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Genotypic Response to *Fusarium* Wilt and Sterility Mosaic Disease and Morphological Characterization of Pigeonpea (*Cajanus cajan* (L.) Millsp.) Genotypes

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Abstract Primary constraints in crop production are a number of biotic and abiotic factors. *Fusarium* wilt and SMD are one of the major biotic constraints affecting the yield. Screening of the genotypes against these diseases provides a clear picture on response and performance of genotypes which helps in planning further breeding programs. Hence, 40 pigeonpea genotypes were screened and the results revealed that the genotype ICP-7035 found asymptomatic for SMD and four genotypes namely GRG-2013, ICPL-15015, ICPH-3762 and GRG-811 were found resistant to both the diseases. In another study a total of 51 genotypes (Includes above 40 genotypes) were used for morphological characterization. It successfully differentiated GC-11-39 and ICPL-87 from rest of the genotypes as they had determinate growth habit and early flowering. Simillarly, BAHAR can be distinguished because of its orange seed color and KARI TOGARI for its dark purple seed color. ICP-7035 can be distinguished for its globular seed shape. Hence, they serve as morphological markers in varietal identification, thus helps in maintaining varietal purity.

Keywords Pigeonpea, *Fusarium* wilt, Sterility Mosaic Disease (SMD).

Introduction

Pigeonpea [*Cajanus cajan* (L.) Millsp.] is an important multi-use shrub legume of the tropics and subtropics. Being a pulse crop the seeds of pigeonpea are rich in protein and therefore make an ideal combination with carbohydrate rich cereals. Primary constraints in crop production are a number of biotic and abiotic factors. *Fusarium* wilt and SMD are one of the major biotic constraints affecting the yield.

Fusarium wilt (FW) and sterility mosaic disease (SMD) are the most important biotic constraints to pigeonpea production worldwide. Wilt disease caused by *Fusarium udum* is the most important problem in all pigeonpea growing areas causing heavy produc-

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Table 1. Reaction of genotypes for *Fusarium* wilt and sterility mosaic diseases under field conditions. WRC = Wilt resistant check, WSC = Wilt susceptible check, SMSC = Sterility mosaic susceptible check, SMRC = Sterility mosaic resistant check, R = Resistant, MR = Moderately resistant, S = Susceptible.

Sl. No.	Entry	% Wilt	Re-action	% SMD	Re-action
Genotypes resistant to both EW and SMD					
1	GRG-2013	7.88	R	4.19	R
2	ICPL-15015	8.12	R	6.56	R
3	ICPH-3762	6.80	R	3.30	R
4	GRG-811 (WRC, SMRC)	2.12	R	9.96	R
Genotypes resistant to FW and moderately resistant to SMD					
5	GRG-140	7.99	R	20.40	MR
6	GRG-177	3.51	R	13.77	MR
7	GRG-152	3.15	R	16.23	MR
Genotypes moderately resistant to FW and resistant to SMD					
8	BRG-3	29.97	MR	2.05	R
9	ICP-7035	20.43	MR	0.00	R
10	BRG-5	12.25	MR	2.00	R
Genotype moderately resistant to both FW and SMD					
11	BSMR-736	13.35	MR	10.30	MR
Genotypes resistant to FW and susceptible to SMD					
12	ICP-8793	5.52	R	72.15	S
13	IC-407476	8.17	R	39.70	S
14	JKM-197	4.22	R	69.20	S
15	ICP-8793-1	6.04	R	72.30	S
16	GRG-222	6.82	R	88.63	S
17	GRG-111	5.55	R	58.90	S
18	GRG-617	8.00	R	100.00	S
19	ICPL-332	8.99	R	87.11	S
20	ICPH-2433	8.10	R	100.00	S
21	TS-3 R (WRC)	5.09	R	57.25	S
22	ICP-8863 (SMSC)	7.14	R	100.00	S
Genotypes moderately resistant to FW and susceptible to SMD					
23	ICP-11320	17.19	MR	71.50	
24	JAMADAR LOCAL	28.72	MR	64.35	S
25	KATTI BEEJA	14.37	MR	30.35	S
26	GPHR-8-11	12.82	MR	30.50	S
27	ICP-13101	10.88	MR	41.00	S
28	ICPL-14001	12.55	MR	73.10	S
29	RAICHUR PINK G	14.38	MR	82.15	S
Genotypes susceptible to FW and resistant to SMD					
30	RAJA	100.00	S	9.20	R
31	BAHAR	42.47	S	1.25	R
Genotypes susceptible to both FW and SMD					
32	AKT-9913	31.39	S	78.80	S
33	KARI TOGARI	30.48	S	92.00 S	
34	BENNUR LOCAL	44.46	S	87.65	S
35	GULYAL WHITE	48.58	S	77.35	S
36	GULYAL RED	39.79	S	75.50	S
37	CHAPLE	78.04	S	71.55	S
38	PGR-176	31.86	S	93.48	S
39	ICPL-161	31.30	S	97.14	S
40	ICP-2376 (WSC)	86.93	S	83.00	S

