

Biological Forum – An International Journal

14(2): 1263-1268(2022)

ISSN No. (Print): 0975-1130 ISSN No. (Online): 2249-3239

Evaluation of Pigeonpea Genotypes against Sterility Mosaic Virus (PPSMV) Disease

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ABSTRACT: The experiment was carried out for screening of Sterility Mosaic Disease (SMD) resistant lines under glasshouse conditions. Seventy-four pigeonpea genotypes were evaluated along with susceptible national check ICP 8863 and resistant check CO(Rg)7 for SMD screening by leaf stapling method. Genotypes were monitored for disease incidence and scoring was done every 15 days interval. Based on the Percent Disease Incidence (PDI), the genotypes were classified into susceptible, moderately resistant and resistant. It was reported that only two genotypes viz., BWR 153 and CRG 16-07 showed resistant reaction with disease incidence ranging from 0.1 to 10%, while genotypes viz., ICP 7919, IC 339057, IC 74016, IPAE 15-05, AL 2250, CRG 16-01, PusaArhar 21-14, PusaArhar 21-27, BWR 253, ICP 9808 and ICP 7234 were moderately resistant with disease incidence ranging from 10.1 to 25%. The remaining genotypes were categorized as susceptible with disease incidence ranging from 25.1 to 100%. Genotypes viz., BWR 153, CRG 16-07, ICP 7919, IC 339057, IC 74016, IPAE 15-05, AL 2250, CRG 16-01, PusaArhar 21-14, PusaArhar 21-27, BWR 253, ICP 9808 and ICP 7234 will be utilized as donors in the production of highvielding pigeonpea varieties.

Keywords: Sterility Mosaic Disease(SMD), Eriophyid mite, Inoculum, Susceptible, Resistant.

INTRODUCTION

Pigeonpea (Cajanus cajan (L.) Millsp is a valuable grain legume crop grown in the tropical and subtropical regions of the world (Varshney et al., 2010). Mature seeds contain 18.8% protein, 53% starch, 2.3% fat, 6.6% crude fiber and 250.3 mg 100 g^{-1} minerals (Ayenan et al., 2017). Productivity of pigeonpea is severely affected by several biotic and abiotic stresses. Of these biotic stresses of pigeonpea could result in complete yield loss. The pigeonpea sterility mosaic virus (PPSMV) causes sterility mosaic disease (SMD) often known as "green plague of pigeonpea". The symptoms include stunted growth, reduction in leaf size, mosaic mottling, chlorotic ring spots and cessation of reproductive structures in Fig. 3 and Fig. 5. PPSMV is one of the key biotic factors that causes high yield losses, poses a big challenge for pigeonpea production in the Indian subcontinent. According to reports, SMD causes an annual economic loss of \$300 million in India alone (Patil and Kumar 2015). Variability in the sterility mosaic pathogen revealed the occurrence of five different isolates in India. Among them, three distinct SMD isolates have been characterized, viz., Patancheru, Bangalore and Coimbatore. Bangalore strains are the most severe, whereas, the Patancheru and Coimbatore variants are Dhanushasree et al.,

mild (Prabhavathi and Ramappa 2018). Pigeonpea is grown with minimal input; although chemical management of disease is effective, it is neither economical nor eco-friendly. Growing resistant varieties is one of the viable options of management to minimize economic losses. For better understanding of SMD, data on mite survival, host, host range and pathogen, as well as seasonal fluctuations in the mite population could be employed (Kaushik et al., 2013). The objective of this study was to find a genotype that confers wide and sustainable resistance to SMD.

