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Evaluation of Pigeonpea Genotypes against Fusarium Wilt and Sterility Mosaic Disease in Gujarat

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ABSTRACT

Background: Fusarium wilt (FW) and sterility mosaic disease (SMD) are two important biotic constraints to pigeonpea production worldwide that can cause loss up to 100 per cent. Host plant resistance is the most durable and economical way to manage these diseases.

Methods: Thirty five pigeonpea genotypes comprises [mid early, mid late, dual and hybrid (mid early) group] were evaluated in a fusarium wilt and sterility-mosaic disease-screening nursery at three location *viz*., Sardarkrushinagar, Bharuch and Vadodara in Gujarat during *kharif* season 2015-16, to identify genotypes having resistance to both the diseases.

Result: Five genotypes identified in each group of pigeonpea *viz;* mid early (SKNP1303, SKNP 1021, SKNP 0805, SKNP 0920, SKNP 1004), mid late (SKNP 1233, SKNP 10-34, AAUVT 07-10, AAUVT 09-24, GJP1207) and dual (SKNP-1119, BP 06-33, BP 08-06, BP 10-03, BP 10-04) and in hybrid (mid early) group only one hybrid *i.e.* SKNPCH 1211 were found combined resistance to Fusarium wilt and SMD (< 10% disease). These diverse genotypes that are resistant to Fusarium wilt and SMD may be useful in pigeonpea disease resistance breeding programme while hybrid identified as resistance to both the diseases may be recommended for commercial cultivation.

Key words: *Cajanus cajan, Fusarium udum,* Fusarium wilt, Host plant resistance, Pigeonpea, Sterility mosaic disease.

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INTRODUCTION

Pigeonpea [*Cajanus cajan* (L.) Millsp.] is the fifth most important grain legume in the world and second most important pulse crop after chickpea in India. It is cultivated in the semi-arid, tropical and sub-tropical regions demarcated between 25° N and 30° S in Asia, Africa and America (Van der Maesen, 1990). Globally, pigeonpea is grown in about 7.02 million hectares with a production of 6.80 million tonnes. In India, the pigeonpea is mainly cultivated under rainfed conditions in varied soils both as the sole and intercropped. India is a major producer of pigeonpea with 4.87 million tonnes from a harvested area of 5.38 million hectares (FAOSTAT, 2017). However, present productivity is very much low (750 kg/ha) compared to its potential productivity (2000-2500 kg/ha) due to several biotic and abiotic constraints.

Among biotic constraint, wilt disease caused by *Fusarium udum* Butler is the major constraint for limiting pigeonpea production in all pigeonpea growing regions (Gwata *et al.* 2006). The disease symptoms usually appear when plants are at the pre-flowering and podding stage (100% loss), at maturity (67%) and at pre-harvest stage (30% loss) but sometimes symptoms also appear in 1-2 month-old plants. The FW incidence increases in the ratoon and perennial crops and causes serious yield losses in susceptible cultivars. In India alone, the annual yield loss due to this disease has been estimated at US $ 71 million (Kannaiyan *et al*. 1984; Reddy *et al.* 1993).

Serility mosaic disease (SMD) is another most important constraint in pigeonpea production in the Indian subcontinent (Singh *et al.* 1999). The disease is caused by pigeonpea sterility mosaic virus (PPSMV) (Elbeaino *et al.* 2014) and is transmitted by *Aceria cajani*, an eriophyid mite in the semi-persistent manner. Symptoms are characterized by no flowering, a mosaic pattern on the leaves, reduced leaf size, excessive vegetative growth and severe stunting. If the infection occurs during the early stage of the crop (<45-day-old), 95-100% loss in yield is estimated. Kannaiyan *et al.* (1984) estimated over 0.2 million tonnes of loss in the production due to SMD alone in India. Environmental factors like temperature (22.44°C), relative humidity (64.30%), rainfall and wind play a crucial role in the development of eriophyid mite. Use of resistant cultivars is the most practical and economical method for any disease management practices. Therefore, the present study was under taken to identify pigeonpea genotypes having combined resistance to fusarium wilt and sterility mosaic disease (SMD) under field condition in Gujarat.

MATERIALS AND METHODS

The experiment was conducted at three locations *viz*., Pulses Research Station, S.D. Agricultural University, Sardarkrushinagar, College of Agriculture, Navsari Agricultural University, Campus Bharuch and Pulses Research Station, Modal Farm, Vadodara, Anand Agricultural University, in Gujarat during *kharif* 2015-16 to identify genotypes having resistance to both the important diseases. Thirty five pigeonpea genotypes including checks were evaluated in a fusarium wilt and sterility-mosaic disease-screening nursery (Table 1).

A threshold level of the wilt pathogen *Fusarium udum* was maintained by incorporating chopped wilted pigeonpea plants in the sick plot every year. Each genotype/hybrids was planted in two rows of 4 m length with a spacing of 60 cm between rows and 20 cm between plants. A highly wilt

Table 1: Evaluation of pigeonpea genotypes.