Table 1. Continued.

tion losses. The *F. udum* is host specific to pigeonpea Patel et al. [1] and can survive in soil under wilted plant stubbles for a long period. The best way of wilt management is by growing resistant varieties.

Similarly, sterility mosaic disease (SMD) is a major biotic constraint in almost all pigeonpea growing areas caused by eriophyid mite (*Aceria cajani*) which transmit pigeonpea sterility mosaic virus (PPSMV). The disease is sometimes referred to as the green plague because at flowering time, affected plants remain green with more vegetative growth and have no flower or pods under congenial conditions Kumar et al. [2].

Screening of the genotypes against these diseases provides a clear picture on response and performance of genotypes which helps in planning further breeding programs.

Morphological characterization helps in varietal identification and helps in maintaining varietal purity.

Materials and Methods

Investigation was carried out during *kharif* 2016 at Agriculture Research Station, Kalaburagi which be-

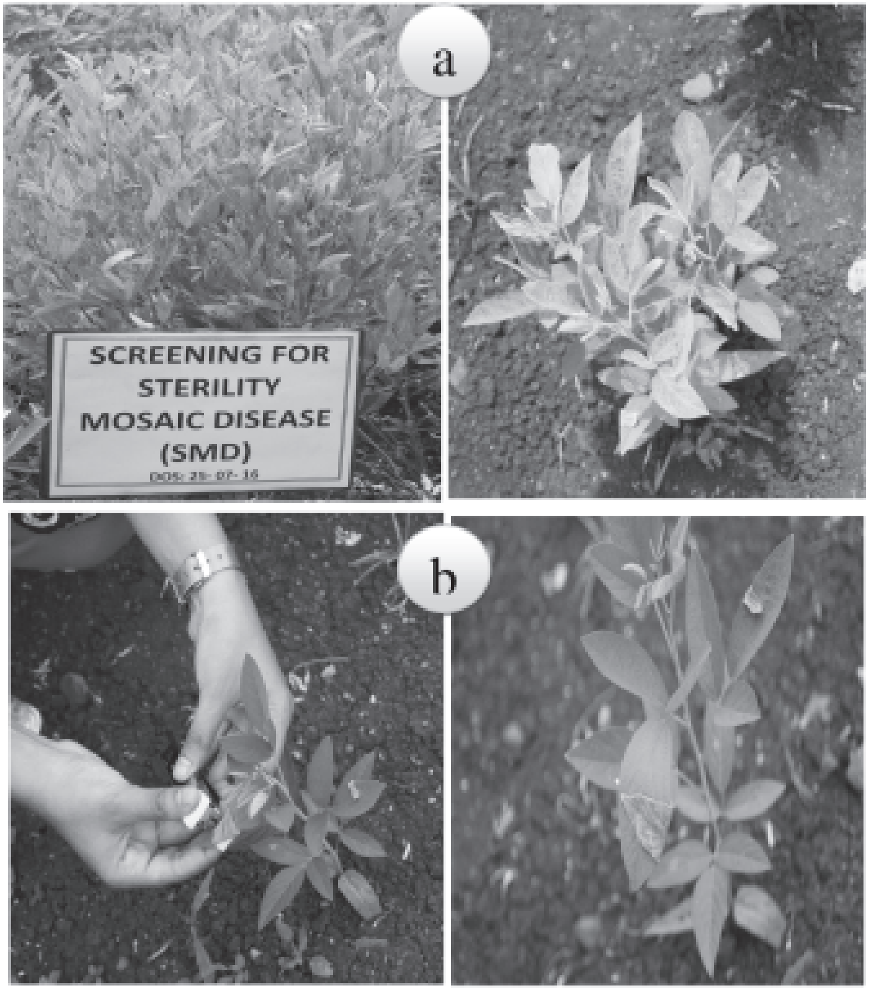

Fig. 1. SMD screening technique in pigeonpea.

longs to the agro-climatic zone-2 (North Eastern Dry Zone) of Karnataka state. Selected 40 genotypes of pigeonpea were studied for their disease resistant reaction for *Fusarium* wilt and SMD.

Fusarium wilt

Experimental layout for screening of *Fusarium* wilt was laid out on National wilt sick plot maintained at Agricultural Research Station, Kalaburagi. The genotypes were sown in single row with two replications along with susceptible check (ICP-2376 for wilt) and resistant check (ICP-8863 for wilt) varieties. Single row of susceptible check was sown after every two test entries. A row length of 4 meters each was maintained with the spacing of 75 cm and 20 cm between the rows and between the plants respectively. The observations on per cent wilt was recorded at flowering (90 days after sowing) and at physiological maturity (150 days after sowing) by counting number of dead plants (due to *Fusarium* wilt) among the total number of plants present per genotype and per cent disease was estimated.

$$\text{Per cent disease incidence (PDI)} = \frac{\text{Number of plants infected in row}}{\text{Total number of plants}} \times 100$$

