GENETIC ANALYSIS OF RESISTANCE TO LINSEED WILT

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ABSTRACT

Six linseed (*Linum usitatissimum* Linn.) types, 3 resistant, R-552, R-556 and G-194, and 3 susceptible, IPI-6, R-17 and G-440, to wilt were subjected to a diallel crossing involving 15 crosses. Out of these, three crosses, IPI-6 \times R-17, IPI-6 \times G-440 and R-17 \times G-440, were with both the susceptible parents; nine crosses, IPI-6 \times R-552, IPI-6 \times R-556, IPI-6 \times G-194, R-17 \times R-552, R-17 \times R-556, R-17 \times G-194, G-440 \times R-552, G-440 \times R-556 and G-440 \times G-194, involved a single resistant parent; and three crosses, R-552 \times R-556, R-552 \times G-194 and R-556 \times G-194, with both resistant parents. Genes governing resistance were worked out by χ^2 test. A monogenic, digenic and trigenic pattern of gene action was recorded for the resistance to linseed wilt (*Fusarium oxysporium*) in the crosses studied.

Key words: Linum usitatissimum, linseed, wilt, inheritance, diallel cross.

Linseed crop suffers considerable yield losses due to fusarial wilt each year. To develop suitable resistant varieties and overcome the losses, genetic analysis of resistance to this disease is required. The present study has been undertaken to obtain this basic genetic information using the wilt-sick plot facilities at the Agriculture College, Indore.

MATERIALS AND METHODS

The material for this study comprised six brown seeded cultivars of linseed (Linum usitatissimum L.). Three cultivars, i.e. IPI-6, R-17 and G-440, were susceptible and the remaining, R-552, R-556 and G-194, were resistant to linseed wilt. All possible crosses among them (excluding reciprocals) were made. The 15 crosses included 3 crosses involving both the susceptible parents, 9 crosses involving a single resistant parent, and 3 crosses with both the resistant parents. The F_1 seeds were sown in 3 m long single rows with 40 cm spacing between the rows. The F_2 progenies of all the 15 crosses along with 6 parents were tested in randomized block design with three replications and plot size 3×0.40 m (5 rows/plot). The plant-to-plant spacing was 10 cm. Observations on wilted plants were recorded as suggested by Jeswani and Upadhyaya [1]. All the plants that survived were recorded as resistant.

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RESULTS AND DISCUSSION

Susceptible parents, IPI-6, R-17 and G-440 showed mortality due to wilt disease to the extent of 98.10%. Some percentage of resistant plants in otherwise susceptible parents might be due to the disease escaping tendency of such parents. Resistance to the tune of 94 to 97% was recorded for the resistant parent R-552, R-556 and G-194.

Reaction to wilt of F_1 hybrids in all the 9 crosses between the 3 susceptible and 3 resistant parents showed that resistance was dominant over susceptibility. The results were in agreement with the findings of [1-3].

 F_2 generation studies. Resistance to wilt was not observed among the F_2 of the crosses in which both parents were susceptible. Thus, no complementation was noticed. The data on inheritance of wilt resistance in susceptible \times resistant crosses are presented in Table 1.

Cross	Parent		Wilt reaction		. 78	Segregation ratio			
	F	M	R	S	X ²	R	S	P	
IPI-6 × R-552	S	R	396	154	2.969	3	1	0.2-0.05	
IPI-6. × R-556	S	R	370	141	1.832	3	1	0.2-0.05	
IPI-6 × G-194	S	R	442	134	0.925	9	· 7	0.5-0.2	
$R-17 \times R-552$	S	R	406	128	0.303	3	1	0.8-0.5	
R-17 × R-556	S	R	423	157	1.324	3	1	0.5-0.2	
R-17 × G-194	S .	R	422	121	2.137	9	7	0.2-0.05	
G-440 × R-552	S	R	444	137	0.625	3	1	0.8-0.5	
G-440 × R-556	S	R	.430	129	1.103	3	1	0.5-0.2	
G-440 × G-194	S	R	373	134	0.553	9	7	0.5-0.2	

Table 1. Inheritance of wilt resistance in susceptible X resistant crosses (F2)

S-susceptible, R-resistant, F-female and M-male.

The results of crosses between wilt susceptible and resistant linseed parents (Table 1) revealed that inheritance of wilt was governed by a single dominant gene in the resistant parents R-552 and R-556. Monogenic inheritance in linseed wilt was reported earlier [1-4].

The results of three other crosses between the resistant parent G-194 and three susceptible parents (IPI-6, R-17 and G-440) revealed that inheritance in these crosses was of complementary type with segregation ratio of 9 resistant: 7 susceptible. It, therefore, indicated the role of two dominant complementary factors in the resistant type G-194. The earlier experiments [3, 5] also revealed similar gene action in linseed.

Observations on the crosses involving both the resistant parents (Table 2) revealed that cross R-552 \times R-556 segregated in a dihybrid ratio, indicating the operation of a single dominant independent gene in both parents. A trihybrid ratio of 57 resistant: 7 susceptible in F_2 of crosses R-552 \times G-194 and R-556 \times G-194

Cross	Read	ction	Segregation ratio				
	R	S -	X ²	R	S	P	
R-552 × R-556	542	27	2.198	15	1	0.2-0.05	
R-552 × G-194	474	68	1.440	57	7	0.5-0.2	
R-556 × G-194	510	70	0.762	57	7	0.5-0.2	

Table 2. Inheritance of wilt resistance in resistant X resistant crosses of linseed

indicated the role of two nonlinked genes in G-194 in relation to the single genes in R-552 and R-556. Resistance to linseed wilt governed by two dominant duplicate factors leading to a segregation ratio of 15 resistant: 1 susceptible has been reported [1, 5]. Observations on the wilt reaction in resistant × resistant crosses revealed that inheritance of this character in crosses R-552 × G-194 and R-556 × G-194 is controlled by three nonlinked dominant genes. Such resistance genes could be combined to obtain better resistance.

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