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Vulnerability studies of okra genotypes to bhendi yellow vein mosaic virus (BYVMV)

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ABSTRACT

India is the leading okra producer globally, but its production suffers due to losses caused by Bhendi yellow vein mosaic virus (BYVMV) disease, transmitted by whitefly. Due to its unstable resistance nature and limited availability of sources for resistance in cultivated types, the crop improvement programme of okra has yet to take a fast pace. In this study, sixty-four distinct okra genotypes were screened for resistance to BYVMV under the natural epiphytotic conditions of Delhi. It was found that the disease incidence (DI), coefficient of infection (CI), vulnerability index (VI), and adult whitefly count (AWC) varied significantly amongst the different okra genotypes. The highest mean DI was recorded in Pusa Sawani (86.5%), and DI was 0 % in the genotypes Pusa Bhindi-5 (DOV-66), DOV-89 and DOV-92. The coefficient of infection (CI) was highest in Pusa Sawani (70.39 %). Maximum VI was recorded in Pusa Sawani (83 %) and 0 % VI in the wild genotypes IC-141040, IC-90560 and cultivated Pusa Bhindi-5, DOV-81 and DOV-92. Similarly, AWC was maximum in Pusa Sawani (30.4) and the lowest number in DOV-26 (1.2). The number of whiteflies peaked at 80 days after sowing and subsequently decreased. Based on this study, Pusa Sawani was the most susceptible genotype, and Pusa Bhindi-5 and DOV-92 were the most resistant genotypes. The resistant genotypes Pusa Bhindi-5 and DOV-92 can be used to transfer BYVMV resistance in other susceptible lines or varieties and for hybrid development in future okra improvement programmes.

Keywords: Okra, YVMV, Disease incidence, Vulnerability index.

INTRODUCTION

Okra (*Abelmoschus esculentus* L. Moench), also known as lady's finger, is a widely cultivated warm season vegetable crop grown in various regions of the world. It is believed to be native to tropical Africa or Asia. Okra is mainly cultivated for its fresh pods and is also a rich source of fibre, minerals and amino acids like lysine and tryptophan, which are a key component for a well-balanced diet. Okra pod contains vitamins A, B, and C and is a rich source of protein, carbohydrates, lipids, minerals, iron, and iodine (Hughes, 9). India is the largest producer of okra in the world accounting more than 72% of production share. Among the vegetables, okra accounts for second highest exchange earning through export after onion. Bhendi yellow vein mosaic virus (BYVMV) disease, transmitted by sap-sucking vector whitefly (*Bemisia tabaci*) is causing serious threats to okra production in India for many years, and recently, it has become a greater problem in various parts of the world (Venkataravanappa *et al*., 21). The BYVMV disease may cause upto 100% of the cumulative crop losses under severe conditions. BYVMV is a type of *Begomovirus* and till now, nine *Begomoviruses* and four different types of beta satellites have been found to be associated with the YVMV (Deshmukh *et al*., 6). Chlorosis and yellowing of veins and veinlets, fewer and smaller yellowish fruits and plants are the major symptoms of BYVMV disease (Fig. 3c and 3e). Dhankhar (7) validated the hypothesis that two complementary dominant genes govern the resistance to yellow vein mosaic disease in okra.

Till date, screening of okra genotypes for BYVMV disease in both cultivated and wild genotypes has been reported by various workers (Badiger and Yadav,3; Mohapatra *et al*., 12; Nirosha *et al*., 14). The unavailability of a large number of polymorphic markers followed by linkage mapping and, very little biotechnological intervention are one of the reasons behind the failure to achieve success in okra resistance breeding programme. The situation is confounded further by variation in chromosome number (2n = 56–196) and the complex polyploidy characteristic of the okra genome (Sastry and Zitter, 18). The most effective technique for managing insect-vector and transmitted plant viruses is to leverage host plant resistance (Legarrea *et al*., 11). Further, evolving of new strains of the virus as well as rapid breakdown of insecticide resistance are

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causing difficulty in the management of BYVMV disease. Thus, precise characterization of the BYVMV infection and, the use of resistant cultivars is the only way to control the disease. Keeping in view of the above facts, the present study was undertaken to identify okra genotypes resistant to BYVMD under field conditions and to determine the possible sources of resistance, that will help in okra improvement programme in the future.