Disease rating was categorized as per the standard wilt scoring format of All India Co-ordinated Research Project (AICRP) on pigeonpea.

Scale	Description	Category
1	0–10 per cent incidence	Resistant
2	10.1–30 per cent incidence	Moderately resistant
3	30.1–100 per cent incidence	Susceptible

Sterility mosaic disease (SMD)

The experiment for screening genotypes for SMD was laid out at Agricultural Research Station, Kalaburagi. Sterility Mosaic disease pressure was created by maintaining four rows of susceptible check (ICP-8863) all around the plot i.e., Infector hedge row technique. The genotypes were sown in single rows with two replications and susceptible check was sown after every 2nd row. Leaf stapling technique was used on 20 days old seedling. SMD infected leaves of test plants at 2–3 leaf stage are shown in Plate 1. As the stapled leaflets from the infected plants get dried, mites from the infected leaves migrate to healthy leaf and inoculates the virus. Scoring was carried out at 60 DAS and 75 DAS by counting the healthy plants (no mosaic symptoms) and diseased plants (with mosaic symptoms). Categorization of genotypes for SMD reaction was carried out following the standard scale Singh et al. [8]. The categorization scale is same as that for wilt.

Per cent disease incidence (PDI) was estimated using formulae

$$\text{Per cent disease incidence (PDI)} = \frac{\text{Number of plants infected in row}}{\text{Total number of plants}} \times 100$$

A total of 51 genotypes of pigeonpea were studied for their morphological characters (Table 2). Seed characters like base seed color and seed shape was recorded using dry seeds after harvest through visual assessment as per categorization of standard guidelines (Fig. 1).

Days to 50% flowering was recorded and categorized as very early, early, medium, late and very late flowering. Plant growth habit was recorded and categorized as determinate and indeterminate. Plant height was recorded as per guidelines and categorized as dwarf, medium and tall.

Base seed color was recorded and categorized as White, Cream, Light brown, Reddish brown, Light grey, Grey, Purple, Dark purple, Dark grey and others.