Genotypes	Wilt incidence (%)				SMD (%)			
	S.K. Nagar*	Bharuch	Vadodara	Mean**	S.K. Nagar*	Bharuch	Vadodara	Mean**
Mid early								
GT 103 (C)	22.03	33.33	5.00	20.12	0.0	0.00	4.00	1.33
GT 101 (C)	8.88	25.00	4.00	12.62	0.0	6.25	5.00	3.75
UPAS120(C)	16.66	5.88	6.00	9.51	0.0	0.00	4.00	1.33
SKNP1303	19.23	0.00	4.00	7.74	0.0	0.00	6.00	2.00
SKNP 1021	17.18	2.52	3.00	7.56	1.66	0.00	3.00	1.55
SKNP 1216	11.53	21.05	3.00	11.86	0.0	5.26	4.00	3.08
SKNP 0615	15.55	20.00	4.00	13.18	2.17	0.00	2.00	1.39
SKNP 0805	17.46	0.00	5.00	7.48	1.56	0.00	4.00	1.85
SKNP 0920	14.28	5.88	5.00	8.38	0.0	0.00	4.00	1.33
SKNP 1004	5.40	5.55	6.00	5.65	2.38	0.00	5.00	2.46
Mid late								
BDN 2 (C)	5.55	18.75	4.00	9.43	0.00	0.00	3.00	1.00
GJP-1 (C)	10.93	6.66	5.00	7.53	0.00	0.00	4.00	1.33
Vaishali (C)	7.54	0.00	6.00	4.51	0.00	5.26	5.00	3.42
AGT 2 (C)	5.55	5.89	7.00	6.14	0.00	0.00	7.00	2.33
SKNP 1233	3.84	13.33	6.00	7.72	0.00	0.00	5.00	1.66
SKNP10-34	14.28	5.88	5.00	8.38	0.00	0.00	4.00	1.33
AAUVT 07-10	8.19	6.25	5.00	6.48	1.63	0.00	4.00	1.87
AAUVT 09-24	10.90	11.11	4.00	8.67	1.78	0.00	3.00	1.59
GJP 1207	1.81	0.00	5.00	2.27	1.78	5.88	5.00	4.22
Dual								
GT1 (C)	12.50	25.00	4.00	13.83	2.77	0.00	4.00	2.25
Vaishali (C)	5.55	16.66	4.00	8.73	0.00	5.55	4.00	3.18
SKNP-1119	0.10	5.88	5.00	3.66	0.00	0.00	5.00	1.66
BP 06-33	0.13	0.00	6.00	2.04	2.70	0.00	5.00	2.56
BP 08-06	4.00	16.67	4.00	8.22	2.00	0.00	3.00	1.66
BP 10-03	0.00	5.88	5.00	3.62	0.00	0.00	6.00	2.00
BP 10-04	2.04	11.76	5.00	6.26	0.00	0.00	5.00	1.66
BP-11-11	10.20	22.22	4.00	12.14	0.00	5.56	5.00	3.52
Hybrids (mid early)								
GT 103 (C)	11.76	5.88	5.00	7.54	5.88	5.88	5.00	5.58
GT 101 (C)	10.00	16.67	6.00	10.89	0.00	0.00	6.00	2.00
UPAS120 (C)	9.52	5.88	6.00	7.13	9.52	0.00	5.00	4.84
GTH 1 (C)	30.43	6.25	5.00	13.89	0.00	0.00	4.00	1.33
SKNPCH 1308	20.68	5.88	4.00	10.18	0.00	0.00	4.00	1.33
SKNPCH 1211	9.09	0.00	5.00	4.69	0.00	0.00	5.00	1.66
SKNPCH 1114	13.33	18.75	6.00	12.69	0.00	0.00	5.00	1.66
SKNPCH 1111	9.67	16.66	7.00	11.11	0.00	0.00	6.00	2.00

*Mean of two replications **Mean of three locations.

susceptible cultivar ICP 2376 was included between every two test rows to serve as an indicator/infector rows. The trial was conducted in randomized complete block design (RCBD) with two replications. All others recommended practices required for cultivation of the crop were followed. Plants were scored for wilt incidence at seedling, flowering and pod formation stages by counting the healthy plants (no wilt symptoms) and diseased plants. Dead plants were examined by splitting open the stems, for characteristic wilt symptoms, *viz;* presence of a purple band on the stem and internal blackening in the wood.

Each of the pigeonpea genotypes/hybrids were evaluated for SMD in the pigeonpea sick plot. An infector hedge of ICP 8863 was imposed on the wilt affected plot to create artificial epiphytotic of sterility mosaic in the trial (Nene *et al.* 1981).The susceptible cultivar ICP 8863 was planted in the sick plot 1 month in advance of the regular planting time to serve as an infector rows in order to have a good source of virus inoculum. A highly susceptible cultivar ICP 8863 was included between every two test rows to serve as an indicator/infector rows. The planting of the test and susceptible cultivars was done across the wind direction in the field to facilitate virus transmission through mites. After transmission of virus from the infected plants to healthy seedlings, seedlings were scored for SMD incidence at 15 days interval up to 75 days by counting the healthy plants and diseased plants (with mosaic symptoms). Plants were regularly monitored for the symptom expression at 15 days interval and PDI is calculated to categorize the genotypes into different disease reactions.

