

Original Research Article

Relationship of Whitefly, *Bemisia tabaci* Population and Mungbean Yellow Mosaic Virus Disease Incidence in Green Gram

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ABSTRACT

The Yellow mosaic disease of green gram is caused by Mungbean Yellow Mosaic Virus. The disease is transmitted by vector, whitefly, *Bemisia tabaci*, which is responsible for the 100 percent loss in susceptible varieties. The present experiments were conducted during Kharif 2014 and 2015 at Agricultural Research Farm, Banaras Hindu University, Varanasi, U.P., India in Randomized Block Design with three replications to find out the relationship between Whitefly, *B. tabaci* population and Mungbean Yellow Mosaic Virus disease incidence in green gram twenty varieties/genotypes. The correlation studies revealed that there was a significant positive correlation ($r=0.992^{**}$) between *B. tabaci* population and Mungbean Yellow Mosaic Virus disease incidence.

Keywords

Whitefly, MYMV,
Green gram,
Incidence

Introduction

Mungbean [*Vigna radiata* (L.) Wilczek] is third most important pulse crop of India after chickpea and pigeonpea (Anonymous, 2017; Sundaram, 2010). The mungbean is native to Indo-Burma (Myanmar) region of South-East Asia and cultivated extensively in Central Asia. Mungbean is commonly known as moong, green gram, oreganpea, etc. The crop suffers with several biotic and abiotic stresses which are responsible for the low production of the crop. Biotic stresses such as insect pests, nematodes and weeds substantially reduce the yield of green gram. According to estimates made in India nearly 10-15% of food legumes production is lost due to diseases alone (Pande *et al.*, 2007; Tikoo *et al.*, 2005). Mungbean is infected by more than eight viruses under field conditions the important one are

Mungbean yellow mosaicvirus, Bean common mosaic virus, Cucumber mosaic virus, Leaf crinklevirus, Leaf curl virus, Mosaic mottle virus and Alfalfa mosaic virus (Nene, 1973; Kaiser *et al.*, 1971).

The yellow mosaic disease of mungbean is caused by mungbean yellow mosaic begomovirus (MYMV). This disease is important, serious, destructive, widespread and inflicts heavy loss annually. It was first identified in India in 1955 and is naturally transmitted by whitefly (*Bemisia tabaci* Genn.), but not by mechanical inoculation or by seed (Nariani, 1960).

Hence, the present study was aimed to find out the relationship between Mungbean yellow mosaicvirus disease and its vector *i.e.* whitefly.

Materials and Methods

The experiment was carried out during the *Kharif* 2014 and 2015 at Agricultural Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, (U.P.) to determine the relationship between the incidence of whitefly (*Bemisia tabaci*) population and yellow mosaic virus disease incidence on 20 promising genotypes of green gram. The recommended agronomic practices without using pesticide were followed in growing of the crop. All the genotypes were grown in Randomized Block Design (RBD) with 3

replications. The row to row and plant to plant distance was maintained as 30 cm and 10 cm, respectively. The unit plot size 4×0.60 m. The infestation of whitefly and incidence of yellow mosaic virus disease incidence was recorded. A correlation coefficient value was obtained with a density of whitefly population and Mungbean Yellow Mosaic Virus disease incidence. MYMV disease incidence was calculated using the following formula.

$$\text{Per cent MYMV disease incidence} = \frac{\text{Total number of infested plants}}{\text{Total number of plants}} \times 100$$

Table.1 Relationship between *B. tabaci* population and incidence of Mungbean Yellow Mosaic Virus disease on different varieties/genotypes during *Kharif* 2014 and 2015