Seed shape was recorded as per guidelines and categorized as Oval (egg shape), Globular (pea shape), Square (angular shape), Elongate and others.

Seed size was recorded and categorized as very small, small, medium, large and very large.

Results and Discussion

Fusarium wilt

In the present study, 45% of the genotypes i.e., 18 out of 40 genotypes was found to be resistant to *Fusarium* with (FW). The per cent disease incidence ranged from 2.12 (GRG-811) to 8.99 (ICPL-332). The genotypes JKM-197, ICP-7035, GRG-177, GRG-617, TS-3 and GRG-152 were wilt resistant. Hence, these varieties can be used as variety or choice of parents for hybridization program. Moderately resistant reaction for FW was observed in 11 out of 40 genotypes (27.5%) (Table 1).

The results are in agreement with Bhaskar [4], two genotypes out of 60 showed resistance to with disease. Sharma et al. [5] found combined resistance of 54 lines out of 3000 germplasm lines screened for resistant to FW and SMD. Muniswamy et al. [6] found three genotypes viz., GRG-811, GRG-2009 and ASHA resistant to both FW and SMD after two years of evaluation.

Table 2. Morphological characterization of 51 pigeonpea genotypes.

Sl. No.	Morphological characters	Types	No. of genotypes	Frequency %	Example of varieties
1	Days to 50% flowering	Early (61–90 days)	02	3.92	GC-11-39, ICPL-87
		Medium (91–130 days)	49	96.08	Almost all the genotypes
2	Plant growth habit	Determinate	02	3.92	GC-11-39, ICPL-87
		Indeterminate	49	96.08	Almost all the genotypes
3	Plant height	Dwarf (< 100 cm)	08	15.69	AKT-9913, GRG-2013, ICPL-161, BDN-711
		Medium (101.1–150 cm)	40	78.43	GRG-140, GPHR-8-11, CHAPLE, TS-3R
		Tall (>250.1 cm)	03	5.88	KATTI BEEJA, LRG-41, BSMR-736
4	Seed color	White	04	7.84	GULYAL WHITE, ICP-2376, BDN-711, TS-3
		Orange	01	1.96	BAHAR
		Light brown	23	45.10	TS-3R, NTH-77, ICPH-2751, CHAPLE
		Reddish brown	22	43.14	ASHA, MARUTI, GRG-177, ICP-7035
		Dark purple	01	1.96	KARI TOGARI
5	Seed shape	Oval	40	78.43	GULYAL WHITE, ICPH-3477, BDN-711, TS-3R
		Globular	01	1.96	ICP-7035
		Square	10	19.61	RAJA, ICPL-332, MARUTI, ICPH-3762
6	Seed size (100 seed weight)	Medium (7.1–9 g)	12	23.53	GRG-2013, BENNUR LOCAL, ICP-2376, GC-11-39
		Large (9.1–11 g)	26	50.98	AKT-9913, ICPH-2751, MPH-10-5, TS-3
		Very large (> 11.1 g)	13	25.49	GRG-140, ICP-7035, BDN-2008-1, NTH-77

Sterility mosaic disease

The results showed that 9 out of 40 genotypes (22.5%) were resistant to SMD with their per cent disease incidence ranging from 0 (immune; ICP-7035) to 9.96 (GRG-811). Four genotypes (viz., GRG-140, GRG-177, GRG-152 and BSMR-736) out of 40 (10%) showed moderate resistance reaction for SMD.

Based on the data collected, ICP-7035 is the only asymptomatic genotype found among 40 genotypes studied for SMD incidence. Other genotypes like BAHAR, BRG-5, GRG-2013 and ICPH-3762 showed high level of resistance to SMD with a mean per cent disease incidence of > 5%.

