gupta et al. (2005) while it was noted to be digenic recessive by Singh (1980), Dwivedi and Singh (1985) and Verma and Singh (1986). The chief objective of this present study was to analyse gene action involved in the inheritance of MYMV resistance in black gram in segregating F₂ populations.

MATERIALS AND METHODS

To study the inheritance pattern of mungbean yellow mosaic

virus resistance we selected susceptible blackgram genotype LBG 759 (female parent) and resistant genotype T9 (male parent) as parent materials. Sowing of parent material and crossing program were performed during kharif 2015-16 season. F₁ seeds are collected and raised to build up segregating F₂ population in rabi 2015-16 season. A total of 125 F₂ plants are examined to analyse the pattern MYMV resistance inheritance.

Evaluation of MYMV reaction

Sowing and estimation of MYMV inheritance in F₂ population was carried in summer 2015-16 season at ARS, MADHIRA which is hot spot for MYMV incidence. For evaluation of the test material against MYMV, pot sowing was done by following the infector row method of sowing two test rows alternating with spreader rows of highly susceptible check 'LBG 759' so as to adequately spread the inoculum at the test location which is hot spot for MYMV. No insecticide was sprayed in a plan to maintain the whitefly population in experimental field. The MYMV occurrence was recorded on all the plants of F₂ population of the cross based on the visual scores on 50th day while the susceptible check LBG 759 recorded scale 9. The rating scale implied by Singh et al. (1988), was used as given below table 1.

Table 1 : Grouping of genotypes into different categories based on 0-9 scale.

Scale	Percentage of plant foliage affected	Reaction
1	Mottling of leaves covering 0.1 to 5.0% of the leaf area	Resistant

3	Mottling of leaves covering 5.1 to 10.0% of the leaf area	Moderately resistant
5	Mottling and yellow discolouration of 10.1 to 25.0% of the leaf area	Moderately susceptible
7	Mottling and yellow discolouration of 25.1 to 50.0% of the leaf area	Susceptible
9	Severe yellow mottling on more than 50.0% and up to 100% of the leaf area	Highly susceptible

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.

Table 2: Chi-square test for inheritance of MYMV resistance in uradbean

Pheno-type	Obs-erved	Value	Expect-ed	Freq. Observed (%)	Freq. expected (%)
a	30	LOW	31.25	24.00	25.00
A	95	HIGH	93.75	76.00	75.00
Totals	125		125.00	100.00	100.00
Chi square calculated value = 0.07 (Mendelian)					
Chi square table value = 3.849					
Confidence level = 0.050					
Calculated p value = 0.796					
Degree of freedom = 1					

Results and discussion

To deduce the inheritance pattern of MYMV resistance blackgram cross LBG 759 × T9 were evaluated and Chi-square test was developed to confirm the expected deviation from the Mendelian segregation ratio of segregating generation F_2 and the results are presented in Table 2. All the accessible information pertaining to MYMV resistance confirmed that the F_1 s of the cross were resistance to MYMV. Resistance type of all the F_1 s of cross marked clearly that the resistance was dominant over susceptibility. With respect to observed: expected F_2 segregation ratio for resistance: susceptible chi-square test showed non-significance chi-square value with chi-square table value between the probability of 0.80 - 0.70 confirmed of the expected ratio, fitted well with 1:3 in F_2 .

The ratio fitted well with different ratios of mendelian in F_2 , B1, B2 populations of five selected cross combinations and revealed the nature of inheritance as duplicate, complementary and inhibitory (Durgaprasad et al 2014). Single dominant gene governing inheritance was conformed in blackgram cultivar "VBN (Bg) 4" (vinoth et al.). The involvement of complementary gene action and interaction of duplicate dominant and duplicate recessive type

of epistasis interactions for MYMV resistance inheritance was noted in different selected crosses (Thamodhran et al. 2016).

The results of the present study are comparable with results obtained by thamodhran in F_2 and BC1 population of the cross MDU1 × PU-31. From the above discussion it was found that inheritance of mungbean yellow mosaic virus resistance is in with ratio of 1 : 3 (resistant: susceptible).

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