MATERIALS AND METHODS

The present study examined sixty-four okra genotypes (Table 1) for resistance to bhendi yellow vein mosaic (BYVMV) disease during the *Kharif* season of 2019 and 2020 at the Indian Agricultural Research Institute, New Delhi (28.6377° N, 77.1571° E). All the genotypes were evaluated for four parameters, namely disease incidence (DI), coefficient of infection (CI), vulnerability index

Table 1. Genotype source, disease incidence, coefficient of infection, vulnerability index and adult whiteflies count of 64 okra genotypes.

Sl. No.	Genotype	Source	Disease Incidence (DI) (%)	Coefficient of infection (CI) (%)	Vulnerability Index (VI) (%)	Whiteflies count (AWC)
1	Pusa Sawani	IARI, New Delhi	86.50	70.39	83	30.4
2	Pusa A4	IARI, New Delhi	41.93	61.15	82	22.8
3	Arka Abhay	IARI, New Delhi	37.16	38.13	68	18.6
4	Arka Anamika	IIHR, Banglore	36.05	37.43	56	17.3
5	Parbhani Kranti	VNMKV, Parbhani	30.49	41.25	53	11.5
6	IC-470737	NBPGR, New Delhi	10.43	5.00	14	6.5
7	IC-90560 (*A. tetraphyllus*)	NBPGR, New Delhi	13.72	22.50	26	7.2
8	(Cut leave)	NBPGR, New Delhi	23.74	29.54	55	6.2
9	IC-90511 (*A. tetraphyllus*)	NBPGR, New Delhi	20.01	29.23	46	5.7
10	IC-90515 (*A. tetraphyllus*)	NBPGR, New Delhi	33.20	42.00	68	6.3
11	IC-141045 (*A. moschatus*)	NBPGR, New Delhi	29.92	37.50	56	3.9
12	IC-90461	NBPGR, New Delhi	27.35	30.00	54	10.1
13	IC-140970	NBPGR, New Delhi	22.21	8.92	22	8.0
14	IC-140	NBPGR, New Delhi	25.07	28.30	47	6.8
15	*A.caillei* Mizoram	NBPGR, New Delhi	9.53	4.25	16	6.6
16	IC-470737	NBPGR, New Delhi	14.25	6.93	13	4.9
17	IC-141040 (*A. moschatus*)	NBPGR, New Delhi	12.23	5.49	0	5.3
18	IC-212557	NBPGR, New Delhi	15.11	20.27	17	4.7
19	*A.caillei*	NBPGR, New Delhi	19.63	26.73	12	4.7
20	*A.caillei* Sikkim	NBPGR, New Delhi	22.58	28.50	38	5.4
21	IC-90560	NBPGR, New Delhi	2.45	1.00	0	6.4
22	IC-90343	NBPGR, New Delhi	10.96	15.23	32	6.4
23	IC-436706	NBPGR, New Delhi	15.41	25.34	29	6.3
24	H-3	IARI, New Delhi	4.32	2.51	5	2.9
25	H-7	IARI, New Delhi	9.28	14.25	12	3.1
26	H-13	IARI, New Delhi	4.82	4.44	23	3.2
27	H-10	IARI, New Delhi	25.40	30.79	56	3.3
28	DOV-26	IARI, New Delhi	4.96	1.97	24	1.2
29	Pusa Bhindi-5 (DOV-66)	IARI, New Delhi	0.00	0.00	0	1.4
30	DOV-92	IARI, New Delhi	0.00	0.00	0	1.5

Contd...

Table 1 contd...

