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Mohammad Irfan
Division of Genetics and Plant Breeding, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir, Shalimar, Jammu and Kashmir, India

M Ashraf Bhat
Division of Genetics and Plant Breeding, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir, Shalimar, Jammu and Kashmir, India

Reyazul Rouf Mir
Division of Genetics and Plant Breeding, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir, Shalimar, Jammu and Kashmir, India

Farooq Ahmed Bhat
Division of Plant Pathology, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir, Shalimar, Jammu and Kashmir, India

Fehim Jeelani
Division of Agri-economics and Statistics, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir, Shalimar, Jammu and Kashmir, India

TA Wani
Division of Plant Pathology, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir, Shalimar, Jammu and Kashmir, India

Corresponding Author:
Mohammad Irfan
Division of Genetics and Plant Breeding, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir, Shalimar, Jammu and Kashmir, India

A study on mungbean germplasm against yellow mosaic virus (MYMV) disease under field conditions

Mohammad Irfan, M Ashraf Bhat, Reyazul Rouf Mir, Farooq Ahmed Bhat, Fehim Jeelani and TA Wani

Abstract
Greater amount of variation was found by screening 110 mungbean accessions against MYMV during *Kharif* season under field conditions at FoA, Wadura Sopore, Jammu and Kashmir. Depending upon the severity of disease, the germplasm was categorized into resistant and susceptible genotypes. Disease severity significantly increased due to prolonged inhabitation of whitefly and remained with it till maturity of crop. Development of insecticide resistance in whitefly increased the frequency of whitefly outbreaks which eventually increased disease incidence. On differential response of germplasm to MYMV, eight (8) genotypes were found highly resistant (HR), thirty four (34) resistant (R), five (5) moderately resistant (MR) to disease. Fourteen (14) were found moderately susceptible (MS), forty seven (47) susceptible (S) and eight (8) highly susceptible (S).

Keywords: Mungbean, mungbean yellow mosaic virus (MYMV), screening, resistance, susceptibility

1. Introduction
Mungbean (*Vigna radiata* L) (2n = 22) is an economically important legume crop, belongs to family fabaceae. Mungbean as a short duration crop and due to its increasing growth rate it is considered as a very predominant legume [1]. It is taken as raw (sprouts) supplement in subtropical zones of the world due to its high protein concentration. It is rich in other mineral composition and dietary fiber which is very essential to human body for better growth and development. Its principal source is India and it is primarily grown in Asia, Southeast Asia. It is India's third most important pulse crop, with 16% of the country's total pulse area and more than 90% of production [2]. It covers 4.5 million hectares land with production and productivity of 2.5 million tonnes and 548 kg/ha accounting only 10% of total pulse production. Despite by making best efforts to improve mungbean cultivars, yield still remains low due to biotic and abiotic factors. Among biotic factors, viral disease like mungbean yellow mosaic virus (MYMV) come across as being a serious threat and broadly distributed in other countries like, India, Pakistan, Bangladesh, Thailand and Phillipines [3]. It has been observed that there are three species of whitefly-transmitted bipartite begomoviruses *viz*., mungbean yellow mosaic India virus (MYMIV), mungbean yellow mosaic virus (MYMV) and horsegram yellow mosaic virus (HgYMV) which are responsible for MYMD in different parts of the world by acting as causal agents [4, 5]. This virus has been found to possess two single stranded DNA molecules (DNA A and DNA B) [6]. This virus causes yellow patches and then turns entire leaf yellow. It causes Chlorosis of leaves followed by necrosis and severe stunting and deformed pods [7]. Plants affected by this virus, blossom sparingly and possess shriveled seeds inside pods. Viral infections in mungbean have the potential to adversely affect the crop and reduce yield by up to 80% in sensitive cultivars [8]. MYMV incidence can only be reduced by lowering the vector, namely the whitefly population, with pesticides, which are ineffective in severe infestations. The most effective way to reduce the occurrence of MYMV disease is to use resistant varieties. It is imperative to test mungbean germplasm against MYMV in order to identify resistant genotypes. Identification and utilization of resistant genotypes act as possible way in alleviating disease severity. Several researchers have previously reported a number of resistant lines, and the current study was meant to screen mungbean germplasm accessions for resistant genotypes utilizing field screening in realistic circumstances using this background knowledge. In this regard, field screening was conducted against mungbean yellow mosaic virus to identify resistant genotypes that could act as a source for resistance in crop improvement program.

