Indian J. Genet., **64**(2): 118-120 (2004)

Inheritance of resistance to sterility mosaic virus in pigeonpea (*Cajanus cajan* (L.) Millsp.)

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(Received: February 2004; Revised: July 2004; Accepted: July 2004)

Abstract

The inheritance of resistance in pigeonpea to the Bangalore strain of Sterility Mosaic Virus (PPSMV) was studied in crosses involving 2 resistant lines (ICP 7035 and MAL 14) with no apparent symptoms and susceptible lines (TTB 7, ICP 8863 and DBN1) with severe mosaic symptoms. The F_1, F_2, BC_1 and BC_2 generations were sown in the field and screened following infector hedge, infector row and leaf stapling techniques. Resistance was recessive and appeared to be governed by two independent non-allelic genes exhibiting complementary epistasis. However, the presence of atleast one gene confering resistance to the disease, in homozygous recessive condition was found to be necessary to express resistance phenotype.

Key words: Pigeonpea, inheritance, sterility mosaic disease, biotic stress resistance

Introduction

Sterility Mosaic Disease (SMD), considered to be the most important disease of pigeonpea, is known to occur in almost all the major pigeonpea growing areas of India and at times can cause yield losses upto 95 per cent [1]. This disease is characterized by a bushy and pale green appearance of plants, excessive vegetative growth, stunting, reduction in leaf size, leaf distortion, mosaic and mottling of leaves and complete or partial cessation of reproductive structures [2]. The disease is caused by the Pigeonpea sterility mosaic virus (PPSMV) [3] and transmitted by an eriophyid mite *Aceria cajani* Channabasavanna [4].

Development of resistant pigeonpea cultivars against the SMD was first initiated by Alam [5]. Systematic resistance breeding was later initiated at International Crops Research Institute for Semi Arid Tropics (ICRISAT), Patancheru, India during 1975 and several resistant and tolerant source(s) for the disease were identified [6]. However, the task of developing resistant varieties has been complicated in view of the reported genetic plasticity of the virus. The presence of PPSMV strains of varying virulence was reported based on the results of pigeonpea multilocation trials [7]. A comprehensive study of the phenomena over a period of four consecutive years, using a set of seven differentials, at nine different locations in India, revealed the occurrence of five different variants of the sterility mosaic virus in India [8]. Breeding of resistant varieties to the existing variants of the PPSMV seems to be the most practical approach. Breeding for resistance, however, depends upon the availability of dependable resistance source(s) and a clear understanding of their genetics. Therefore, the present investigation was undertaken to elucidate the inheritance pattern of resistance for the Bangalore strain of the Sterility Mosaic.

Materials and methods

The study was conducted at UAS, Bangalore during 2001-2003. Parents for the inheritance of resistance to SMD of pigeonpea were selected from the preliminary screening experiment in which 89 genotypes were evaluated against Bangalore strain. The lines ICP 7035 and MAL 14, which were resistant to SMD, confirmed through ELISA, were used as lines and highly susceptible lines TTB 7, ICP 8863 and BDN 1 were used as testers. The selected SMD resistant and susceptible lines were crossed in Line × Tester fashion during *Kharif* 2001. Hybridization was carried out under bee proof nylon net to prevent contamination by natural out crossing. Sufficient F_1 seeds were produced in each cross. Parts of the F_1s were used for generation advancement and back crossing and the rest part was retained for screening.

Off-season advancement of F_1s was taken up during November 2001, to facilitate the rapid advancement of generations. Morphological traits such as flower initiation, flower colour, seed size and other contrasting characters among parents were used as markers to check the trueness of F_1 plants. Only true

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F_1s were used for back crossing and advancement to F_2 generation. Backcrossing of F_1s with their respective parents and advancement of F_1 generation were carried out simultaneously. The parents, F_1, F_2 and backcrosses of the resistant × susceptible crosses (single plant progenies) were screened for their reaction to Sterility Mosaic Disease during *Kharif* 2002 in the field following infector row, infector hedge and leaf stapling techniques. Observations on disease reaction were recorded at 75 DAS. The plants were classified as resistant (no apparent symptoms) or susceptible (severe mosaic symptoms). The goodness of fit to Mendelian segregation of resistant and susceptible plants in the segregating population was tested by Chi-square test. The significance of Chi-square value was tested against the table value with (n-1) degrees of freedom, where n is the total number of segregating classes [9].

Results and discussion

The susceptible checks TTB 7 planted as infector hedge and ICP 8863 planted at frequent intervals (as infector row) between the test entries exhibited 100 per cent infection, indicating good disease spread. ICP 7035 and MAL 14 were 100 per cent resistant with no apparent symptoms, while TTB 7, ICP 8863 and BDN 1 were highly susceptible with severe mosaic symptoms.