Sl. No.	Genotype	Source	Disease Incidence (DI) (%)	Coefficient of infection (CI) (%)	Vulnerability Index (VI) (%)	Whiteflies count (AWC)
31	DOV-89	IARI, New Delhi	0.00	0.00	14	1.3
32	DOV-77	IARI, New Delhi	1.90	0.64	12	1.6
33	DOV-28	IARI, New Delhi	1.78	0.67	14	1.9
34	DOV-81	IARI, New Delhi	0.00	0.00	0	1.7
35	DOV-19	IARI, New Delhi	19.55	30.75	30	1.9
36	DOV-31	IARI, New Delhi	5.56	1.99	4	5.0
37	*A. caillei* × *A. grandiflorus*	NBPGR,New Delhi	9.26	3.70	4	3.4
38	C-350	NBPGR, New Delhi	8.14	4.15	4	3.3
39	DOV-68	IARI, New Delhi	7.27	3.64	10	3.3
40	KR-19506490	IARI, New Delhi	21.94	31.50	32	2.4
41	DOV-68-1	IARI, New Delhi	3.88	1.26	16	4.7
42	DOV-8063	IARI, New Delhi	15.53	21.85	12	3.5
43	DOV-862	IARI, New Delhi	6.27	2.89	4	3.5
44	YVRES-6	IARI, New Delhi	23.10	33.14	54	4.6
45	DOV-693	IARI, New Delhi	27.89	32.25	54	4.9
46	DOV-22	IARI, New Delhi	9.78	3.70	16	4.6
47	DOV-10	IARI, New Delhi	4.48	2.41	6	4.0
48	DOV-9	IARI, New Delhi	5.85	2.47	7	4.3
49	YVRES-9	IARI, New Delhi	0.00	0.00	0	3.6
50	CO-4	TNAU, Coimbatore	4.25	2.63	4	4.4
51	DOV-8999	IARI, New Delhi	6.04	2.82	4	4.1
52	DOV-15	IARI, New Delhi	7.66	3.00	2	4.1
53	DOV-33	IARI, New Delhi	4.98	2.00	6	3.3
54	DOV-47	IARI, New Delhi	3.31	1.06	6	3.7
55	DOV-319	IARI, New Delhi	15.03	13.65	46	3.7
56	SW-002	IARI, New Delhi	11.58	9.71	24	3.0
57	SW-005	IARI, New Delhi	15.66	16.50	24	2.6
58	SW-003	IARI, New Delhi	19.53	17.08	12	1.7
59	SW-001	IARI, New Delhi	25.98	29.24	54	1.9
60	SW-004	IARI, New Delhi	15.51	12.05	33	2.2
61	Perkins Long Green	IARI, New Delhi	26.79	30.63	51	10.0
62	Pusa Makhmali	IARI, New Delhi	36.28	49.90	78	20.5
63	Kashi Vardhan	IIVR, Varanasi	29.42	30.29	54	10.1
64	DOV-1	IARI, New Delhi	24.59	16.08	46	10.6
		Mean	**16.05**	**16.92**	**27**	**5.9**

(VI), and adult whiteflies count (AWC). The infector row approach was used to screen the genotypes in natural epiphytotic conditions. Pusa Sawani, a susceptible variety, was used as an infector line for every genotype to ensure an equal distribution of viral disease pressure in the experimental block. The disease incidence was recorded at 15 days intervals during the crop-growing season. The disease incidence was calculated in percentage using the formula: DI = (Number of diseased plants/

Total number of plants) × 100. Symptom severity grade, response value, and co-efficient of infection were determined as per Appiah *et al*. (1) (Table 2). The coefficient of infection was calculated as per the formula of CI (%) = DI × RV. The vulnerability index (VI) of the genotypes were calculated using a six-point scale varying from 0 to 5 (Table 3; Fig. 3a) and using the formula given by Gonde *et al*. (8). Adult whiteflies count (AWC) on each genotype was calculated as per Borad *et al*. (5) and genotypes were classified as suggested by Benchasri (4). All the 64 genotypes were classified and grouped according to their response to BYVMD based on the above four parameters studied and represented in a tabular form. To verify the results and to know the interaction of all the four parameters studied, a factorial grouping of the genotypes was done using DARwin6 software (Perrier, 16).