MATERIALS AND METHODS

Screening of pigeonpea genotypes for SMD resistance was carried out in Department of Pulses, Tamil Nadu Agricultural University during rabi 2021-22. The materials used for the investigation includes seventyfour pigeonpea germplasms along with susceptible national check (ICP 8863) and resistant check (CO(Rg)7) obtained from Ramiah gene bank. The genotypes were sown in pots under glass house conditions given in Fig. 2a. Inoculum for Eriophyid mite was collected from susceptible check entry ICP 8863 (Maruthi) maintained at Department of Plant pathology, Tamilnadu Agricultural University, Coimbatore. The disease was transmitted through leaf

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stapling approach (Nene *et al.*, 1976) shown in Fig. 2b. SMD infected leaf samples were gathered and examined under stereo zoom microscope for presence of Eriophyid mites (*Aceria cajani*), which transmits the SMD virus in Fig. 1. Collected leaf samples were stapled to the primary leaves of genotypes under screening. Mites from the diseased leaves moves towards healthy leaflets when the stapled leaf got dried. Plants were monitored for SMD incidence at 15 days interval from day after the first inoculation up to 90 days by counting the healthy plants (no mosaic symptoms) and diseased plants (with mosaic symptoms). Based on the disease development, the PDI was calculated using the formula

Number of infected plants

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

AICRP scale was assessed to evaluate the genotypes against SMD and classified as resistant, moderately resistant and susceptible based on disease reactivity listed in Table 1.



Fig. 1. Stereo zoom microscopic image of Eriophyid mite (Aceria cajani).





Fig. 2. Glasshouse screening of SMD (2a) and leaf stapling technique (2b).

RESULTS AND DISCUSSION

Among the seventy-four genotypes screened for SMD along with national susceptible check ICP 8863 (Maruthi) and resistant (CO(Rg) 7) check with percent disease incidence given in Table 2. All the genotypes showed mild to severe mosaic ranging from 30 to 100 percent except CRG 16-07 and BWR 153. The genotypes viz., ICP 7919, IC 339057, IC 74016, IPAE 15-05, AL 2250, CRG 16-01, PusaArhar 21-14, PusaArhar 21-27, BWR 253, ICP 9808 and ICP 7234 were classified as moderately resistant with PDI ranging from 10.10 to 30 percent. Only two genotypes showed resistance reaction with 0-10 percent PDI listed in Table 3. Rest seventy-two genotypes showed mild to severe mosaic symptoms and were classified as susceptible ones. Relative and Absolute frequency were observed for seventy-four genotypes grouped into three reaction types listed in Table 3. Nearly 2.63 percent genotypes showed resistant reaction, 14.86 percent genotypes were found to be moderately resistant and 82.43 percent genotypes were classified under susceptible entries graphically represented in Fig. 4. Sharma et al. (2015) reported that eleven entries viz., ICP 3576, ICP 7869, ICP 9045, ICP 11015, ICP 11059, ICP 11230, ICP 11281, ICP 11910, ICP 14819, ICP 14976, and ICP 15049 were resistant to sterility mosaic

disease. Joshi et al. (2017) discovered that out of total 188 RILs screened, 90 RILs showed resistant reaction to SMD infection, 98 RILs were susceptible and 33 RILs categorized as resistant lines which consistently showed 0 percent PDI. Bhaskar (2016) found that out of 60 entries screened for SMD resistance, eight entries viz., ICPL-87119, ICPL-2376, BDN-2, PT-4-307, CORG-9701, BSMR-736, GRG-811 and BSMR-853 showed resistant to sterility mosaic disease. Prabhavathi and Ramappa (2018) reported that all twenty-two IVT medium duration entries were susceptible to SMD, except Bahar, however only one IVT early duration entry, RKPV405-10, showed resistant reaction, while the others showed susceptible reaction. According to Tharageshwari et al. (2019), out of the ninety-four genotypes studied, only four genotypes, DPP 2-89, DPP 3-182, IC 22557, and ICP 3666 showed highly resistant reaction to SMD infection, whereas fifty-four genotypes showed highly sensitive reaction. Genotypes viz., CRG 16-07, BWR 153, ICP 7919, IC 339057, IC74016, IPAE 15-05, AL 2250, CRG 16-01, PusaArhar 21-14, PusaArhar 21-27, BWR 253, ICP 9808 and ICP 7234 were found to be SMD resistant ones and can be utilized as donors for resistant breeding program to reduce yield loss as compared to susceptible types.

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Table 1: Classification based on percent disease incidence (PDI).

Percent Disease Incidence (PDI)%	Reaction
0.0-10.00	Resistant
10.10-30.00	Moderately resistant
>30.00	Susceptible

Table 2: Disease	Incidence on	different	pigeonpea	genotypes.

