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Development of Mungbean Yellow Mosaic Virus (MYMV) Resistant Genotypes in Greengram through Introgression of Wild Genotypes

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A B S T R A C T

Two hundred and twenty-five F_2 derivatives of a greengram crossed between the MMYMV susceptible genotype VRM(Gg)1 and wild *Vigna* species *Vigna umbellata* of Ricebean resistant genotypes were taken for the MYMV screening study for which the variety CO-5 greengram was used as susceptible check variety. Augmented design was imposed in the trial for test verifies the MYMV introgrossed lines of greengram derivatives. Out of 225 introgressed lines studied, the result indicated that 18 green gram genotypes viz., P- 8, P- 18, P- 30, P- 45, P- 53, P- 62, P- 72, P- 88, P- 103, P- 113, P- 124, P- 135, P- 149, P- 166, P- 174, P- 183, P- 207, P- 214 shown the negative reaction for MYMV for VMGG012 x VRM (Gg)1 greengram cross derivatives lines showed complete resistance to MYMV while other entries showed 16 percent to 100 percent MYMV infection.

Introduction

Greengram is one of the most important pulse crops consumed by the whole world through which cheapest protein get into the body for their growth and development finally good health. The yield is reduced upto 80 percent by devasting disease of Mungbean Yellow Mosaic Virus (MYMV). All over the world mungbean is not having complete resistant due seasonal and geographical variation. To generate durable resistance into the greengram improvement by using wild *Vigna* species. In wild *Vigna* species like *Vigna umbellata* (Rice bean) is having 100 percent MYMV resistant. *Vigna umbellata* is only durable donor for MYMV resistant which is included for greengram improvement.

The aim of the study is to develop MYMV resistant geneotypes in greengram crossed with rice bean resistant genotypes. To overcome the susceptibility through this crosses combination wild *Vigna* species.

Materials and Methods

Two hundred and twenty- five F2 genotypes of greengram -VRM(Gg)1 (MYMV susceptible donor) with wild (Rice bean resistant donor) cross derivatives taken for the MYMV screening. All 225 plants were raised in single plant covering both side male and female parents were sown at Agricultural Research Station, TNAU, Virinjipuram, Vellore. The spacing adopted for the plant to plant was 30 x 10 cm. Row to row 50 cm was maintained. Every ten rows or genotypes, variety Co5 greengram susceptible check considered as one block (total 22 blocks) was raised to monitor the MYMV resistant genotypes in F2 segregants. The observation was taken in leaf area affected in a plant. Augmented design imposed in the trial for test verify the introgressed lines of greengram This interspecific cross and their parent's resistance study was carried out. The disease intensity was recorded by observing the percentage of infected plants to the total number of plants and assigned a rating scale. The rating was done as followed by Singh *et al.,* (1988) and greengram is concern for this study only two category is followed zero percent infected and more than zero percent infected. Zero percent infection is considered to be – and above zero percent MYMV infection is considered to be + since there no stability of MYMV infection in greengram genotypes having seasonal variation.

Results and Discussion

In the F_2 generation of interspecific crosses between greengram and rice bean, sufficient plant population of 225 plants recovered. The disease score was recorded for each ten rows. Among the 22 blocks genotypes, 18 genotypes or rows only exhibited the 100 per cent resistance to MYMV namely plant no 8,18,30 45, 53, 62, 72,88, 103, 113,124,135,149, 166,174, 183,207 and 214 was marked as + while severe infection (100 per cent) and lowest infection below 1 was observed in the susceptible lines marked as in Table 1. In a particular season a single plant affected below 0.1 percent infection is considered to be probability of MYMV susceptibility in subsequent season since, greengram showing seasonal variability for MYMV resistance. One season one genotype showing resistance and same genotypes showing susceptibility to subsequent season. In this situation exploring the complete resistant genotypes is required that means 0.0 percent MYMV infection lines may be selected for future crop improvement programme such genotypes used as MYMV donor .

The present investigation is to assess MYMV resistant potentiality in the interspecific F_2 population of (VMGG 012-05 x VGGru1) x *V.umbellata* derivatives. Mung Bean Yellow Mosaic Virus incidence of MYMV varied from 0.00 to 95.00 per cent among the 215 plants. The accessions were grouped based on the reaction of MYMV present in rows (population) and complete resistant reaction of MYMV by its expression. 100 per cent no incidence was taken as complete resistant and above 0.1 percent infections that is lowest incidence to highest 100 percent incidence considered to be susceptible genotypes. The disease intensity was recorded by observing the percentage of infected plants to the total number of plants and assigning a rating scale. Among the parents V. *umbellata* had a score 0 with rating of 1 indicated as resistance to MYMV where as *Vigna radiata* VMGG012-005 had susceptible score 25 percent. The recombinants of segregating genotypes in F2 generation involving *V. radiata x V. umbellata 18* entires found as immune to MYMV while other row or genotypes showed moderate resistant to susceptible.