Table 1. Reaction of parents and F_1 hybrids to pigeonpea sterility mosaic virus

Material	Total no. of plants	Resistant plants	Susceptible plants	% disease incidence	Reaction
Parents:					
ICP 7035	26	26	-	0	R
MAL 14	19	19	-	0	R
TTB 7	24	-	24	100	S
BDN 1	23	-	23	100	S
ICP 8863	21	-	21	100	S
Hybrids:					
ICP 7035 × TTB 7	25	-	25	100	S
ICP 7035 × ICP 8863	25	-	25	100	S
ICP 7035 × BDN 1	21	-	21	100	S
MAL 14 × TTB 7	24	-	24	100	S
MAL 14 × ICP 8863	23	-	23	100	S
MAL 14 × BDN 1	22	-	22	100	S

R-Resistant, S-Susceptible

All the F_1's were susceptible (Table 1), indicating the susceptibility to be dominant over resistance. Similar observations on susceptibility being under the influence of dominant genes have also been reported in studies involving many crosses of resistant and susceptible pigeonpea genotypes [10, 11, 12 & 13].

The reactions of the F_2 and backcross generations are presented in Table 2. The F_2 segregation pattern of the resistant × susceptible crosses revealed digenic ratios of 7 resistant : 9 susceptible for four crosses involving resistant parents ICP 7035 and MAL 14 with susceptible parents, ICP 8863 and BDN 1. In contrast, the crosses ICP 7035 × TTB 7 and MAL 14 × TTB 7, monogenic segregation ratio of 1 resistant : 3 susceptible was obtained. The backcrosses corroborated the segregation pattern of F_2 generation. The resistant parents, ICP 7035 and MAL 14, thus appeared to differ from the susceptible parents, ICP 8863 and BDN 1 in respect of two gene pairs. While, the resistant parents differed from the susceptible parent, TTB 7 in respect of a signle gene pair. Singh *et al* [10]; Sharma *et al.* [11] and Srinivas *et al.* [14] also reported a variation among different crosses in the number of genes governing the resistance trait for Sterility Mosaic Disease. Singh *et al.* (1983) reported the involvement of two genes in crosses involving the resistant parents Pant 43 and ICP 6999 and three genes in crosses involving ICP 3783, ICP 7035 and ICP 7119 resistant parents with the susceptible Pant A_2, UPAS 120 and T 21. However, Sharma *et al.* (1984) reported the involvement of two genes governing resistance in ICP 7035 parent and tolerance in ICP 2376 in cross combinations with the susceptible parent BDN 1. Srinivas *et al.* (1997) reported that inheritance of resistance to the Patancheru isolate 2 of the Sterility Mosaic Disease was recessive and appeared to be governed by two independent non-allelic genes exhibiting complementary epistasis in crosses involving five resistnat lines (ICP 7035, ICP 7349, ICP 8006, ICP 8136 and ICP 8850) with a susceptible line (ICP 8863). Resistance was dominant in two crosses *viz.* ICP 7035 × ICP 8863 and ICP 7349 × ICP 8136 and susceptibility in ICP 8850 × ICP 8863. The disease reaction for isolate 2 appeared to be governed by a single gene with 3 alleles, with one resistant allele exhibiting dominance and the other being recessive over the allele for susceptibility.

When the cross-involving resistant parent, ICP 7035 or MAL 14 segregates for one of the genes, a monogenic ratio of 3 susceptible : 1 resistant was obtained. However, when parents differ by two genes a digenic ratio of 9 susceptible : 7 resistant were obtained, indicating the complementary nature of the two dominant genes for susceptibility. It is therefore postulated that susceptibility to Bangalore strain is under the control of two independent loci exhibiting complementary gene action. When locus 1 or 2 or both occur in homozygous recesive state resistance reaction occurs, while dominant alleles at both loci would be necessary to result in susceptibility. Accordingly, resistance is expressed in the presence of recessive alleles in homozygous state at least at one locus.

Table 2. Reaction of segregating generations of resistant × susceptible crosses to pigeonpea sterility mosaic virus

