Indian J. Genet., **53** (2): 115–117 (1993)

INHERITANCE OF RESISTANCE TO ALTERNARIA LEAF BLIGHT IN PIGEONPEA (*CAJANUS CAJAN* (L.) MILLSP.)

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(Received: October 3, 1989; accepted: February 4, 1992)

ABSTRACT

The inheritance of resistance to leaf blight caused by *Alternaria tenuissima* was studied in pigeonpea (*Cajanus cajan*). The F_1, F_2, BC_1 and BC_2 generations involving seven resistant and a susceptible parents were evaluated. The dominance of susceptibility in F_1 generation and segregation into 3S:1R ratio in F_2 indicated that resistance is governed by single recessive gene in each of the varieties used in this study. The monogenic nature of disease resistance was confirmed by back-cross analysis.

Key words: Pigeonpea, *Alternaria* blight, inheritance, genetics.

Alternaria leaf blight is a serious disease of the post-rainy season (pre-rabi) crops of pigeonpea in the north eastern state of India. It is caused by *Alternaria tenuissima* (Kunse, ex Pers) Wiltshire. The disease causes extensive damage to the aerial parts of the plants, resulting in complete blightening of the crop. Yield losses may reach 95% if the disease strikes in the early stages of the crop. The yield losses in yield of pigeonpea due to this disease are more pronounced in the postrainy crop although it may also occur in kharif. The variety Bahar, which was initially recommended for postrainy season, was found to be highly susceptible to this disease soon after the postrainy season pigeonpea technology became popular in eastern India. Total crop failure due to this disease was recorded during 1979-80 at the Research Farm, Dholi [1]. Very little information is available on the genetics of resistance to *Alternaria*.

MATERIALS AND METHODS

Seven blight resistant lines DA-2, DA-6, DA-9, DA-11, DA-12, DA-16, D-1301 were crossed with the susceptible cultivar Bahar. Among the parents used DA (Dholi-Arhar)-2 is

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a derivative of cross Bahar x Gwalior-3. DA-6 and DA-9 are the sister lines of a cross UPAS 120 x Prabhat. DA-11 (Bahar x PS 66 x NPWR-15) is an outstanding variety released for cultivation in pre-rabi planting in Bihar. The other lines, i.e. DA-12, DA-16 and D-1301, are the promising lines selected at Dholi Centre. Crosses were also made among the resistant parents. BC_1 and BC_2 were raised to confirm the nature of inheritance. The F_1, F_2, BC_1 and BC_2 materials were planted along with the parents at the research farm of the Tirhut College of Agriculture, Dholi (Muzaffarpur) during the postrainy seasons. The F_1 and backcrosses were grown in single-row plots each, F_2 in 20 rows, and the parents in 3 rows of 4 m length spaced at 30 cm. Disease epiphytotic was developed by spraying the disease inoculum 70 days after sowing the crop (first week of November). All the plants of each population were studied for disease reaction. The diseased plants started to show disease symptoms within 10–12 days after inoculation. The disease score was recorded three weeks after inoculation when the symptoms were fully expressed. The disease rating was done on the 0–9 scale. Although a few spots were noticed even on the leaves of resistant parents, the disease intensity did not exceed 5% in such genotypes whereas the plants of susceptible genotypes were heavily covered with disease. The expected segregation of resistant annd susceptible plants in F_2, BC_1 and BC_2 was confirmed by χ^2 test.

RESULTS AND DISCUSSION

In the resistant x susceptible crosses, the F_1s were always susceptible indicating that resistance is governed by recessive gene(s). The F_2 populations comprising 244 to 366 plants in different crosses segregated in the ratio of 3 susceptible : 1 resistant, indicating a single

Table 1. Number of leaf blight resistant and susceptible plants in F_2, BC_1 and BC_2 generations of pigeonpea

Cross	Reaction in F_1	F_2 plants		Expected ratio		χ^2	P
		susceptible	resistant	total	S : R		
DA-2 x Bahar	S	250	86	336	3 : 1	0.0064	0.09–0.80
DA-6 x Bahar	S	210	72	282	3 : 1	0.0425	0.90–0.80
DA-9 x Bahar	S	180	64	244	3 : 1	0.1967	0.70–0.50
DA-11 x Bahar	S	288	94	382	3 : 1	0.0314	0.90–0.60
DA-12 x Bahar	S	235	80	315	3 : 1	0.0264	0.90–0.90
DA-16 x Bahar	S	290	98	388	3 : 1	0.0131	0.95–0.90
D-1301 x Bahar	S	228	77	305	3 : 1	0.0098	0.95–0.90
DA-2 x DA-6	R			No segregation in F_2 generation			
DA-2 x D-1301	R			-do-			
DA-6 x DA-11	R			-do-			
DA-6 x DA-9	R			-do-			
DA-11 x DA-16	R			-do-			
DA-16 x D-1301	R			-do-			

recessive gene controlling resistance (Table 1). All the BC_1 plants (F_1 x susceptible parent) were susceptible (Table 2). The BC_2 (F_1 x resistant parent) populations segregated in the ratio of 1S : 1R which confirmed the monogenic recessive nature of resistance to *Alternaria* blight in this crop. Similar results were reported by Singh et al. [2] in a cross involving two parents.

Table 2. Segregation pattern for *Alternaria* blight resistance in back-crosses of pigeonpea

Back-cross population	Cross	Phenotypic groups		Expected ratio	χ^2	P
		susceptible	resistant	S : R		
BC_1	(DA-2 x Bahar) x Bahar	24	0	—	—	—
	(DA-6 x Bahar) x Bahar	22	0	—	—	—
	(DA-9 x Bahar) x Bahar	20	0	—	—	—
	(DA-11 x Bahar) x Bahar	19	0	—	—	—
	(DA-12 x Bahar) x Bahar	23	0	—	—	—
	(DA-16 x Bahar) x Bahar	18	0	—	—	—
	(D-1301 x Bahar) x Bahar	18	0	—	—	—
BC_2	(DA-2 x Bahar) x DA-2	18	12	1 : 1	1.200	0.50–0.25
	(DA-6 x Bahar) x DA-6	15	9	1 : 1	1.500	0.25–0.10
	(DA-9 x Bahar) x DA-9	24	21	1 : 1	0.200	0.75–0.50
	(DA-11 x Bahar) x DA-11	15	18	1 : 1	0.272	0.75–0.50
	(DA-12 x Bahar) x DA-12	18	14	1 : 1	0.500	0.50–0.25
	(DA-16 x Bahar) x DA-16	12	10	1 : 1	0.182	0.75–0.50
	(D-1301 x Bahar) x D-1301	7	9	1 : 1	0.250	0.75–0.50

R—resistant, S—susceptible.

The F_1s from the crosses between resistant parents, viz DA-2 x DA-6, DA-6 x DA-9, DA-6 x DA-11, DA-2 x D-1301, DA-11 x DA-16 and DA-16 x D-1301, were always resistant. No segregation was observed for disease reaction in F_2 generation of these crosses. It was, therefore, concluded that all resistant parents used in this study carry the same gene for resistance to *Alternaria* blight.

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