Indian J. Genet., **61**(3): 250-252 (2001)

Inheritance of white rust resistance in Indian mustard incorporated from *Brassica napus*

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(Received: October 2000; Revised: June 2001 ; Accepted: June 2001)

Abstract

The mode of inheritance of white rust (*Albugo candida*) resistance in three strains S-II, S-IV (R) and S-VI incorporated from *Brassica napus* and stabilized as *Brassica juncea* was studied by crossing with susceptible strains S-VIII, Pusa Bold and S-IX(S) and raising their F_1, F_2, B_1 and B_2 generations. The F_2 and backcross populations from all the three crosses segregated for a dominant gene. These results were also confirmed when tested at two hotspots Wellington and Kukumseri. It was concluded from the segregation pattern of inter-crosses between resistant strains that the same gene for white rust resistance is operating in all the three parents. The monogenic dominant inheritance was also confirmed when resistant strains were crossed with white rust resistance gene carrier strain deriving resistance from *B. carinata*.

Key words : Indian mustard, white rust, resistance, inheritance, dominant

Introduction

White rust, caused by *Albugo candida* (Pers. ex Lev.) Kuntze is most important disease of Indian mustard present in all mustard growing areas, and most regularly causing extensive damage in recent years due to congenial agro-climatic conditions. Depending upon the intensity of staghead formation and late sown conditions of the crop, yield losses up to the extent of 50 percent have been reported [1]. Most of the available cultivars of Indian mustard are susceptible to white rust, however, a high degree of resistance is available in *Brassica napus* and *Brassica carinata*. Therefore, breeding of the resistant varieties incorporating genetic resistance is the most economical and preferable way of reducing yield losses due to white rust. Knowledge of the nature and mode of inheritance of the resistant genes and their stability under different agroclimatic conditions is imperative for effective utilization of resistance in the breeding programme.

Keeping this in view, the present study was undertaken to understand the inheritance in three stable resistant strains of *B. juncea* deriving resistance from *Brassica napus* and their test of allelism with resistance derived from *Brassica carinata*.

Materials and methods

All the resistant and susceptible strains used were developed at the Division of Genetics, IARI, New Delhi

Three white rust resistant strains designated as S-II, S-IV(R) and S-VI were developed from the crosses Varuna × WR16-3-1, EC287711 × WR16-3-6 and VSL-1 × WR16-3-6 respectively. While Varuna is widely cultivated variety of brown seeded mustard, EC 287711 is an exotic introduction for low erucic acid and VSL-1 is a high yielding strain developed by crossing Varuna with synthetic *Brassica juncea*. The lines EC 287711, VSL-1 and cultivar Varuna are susceptible to white rust. Resistant lines WR 16-3-1 and WR 16-3-6 were obtained from interspecific hybridization of *B. juncea* with *B. napus* and stabilized as *B. juncea*.

An another white rust resistant strain S-III, reported to carry monogenic recessive resistance [2] was also developed from a cross EC 287711 × AB-5, where AB-5 is white rust resistant strain developed from interspecific hybridization between *B. juncea* and *B. carinata* and stabilized as *B. juncea*.

Two strains, S-VIII and S-IX(S) derived from the crosses PSR-7 × AB-5 and Varuna × PCR05 respectively and a popular bold seeded variety Pusa Bold, were used as susceptible parents.

Three crosses [S-II × S-VIII, S-IV(R) × Pusa Bold and S-VI × S-IX(S)] were made between resistant strains S-II, S-IV(R), S-VI and susceptible strains S-VIII, S-IX(S), Pusa Bold. Two crosses i.e. S-II × S-IV(R) and S-VI × S-II were also made between the resistant parents. Using a *B. carinata* derived resistant strain S-III, two crosses i.e. S-III × S-II and S-III × S-IV(R)

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Table 1. Inheritance of white rust resistance in different crosses of *Brassica juncea*

