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Field screening of okra (*Abelmoschus esculentus* L. Moench) genotypes against okra yellow vein mosaic virus disease

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Abstract
Yellow Vein Mosaic Virus (YVMV) is a major disease in okra which is transmitted by the vector whitefly (*Bemisia tabaci*). Five diverse okra genotypes namely AE 64, AE 65, AE 66, Kashi Pragati and VRO 106 were crossed in full diallel fashion. A total of twenty five cross combinations (five parents and twenty hybrids) were raised in randomized block design in two replications during the *Rabi* - Summer, 2015 at Department of Vegetable Crops, Horticultural College and Research Institute, Tamil Nadu Agricultural University, Coimbatore. The severity of YVMV disease was recorded and the percent disease incidence (PDI) was calculated. The genotypes AE 64, AE 65 and AE 66 were found to be immune to the disease which could be exploited for further breeding programme due to their resistant disease reaction towards YVMV. Among the hybrids, the cross combinations of AE 64 x AE 65, AE 64 x AE 66, AE 65 x AE 64, AE 65 x AE 66 and AE 66 x AE 64 did not express any disease symptoms whereas the susceptible check COBhH 1 showed highly susceptible reaction.

Keywords: Okra, Percent Disease Incidence (PDI), whitefly, Yellow Vein Mosaic Virus (YVMV)

Introduction
Okra (*Abelmoschus esculentus* (L.) Moench), is an economically important vegetable crop grown in tropical and sub-tropical parts of the world. It is one of the important member of Malvaceae family having higher chromosome number of 2n=8x=72 or 144 and polyploidy in nature. Though okra is native of tropical Africa, it is a priced vegetable grown for its tender fruits in India. Okra has good nutritional value, particularly high content of vitamin C (47 mg/100g), vitamin A (0.18 mg/100g), calcium (84 mg/100g), iron (1.20 mg/100g) and fibre (1.70 g/100g) in the edible fruit (Benchasri *et al*., 2012) [4].

In Okra, yellow vein mosaic virus disease (YVMV) is the most devastating disease which is transmitted by whiteflies (*Bemisia tabaci*) (Magar and Nirmal 2010) [9]. YVMV belongs to the genus Begomovirus, family Geminiviridae. In India, the occurrence of this disease was first reported by Kulkarni (1924) [8] in the province of Bombay. A plant with yellow vein mosaic virus has yellowish mosaic on the leaves, prominent yellow veins and crinkled leaves. If infection is severe, plants become stunted with poor quality pods and upto 100 per cent infection in the field oocur with yield losses ranging from 50 to 94 per cent depending on the stage of crop growth at which infection occurs (Sastry and Singh, 1974) [14]. The application of pesticides for controlling the whiteflies is commonly practiced by the farmers but this poses a threat and pesticide residues to the consumers. Uprooting of infected plants is also done when infection is heavy in the field. The only practical solution for this problem is to develop resistant cultivars, identification and transfer of genes for resistance to YVMV from related wild species to susceptible high yielding cultivated varieties (Jambhale and Nerkar, 1985) [6]. Therefore, the present study aims at searching the source of resistance towards yellow vein mosaic virus resistance.

Material and methods
Plant material: Five diverse okra genotypes namely AE 64, AE 65, AE 66 collected from Tamil Nadu Agricultural University, Coimbatore, Kashi Pragati and VRO 106 collected from Indian Institute of Vegetable Research, Varanasi were used for the present study. They were maintained through selfing during *kharif* season of 2014 and were crossed in full diallel mating design to develop twenty F1 hybrids during *Rabi*- summer of 2015.

Planting and experimental design: During *Rab*i - Summer of 2015, the five parental lines, twenty F1 hybrids along with susceptible line CoBhH 1(border crop) were raised in a randomized block design with two replications at the Vegetable Orchard,

Department of Vegetable Crops, Tamil Nadu Agricultural University, Coimbatore. All the entries were sown in plot size of 4 m^2 and spacing of 60 x 30 cm was followed.

Per cent disease incidence (PDI) at 15 days interval: The per cent disease incidence was recorded at 15 days interval up to 105 days after sowing based on the scale given in Table 1 (Ali *et al*., 2005) [1].

Table 1: Disease rating scale.

Rating scale	Type	Disease incidence (%)
0	Immune	0
1	Highly resistant	1-10
2	Moderate resistant	11-25
3	Tolerant	26-50
4	Moderate susceptible	51-60
5	Susceptible	61-70
6	Highly susceptible	71-100

Per cent disease incidence (PDI) is calculated as under:

$$PDI = \frac{\text{Number of infected plants}}{\text{Total number of plants observed}} \times 100$$

Results and discussion

To develop and evolve new hybrids, it is necessary to understand the genetic architecture of quantitative characters for formulating an efficient breeding programme. Selection of suitable parent is one of the important steps in the hybridization programme. It is essential that the parents should be chosen on the basis of this genetic value because phenotypically superior lines may also yield poor combinations. Okra is very much susceptible to whitefly transmitted yellow vein mosaic virus and several attempts had been made by several workers to reduce the disease through vector control, resistance screening and other breeding strategies. Emphasis needs to shift towards development of yellow vein mosaic virus resistant cultivars. This study was undertaken to find out the potential source of resistance of okra to yellow vein mosaic virus under natural epiphytic condition.

