Indian J. Genet., **58**(3): 319-322 (1998)

DIFFERENTIAL EXPRESSION OF WHITE RUST RESISTANCE IN INDIAN MUSTARD (*BRASSICA JUNCEA*)

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(Received: January 15, 1997; accepted: October 15, 1998)

ABSTRACT

Genes for white rust (*Albugo candida*) resistance derived from different species and tested using various genotypes of *Brassica juncea* exhibited differential expression. The inheritance pattern was monogenic showing complete dominance in four crosses and lack of dominance (haplo insufficient) in seven crosses resulting in ratios of 3R :IS or IR : 3S, respectively.

Key words : Indian mustard, white rust, resistance, differential expression

Most of the cultivars of Indian mustard (*Brassica juncea*) the predominantly cultivated oilseed crop of India is generally susceptible to white rust (*Albugo candida*). This disease causes 17-34 percent yield loss particularly due to stag head phase [1,2] and upto 50% yield loss under late sown conditions [3]. Use of resistant varieties is the most acceptable way of reducing losses due to diseases. Absolute resistance or very high degree of resistance is not available in any of the existing cultivars of *B. juncea* in India. Some exotic *B juncea* cultures are immune or highly resistant to white rust. These are, however, late maturing with low yield potential. Other sources of resistance are available in the related species of *B. napus* and *B. carinata*. Breeding lines of *B. juncea* are available where resistance genes from these species have been transferred. For incorporating the genes responsible for disease resistance into otherwise desirable genetic background, the mode of inheritance of white rust resistance was studied in different crosses of *B. juncea*.

MATERIALS AND METHODS

In this study, Varuna, VSL-1, PSR-7 and EC 287711 were used as female parents. Varuna is most widely cultivated variety in India. VSL-1 and PSR-7 are two recently evolved strains with high yield potential and EC 287711 has low erucic acid in its

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*Present address : Scientist, Seed Technology Division, IGFRI, RRS, UAS Campus, Dharwad 580 005 oil. The male (resistance donor) parents used were five different sources, two from exotic introductions [WR 16-3-6 and WR (D313 × YSJ)] and three (AB-4-3, AB-5 and AB-10-1) derived from inter specific hybridization of *B. juncea* with *B. napus* and *B. carinata*. Parental and F_1 generations were sown in one row each and F_2 was sown in 4-6 rows each during rabi 1994-95 at IARI, New Delhi. To ensure disease incidence artificial inoculation was done in the month of January 1995. The plant populations were screened for white rust depending on the presence or absence of infection, without grading them further for intensity of the disease. Observations were recorded in vegetative stage only. The data was subjected to Chi-square test to fit into appropriate genetic ratios as per the standard statistical procedures [4].

RESULTS AND DISCUSSION

Of the 11 crosses studied for their segregation pattern in F_2 against white rust disease (Table 1) 7 crosses namely, Varuna × AB-5, Varuna × AB-4-3, EC 287711 × AB-5, EC 287711 × WR (D313 XYSJ), VSL-1 × AB-5, VSL-1 × WR (D 313 × YSJ) and PSR-7 × AB-5 showed IR: 3S ratio whereas the remaining four crosses showed 3R :1S irrespective of the female parents (Varuna, EC287711 and VSL-1) used. This indicates monogenic dominant behaviour for white rust resistance. The male parent used was an exotic introduction. Besides this, F_2 population in the cross PSR-7 × AB10-1 also showed 3R : 1S ratio. The resistance donor in this cross was a derivative from interspecific crosses. An earlier study [5] showed the resistance to white rust as monogenic which could be easily transferred to adaptable susceptible genotypes via back crossing. A more recent study [6] also showed that resistance was governed by a dominant nuclear gene pair for white rust in Indian mustard.

Table 1. Inheritance of White Rust resistance in different crosses of *Brassica juncea*

S. No.	Cross	Generation	No. of plants showing			Chi-square	Probability	Ratio
			R	S	Total			
1	2	3	4	5	6	7	8	9
1.	Varuna × AB-5	P1	0	16	16			
		P2	18	0	18			
		F1	0	16	16			
		F2	10	37	47	0.348	0.70-0.50	1R:3S
2.	Varuna × AB-4-3	P1	0	16	16			
		P2	14	0	14			
		F1	0	17	17			
		F2	14	40	54	0.025	0.90-0.80	1R:3S

(*Table 2 contd.*)

3.	Varuna × WR 16-3-6	P1	0	14	14			
		P2	17	0	17			
		F1	18	0	18			
		F2	62	20	82	0.016	0.90-0.80	3R:1S
4.	EC287711 × AB-5	P1	0	14	14			
		P2	16	0	16			
		F1	0	12	12			
		F2	11	31	42	0.032	0.90-0.80	1R:3S
5.	EC287711 × WR 16-3-6	P1	0	14	14			
		P2	16	0	16			
		F1	18	0	18			
		F2	76	24	100	0.053	0.90-0.80	3R:1S
6.	EC 287711 × WR(D313×YSJ)	P1	0	16	16			
		P2	14	0	14			
		F1	0	17	17			
		F2	16	46	62	0.021	0.90-0.80	IR:3S
7.	VSL-1 × AB-5	P1	0	22	22			
		P2	14	0	14			
		F1	0	19	19			
		F2	25	72	97	0.031	0.90-0.80	IR:3S
8.	VSL-1 × WR 16-3-6	P1	0	20	20			
		P2	20	0	20			
		F1	20	0	20			
		F2	37	13	50	0.027	0.90-0.80	3R:1S
9.	VSL-1 × WR(D313×YSJ)	P1	0	17	17			
		P2	14	0	14			
		F1	0	18	18			
		F2	15	48	63	0.048	0.90-0.80	IR:3S
10.	PSR-7 × AB-10-1	P1	0	22	22			
		P2	12	0	12			
		F1	15	0	15			
		F2	43	15	58	0.028	0.90-0.80	3R:1S
11.	PSR-7 × AB-5	P1	0	15	15			
		P2	12	0	12			
		F1	0	23	23			
		F2	19	53	72	0.075	0.80-0.70	1R:3S

R : Resistant; S : Susceptible

In the remaining seven crosses, F_2 showed a segregation ratio of IR : 3S. Since the plants were classified based on the presence or absence of infection without grading them further, the plants which could have been categorized under moderately resistant/ tolerant have been scored under the susceptible category. Therefore, the homozygous dominant plants free from disease were scored as resistant and heterozygous and homozygous recessive as susceptible plants, respectively. Therefore, it can be concluded that the resistance to white rust is controlled by a single dominant gene with differential expression, sometimes giving complete dominance with 3 : 1 ratio and in other cases giving incomplete dominance ratio of 1:2:1. For breeding purpose the gene showing complete dominance may be more desirable.

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