S. No.	Cross	Generation	Locations	No. of plants			Ratio (R:S)	Chi-square	P-value
				R	S	Total			
Resistant × susceptible crosses									
1.	S-II × S-VIII	P_1	Delhi	19	0	19			
		P_2	Delhi	0	17	17			
		F_1	Delhi	21	0	21			
		F_2	Wellington	62	26	88	3:1	0.755	0.30-0.50
			Kukumseri	38	18	56	3:1	1.167	0.20-0.30
			Delhi	170	67	237	3:1	1.183	0.20-0.30
			Heterogeneity					0.370	0.80-0.90
		B_1	Delhi	24	0	24	all R	-	-
		B_2	Delhi	17	15	32	1:1	0.001	0.99
2.	S-IV(R) × Pusa Bold	P_1	Delhi	20	0	20			
		P_2	Delhi	0	23	23			
		F_1	Delhi	21	0	21			
		F_2	Wellington	65	29	94	3:1	1.419	0.20-0.30
			Kukumseri	35	17	52	3:1	1.256	0.20-0.30
			Delhi	163	49	212	3:1	0.308	0.50-0.70
			Heterogeneity					2.940	0.20-0.30
		B_1	Delhi	25	0	25	all R		
		B_2	Delhi	25	21	46	1:1	0.348	0.50-0.70
3.	S-VI × S-IX(S)	P_1	Delhi	23	0	23			
		P_2	Delhi	0	20	20			
		F_1	Delhi	21	0	21			
		F_2	Wellington	53	22	75	3:1	0.537	0.30-0.50
			Kukumseri	36	16	52	3:1	0.641	0.30-0.50
			Delhi	127	54	181	3:1	2.005	0.10-0.20
			Heterogeneity					0.034	0.98-0.99
		B_1	Delhi	34	0	34	all R		
		B_2	Delhi	15	12	27	1:1	0.333	0.50-0.70
Resistant × resistant crosses									
4.	S-II × S-VI	P_1	Delhi	19	0	19			
		P_2	Delhi	22	0	22			
		F_1	Delhi	19	0	19			
		F_2	Delhi	153	0	153	all R		
5.	S-II × S-IV(R)	P_1	Delhi	24	0	24			
		P_2	Delhi	20	0	20			
		F_1	Delhi	19	0	19			
		F_2	Delhi	141	0	141	all R		
Crosses for test of allelism									
6.	S-III × S-II	P_1	Delhi	22	0	22			
		P_2	Delhi	24	0	24			
		F_1	Delhi	32	0	32			
		F_2	Delhi	190	31	221	13:3	5.858	0.01-0.02
7.	S-III × S-IV(R)	P_1	Delhi	18	0	18			
		P_2	Delhi	21	0	21			
		F_1	Delhi	29	0	29			
		F_2	Delhi	227	49	276	13:3	0.320	0.50-0.70

R = Resistant, S = Susceptible

were attempted for test of allelism. The F_1, F_2 and backcross generations, B_1 (with resistant parent) and B_2 (with susciptible parents) were raised. Parents, F_1, F_2, B_1 and B_2 generations of these crosses were tested at IARI, New Delhi under artificial epiphytotic conditions. The F_2s of these crosses were also tested under natural epiphytotics at off-season nurseries at Wellington (T.N.), South India and Kukumseri (H.P.), North India. Observations for white rust were recorded using 0-5 visual disease scoring scale [3] at vegetative and full podding stages. Categories 0-2 were defined as resistant with complete absence of white rust pustules or with very low hypersensitive infection. Other categories 3-5 were classified with moderate to high infection of disease with more rust pustules and development of stagheads at later stages, as susceptible. The data was subjected to test the goodness of fit with the appropriate genetic ratios as per the procedure given by Panse and Sukhatme [4].

Results and discussion

The observations on P_1, P_2, F_1, F_2, B_1 and B_2 generations of these crosses are given in Table 1. Resistance of the parental lines S-II, S-IV(R) and S-VI falls in the categories 0 and 1 in contrast to susceptible parents S-VIII, S- IX(S) and Pusa Bold (categories 4 and 5). The F_1 plants of these crosses S-11 x S-VIII, S-IV(R) x Pusa Bold and S-VI x S-IX(S) were resistant indicating the dominant nature of resistance to white rust. The segregation pattern in F_2 generation of these three crosses fits very well in 3 Resistant : 1 Susceptible ratio of monogenic inheritance at all three locations (Table 1) suggesting that there is no effect of location on expression of resistance gene. This monogenic dominant nature of the resistance gene to white rust was confirmed when backcross populations were tested In the backcrosses (B_1) with resistant parents, all the plants were resistant while backcrosses (B_2) with susceptible parents segregated in 1R:1S ratio.

All the plants in F_2 generations of inter-resistant crosses [S-II × S-IV(R) and S-II × S-VI] were resistant, suggesting that all the three resistant strains S-II, S-IV(R) and S-VI carry the same gene for resistance to white rust.

When the F_2s of crosses between strain S-III deriving a recessive resistance gene from *B. carinata* and resistant strains S- II and S-IV (R) were tested, they showed segregation in 13R:3S ratio. The digenic ratio suggested the interaction of one recessive and a dominant gene. The monogenic dominant nature of resistance in strains S-II, S-IV(R) and S-VI, deriving resistance from *B. napus*, was further corroborated by the fact that strain S-III carries single recessive gene for white rust resistance [2]. The dominant gene for resistance carried by S-II, S-IV(R) and S-VI is epistatic to dominant allelic form of single recessive gene for resistance carried by strain S-III. The single dominant gene for resistance to *Albugo candida*, derived from *B. napus* is tentatively designated as "ac-napus". These results of monogenic dominant nature of resistance to white rust are in agreement with the findings of earlier workers [5, 6, 7].

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