RESULTS AND DISCUSSION

This experiment aimed to find out a source of BYVMV resistance in the available okra germplasm and to classify them according to their response to the particular viral disease. Out of the sixty-four genotypes screened for BYVMD, disease incidence (DI) varied from 0 to 86.5 %, and the maximum mean DI was recorded in Pusa Sawani (86.5 %) followed by Pusa A4 (41.93%), while there was 0% DI in the cultivated genotypes Pusa Bhindi-5 (DOV-66), DOV-89, and DOV-92 which showed their high level of resistance to BYVMV. The mean DI of all the genotypes studied in this experiment was 16.05 %. The mean DI at different intervals increased gradually from 45 days after sowing (DAS) (5.33 %), 60 days after sowing (11.71 %), 75 days after sowing (18.84 %) and 90 days after sowing (25.62 %) (Fig. 1). This showed that infection of BYVMV disease in okra increases rapidly with advancement of crop growth from the initial infection. Similar findings were also reported by Benchasri (4). The variation in DI observed in various genotypes may be due to unique interaction between the particular virus strain and plant genotype or altered feeding conditions of the vector. Cross-protection is another mechanism that can confer plant resistance against viruses in these resistant genotypes (Seth *et al*., 19). It was noticed that genotypes with thick and rough leaves with dark green leaves (DOV-92, DOV-89 and Pusa Bhindi-5) showed less DI. So, these morphological features can be taken as selection criteria in the screening of okra genotypes against BYVMV disease. First and earliest appearance of yellow vein mosaic virus symptom was noticed in variety Pusa Sawani after 20 days of sowing (Fig.1). This led to highest level of disease incidence (86.5%) in this variety, which clearly showed that the early incidence of YVMV disease in okra causes high level of incidence and may cause higher crop yield loss provided the variety is susceptible.

The coefficient of infection ranged from 0-70.39%. The coefficient of infection was highest

Table 2. Response value, severity grade and reaction of 64 okra genotypes used for the calculations of CI.

Symptoms	Severity grade	Response value	CI	Reaction
Symptom absent	0	0.00	0-4	HR (Highly resistant)
very mild symptoms upto 25% of leaves	1	0.25	4-9	R (Resistant)
The appearance of symptoms in 26-50% leaves	2	0.50	9-19	MR (Moderately resistant)
Appearance of symtoms in 51-75% leaves	3	0.75	19-39	MS (Moderately succeptible)
Severe disease infection in symptoms (>75%)	4	1.00	39-100	S (Succeptible)

Table 3. Vulnerability index (VI) based on score categories, symptoms and reaction of 64 okra genotypes.

Score	Symptom	Genotype class
0	No symptoms	Immune (I)
1	Mild mosaic of young leaves covering < 10% of the surface	Resistant (R)
2	Mosaic of young leaves covering < 25% of the surface	Moderately Resistant (MR)
3	Mosaic of young leaves covering < 50% of the surface, blistering and puckering of leaves	Moderately Susceptible (MS)
4	Severe mosaic of young leaves covering < 75% of the surface, distortion of leaves	Susceptible (S)
5	Severe mosaic of young leaves covering > 75% of the surface, distortion of leaves and stunting of the plants	Highly Susceptible (HS)

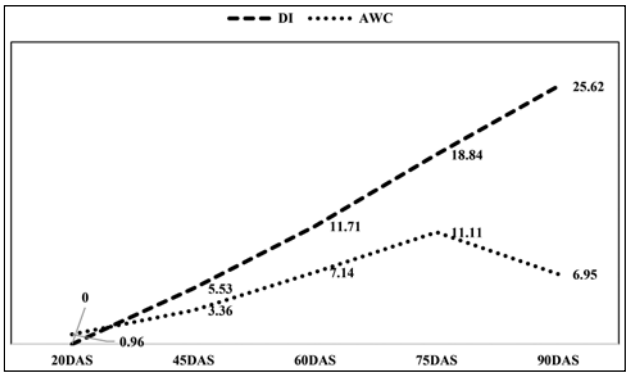

Fig. 1. Correlation between BYVMV disease incidence (DI) and adult whiteflies count (AWC) at different intervals in okra.

in Pusa Sawani (70.39 %), followed by Pusa A4 (61.15%) and Pusa Makhmali (49.90%) compared to 0% in genotypes Pusa Bhindi-5 (DOV-66), DOV-89, DOV-92, DOV-81, and DOV-9. The average CI was 16.92 %. These results were in confirmity with the findings of Patel *et al*. (15). The value of CI in resistant lines were very low while, high in susceptible varieties. This type of resistance in some genotypes may also related to the coat protein expression level as reported by Pun *et al*. (17).

