Characterization of an Indian Mustard *(Brassica juncea)* Indigenous Germplasm Line Bio-YSR for White Rust Resistance

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(Received: 9 November 2010; Accepted: 3 December 2010)

White rust, caused by *Albugo candida* is one of the major diseases of Indian mustard in India, causing heavy yield losses ranging from 17 to 34%. The breakdown of resistance is the prime concern to search for new genes to develop a durable resistance against white rust in mustard. A stable donor Bio-YSR (INGR No. 04099) has been developed indigenously, which need genetical characterization. Bio-YSR, the resistant donor germplasm line was crossed with popular, widely grown and high yielding susceptible cultivars Varuna and Bio-902 (Pusa Jai Kisan), to study the mode of inheritance of white rust resistance gene. The F_1 plants of these crosses were resistant indicating the dominant nature of the resistance. The segregation pattern in F_2 of the crosses fits well in 3 resistant (R): 1 susceptible (S) ratio indicating Bio-YSR carries a single dominant gene. This monogenic dominant nature was confirmed from the results of backcross populations as well. Hence, the major gene governing white rust resistance in the indigenous germplasm line Bio-YSR, will be of immense use in breeding for durable resistance by the way of diversification of resistant sources and gene pyramiding.

Key Words: Indian mustard, Indigenous germplasm, Inheritance, Resistance, White rust

Introduction

White rust, caused by *Albugo candida*, is a common disease of many economically important cruciferous vegetables and oilseed crops. It is most wide-spread and highly destructive to *Brassica juncea*, reported to cause 17–34 % yield losses (Kolte, 1985). The Indian genotypes are highly susceptible to white rust (Li *et al*., 2008) and an appreciable loss in seed yield has been reported to the extent of 50% under late sown conditions (Saharan *et al.*, 1984). Amongst the four oleiferous *Brassica spp.* grown in India, *B. juncea* is the predominant one and occupies more than 80% of the total area under rapeseed-mustard. Though, *B. juncea* is hardy in comparison to other oilseed Brassicas, yet it is highly susceptible to white rust. This disease is recurring every season with different degrees of intensity at different stages of crop growth, causing significant reduction in yield. The disease is characterized by the formation of white pustules on the cotyledons, leaves, stems and inflorescence. Systemically infected inflorescence becomes hypertrophied, causing the characteristic staghead galls (Verma and Petrie, 1980). It has been estimated that combined infection of leaf and inflorescence causes yield losses to the extent of 62.7%, the loss being more severe (89.8%) as a result of staghead formation in the susceptible cultivars (Lakra and Saharan, 1989). The most cost-effective way of protecting mustard plants from white rust is through introgression of genetic resistance. Identification of different sources of resistance to white rust is an important prerequisite in managing this disease by means of effective and durable genetic resistance.

Genetic analysis of available white rust resistance has elucidated a digenic mode of inheritance with duplicate gene action in *B. napus* (Fan *et al*., 1983; Verma and Bhowmik, 1989) and monogenic dominant resistance in *B. juncea* (Tiwari *et al*., 1988; Bansal *et al*., 1999; Sachan *et al*., 2000; Chauhan and Sharma, 2001) as well as in *B. rapa, B. carinata and B. nigra* (Delwiche and Williams, 1974; 1981). The earlier studies were based on the exotic sources of white rust resistance. A stable donor Bio-YSR has been developed indigenously, and the genetics of this resistance source has not been studied. In comparison to the different exotic sources taken for genetic studies and used in white rust resistance breeding programme, Bio-YSR is agronomically superior and also stable under Indian conditions (Katiyar and Chopra, 1990).

Dynamic changes in race composition of the pathogen have often resulted in short-lived efficiency of host resistance in the improved varieties which necessitates identification and characterization of new sources of white rust resistance. Hence, the present study was undertaken to investigate the nature and inheritance of white rust

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resistance in an indigenous germplasm for their use in future crop improvement programme for breeding for durable resistance for this disease.

Materials and Methods

Development of experimental material

The experimental material used in the study includes two popular, widely grown, high yielding cultivars *viz*., Varuna and Bio-902 (Pusa Jai Kisan) of *B. juncea*, which are highly susceptible to white rust. The resistant source used was Bio-YSR, a somaclone of *B. juncea* developed by NRCPB, IARI, New Delhi, and registered with NBPGR (INGR No. 04099). Bio-YSR, the resistant donor of *B. juncea*, was crossed with susceptible cultivars Varuna and Bio-902, during *rabi* 2006–07 at IARI Experimental Farm, New Delhi to study the mode of inheritance of white rust resistance gene. The F_1s, thus, obtained were advanced during *rabi* 2007–08 to derive F_2 population by selfing, and backcrossed to both the parents to obtain Backcross1(B_1) (with susceptible parent, $F_1 \times P_1$) and Backcross2 (B_2) (with resistant parent, $F_1 \times P_2$) generations for studying the genetics of white rust resistance.