Data on disease incidence (FW and SMD) was collected from each replication. Based on the disease reaction, for wilt, the genotypes were grouped as resistant (0-10% of plants mortality); moderately resistant (10.1-20% plant mortality); susceptible (20.1-40% plant mortality) and highly susceptible (>40%). AICRP scale was adopted to evaluate the genotypes against SMD and categorize the genotypes as resistant (0-10.0%); moderately resistant (10.1-30.0%) and susceptible (>30.0%).

RESULTS AND DISCUSSION

Data presented in Table 1 revealed that in mid early group, mean data of wilt incidence showed that five genotypes *i.e.* SKNP 1303, SKNP 1021, SKNP 0805, SKNP 0920 and SKNP 1004 were showed resistant reaction (<10.0% wilt incidence) at all the three locations. Similarly, all the test genotypes at all the locations showed resistant reaction against SMD. In mid late genotypes, mean data of wilt incidence revealed that all the five genotypes *i.e.* SKNP 1233, SKNP 10-34, AAUVT 07-10, AAUVT 09-24 and GJP1207 were showed resistant reaction while, all the test genotypes at all locations showed resistant reaction against SMD. In dual group, mean data of wilt incidence showed that out of six genotypes five genotypes (SKNP-1119, BP 06-33, BP 08-06, BP 10-03 and BP 10-04) were showed resistant reaction while all the six genotypes showed resistant reaction against SMD. Apart from this, in hybrid group mean data of wilt incidence revealed that out of four hybrids only one hybrid *i.e.* SKNPCH 1211 was showed resistant reaction. As far as SMD is concerned, all the four test hybrids (SKNPCH 1308, SKNPCH 1211, SKNPCH 1114 and SKNPCH 1111) showed resistant reaction at all locations.

Five genotypes in mid early group of pigeonpea (SKNP1303, SKNP 1021, SKNP 0805, SKNP 0920, SKNP 1004), five in mid late (SKNP 1233, SKNP 10-34, AAUVT 07-10, AAUVT 09-24,GJP1207), five in dual (SKNP-1119, BP 06-33, BP 08-06, BP 10-03, BP 10-04) and in hybrid (mid early) only one hybrid *i.e.* SKNPCH 1211were found combined resistance to Fusarium wilt and SMD (Table 2). Sources of resistance to FW and SMD has been reported in germplasm and breeding lines of pigeonpea by various workers (Nene *et al*., 1989; Rangaswamy *et al.* 2005 ; Gwata *et al.* 2006), but no sources of resistance to these diseases are reported particularly in vegetable pigeonpea. Identification of vegetable pigeonpea genotypes with resistance against single disease and/or select combination of two diseases (FW and SMD) would permit use of diverse sources for future breeding efforts and ensure a better

Table 2: Details of the genotypes showing resistance to disease identified from the pigeonpea group.

Pigeonpea group	Resistant genotypes*(< 10% disease)		
	Fusarium wilt	SMD	Combined (FW + SMD)
Mid early (151-165 days)	SKNP1303, SKNP 1021, SKNP 0805, SKNP 0920, SKNP 1004	SKNP1303, SKNP 1021, SKNP 0805, SKNP 1216, SKNP 0615,SKNP 0920, SKNP 1004	SKNP1303, SKNP 1021, SKNP 0805, SKNP 0920, SKNP 1004
Mid late (165-190 days)	SKNP 1233, SKNP 10-34, AAUVT 07-10, AAUVT 09-24, GJP1207	SKNP 1233, SKNP 10-34, AAUVT 07-10, AAUVT 09-24, GJP1207	SKNP 1233, SKNP 10-34, AAUVT 07-10, AAUVT 09-24, GJP1207
Dual (151-180 days)	SKNP-1119, BP 06-33, BP 08-06, BP 10-03, BP 10-04	SKNP-1119, BP 06-33, BP 08-06, BP 10-03, BP 10-4,BP-11-11	SKNP-1119, BP 06-33, BP 08-06, BP 10-03, BP 10-04
Hybrid (Mid early) (151-165 days)	SKNPCH 1211	SKNPCH 1308, SKNPCH 1211, SKNPCH 1114, SKNPCH 1111	SKNPCH 1211

chance of success in improving the disease resistance of vegetable pigeonpea. Resistant lines to one or both the disease should be very useful to introgress the resistance to FW and/or SMD while developing superior pigeonpea varieties through classical breeding.

CONCLUSION

The information presented in this paper will be of great value to plant breeders in their efforts to develop resistance breeding programs for pigeonpea. The genotypes identified for resistant against both the diseases (Fusarium wilt and SMD) may be useful in pigeonpea disease resistance breeding programme.

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