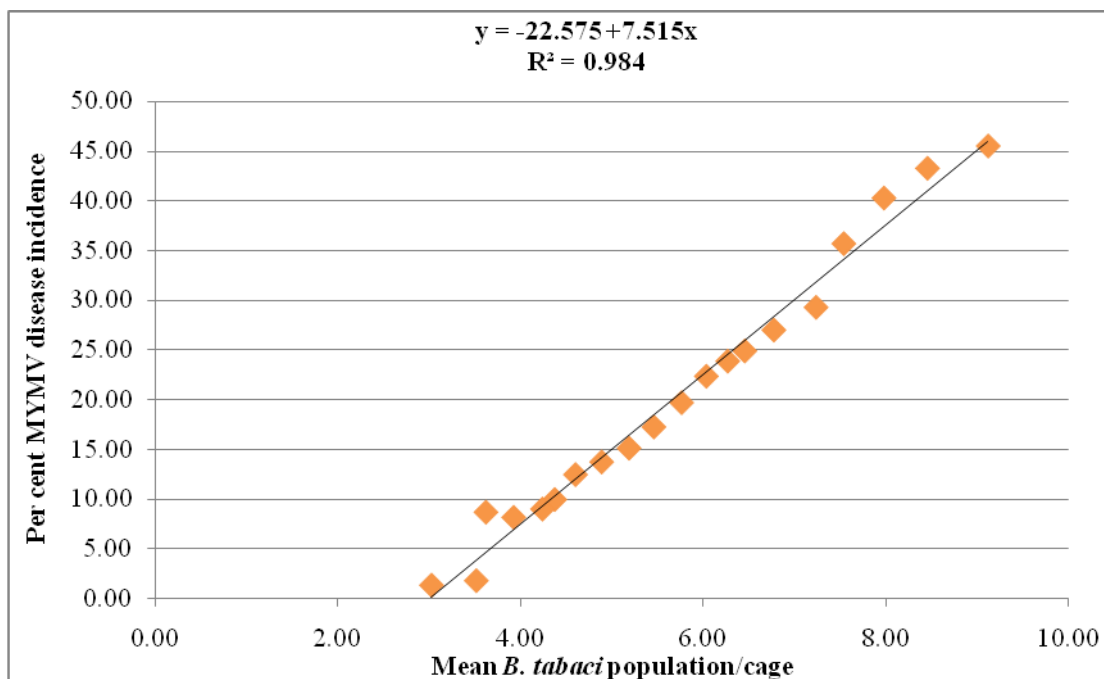
Tr. No.	Varieties/Genotypes	Mean <i>B. tabaci</i> population/cage	Mean MYMV incidence (%)	Ratio	Yield (q/ha)
T ₁	PM-5	3.02	1.29	1:0.43	7.72
T ₂	IPM 2K 14-9	4.37	9.90	1:2.27	6.22
T ₃	HUM-1	3.62	8.63	1:2.38	6.40
T ₄	ML 1257	5.76	19.65	1:3.41	4.73
T ₅	Pusa 672	4.89	13.68	1:2.80	5.77
T ₆	IPM 306-6	7.54	35.64	1:4.73	3.11
T ₇	SM 48	8.45	43.22	1:5.11	3.33
T ₈	IPM 05-3-22	6.03	22.30	1:3.70	3.23
T ₉	Pusa Bold 2	4.60	12.41	1:2.70	5.99
T ₁₀	IPM-9901-10	5.46	17.21	1:3.15	5.09
T ₁₁	HUM-16	3.92	8.12	1:2.07	6.58
T ₁₂	IPM 306-1	3.51	1.74	1:0.49	6.96
T ₁₃	PM 4	4.24	8.95	1:2.11	5.26
T ₁₄	ML 5	9.12	45.46	1:4.99	3.30
T ₁₅	ML 1256	5.19	15.07	1:2.91	5.54
T ₁₆	ML 1059	7.98	40.24	1:5.04	4.41
T ₁₇	SML 191	6.77	26.95	1:3.98	4.04
T ₁₈	ML 515	6.27	23.82	1:3.80	4.17
T ₁₉	PDM 288	7.23	29.24	1:4.04	3.78
T ₂₀	HUM-12	6.45	24.85	1:3.85	4.13

Table.2 Simple correlation coefficient between mean *B. tabaci* population and incidence of Mungbean Yellow Mosaic Virus disease on different varieties/genotypes during *Kharif* 2014 and 2015

Variables	Correlation coefficient (r)	Regression equation	R ² Value
Mean <i>B. tabaci</i> population (x) Vs MYMV incidence (y)	0.992**	$y = -22.575 + 7.515x$	0.984

** Significant at 1%

Fig.1 Relationship between *B. tabaci* population and incidence of Mungbean yellow mosaic virus disease observed under green gram during *Kharif* 2014 and 2015



Results and Discussions

The relationship between the *B. tabaci* population and Mungbean Yellow Mosaic Virus disease incidence in green gram varieties/ genotypes

The data of both the year of experimentation i.e. *Kharif* 2014 and 2015 depicted a clear picture of the relationship between *B. tabaci* population MYMV disease incidences. The pooled data revealed that in PM-5, lowest *B.*

tabaci population (3.02 whitefly/cage) was recorded and also lowest MYMV incidence (1.29%). The maximum *B. tabaci* population (9.12 whitefly/cage), as well as maximum MYMV incidence (45.46%), was found in ML 5. In the pooled data also the highest ratio between *B. tabaci* population and MYMV incidence was highest in SM 48 (1:5.11), while lowest in PM-5 (1:0.43). The correlation studies revealed that there was a significant positive correlation ($r = 0.992^{**}$) between *B. tabaci* population and MYMV

incidence (Table 2). The study revealed that increased the density of vector there is an increase in the incidence of MYMV disease (Table 1 and Fig. 1). The present findings are in agreement with Sahoo and Sahoo (1991) who reported that positive correlation between the population of whitefly and incidence of yellow mosaic virus disease irrespective of the variety.

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