The vulnerability index was measured in the middle of the crop season or active vegetative growth (60 DAS) from all the genotypes when okra is most sensitive to insects and diseases. The vulnerability index (VI) of all the genotypes was in the range of 0 to 83, with the highest vulnerability index (91%) in Pusa Sawani followed by Pusa A4 (82%) and vulnerability index was recorded 0% in the genotypes IC-141040, IC-90560, Pusa Bhindi-5, DOV-81, and DOV-92. The mean value of the vulnerability index of all the genotypes studied was 27.25%. The genotypes recording less or 0% vulnerability index (IC-141040, IC-90560, Pusa Bhindi-5, DOV-81, and DOV-92.) had higher level of resistance and can be used for development of resistant lines/hybrids for new areas which are prone to BYVMV disease directly. However, genotypes showing high vulnerability index (Pusa Sawani and Pusa A4) should be avoided or can be used with utmost care or cautiously. Less vulnerability in resistant genotypes may be due to production of new allergens or toxic proteins compared to the susceptible genotypes (Seth *et al*., 19). The adult whiteflies populations recorded in all sixty-four genotypes showed a wide range from 1.2 to 30.4 whiteflies per plant. In our investigation, the highest mean number of whiteflies were observed on Pusa Sawani (30.4), followed by Pusa A4 (22.8) and the lowest number in the genotypes DOV-26 (1.2). The whiteflies per plant were recorded from 20 DAS to 100 DAS, where we found that there was a steady increase in number of whiteflies from 20 DAS (0.96) to 80 DAS (11.11) and thereafter, decrease in number to 6.95 at 100 DAS (Fig. 1). Mean whitefly population in different time intervals was recorded as 5.90. These results were in the same line with the findings established by Borad *et al*. (5) where they correlated the BYVMV disease with a population density of adult whitefly. As per the report of Patel *et al*. (15) and Gonde *et al*. (8), the cultivar Pusa Sawani is highly vulnerable to the whiteflies attack. Several reports on the BYVMV disease and whiteflies found that there is a clear correlation between a vector peak and BYVMV disease severity. Biochemical defence line, which directly limits oviposition and feeding site development is an important feature of host plant resilience (Siddique *et al*., 20).

In an earlier study, Kennedy (10) found that the presence of a vector-resistant host plant significantly influences the virus infection due to the presence of fewer *B. tabaci* individuals as well as lower inoculum concentration. The resistant genotypes have a comparatively lower *B. tabaci* population than susceptible ones (Seth *et al*., 19). Our study also found a strong association between disease incidence (DI) and adult whiteflies count as well as an increase in values at different intervals. At 45 DAS, the mean DI was only 5.53 % in all genotypes, and it reached the peak of 25.62 % at 90 DAS while at 40 DAS the mean of adult whiteflies population was only 3.36. Thereafter, the number of adult whiteflies gradually increased and it was found to the maximum at 80 DAS (11.11) (Fig.1). It was found that the DI increased with the increase in whitefly populations. The symptoms emerged simultaneously in all vulnerable lines but only intermittently in resistant lines. The DI and VI variations between okra varieties might be caused by the increase in *B. tabaci* population density, build-up in inoculum since the beginning of the season's initial weeks, and each variety's susceptibility to infection by BYVMV disease (Appiah *et al*., 1).

Wild okra species *A. caillei* and *A. moschatus* (IC-141040) and *A. tetraphyllus* (IC-90560) showed highest resistance to whiteflies whereas, few genotypes belonging to species *A. esculentus, A. ficulneus,* and *A. tuberculatus* showed considerable resistance. This might be due to the presence of abundant hairs on stems and both upper and lower surface of a leaf obstructing the activity of whiteflies (Arora *et al*., 2; Narayanan *et al*., 13). Further, resistance to *B. tabaci* and BYVMV disease could

be due to the presence of the R-gene in the genome (Siddique *et al*., 20).

Classification of genotypes based on their reaction to the number of whiteflies attack was summarized (Table 4). This classification is in the same line with the pattern observed based on factorial analysis computed using DARWin6 software. All the 64 genotypes were distributed into 4 quarters in the factorial graph, *i.e*., the first and second quarter containing susceptible and moderately susceptible genotypes (20), respectively, and the third and fourth quarter consists of resistant and moderately resistant genotypes (44), respectively (Fig. 2). Badiger and Yadav (3) also categorized okra genotypes in different groups of resistance and susceptibility based on disease reaction.

The current study concluded that the transmission of the BYVMV disease in okra is directly linked to the presence of the vector *B. tabaci*. BYVMV infection was found severe because of the increased population

Table 4. Classification of sixty-four okra genotypes based on their responses to different disease parameters.