In this study, the parents AE 64, AE 65 and AE 66 did not express any symptom of yellow vein mosaic virus disease and are immune to the disease (Vinod *et al*., 2000; Debnath and Nath, 2003; Tiwari *et al*., 2012) [16, 5, 15]. Kashi Pragati and VRO 106 showed increase YVMV incidence of 60.40 and 65.46 per cent respectively at 90 DAS. At 105 DAS both the parents showed severe increase of YVMV incidence of 82.31 and 88.57 per cent respectively and are referred as highly susceptible parent (Rashid *et al*., 2002; Nizar *et al*., 2004) [11, 10]. Among the twenty hybrids, five hybrids namely AE 64 x AE 65, AE 64 x AE 66, AE 65 x AE 64, AE 65 x AE 66 and AE 66 x AE 64 did not express any disease symptoms whereas AE 66 x AE 65 is highly resistant with the disease incidence of 7.14 per cent (Rattan and Bindal, 2000; Batra *et al*., 2000) [12, 3]. Seven hybrids *viz*., AE 64 x Kashi Pragati, AE 64 x VRO 106, AE 65 x Kashi Pragati, Kashi Pragati x AE 64, Kashi Pragati x AE 66, VRO 106 x AE 64 and VRO 106 x Kashi Pragati were tolerant to YVMV with the incidence of 29.71, 42.87, 41.78, 45.89, 34.65, 29.50 and 28.57 per cent respectively at 105 DAS (Sankara *et al*., 2012) [13].

Four hybrids *viz*., AE 65 x VRO 106, AE 66 x Kashi Pragati, Kashi Pragati x AE 65 and VRO 106 x AE 65 were moderately resistant to the yellow vein mosaic virus disease with the incidence of 21.43, 17.28, 21.23 and 21.43 per cent respectively at 105 DAS (Kamalpreet *et al*., 2013) [7] The remaining cross combination of AE 66 x VRO 106, Kashi Pragati x VRO 106, VRO 106 x AE 66 along with the check COBhH 1 show high degree of disease incidence. It is clear that the disease incidence varies in different genotypes as well as the hybrid combination which may be due to the preference of insects in cultivars due to the presence of biochemical substances or metabolites which includes phenols, terpinoids, flavonoids, alkaloids, catalase, etc. which plays a vital role in imparting resistance to insects/pests (Baldwin, 2010) [2].

Table 2: Percent disease incidence (PDI) of YVMV in okra at 15 days interval during Rabi- Summer, 2015

Parents and Hybrids	YVMV incidence (PDI)					
	Days after sowing					
	45	60	75	90	105	Score
AE 64	0	0	0	0	0	I
AE 65	0	0	0	0	0	I
AE 66	0	0	0	0	0	I
Kashi Pragati	4.78	10.34	25.21	60.40	82.31	HS
VRO 106	3.87	7.87	18.89	65.46	88.57	HS
AE 64 x AE 65	0	0	0	0	0	I
AE 64 x AE 66	0	0	0	0	0	I
AE 64 x Kashi Pragati	0	0	0	12.54	29.71	T
AE 64 x VRO 106	0	0	12.32	26.45	42.87	T
AE 65 x AE 64	0	0	0	0	0	I
AE 65 x AE 66	0	0	0	0	0	I
AE 65 x Kashi Pragati	0	0	13.16	27.61	41.78	T
AE 65 x VRO 106	0	0	0	10.71	21.43	MR
AE 66 x AE 64	0	0	0	0	0	I
AE 66 x AE 65	0	0	0	0	7.14	HR
AE 66 x Kashi Pragati	0	0	0	7.10	17.28	MR
AE 66 x VRO 106	0	10.71	42.86	60.71	82.14	HS
Kashi Pragati x AE 64	0	0	10.27	31.67	45.89	T
Kashi Pragati x AE 65	0	0	0	8.67	21.23	MR
Kashi Pragati x AE 66	0	0	10.56	21.28	34.65	T
Kashi Pragati x VRO 106	0	0	21.78	58.87	81.46	HS
VRO 106 x AE 64	0	0	3.57	17.81	29.50	T
VRO 106 x AE 65	0	0	0	6.89	21.43	MR
VRO 106 x AE 66	0	0	14.29	28.57	64.29	S
VRO 106 x Kashi Pragati	0	0	10.71	18.76	28.57	T
COBhH 1	0	15.76	35.87	60.11	74.87	HS

Conclusion

Future research must be directed towards identification of resistant sources and mechanism as well exploitation of wild relatives of the genus *Abelsmoschus* for identification of resistant genes which can be utilize in future breeding programmes.

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