2. Methodology

Screening of 110 mungbean germplasm lines was done against MYMV under field conditions at FoA, Wadura Sopore. All accessions were sown in ABD block design with 2m row length, row to row and plant to plant distance of 50 × 10 cm, respectively. After every 2 rows, a susceptible check as a spreader row was sown for uniform spread of disease. The experiment was maintained by adopting all the cultural practices. Insecticidal sprays were avoided to encourage natural spread of disease. Assessment of different germplasm lines were carried out at reproductive stage from 10 randomly selected and tagged plants of each plot.

Data was recorded from each accession based on total plant stand after infection. Depending on severity of MYMV prevalence, classification of germplasm was done on the basis of rating scale (0-5) given by Bashir *et al.* [3] as shown in Fig. 1.

Table 1: Disease rating scale

Score	Symptom Description	Severity Index	Response
0	Immune	0	Highly resistant
1	Small yellow spots on leaves	0.01-1.4	Resistant
2	Coalesced bright yellow spots on leaves	1.5-2.4	Moderately Resistant
3	Mostly coalesced bright yellow spots on leaves	2.5-3.4	Moderately Susceptible
4	Coalesced bright yellow specks on leaves, with minor stunting and few normal pods	3.5-4.4	Susceptible
5	Yellowing of leaves, severe stunting, small, immature and shriveled seeds	4.5-5.0	Highly Susceptible

Fig 1: Disease rating scale [0, Highly resistant; 1, Resistant; 2, Moderately resistant; 3, Moderately susceptible; 4, Susceptible; 5, Highly susceptible]

3. Results

Great amount of variation was observed among the genotypes by screening under field conditions at FoA, Wadura against mungbean yellow mosaic virus (MYMV). Based on disease severity, the germplasm was classified into 6 different classes. Out of 110 tested genotypes, the MYMV incidence ranged from 0 to 84.3%, Eight (8) genotypes were observed to have high resistance level, Thirty four (34) genotypes were resistant, Five (5) genotypes were at level of moderate resistance, fourteen (14) genotypes were moderately susceptible, Forty four (44) were susceptible and only five (5) genotypes were found highly susceptible against MYMV. More importantly, sufficient amount of incidence to MYMV was recorded in genotype SKUA-WMB-103 (84.3%) followed by SKUA-WMB-33 (81.2%), SKUA-WMB-110 (76.3%), SKUA-WMB-31 (73.4%) and SKUA-WMB-85 (73.2%) and was observed highly susceptible to MYMV. Similarly, for resistant genotypes MYMV incidence ranged from 5.3 to 9.2%, 17.2 to 18.6% for moderately resistant genotypes, 25.4% to 29.8% for moderately susceptible genotypes and for susceptible genotypes incidence ranges from 33.9% to 49.2% as shown in Table 2. Pie chart revealed 7% genotypes were highly resistant, 31% resistant, 4% moderately resistant, 13% moderately susceptible, 40% susceptible and 5% highly susceptible against mungbean yellow mosaic virus (MYMV).

Table 2: Reaction of mungbean germplasm against MYMV disease

Disease	Reaction Group	Genotypes	Number	MYMV Incidence
Mungbean Yellow Mosaic virus disease	Highly Resistant	SKUA-WMB: 9, 10, 21, 28, 47, 53, 79, 107.	8	0
	Resistant	SKUA-WMB: 1,5,18,19,20,22,26,27,29,32,36,37,46,48,49,54,56,58,59,62,64,66,70,75,78,80,82,86,89,93,98,99,108,109	34	5.3-9.2
	Moderately Resistant	SKUA-WMB: 69,74,83,97,100	5	17.2-18.6
	Moderately Susceptible (MS)	SKUA-WMB: 3,4,6,8,14,25,43,44,67,72,77,87,92,96	14	25.4-29.8
	Susceptible (S)	SKUA-WMB: 2,7,11,12,13,15,16,17,23,24,30,34,35,38,39,40,41,42,44,50,51,52,55,57,60,61,63,65,68,71,73,76,81,84,88,90,91,94,95,101,102,104,105,106	44	34.4-48.2
	Highly Susceptible (HS)	SKUA-WMB: 103,85,33, 31, 110	5	67.9-86.1

