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INHERITANCE OF PHENOLS AND PROTEIN IN RELATION TO WHITE RUST (*ALBUGO CANDIDA*) RESISTANCE IN INDIAN MUSTARD

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ABSTRACT

Studies on the relationship of phenols and protein with white rust severity showed that phenols imparted resistance whereas more protein led to higher disease severity at vegetative and reproductive stages in Indian mustard. Inheritance studies indicated the importance of both additive and dominance components of variance, with the preponderance of latter, in the genetic control of phenols and protein. Genotypes EC126743, EC 126745, Domo-4 and EC 126746-1 were identified as good combiners. Six crosses have been identified on the basis of their high SCA effects and per se performance for further studies.

Key words: *Brassica juncea*, white rust, combining ability, phenols, proteins.

White rust (*Albugo candida* Lav.), one of the most severe diseases of Indian mustard (*Brassica juncea* L. Czern & Coss), causes substantial degree of losses in seed yield [1, 2]. Chemical control of the disease has not been very effective. Thus, cultivation of disease resistant varieties seems to be only practical and effective control measure.

To evolve disease resistant cultivars, breeding efforts hitherto have been planned on the basis of available knowledge in respect of inheritance of disease. At present, however, greater emphasis is being laid on role of phenols and protein in disease resistance. Dhawan et al. [3] reported higher content of phenols in white rust resistant lines of Indian mustard. However, the information regarding inheritance of phenols and protein is lacking. The present study was therefore, conducted to get further information on the role of phenols and protein in white rust resistance/susceptibility and their genetic control.

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MATERIALS AND METHODS

Among the 10 lines selected for this study five, viz. Prakash, Varuna, Kranti, RLC 1357 and RLC 1359 were susceptible, while four varieties, i.e. EC 126743, EC 126745, EC 126746-1 (Russian origin) and Domo-4 (Canadian origin) were resistant to white rust. The line RC 781 was moderately resistant. These ten lines were crossed in diallel fashion excluding reciprocals. The resulting 45 F_1 hybrids and 10 parents were grown in randomized block design with three replications under epiphytotic conditions at Haryana Agricultural University, Hisar during rabi 1987–88. Each genotype was grown in a single row of five metres. The inter- and intra row spacing of 45 and 15 cms, respectively, was maintained.

Inoculum was sprayed five times, starting three weeks after sowing and then at weekly intervals during evening hours to get adequate pressure of white rust in the experimental area. The inoculum was prepared by collecting white rust infected leaves from highly infested areas and putting them in a pure water to get sporangia dissolved in it. This sporangial suspension was kept for three hours to allow germination of fungal spores. The concentration of spores was adjusted to 2.5×10^4 per ml. High humidity was maintained by providing irrigations at regular intervals.

Five leaves from each of five plants per plot were plucked at vegetative (six weeks after sowing) and reproductive (twelve weeks after sowing) stages represented by S_1 and S_2, respectively. The leaves were scored using 0 to 5 rating scale. Disease severity was calculated as:

$$\frac{\text{Sum of all numerical ratings}}{\text{Total number of leaves scored}} \times \frac{100}{\text{Highest rating}}$$

The leaves after scoring for disease severity were utilized for determination of total phenols (mg/g) [4] and per cent protein [5]. The data thus recorded were subjected to biometrical analysis [6, 7].

RESULTS AND DISCUSSION

Resistant lines EC 126743, EC 126745, EC 126746-1 and Domo-4 contracted no disease at S_1 and showed 0–2% white rust severity at S_2 (Table 1). On the other hand susceptible genotypes exhibited 21–42% and 28–57% rust severity at S_1 and S_2, respectively indicating effectiveness of the inoculation technique used. Resistant genotypes had higher content of phenols and lower content of proteins than susceptible genotypes at both the stages. Dhawan et al. [3] had earlier reported more phenols in resistant material. It was further noted that at S_2, where the disease severity was more, there was decrease in phenols and increase in protein content in all the genotypes from what they contained at S_1 (Table 1).

Table 1. White rust severity (%), total phenol (mg/g) and protein (%) content at two stages

Genotype	Vegetative stage (S_1)			Reproductive stage (S_2)		
	white rust	total phenols	protein	white rust	total phenols	protein
Prakash	21.5	2.08	25.75	57.1	0.45	32.46
Varuna	21.1	2.40	26.72	28.8	0.75	32.10
Kranti	22.8	2.31	24.57	33.3	1.00	29.96
EC 126743	0.0	3.46	17.57	0.7	1.79	20.30
EC 126745	0.0	3.63	18.15	1.3	1.39	19.61
EC 126746-1	0.0	3.74	17.55	2.0	1.13	21.52
Domo-4	0.0	3.64	18.72	0.0	1.11	20.17
RC 781	4.2	3.14	20.94	10.0	1.19	21.55
RLC 1359	24.2	2.15	25.88	39.8	0.74	30.25
RLC 1357	42.8	2.11	27.89	49.9	0.69	31.00

Thus, it seems that phenols provide resistance whereas more protein content increases the susceptibility to white rust. It was further substantiated by high negative correlation ($r = -0.92^{**}$ and -0.86^{**} at S_1 and S_2, respectively) of white rust severity with phenols and positive correlation ($r = 0.94^{**}$ at both the stages) with protein. These findings were in confirmity with Gupta et al. [8].

The estimates of additive (D) and dominance (H_1 and H_2) components were significant for both the traits (Table 2) showing importance of both type of variances. Significant mean squares due to general combining ability (gca) and specific combining ability (sca) (Table 3) also indicated importance of additive and dominance components of variance. The value of parameter F was significant and positive for protein indicating the excess of dominant genes among the parents (Table 2). Contrarily, equal proportion of dominant and recessive genes was observed for phenols as indicated by nonsignificant value of F. The environmental variation (E) was not important for both the traits. Average degree of dominance $(H_1/D)^{0.5}$ indicated more importance of dominance component for phenols at both the stages and protein at S_2.