Inoculum preparation and incubation conditions

The inoculum was prepared by collecting the white rust zoosporangia from heavily infected fresh leaves of the susceptible *B. juncea* cultivar Varuna and Pusa Bold maintained in the National Phytotron Facility, IARI, New Delhi. The zoosporangia were collected in sterile distilled water and allowed to germinate for 4 hours at 8ºC. The zoospore suspension was sprayed on the foliage with a hand automizer until runoff. Dark conditions were maintained for 24 hrs after the spray for development of the disease by covering the entire plot with light blocking PVC sheet. To maintain high humidity, which is congenial for the disease development, experimental plot was irrigated frequently and water was kept standing in the channels surrounding the plots during the period of inoculation.

Phenotyping for white rust resistance

The parents, F_1, B_1, B_2 and F_2 generations of these crosses were grown and their white rust reaction was observed during Rabi, 2008–09. Two rows of parents and F_1, five rows of B_1 and B_2 and ten rows of F_2 were planted with a spacing of 30 cm between rows, and 10 cm between plants within row. Recommended package of practices were followed to raise a good crop. The plants were rated for white rust reaction two weeks after inoculation. For recording the observations for white rust a minimum of 20 plants each from P_1, P_2, F_1, 100 plants in B_1 and B_2 and 250 plants in F_2 were taken. The plants on which observations for white rust were recorded, were tagged from seedling stage and scoring was done upto the stage of staghead formation. The disease scoring was done as per the method described by Fox and Williams (1984). Chi-square (χ^2) test was employed to test goodness of fit of observed and expected frequency in segregating generations.

Results and Discussion

The results of the present study are based on the observations recorded and analysis carried out for inheritance of white rust resistance in Parents, F_1, B_1, B_2 and F_2 generations of the two crosses involving Bio-YSR as a white rust resistance donor.

Mode of inheritance

Disease scores of parental lines indicated that the indigenous germplasm line Bio-YSR was resistant to local *A. candida* population. The observations on P_1, P_2, F_1, B_1, B_2, and F_2 generations of these crosses are given in the Table 1. The F_1 plants of these crosses Varuna × Bio-YSR and Bio-902 × Bio-YSR were resistant to white rust indicating the dominant nature of the resistance.

The segregation pattern in F_2 of the two crosses fits well in 3 resistant (R):1 susceptible (S) ratio ($\chi^2 = 1.58$, and 0.79, respectively) (Table 1) indicating that the donor carries a single dominant gene. This monogenic dominant nature of the resistance gene to white rust was confirmed from the results of backcross populations as well. In the backcrosses 2 (B_2) with the resistant parent, all the plants were resistant, whereas, in the backcrosses1 (B_1) with susceptible parents, test cross progenies segregated in 1R:1S ratio. These results of monogenic dominant nature of resistance to white rust are in agreement with the earlier findings (Tiwari *et al*., 1988; Bansal *et al*., 1999; Sachan *et al*., 2000; Chauhan and Sharma, 2001).

The study revealed that the resistance is monogenic in the indigenous resistant source Bio-YSR. Hence, the major gene governing white rust resistance could be easily transferred to the well adapted, high yielding but susceptible genotypes by backcross breeding. The presence of monogenic resistance gene in the indigenous source Bio-YSR will be very useful in breeding for durable resistance by the diversification of resistant sources and gene pyramiding. However, more detailed studies would have to be conducted to analyse the virulence spectra and diversity in the pathogen population through controlled experiments.

Table 1. Segregation pattern for white rust resistance in the crosses between Bio-YSR and susceptible genotypes

Cross	Generations	Total plants	Observed		Expected ratio	Expected		χ^2	P value
			Resi.	Susc.		Resi.	Susc.		
Varuna x Bio-YSR	P_1	27	0	27	–	0	27	–	–
	P_2	21	21	0	–	21	0	–	–
	F_1	23	23	0	–	23	0	–	–
	F_2	257	184	73	3:1	192.75	64.25	1.58	0.20 – 0.30
	B_1	112	64	48	1:1	56	56	2.28	0.10 – 0.20
	B_2	109	109	0	1:0	109	0	–	–
Bio-902 x Bio-YSR	P_1	25	0	25	–	0	25	–	–
	P_2	22	22	0	–	22	0	–	–
	F_1	20	20	0	–	20	0	–	–
	F_2	263	191	72	3:1	197.25	65.75	0.79	0.30 – 0.50
	B_1	119	52	67	1:1	59.5	59.5	1.89	0.10 – 0.20
	B_2	113	113	0	1:0	113	0	–	–

Acknowledgements

The first author is thankful to the Indian Council of Agricultural Research, New Delhi, India for the grant of Junior Research Fellowship for the master's degree programme. The financial support from the Department of Biotechnology, Government of India, is also duly acknowledged by the authors.

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