

Original Research Article

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Genetics of Mungbean Yellow Mosaic Virus (MYMV) Resistance in Blackgram (*Vigna mungo* (L.) Hepper)

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ABSTRACT

Keywords

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Blackgram is one of the most highly profitable pulse crop, cultivated in almost all parts of India. Beside different constraints, viral diseases mostly yellow mosaic virus disease is the prime hazard 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 breakdown diseases of blackgram. Genetics of resistance to YMV was studied in F₂ population of a cross LBG 759 (Susceptible parent) × T9 (Resistant parent). Goodness of fit test (chi square test) relevant to test the deviation of observed ratio to mendelian segregation ratio for MYMV in the segregating population suited well with 1:3 (Resistance: Susceptible). It indicates a typical monogenic recessive gene is governing resistance and susceptibility reaction against MYMV in blackgram.

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. 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.

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.*, 1980).

The virus is transmitted by white flies (*Bemisia tabaci*). The awareness on mode of inheritance of MYMV resistance is crucial to develop relevant breeding strategy targeted to incorporate 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 Gupta *et al.*, (2005) while it was noted to be digenic recessive by 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 programme 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 Shad *et al.*, 2006, was used as given below table 1.

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

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 F₂ and the results are presented in Table 2. All the accessible information pertaining to MYMV resistance confirmed that the F₁s of the cross were shown no symptoms to MYMV and this marked clearly that the resistance was susceptible over dominance. With respect to observed: expected F₂ 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 (resistance: susceptible) in F₂. It indicates a typical monogenic recessive gene is governing resistance and susceptibility reaction against MYMV in blackgram.

The ratio fitted well with different ratios of Mendelian in F₂, 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 confirmed in blackgram cultivar "VBN (Bg) 4" (Vinoth *et al.*, 2014).

Table.1 Grouping of genotypes into different categories based on 0-5 scale

SEVERITY	% INFECTION	INFECTION CATEGORY	REACTION GROUP
0	All plants free of virus symptoms	Highly Resistant	HR
1	1-10% infection	Resistant	RR
2	11-20% infection	Moderately resistant	MR
3	21-30% infection	Moderately Suseptible	MS
4	30-50% infection	Susceptible	S
5	More than 50%	Highly susceptible	HS

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

Phenotype	Observed	Value	Expected	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						

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).

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