Symmetrical or asymmetrical distribution of genes is indicated by the ratio $H_2/4H_1$. The equal distribution of genes in the parents helps the breeder for selecting a particular trait without loosing any other desirable trait. But in the present study symmetrical distribution of genes with positive and negative effects in the parents was not observed for

Table 2. Estimates of genetic components of variance with respect to total phenols and protein at vegetative (S_1) and reproductive (S_2) stages

Components of variance/ratios	Total phenols		Protein	
	S_1	S_2	S_1	S_2
D	0.51* ± 0.08	0.15* ± 0.01	17.48* ± 0.97	31.61* ± 1.46
H_1	1.17* ± 0.17	0.16* ± 0.03	15.80* ± 2.06	37.50* ± 3.11
H_2	1.10* ± 0.15	0.10* ± 0.03	13.71* ± 1.75	31.57* ± 2.64
h^2	0.04 ± 0.10	0.05* ± 0.02	24.42* ± 1.17	37.97* ± 1.77
F	− 0.11 ± 0.19	0.03 ± 0.03	10.31* ± 2.23	22.81* ± 3.57
E	0.00 ± 0.02	0.00 ± 0.01	0.02 ± 0.29	0.04 ± 0.44
$(H1/D)^{1/2}$	1.51	1.07	0.95	0.09
$(H2/4H_1)$	0.23	0.17	0.22	0.21
$\frac{(4DH1)^{1/2} + F}{(4DH2)^{1/2} - F}$	1	1	1.90	1.99
$h^2/H2$	0.04	0.50	1.78	1.20
Heritability (n.s.)	0.55	0.77	0.57	0.48
t^2	3.21	2.89	1.70	3.43

*Significant at P = 0.05.

any of the trait as the ratio deviated from the theoretical value of 0.25. The ratio $(4DH_1)^{0.5}$ + $F/(4DH_1)^{0.5}$-F was greater than unity due to positive value of F for protein indicating that it was controlled by more of dominant genes in the parents. Therefore, it is likely to show a slow progress through selection.

The ratio h^2/H_2 indicated two groups of genes for protein and one group of genes for phenols but it might have been underestimated due to asymmetry of genes in the parents. Moderate estimates of heritability indicated that both the traits are amenable for further improvement by simple selection procedures.

Study of gca effects (Table 4) revealed that line EC 126743 was best general combiner both for phenol and protein content followed by EC 126745,

Table 3. Analysis of variance (MS) for total phenols and protein at vegetative (S_1) and reproductive (S_2) stages.

Source	d.f.	Total phenols		Protein	
		S_1	S_2	S_1	S_2
Gca	9	1.95*	0.47*	31.04*	50.19*
Sca	45	0.28*	0.03*	4.23*	9.37*
Error	108	0.001	0.0002	0.019	0.038

*Significant at P = 0.05.

Domo-4 and EC 126746-1. They are thus worth utilizing in future breeding programmes. Significant correlations ($r = 0.9^{**}$) between gca effects and per se performance of parents indicated that the parents can be selected on the basis of latter for their further use in breeding programmes.

The sca effects of all the crosses were computed. It was observed that number of crosses involving both the parents as good combiners was very low or not at all (Table 5). On the other hand, high x low combinations gave high sca effects again revealing the more importance of dominance gene effects.

From practical point of view, high sca effects of crosses alone will not lead to much improvement unless it is coupled with high per se performance. Therefore, selection of crosses for further breeding programmes should be based on higher values of both of these parameters. In the present study, six such crosses, viz. Varuna x EC 126743, Varuna x EC 126745, Varuna x Domo-4, Kranti x EC 126745, RLC 1359 x EC 126745 and RLC 1359 x EC 126746-1, have been identified to be utilized as base material for further improvement.

Table 4. General combining ability (gca) effects of parents for total phenols and protein at vegetative (S_1) and reproductive (S_2) stages in Indian mustard

Genotype	Total phenols		Protein	
	S_1	S_2	S_1	S_2
Prakash	-0.55^{**}	-0.28^{*}	1.17^{*}	1.87^{*}
Varuna	-0.34^{*}	-0.17^{*}	1.82^{*}	2.71^{*}
Kranti	-0.17^{*}	-0.12^{*}	1.45^{*}	2.26^{*}
EC 126743	0.46^{*}	0.26^{*}	-1.99^{*}	-2.18^{*}
EC 126745	0.44^{*}	0.25^{*}	-1.67^{*}	-2.42^{*}
EC 126746-1	0.34^{*}	0.14^{*}	-1.39^{*}	-1.54^{*}
Domo-4	0.46^{*}	0.21^{*}	-1.64^{*}	-2.37^{*}
RC 781	0.09^{*}	-0.03^{*}	-0.63^{*}	-0.59^{*}
RLC 1359	-0.28^{*}	-0.12^{*}	0.92^{*}	0.87^{*}
RLC 1357	-0.44^{*}	-0.15^{*}	1.96^{*}	1.40^{*}

*Significant at P = 0.05.

Table 5. SCA performance of crosses for phenols and protein at vegetative (S_1) and reproductive (S_2) stages in Indian mustard

Item	Total phenols		Protein	
	S_1	S_2	S_1	S_2
Number of crosses showing significant sca effects	22	21	25	24
High x high	1	0	1	0
High x low	19	17	19	18
Low x low	2	4	5	6

Note. High — good general combiner.
Low — poor general combiner

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