ICP-7035 was found to be resistant to SMD by research conducted by Nagaraj et al. [7], Rangaswamy et al. [8], Saifulla et al. [9], Ganapathy [10], Ganesh et al. [11] and Ganapathy et al. [12]. GRG-811 which showed resistant reaction in the present investigation, showed similar results in study conducted by Bhaskar [4] but was reported to be moderately resistant by Muniswamy et al. [6]. BRG-3 which was reported resistant by Saifulla et al. [9], Ganapathy [10] and Ganapathy et al. [12] showed similar results in the present investigation. BSMR-736 was reported to be resistant by Abhijit et al. [13] and Bhaskar [4] obtained moderately resistant reaction for the genotype.

Sharma et al. [14] showed that 24 accessions to show high level of resistance to SMD out of 146 accessions screened. Dipshikha et al. [15] showed that 18 genotypes resistant to SMD out of 36 screened. Abhijit et al. [13] concluded that the inheritance of pigeonpea sterility mosaic disease resistance was controlled by two genes, SVI and SV2 with inhibitory gene interaction. Udikeri [16] evaluate mini core accessions of pigeonpea of which 16 were found to be moderately resistant. Bhaskar [4] showed that reported 8 entries out of 60 entries screened to be resistant to SMD.

Multiple disease resistance reaction for FW and SMD

In the present study a total of four genotypes (GRG-2013, ICPL-15015, ICPH-2433 and GRG-811) out of 40 showed multiple disease resistance reaction for FW and SMD. BSMR-736 showed moderate resistance to both FW and SMD. Three genotypes GRG-140, GRG-177 and GRG-152 were found resistant to FW and moderately resistant to SMD. In contrast,three genotypes BRG-3, ICP-7035 and BRG-5 were found to be resistant to SMD and moderately resistant to FW (Table 1).

Sharma et al. [14] showed that 5 accessions out of 146 to show combined resistant reaction for FW and SMD. Sharma et al. [5] found 54 lines showing combined resistance out of 3000 germplasm lines screened. Bhaskar [4] mentioned ICPL-87119 to be resistant to both FW and SMD. Three genotypes (GRG-811, GRG-2009 and ASHA) were found to be resistant to FW and moderately resistant to SMD.

Morphological characterization

Morphological characterization indicated that characters like determinate growth habit can be successfully used to differentiate ICPL-87 and GC-11-39 from rest of the genotypes. Further, the carliness in days to 50% flowering could separate ICPL-87 and GC-11-39 from rest of the genotypes. Similarly the characters like tall plant type (> 150.1 cm), orange seed color (BAHAR), dark purple seed color (KARI TOGARI), globular seed shape (ICP-7035) were found in limited number of genotypes. Seed characters like seed color and seed shape were used to characterize genotypes, which helps in varietal or genotype identification and serves as morphological indicators in breeding at field level. As there is less influence of environment on morphological characters compared to quantitative characters, they can be used as morphological markers to identify the variety and rogue out the off types.

Awnindra Kumar et al. [17] experimented on agro-morphological characterization of Bay Islands pigeonpea (*Cajanus cajan*) landraces and advanced lines under Islands conditions. There were significant genetic variability recorded for days to 50% flowering, days to maturity, plant height and seed yield per plant. Manyasa et al. [18] studied 16 qualitative traits in 123 genotypes and identified significant polymorphism in qualitative traits for base flower color, pod color, flowering pattern, streak pattern and seed color. Philip [19] evaluated 28 accessions of pigeonpea for 23 descriptors and observed stem color, flower color, pod color, pattern of streaks and color of the seed coat to be important components of variability.

Conclusion

Field screening of 40 genotypes for *Fusarium* wilt yielded 18 resistant genotypes (including two check varieties), of which GRG-152, GRG-617, ICPL-332, GRG-811, ICPH-3762 and ICPH-2433 were promising based on visual observations. Sterility mosaic disease (SMD) screening yielded nine resistant genotypes viz., GRG-2013, RAJA, BRG-3, BAHAR, ICP-7035, ICPL-15015, BRG-5, ICPH-3762 and GRG-811. The genotype ICP-7035 found asymptomatic for SMD, hence it can be used either as donor parent for resistant variety development or contrasting parent in developing mapping population for DNA marker identification. Different morphological features helps in maintaining varietal purity.

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