Parameter	Reaction		Genotypes	
Coefficient of infection (CI)	I.	Highly resistant	I.	H-3, DOV-26, DOV -66, DOV -92, DOV -89, DOV -77, DOV -28, DOV -81, DOV-31, *A. caillei*× *A. grandiflorus*, DOV-68, DOV-68-1, DOV-862, DOV-22, DOV-10, DOV-9, YVRES-9, CO-4, DOV-8999, DOV-15, DOV-33, DOV-47
	II.	Resistant	II.	IC-470737, IC-140970, IC-141040, IC-90560, IC90343, H-7, H-13, C-350 33-2
	III.	Moderately resistant	III.	IC90343, H-7, H-13, C-350 33-2, KR-19506490, DOV-319, SW-002, SW-005, SW-003, SW-004, DOV-1
	IV.	Moderately susceptible	IV.	IC-90560, IC-47073, IC-90511, IC-90515, IC-141045, IC-90461, IC-140S, IC-212557, *A. caillei*, *A. caillei* Sikkim, IC436706, H-10, Dov-19, 8063, YVRES-6, DOV-693, SW-001, Perkins Long Green, Kashi Vardhan
	V.	Susceptible	V.	Pusa Sawani, Pusa A4, Arka Abhay, Arka Anamika, Parbhani Kranti, Pusa Makhmali
Vulnerability index (VI)	I.	Highly resistant	I.	H-3, DOV-26, DOV -66, DOV -92, DOV -89, DOV -77, DOV -28, DOV -81, DOV-31, *A. caillei* × *A. grandiflorus*, C-350, DOV-68, DOV-68-1, DOV-862, DOV-10, DOV-9, YVRES-9
	II.	Resistant	II.	IC-470737, IC-140970, Catleev, IC-470737, IC-141040, IC-90560, H-3, DOV-26, DOV-66, DOV-92, DOV-89, DOV-77, DOV-28, DOV-81, DOV-31, *A. caillei* × *A. grandiflorus*, C-350, DOV-68, DOV-68-1, DOV-862, DOV-10, DOV-9, YVRES-9, CO-4, DOV-8999, DOV-15, DOV-33, DOV-47
	III.	Moderately resistant	III.	IC-90560, IC-90511, IC-140S, IC-212557, *A. caillei*, *A. caillei* Sikkim, IC90343, IC436706, H-7, H-13, Dov-19, KR-19506490, 8063, DOV-22, DOV-319, SW-002, SW-005, SW-003, SW-004, DOV-1
	IV.	Moderately Succeptible	IV.	Arka Abhay, Arka Anamika, Parbhani Kranti, IC-47073, IC-90515, IC-141045, IC-90461, H-10, YVRES-6, DOV-693, SW-001, Perkins Long Green, Kashi Vardhan
	V.	Succeptible	V.	Pusa Sawani, Pusa A4, Pusa Makhmali
Adult whitefly count (AWC)	I.	Resistant	I.	IC-141045, IC-90461, IC-470737, IC-212557, *A. caillei*, H-3, H-7, H-13, H-10, DOV -26, DOV -66, DOV -92, DOV -89, DOV -77, DOV -28, DOV -81, DOV -19, *A. caillei* × *A. grandiflorus* , C-350, DOV-68, KR-19506490, DOV-68-1, 8063, DOV-862, YVRES-6, DOV-693, DOV-22, DOV-10, DOV-9, YVRES-9, CO-4, DOV-8999, DOV-15, DOV-33, DOV-47, DOV-319, SW-002, SW-005, SW-003, SW-001, SW-004
	II.	Moderately resistant	II.	IC-470737, IC-90560, IC-47073, IC-90511, IC-90515, IC-140970, IC-140S, Catleev, IC-141040, *A. caillei* Sikkim, IC-90560, IC90343, IC436706, DOV-31
	III.	Moderately Succeptible	III.	Arka Abhay, Arka Anamika, Parbhani Kranti, IC-90461, Perkins Long Green, Kashi Vardhan, DOV-1
	IV.	Succeptible	IV.	Pusa A4, Pusa Makhmali
	V.	Highly Succeptible	V.	Pusa Sawani