Table.1 MYMV reactions for VMGG012 X *VGG ru 1* cross derivatives

Plant Name	MYMV REACTION	Plant Name	MYMV REACTION	Plant Name	MYMV REACTION
P1	+	P41	+	P81	+
P2	+	P42	+	P82	+
P3	+	P43	+	P83	+
P4	+	P44	+	P84	+
P5	+	P45	-	P85	+
P6	+	P46	+	P86	+
P7	+	P47	+	P87	+
P8	-	P48	+	P88	-
P9	+	P49	+	P89	+
P10	+	P50	+	P90	+
P11	+	P51	+	P91	+
P12	+	P52	+	P92	+
P13	+	P53	-	P93	+
P14	+	P54	+	P94	+
P15	+	P55	+	P95	+
P16	+	P56	+	P96	+
P17	+	P57	+	P97	+
P18	-	P58	+	P98	+
P19	+	P59	+	P99	+
P20	+	P60	+	P100	+
P21	+	P61	+	P101	+
P22	+	P62	-	P102	+
P23	+	P63	+	P103	+
P24	+	P64	+	P104	+
P25	+	P65	+	P105	+
P26	+	P66	+	P106	+
P27	+	P67	+	P107	+
P28	+	P68	+	P108	+
P29	+	P69	+	P109	+
P30	-	P70	+	P110	+
P31	+	P71	+	P111	+
P32	+	P72	-	P112	+
P33	+	P73	+	P113	+
P34	+	P74	+	P114	+
P35	+	P75	+	P115	+
P36	+	P76	+	P116	+
P37	+	P77	+	P117	+
P38	+	P78	+	P118	+
P39	+	P79	+	P119	+

P40	+	P80	+	P120	+
P121	+	P161	+	P201	+
P122	+	P162	+	P202	+
P123	+	P163	+	P203	+
P124	-	P164	+	P204	+
P125	+	P165	+	P205	+
P126	+	P166	-	P206	+
P127	+	P167	+	P207	-
P128	+	P168	+	P208	+
P129	+	P169	+	P209	+
P130	+	P170	+	P210	+
P131	+	P171	+	P211	+
P132	+	P172	+	P212	+
P133	+	P173	+	P213	+
P134	+	P174	-	P214	-
P135	-	P175	+	P215	+
P136	+	P176	+		
P137	+	P177	+		
P138	+	P178	+		
P139	+	P179	+		
P140	+	P180	+		
P141	+	P181	+		
P142	+	P182	+		
P143	+	P183	-		
P144	+	P184	+		
P145	+	P185	+		
P146	+	P186	+		
P147	+	P187	+		
P148	+	P188	+		
P149	-	P189	+		
P150	+	P190	+		
P151	+	P191	+		
P152	+	P192	+		
P153	+	P193	+		
P154	+	P194	+		
P155	+	P195	+		
P156	+	P196	+		
P157	+	P197	+		
P158	+	P198	+		
P159	+	P199	+		
P160	+	P200	+		

+ indicates MYMV infection, – indicates MYMV complete no infection

Similar result was reported by Nath (1994) and Gupta (2003), (Pandiyan *et al.,* 2007). The genotypes grouped into resistant may be further used in MYMV resistance breeding programme. Balaji *et al.,* (2004) revealed the result as that of present study for agroinoculation in mungbean.

The Virus resistance and gene silencing in plants infected with begomovirus is derived from *V.umbellata* resistant source derived into derivatives of greengram and ricebean crosses (Dhakar, *et al.,* 2010) as that of present result. Resistance to Mung bean yellow mosaic virus, phenotypic characters and yield components in urd bean the present study obtained in green gram **(**Kang *et al.,* 2005). Genetics of plant virus resistance explained the genetical reaction agree with present study. Karthikeyan *et al.,* (2012) obtained the similar results supported to the present study support for greengram Mungbean Yellow Mosaic Virus (Karthikeyan *et al.*, 2014).

Mungbean Yellow Mosaic Virus (MYMV) resistant geneotypes derived from intraspecific crosses agree with interspecific crosses of mungean with rice bean. Mariyammal *et al.,* (2019) studied the same genotypes of population for bruchids resistant which was developed for MYMV resistant study in mungbean and umbellata crosses (Pandiyan *et al.,* 2005). Cross between *V.radiata x V.umbellata* for MYMV resistant geneotypes Cytological irregularities happened as the same result obtained in this study. Pandiyan *et al.,* (2006) reported that the Mungbean Yellow Mosaic Virus Resistance in *Vigna* species agreed with same kind of result obtained.

Pandiyan *et al.,* (2018) in blackgram same types of result obtained in green gram. Selvi, *et al.,* (2006) reported the similar result in greengram (Singh *et al.,* 1988). reported Multiple disease resistance in mung bean with special emphasis on mung bean yellow mosaic virus (Sudha *et al.,* 2013 and 2013 b). Inheritance studies regarding mungbean yellow mosaic virus (MYMV) in inter and intra specific crosses of mungbean (*Vigna radiata*) is endorse with present study results (Sudha *et al.*, 2015).

Vigna species resistance to mungbean yellow mosaic virus in mungbean conferring study also similar to present study. The hybrids grouped under resistant may be subjected further screening in subsequent generation. Even in the smaller population of F_2 segregants, there was resistance reaction registered by *V.radiata x V. umbellata* reported by Pandiyan *et al.,* (2020) hence selection for resistance may be employed at later generation when plant population is high.

The green gram genotypes viz., P- 8, P- 18, P- 30, P- 45, P- 53, P- 62, P- 72, P- 88, P- 103, P- 113, P- 124, P- 135, P- 149, P- 166, P- 174, P- 183, P- 207, P- 214 for MYMV reactions for VMGG012 X VRM (Gg)1 greengram cross derivatives can be utilized for different breeding programmes to develop a variety resistant to Mungbean yellow mosaic virus. The greengram gentotypes seeds can be preserved for the future plant breeding work.

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