Sr. No.	Genotypes	Percent of Disease Incidence (PDI)	Arc sine values	Reaction type
1.	ICPL 90047	44.44	41.81	S
2.	ICP 13271	44.44	41.81	S
3. 4.	ICP 2391 ICP 245507	66.67 66.67	54.74 54.74	S S
5.	ICP 245531	27.78	31.81	<u> </u>
6.	ICP 7919	16.67	24.09	MR
7.	ICP 92047	38.89	38.58	S
8.	IC 123325	38.89	38.58	S
9.	IC 339057	22.22	28.13	MR
10.	IC 342747	16.67	24.09	MR
11.	IC 74016	25.00	30.00	MR
12. 13.	ACP 1225 AL 1685	33.33 100.00	35.26 99.66	S S
14.	AL 1603	46.67	43.09	S
15.	CO 5	33.33	35.26	Š
16.	DPP 2-52	41.67	40.20	S
17.	DPP 3-81	66.67	54.74	S
18.	DPP-2-188	33.33	35.26	S
19.	DPP-3-2	55.56	48.19	S
20.	DPP-3-244	40.00	39.23	S
21.	PA 509 AL 2184	44.44 33.33	41.81 35.26	S S
22.	IPAE 15-05	25.00	30.00	MR
24.	IPAE 18-04	33.33	35.26	S
25.	AL 2250	20.00	26.57	MR
26.	AL 2276-1	40.00	39.23	S
27.	PA 669	50.00	45.00	S
28.	PusaArhar 21-45	50.00	45.00	S
29.	CRG 16-01	16.67	24.09	MR
30.	PusaArhar 21-14	33.33	35.26	S
31. 32.	PusaArhar 21-27 PusaArhar 21-24	25.00 29.63	30.00 32.98	MR
33.	PusaArhar 21-24 PusaArhar 21-29	53.33	46.91	S
34.	PA 291	77.78	61.87	s
35.	UPAS 120	33.33	35.26	Š
36.	AL2324	66.67	54.74	S
37.	PA 21-57	33.33	35.26	S
38.	IC 525443	66.67	54.74	S
39.	IC 525520	100.00	99.66	S
40.	IC 525468 IC 73895	100.00 72.22	99.66 58.19	S S
42.	AL 1727	66.67	54.74	<u> </u>
43.	AL 1730	33.33	35.26	S
44.	AL 1736	100.00	99.66	S
45.	AL 1739	73.33	58.91	S
46.	C 11	100.00	99.66	S
47.	C 2542	75.00	60.00	S
48.	DPP-2-183	77.78	61.87	S
49.	RVKT 333	100.00	99.66 49.80	S
50. 51.	PA 21-61 CRG 16-12	58.33 100.00	49.80 99.66	S S
52.	TJT 501	33.33	35.26	<u> </u>
53.	BDN 711	33.33	35.26	S
54.	BWR 243	50.00	45.00	S
55.	BWR 853	33.33	35.26	S
56.	BSMR 26	40.00	39.23	S
57.	BWR 253	25.00	30.00	MR
58.	BWR 553	41.67	40.20	S
59. 60.	BWR 316 BSMR 2	33.33 50.00	35.26 45.00	S S
60.	BSMR 2 BSMR 65	29.63	32.98	<u> </u>
62.	BSMR 05	29.03	31.09	S
63.	BSMR 399	46.67	43.09	S
64.	BWR 23	53.33	46.91	S
65.	BWR 164	33.33	35.26	S
66.	BWR 153	0.00	0.34	R
67.	BWR 134	100.00	99.66	S
68.	ICPL 11301	33.33	35.26	S
69. 70.	ICPL 20325	33.33 0.00	35.26 0.34	S
70.	CRG 16-07 ICP 9808	22.22	28.13	R MR
72.	ICP 9808 ICP 7234	25.00	30.00	MR
73.	ICP 2387	33.33	35.26	S
74.	ICP 3215	100.00	99.66	s

S=Susceptible MR=Moderately Resistant R=Resistant

Table 3: Categorization of genotypes based on reaction type.