Generation	Observed frequencies			Expected frequencies		Ratio R:S	χ^2	Probability
	Total plants	Resistant plants	Susceptible plants	Resistant plants	Susceptible plants			
ICP 7035 × TTB 7								
F_2	225	66	189	63.75	191.25	1:3	0.105	0.70-0.50
$BC_1 = F_1 \times$ ICP 7035	88	41	47	44	44	1:1	0.408	0.60-0.50
$BC_2 = F_1 \times$ TTB 7	51	0	51	6	51	-	-	-
ICP 7035 × ICP 8863								
F_2	198	91	107	86.62	111.37	7:9	0.391	0.60-0.50
$BC_1 = F_1 \times$ ICP 7035	105	21	72	26.25	78.75	3:1	1.628	0.07-0.05
$BC_2 = F_1 \times$ TTB 7	72	0	72	0	72	-	-	-
ICP 7035 × BDN 1								
F_2	144	57	87	63	81	7:9	1.015	0.35-0.25
$BC_1 = F_1 \times$ ICP 7035	96	19	65	24	72	3:1	1.721	0.20-0.10
$BC_2 = F_1 \times$ TTB 7	41	0	41	0	41	-	-	-
MAL 14 × TTB 7								
F_2	248	73	175	62	186	1:3	2.60	0.15-0.10
$BC_1 = F_1 \times$ ICP 7035	73	34	39	36.5	36.5	1:1	0.342	0.65-0.50
$BC_2 = F_1 \times$ TTB 7	42	0	42	0	42	-	-	-
MAL 14 × ICP 8863								
F_2	229	69	160	57.25	171.75	7:9	3.213	0.10-0.05
$BC_1 = F_1 \times$ ICP 7035	97	42	55	48.5	48.5	3:1	1.742	0.20-0.10
$BC_2 = F_1 \times$ TTB 7	53	0	53	0	53	-	-	-
MAL 14 × BDN 1								
F_2	197	79	118	86.18	110.81	7:9	1.119	0.35-0.25
$BC_1 = F_1 \times$ ICP 7035	110	36	74	27.5	82.5	3:1	3.502	0.25-0.10
$BC_2 = F_1 \times$ TTB 7	72	0	72	0	72	-	-	-

References

1. **Reddy M. V. and Nene Y. L.** 1981. Estimation of yield losses due to sterility mosaic, *In*: Proceedings of International Workshop on Pigeonpea. 15-19, Dec., 1980. ICRISAT, Patancheru, A.P., India, Vol. 2, p. 305-312.
2. **Reddy M. V., Sharma S. B. and Nene Y. L.** 1990. Pigeonpea disease management. *In*: The Pigeonpea. (eds. Y.L. Nene, S.D. Hall and V.K. Sheila), CAB International U.K. and ICRISAT, Patancheru, A.P., India, p. 310-316.
3. **Kumar P. L., Jones A. T. and Reddy D. V. R.** 2003. A novel mite- transmitted virus with a divided RNA genome closely associated with pigeonpea sterility mosaic disease. Phytopath., **93**: 81-91.
4. **Seth M. L.** 1962. Transmission of pigeonpea sterility by an eriophyid mite. Indian Phytopath., **15**: 225-227.
5. **Alam M.** 1931. Administration report of the botanical section 1930-31. Department of Agriculture, Bihar and Orissa, India, p. 42-65.
6. **Nene Y. L., Kannaiyan J. and Reddy M. V.** 1981. Resistance to major pigeonpea diseases. *In*: Proceedings of International Workshop on Pigeonpea. 15-16 Dec., 1980, ICRISAT, Patancheru, A.P., India, p. 121-128.
7. **Nene Y. L., Reddy M. V., Beniwal S. P. S., Mahmood M., Zote K. K., Singh R. N. and Sivaprakasam K.** 1989. Multilocational testing of pigeonpea for broad based resistance. Indian Phytopath., **42**: 44-48.
8. **Reddy M. V., Raju T. N., Nene Y. L., Ghanekar A. M., Amin K. S., Arjunan G., Astaputra J. V., Sinha B. K., Muniyappa V., Reddy S. V., Supta R. P. and Gangadharan K.** 1993. Variability in sterility mosaic pathogen in India. Indian Phytopath., **46**: 206- 212.
9. **Stansfield W. D.** 1986. Theory and Problems of Genetics, McGraw- Hill Inc., pp. 452.
10. **Singh B. V., Pandeya B. P., Gautam P. L., Beniwal S. P. S. and Pandey M. P.** 1983. Inheritance of resistance to sterility mosaic virus in pigeonpea. Indian J. Genet., **43**: 487-493.
11. **Sharma D., Gupta S. C., Rai S. and Reddy M. V.** 1984. Inheritance of resistance to sterility mosaic disease in pigeonpea. Indian J. Genet., **44**: 84-90.
12. **Amala Balu P.** 1992. Studies on genetic analysis of biometric traits and inheritance of sterility mosaic disease resistance in pigeonpea [*Cajanus cajan* (L.) Millsp]. M.Sc. (Agri.) Thesis, Tamil Nadu Agric. Univ., Coimbatore.
13. **Srinivas T., Reddy M. V., Jain K. C. and Reddy M. S. S.** 1997a. Studies on inheritance of resistance and allelic relationships for strain 2 of pigeonpea sterility mosaic pathogen. Ann. Appl. Biol., **130**: 105-110.
14. **Srinivas T., Reddy M. V., Jain K. C. and Reddy M. S. S.** 1997b. Genetics of resistance for the Patancheru isolate of sterility mosaic pathogen in pigeonpea [*Cajanus cajan* (L.) Millsp]. Crop Improv., **24**: 183-188.