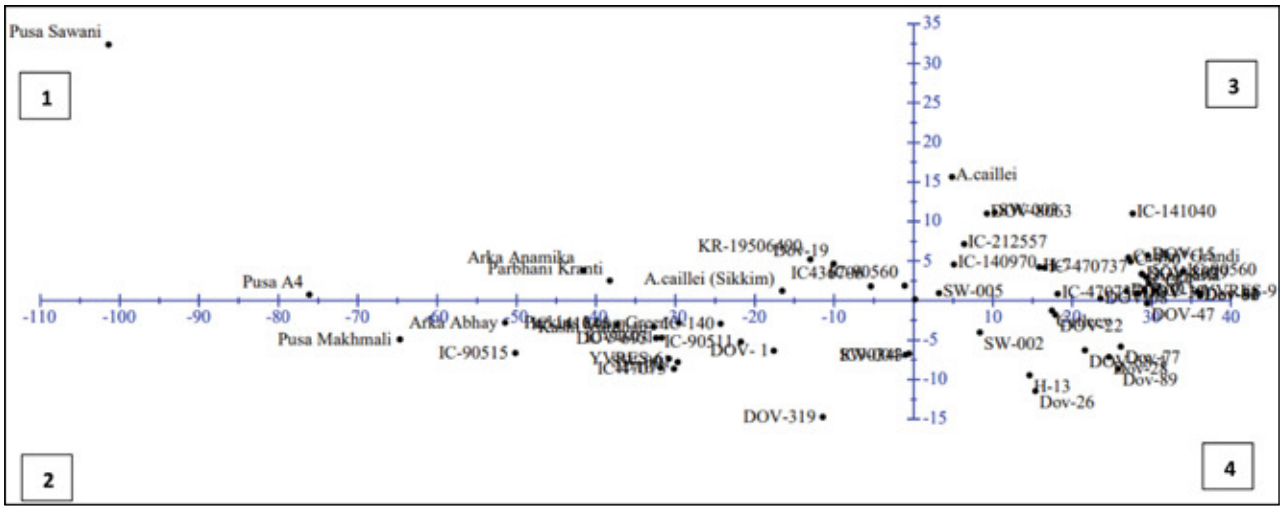

Fig. 2. Factorial correlation between 64 genotypes and different parameters studied related to vulnerability study in okra.

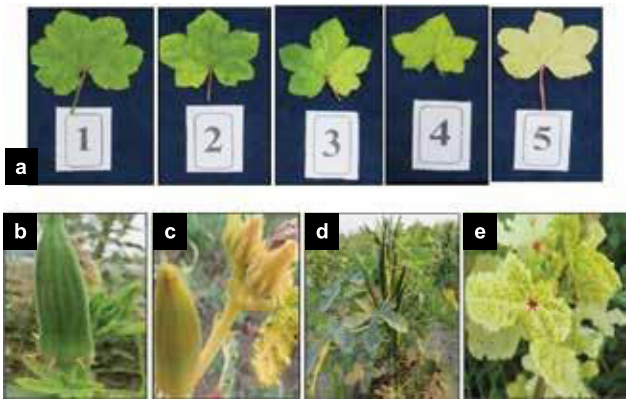

Fig. 3. a) Okra BYVMV disease scale from 1 to 5 b) Healthy fruit of okra c) BYMV disease affected fruit. d) Healthy plant of okra e) Okra leaves infected with BYMV.

of whiteflies as well as vulnerable genotypes. Pusa Sawani and Pusa A4 were the most susceptible, while Pusa Bhindi-5 (DOV-66), DOV-92, and DOV-89 were the most resistant cultivated genotypes and *A. caillei*, *A. moschatus* (IC-141040) and *A. tetraphyllus* (IC-90560) most resistant wild genotypes to BYVMV infection. Based on these findings, it was suggested that the *B. tabaci* population should be monitored from the beginning of the season and the actions needed for controlling the disease must be implemented before the whitefly population reaches the economic threshold level (ETL). However, their response to additional BYVMV strains must be determined to have the varieties, which are stable across different climatic conditions. Identified resistant sources in this study can be effectively used directly as a variety or as a source of resistance for transfer in other lines/ varieties or as a parent of hybrids in future okra breeding programmes.

AUTHORS' CONTRIBUTION

Conceptualization of research, editing and designing of the experiments (RKY); Contribution of experimental materials (RKY, AG); Execution of field/lab experiments and data collection (PVP, AT, GB); Analysis of data and interpretation (PVP, HC, BST and AD); Preparation of the manuscript (PVP, AD and SL).

DECLARATION

The authors declare that they have no conflict of interest.

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