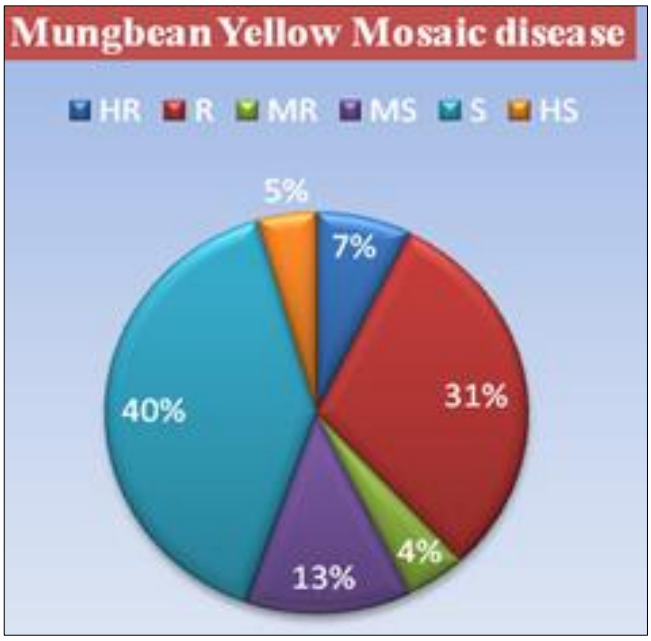

Fig 2: Response of genotypes against MYMV

HR =highly resistant, R = resistant, MR = moderately resistant, MS = moderately susceptible, s = susceptible, HS = highly susceptible.

4. Discussion

From previous studies it has been observed that MYMV potentially decrease the yield of number of legume crops. Greater susceptibility rate was observed for some accessions to MYMV that may be conceivably related to more conducive environmental factors and susceptible checks which lead to infection due to large vector population availability in the field. Disease severity significantly increased due to prolonged inhabitation of whitefly and remained with it till maturity of crop. Development of insecticide resistance in whitefly increased the frequency of whitefly outbreaks which eventually increased disease incidence [9] and therefore resistant cultivars which is environmentally compatible and imperative tool for an effective disease control. So identification of sources resistant to MYMV needs an accuracy assessment technique for successful plant breeding program [10, 11].

It is quite obvious from the results that out of one hundred ten tested genotypes, Eight (8) genotypes have shown high resistance level, Thirty four (34) genotypes as resistant; Five (5) were at the level of moderate resistance. Therefore such germplasm lines could be used in breeding program as donors for disease resistance and help in improving the resistance level of adapted cultivars. However, from last few decades the increasing trend in incidence and epidemic conditions of MYMV may trigger and increase the probability of resistance breakdown to MYMV disease [12]. So there is a need to pressure and give priority in finding more reliable, resistant and potential source to widen the genetic base of MYMV disease resistant source for crop improvement. Knowledge of resistant sources can be useful in germplasm selection so that can be utilized in breeding program [13].

5. Conclusion

From the results it has been concluded that there is high amount of variability present in our germplasm and to further screen these lines under natural and artificial conditions will help in better understanding of this crop. The resistant lines identified while screening can be used as donor source for future breeding program and can also be utilized to develop a mapping population for tagging and mapping of MYMV resistant gene.

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7. Competing interests

Authors have declared that no competing interests exist.

8. Author's contribution

Mohammad Irfan, M. Ashraf Bhat conceptualized and conducted this research. Reyaz ul Rouf Mir, Farooq Ahmed Bhat facilitated collection of germplasm. Fehim Jeelani, T. A. Wani helped in writing and editing of the manuscript. All authors contributed to manuscript revision.

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