



E-ISSN: 2278-4136
P-ISSN: 2349-8234
JPP 2018; 7(1): 660-662
Received: 25-11-2017
Accepted: 26-12-2017

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Screening of okra genotypes against yellow vein mosaic virus disease (OYVMV) under Field conditions in Allahabad

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Abstract

The present study was conducted at central research farm of Sam Higginbottom University of Agriculture, Technology and Sciences, Allahabad during *Rabi* season 2017. The experiment was conducted during March, to June, 2017 at Field of central field of SHUATS, Allahabad. There were 8 okra genotypes with diverse morphological characters collected from IIVR, Varanasi. The experiment consisted of 8 treatments and 3 replications in randomized block design. Based on disease scale, the data presented of screening of 8 different genotypes on okra against YVMV showed completely free/immune in (VRO-5) to Yellow vein mosaic virus incidence with 6.6 % disease and yield 40.23 q/ha, whereas genotypes (IC117216, IC140934 and Parbhani Kranti (check) were Moderate resistant while two genotypes (IC433695, and IC140906) were Tolerant against YVMV, and genotype (VRO-4) was Susceptible. The highest Susceptibility reach as was observed in IIVR-10, yield 53.12 q/ha.

Keywords: Okra, yellow vein mosaic virus, Immune, resistant, Susceptibility, tolerant

Introduction

Okra [*Abelmoschus esculentus* (L.) Moench] is placed in Malvaceae family and originated in tropical Africa but can be grown in tropical and sub-tropical regions of the world (Ali *et al.*, 2012) [2]. It is a most edible vegetable crop and popular for its green tender fruits grown throughout India during summer and rainy seasons (Solankey *et al.*, 2016) [16]. India is the largest producer of okra in the world with the total area 0.533 million ha, production of pods 6.346 million tonnes and productivity 11.9 metric tonnes/ ha (Anonymous 2014) [3]. Among the various biotic diseases yellow vein mosaic virus YVMV is a most serious disease and caused substantial yield losses (80-90%) in okra crops (Sastry and Singh 1974, Ali *et al.*, 2005) [13, 1]. The disease is characterized by a homogenous knotted, yellow veins and yellowish or creamy color of green leaf, stunted plant growth and bear very few deformed small fruits (Ali *et al.*, 2005, 2012) [1, 2]. This YVMV disease of okra is spread in the humid and heavy rainfall areas and transmitted by a vector whitefly (*Bemisia tabaci* Gen.) belonging to genus begomovirus and family of geminiviridae (Chakraborty *et al.* 1999) [8]. A cultivar Pusa Sawani developed as a tolerant to YVMV by using a resistance gene from strain IC-1542 (Singh and Joshi 1960) [14] but now days this is indicated to be susceptible for this disease. In a study, it was found that the infection rate has reached up to 100% if field yield loss ranges between 50% and 94% (Ali *et al.* 2012) [2]. Today, availability of little resistance stock of cultivars/varieties of okra is available which may be due to change of strain in virus (Singh *et al.* 1962) [15]. The major problem in okra cultivation is lack of high-yielding varieties along with location specific and resistant/tolerant hybrids. The transfer of OYVMV resistant gene through breeding has another best way of getting resistant and high yielding cultivars/ variety in often cross-pollinated crops like okra, which is need of breeders (Nerkar and Jambhale 1985) [11]. Heterosis is a special genetic mechanism wherein the distant genotypes are brought together in a specific pattern to express their ability to make a dramatic shift in the magnitude of a particular trait (Mehta *et al.* 2007) [10]. However, there has been a pressing demand for a high yielding variety, coupled with resistance to YVMY. Therefore, efforts have been made on selected hybrids to see the performance of good F1s in relation to YVMV disease occurrence with the aim to classify the hybrids on the basis of the occurrence of YVMV under natural condition.

Materials and methods

The present investigation was conducted at the Central Field (Entomology field) of "Sam Higginbottom University of Agriculture, Technology and Sciences" Allahabad, Uttar Pradesh during *Rabi* under late season 2017. There were 8 genotypes with diverse morphological

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characters collected from IIVR, Varanasi. The experiment consisted of 8 treatments and 3 replications in randomized block design.

In each plot five plants were randomly selected and tagged for recording observation on whitefly incidence (YVMV). The observations were recorded from the 3 leaves of each plant viz., bottom, from the middle and one from the top of the plant and mean number of nymphs' and adult fly per leaf were worked out.