Percent Disease Incidence (PDI)%	Reaction types	Absolute frequency	Relative frequency	Genotypes	Symptoms observed
0.0-10.00	Resistant	2	2.63	BWR 153, CRG 16-07	
10.10-30.00	Moderately resistant	11	14.86	ICP 7919, IC 339057, IC 74016, IPAE 15-05, AL 2250, CRG 16-01, PusaArhar 21-14, PusaArhar 21-27, BWR 253, ICP 9808, ICP 7234.	
>30.00	Susceptible	61	82.43	ICPL 90047, ICP 13271, ICP 2391, ICP 245507, ICP 245531, ICP 92047, IC 123325, IC 342747, ACP 1225, AL 1685, AL 1692, CO 5, DPP 2-52, DPP 3-81, DPP-2-188, DPP-3-2, DPP-3-244, PA 509, AL 2184, IPAE 18-04, AL 2276-1, PA 669, PusaArhar 21-45, PusaArhar 21-24, PusaArhar 21-29, PA 291, UPAS 120, AL2324, PA 21-57, IC 525443, IC 525520, IC 525468, IC 73895, AL 1727, AL 1730, AL 1736, AL 1739, C 11, C 2542, DPP-2-183, RVKT 333, PA 21-61, CRG 16-12, TJT 501, BDN 711, BWR 243, BWR 853, BSMR 26, BWR 553, BWR 316, BSMR 2, BSMR 65, BSMR 1, BSMR 399, BWR 23, BWR 164, BWR 134, ICPL 11301, ICPL 20325, ICP 2387, ICP 3215.	



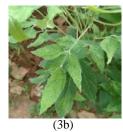
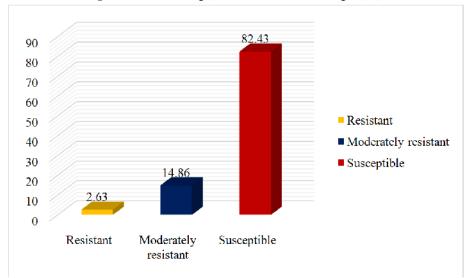
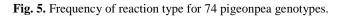


Fig. 3. Mosaic mottling (3a) and distorted leaf margin (3b).





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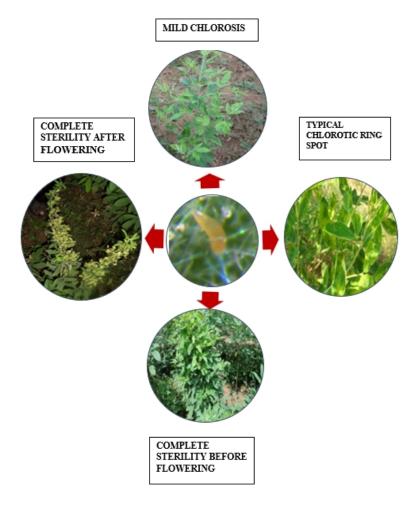


Fig. 4. Symptom variability of SMD.

CONCLUSION

The above study concludes that out of seventy-four pigeonpea genotypes used for SMD screening, two genotypes were categorised as resistant ones, eleven genotypes were classified into moderately resistant and remaining sixty-one genotypes showed susceptible reaction as per the Percent Disease Incidence given by AICRP scale. Genotypes that had shown resistance to SMD will be used as prospective donors for the production of high-yielding pigeonpea varieties.

FUTURE SCOPE

Conventional plant breeding has been substantially facilitated by genomic tools such as molecular markers, genetic maps and other tools, resulting in the establishment of improved genotypes/varieties with enhanced resistance/tolerance to pests and diseases. Hence, the resistant genotypes obtained from the glasshouse screening should be subjected to molecular confirmation for SMD resistance which will be available as a useful donor material for future resistant breeding programmes.

Acknowledgement. I am grateful to all professors of Department of Pulses, Tamilnadu Agricultural University, Coimbatore for their immense support to complete the research work successfully.

Conflict of Interest. None.

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How to cite this article: M. Dhanushasree, A. Thanga Hemavathy, R.P. Gnanamalar and L. Karthiba (2022). Evaluation of Pigeonpea Genotypes against Sterility Mosaic Virus (PPSMV) Disease. *Biological Forum – An International Journal*, *14*(2): 1263-1268.