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INHERITANCE OF WILT RESISTANCE IN PIGEONPEA

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ABSTRACT

Inheritance of resistance to *Fusarium* wilt in the F_1, F_2 and F_3 generations of the cross TT 6 x ICP 8863 in pigeonpea was studied by pot and laboratory screening methods using *Fusarium udum* isolate 8801. The survival of the susceptible and resistant parents ranged between 0–7% and 87–94%, respectively in the wilt sick pots and between 3–8% and 94–100% in the laboratory. The reaction of the F_1 plants indicated dominance of resistance over susceptibility. Segregations in the F_2 and F_3 generations indicated dominant monogenic inheritance of wilt resistance. It is inferred that ICP 8863 has one dominant gene (*FuR1*) for resistance against the pathogen isolate 8801.

Key words: *Cajanus cajan, Fusarium udum,* inheritance, resistance.

The wilt caused by *Fusarium udum* is the most important soil borne disease of pigeonpea (*Cajanus cajan*) in the Indian subcontinent [1]. Different studies on the genetics of resistance reported one dominant [2], two complementary [3, 4], duplicate [5] and multiple [6] genes for wilt resistance in pigeonpea. This is possibly due to different sources of resistance and *Fusarium* isolates used in the studies. In order to make rational use of the resistance gene(s) available, it is necessary to identify them against different isolates of the pathogen in the available wilt resistant genotypes. To achieve this objective, the inheritance of resistance in ICP 8863 against *Fusarium udum* isolate 8801 was studied by pot screening and an improved laboratory method.

MATERIALS AND METHODS

ICP 8863 (Maruthi), identified as wilt resistant in the ICRISAT programme, was earlier found to be the highly resistant in our experiments. The wilt susceptible cultivar TT 6 (Trombay Vishakha-1) was crossed with resistant ICP 8863. The F_1, F_2 and F_3 populations were screened in the *Fusarium* infected (wilt sick) pots in rabi seasons and in the laboratory during the years of 1991–93. The sick pots were developed as per the procedure described by Nene et al. [7]. The four isolates of *Fusarium udum*; 8801 from PDKV Akola, 8802 from MKV Badnapur, 8803 from IARI New Delhi and 8804 from ICRISAT Hyderabad were used for identifying the resistant sources in pigeonpea germplasm. The wilt reaction of the resistant genotype ICP 8863 and susceptible genotype TT 6 was found to be similar with all the four isolates. Therefore isolate 8801 from Dr. Punjabrao Deshmukh Krishi Vidyapeeth Akola was used in the present studies. In the sick pots, the mortality of the resistant and susceptible parents ranged between 6–13% and 93–100%, respectively, in different experiments.

Eight F_1 seed of the cross TT 6 x ICP 8863 obtained from individual pollinations were sown in the infected pots, one seed per pot. The F_2 seeds obtained from a single F_1 plant were sown in six sick pots, keeping 25–30 seeds per pot. The number of seedlings in each pot was recorded two weeks after sowing. Number of wilted plants was periodically recorded. The final count of the surviving plants was taken at the time of harvest. Individual progenies of 25 plants from the resistant F_2 plants were further tested in the infected pots in F_3 generation. Seeds from each progeny were sown in individual pots, keeping one progeny per pot.

Screening in the laboratory was carried out by an improved method over the one described by Nene and Kannaiyan [8]. It involves growing of 15-day-old seedlings in test tubes containing 20 ml of the pathogen spore suspension (10^7 spores/ml) in a BOD incubator at 28 ± 1°C for 28 days [9]. Seedlings were raised on filter paper folders and screened in batches. A set of 10 seedlings of the susceptible cultivar TT 6 was always included as check in each experiment to monitor the virulence of *Fusarium* spores. Under these conditions, the survival of the resistant and susceptible parents ranged between 94–100% and 3–8%, respectively.

Ten seedlings raised from the F_1 seeds of 10 different crosses were tested for resistance. Seedlings of the F_2 and F_3 families were also screened similarly. Segregation pattern was followed by individual F_2 and F_3 families and pooled data were used to estimate the overall segregation pattern.

The surviving F_2 plants were transferred to soil, first in plastic cups at 24 ± 1°C for about three weeks for hardening, and then in the pots.

RESULTS AND DISCUSSION

POT SCREENING

Seven out of eight F_1 plants survived in sick pots till maturity. One plant wilted three months after sowing. The total number of surviving (resistant) and wilted (susceptible) plants in the F_2 generation was 93 and 40, respectively, at maturity. The segregation fits into

3:1 ratio, $\chi^2 = 1.827$ (Table 1). The segregation pattern of the pooled data of 16 F_3 progenies gave good fit to the ratio of 3:1, $\chi^2 = 0.127$. The ratio of 9 true breeding resistant and 16 segregating progenies fits also in 1:2 ratio, $\chi^2 = 0.081$ (Table 1).

LABORATORY SCREENING

Out of the 10 F_1 seedlings screened, eight survived. In F_2 generation, 189 seedlings were resistant and 51 susceptible, which fits in ratio of 3 R : 1 S, $\chi^2 = 1.800$ (Table 1). Out of 14 F_3 progenies, 5 were true breeding resistant and 9 segregated for resistance and susceptibility. The ratio between true breeding and segregating progenies was 1:2, $\chi^2 = 0.357$ (Table 1). Segregation of F_3 plants in 9 progenies was in the ratio of 3:1 (118 R : 45 S; $\chi^2 = 0.591$).

Table 1. Segregation for resistance and susceptibility in the F_2 and F_3 generations of the cross TT 6 x ICP 8863 in pot and laboratory screening

Generation	No. of progenies studied	Frequency of phenotypes			Ratio tested	χ^2	P
		R	S	total			
Pot screening							
F_2	1	93	40	133	3:1	1.827	0.10–0.20
F_3	9	125	—	125	—	—	—
	16	235	82	317	3:1	0.127	0.70–0.80
Total F_3 progenies	25	9	16 (segr.)		1:2	0.081	0.70–0.80
Laboratory screening							
F_2	4	189	51	240	3:1	1.800	0.10–0.20
F_3	5	65	—	65	—	—	—
	9	118	45	163	3:1	0.591	0.30–0.50
Total F_3 progenies	14	5	9 (segr.)		1:2	0.357	0.50–0.70
Pooled over pot and laboratory experiments							
	30	635	218	853	3:1	0.141	0.70–0.80

The pooled F_2 and F_3 data of segregating progenies from pot and laboratory screening experiments also showed a good fit to the ratio of 3 R : 1 S, $\chi^2 = 0.141$ (Table 1). Thus the resistant reaction of the F_1 plants in pots as well as in laboratory screening indicated dominance of resistance over susceptibility. The segregation pattern observed in the F_2 and F_3 generations confirmed the monogenic inheritance of wilt resistance. This confirms the findings of Pawar and Mayee [2]. Monogenic dominant control of *Fusarium* wilt has been reported in other pulse crops like pea [10] and field bean [11].

The wilt resistance gene in ICP 8863 is designated as *FuR1*. Efforts are in progress to identify the gene(s) for *Fusarium udum* resistance in other known wilt resistant genotypes of pigeonpea.

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