The per cent disease incidence (PDI) will calculated by the following formula, Tiwari *et al.* (2012) [17].

$$\text{PDI} = \frac{\text{Number of diseased plant}}{\text{Total no. plant observed}} \times 100$$

Following by self-made disease rating scale by Ali *et al.*, (2005) [1] tables

Result and discussion

Screening against Whitefly, *B. tabaci* and YVMV disease incidence

The genotypes Prasant YVMV disease per cent IC117216 (26.66 %), IC140934 (23.43 %), VRO-5 (6.6 %), Parbhani Kranti (check) (13.3 %), IC433695 (48.52 %), IC140906 (46 %), VRO-4 (63.51 %), IIVR-10 (90.88 %) infested. The genotypes yield whereas IC117216 (43.3 q/ha), IC140934 (47.8 q/ha), VRO-5 (40.23 q/ha), Parbhani Kranti (check) (44.12 q/ha), IC433695 (52.31 q/ha), IC140906 (61.42 q/ha), VRO-4 (51.22 q/ha), IIVR-10 (53.12 q/ha) recorded.

Symptomatology

During the observation, it was noted that affected okra plants were showing number of typical symptoms with varying intensity.

Based on disease scale, the data presented in (Table.1) of screening of 8 different genotypes of okra against YVMV under field condition revealed that out of 8 genotypes tested, the genotypes were found in completely free (immune) on (VRO-5) to Yellow vein mosaic virus incidence. Similar results were also reported by Benchasri (2011) [6] and Venkataravanappa *et al.*, (2013) [18].

Were 3 genotypes or (IC117216, IC140934 and Parbhani Kranti (check) Moderate resistant while two genotypes (IC433695, and IC140906) was Tolerant against YVMV, one genotype (VRO-4) Susceptibility, while the remaining one genotype (IIVR-10) was High Susceptibility reaction. The genotypes IIVR-10 earlier showed to be resistance to BYVM (Borah *et al.*, 1992) [7], were High Susceptible with much faster development of disease symptoms than other tested genotype (Venkataravanappa *et al.*, 2013) [18]. The variation in symptoms observed in various genotypes may be due to unique interaction between the particular virus strain and plant genotype or vector and genotype or altered feeding conditions of the vector (Polston and Anderson, 1997; Delatte *et al.*, 2006; Azizi *et al.*, 2008; Venkataravanappa *et al.*, 2013) [12, 9, 4, 18] has reported the incidence of Yellow vein mosaic virus in okra. In case of hybrids disease incidence ranged between 19.26 and 69.13 per cent plants, it ranged from 19.95 to 51.16 per cent. Batra and Singh (2000) [5] screened eight okra varieties against OYVMV.

Table 1: Scale for classifying disease reaction against Yellow vein mosaic virus

Severity Grade	Rating Scale	Severity Range (%)
0	Immune	0%
1	Highly resistant	1-10 %
2	Moderate resistant	11-25 %
3	Tolerant	26-50 %
4	Moderate Susceptibility	51-60 %
5	Susceptibility	61-70 %
6	High Susceptibility	71-100 %

Table 2: Performance of different genotypes of Okra against Yellow vein mosaic virus under late Rabi field conditions Allahabad.

Sr.no	Genotypes	Severity Grade	Disease (%)	Reaction of genotypes	Fruit yield (q/ha)
T1	IC117216	2	26.66	Moderate	43.3
T2	IC140934	2	23.43	Moderate	47.8
T3	VRO-5	0	6.6	Mild (immune)	40.23
T4	PK(check)	2	13.3	Moderate	44.12
T5	IC433695	3	48.52	Tolerant	52.31
T6	IC140906	3	46	Tolerant	61.42
T7	VRO-4	5	63.51	Susceptibility	51.22
T8	IIVR-10	6	90.88	High Susceptibility	53.12

The okra genotypes are screening to against YVMV resistant (check) on Parbhani Kranti okra genotype Moderate resistant on YVMV. The genotype VRO-5 (6.6%) disease immune (mild) recorded. IC140934 (23.43%) Moderate resistant recorded and followed by IC11716 (26.66%) recorded. IC33695 (48.52%) Tolerant and followed by IC140906 (46%) recorded. VRO-4 (63.51%) Susceptibility. IIVR-10 (90.88%) High Susceptibility recorded.

The better on Parbhani Kranti (check) VRO-5 genotype scale of disease lowest recorded its better in against YVMV infested locations. Better IC140934 and followed by IC117216 genotype in Allahabad field conditions.

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