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An Analysis of Genes for Resistance Against Two Indian Cultures of Stem Rust Races of Two Bread Wheats

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Summary. Two bread wheat accessions, E5008 and E6160, have been genetically analysed for resistance genes effective against Indian cultures of stem rust races, 15C and 122. The inheritance of resistance to each race has been determined from the F1 and F2 of the crosses (resistant parents with the susceptible variety, 'Agra Local') and F2 progenies from the backcross to 'Agra Local'. Tests have been performed to see if the two varieties carry common genes/s for resistance. The identity of the genes for resistance has been established from relevant crosses with single gene lines carrying known genes for resistance.

A single dominant gene effective to race 15C in E5008 has been demonstrated to be *Sr*9b. Of the two recessive genes, each producing distinct infection types (0; and 1-3) against race 122, one gene has been inferred to be *Sr*12 and the second to be a hitherto undesignated gene.

The resistance of E6160 against race 15C is controlled by two genes, one dominant and one recessive. The dominant gene has been identified as *Sr*9b. The recessive gene has been inferred to be a new gene. Similarly, a dominant gene effective against race 122 in E6160 has been observed to be different from those so far designated. In addition, the presence of modifier gene/s in the variety, E6160 has been suggested.

Key words: *Triticum aestivum* – Wheat – *Puccinia graminis* – Stem rust resistance – Inheritance

Introduction

The utilisation of specific genes for resistance has been the major approach for resistance breeding in wheat against rust pathogens. This kind of resistance is normally short-lived but several methods have been suggested for prolonging the effective field life of race specific resistance genes. Basic to all these methods is the need of a genetic diversification of the resistance base, which requires identification and characterisation of as many different genes as possible. In this paper we report genetic analysis in terms of number, nature and identity of resistance genes present in two highly resistant genotypes against two races of stem rust.

Materials and Methods

Two varieties from the International Spring Rust Nurseries bearing the Indian Agricultural Research Institute accession numbers E5008 and E6160 were selected for the analysis of resistance genes. E5008 is a line developed at Minnesota from the cross ('Frontana' – 'Kenya 58' – 'Newthatch') × ('Red Egyptian' – 'Frontana'). The variety is resistant to all stem rust races except race 295. At an adult plant stage it shows a trace infection of stem rust. E6160 is a Canadian line evolved from the cross 'Thatcher' – 'Mida' – 'McMurachy' – 'Erechim', 60 GRS57. It is a tall and late maturing variety. At the seedling stage, it is resistant to all races of stem rust. It shows complete freedom from all the rusts at the adult plant stage. The resistant parents E5008 and E6160 were crossed with a susceptible parent, 'Agra Local'. The parents, F1, F2 and F2 backcross (Resistant × susceptible) × (susceptible) progenies were tested for determining the number and nature of genes for resistance against stem rust races, 15C and 122. The same set of F2 backcross families was tested with the two races to find out the independence or non-independence of genes operating for resistance against the two races by using the association chi-square test. (Mather 1963). The identity of the genes in the resistant parents was established from the segregation pattern in F2 of crosses between the resistant parent and effective *Sr* gene lines in 'Marquis' background. The relationship between the genes for resistance in the two parents were analysed in the F2 and F3 of cross between the resistant parents. Inoculations were done according to procedure suggested by Stakman et al. (1944); scoring of infection type was done according to Stakman et al. (1962). The minimum and maximum temperature in the glass house was recorded daily and the testing of material was conducted at an average temperature not exceeding 22° C.

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Results

Analysis of E5008

E5008 gave a highly resistant (0; 1T) reaction to races 15C and 122.

The F2 data (Table 1) provides evidence that the resistance of E5008 is controlled by a single dominant gene against race 15C and by two independently acting recessive genes against race 122.

Data on 45 F2 backcross families tested both against race 15C and 122 are set out in Table 2. The expected ratio of 1 segregating: 1 susceptible was observed for race 15C. Further, the 3 resistant: 1 susceptible segregation within F2 backcross families confirmed the operation of a single gene. For race 122, 34 families segregated while the remaining 11 were susceptible. This is a close fit to 3 segregating families: 1 susceptible family, a ratio expected from a 2 gene segregation. The segregating families could be divided into two classes: those segregating in a 1 resistant: 3 susceptible ratio and those segregating in a 7 resistant: 9 susceptible ratio. Since the F1 seedlings were susceptible, both these genes should be recessive. This was confirmed by the results from segregation within the F2 backcross families. The number of families showing 1 resistant: 3 susceptible ratio were twice as frequent as those showing the 7 resistant; 9 susceptible ratio. Of the families segregating against race 122, 18 segregated with seedlings showing 1-3 IT; 8 having 0; IT and the remaining 8 showed seedling reaction 0; as well as 1-3 IT. This indicates the operation of two distinct genes, one conferring 0; IT and the other producing 1-3 IT to race 122.

A chi-square test for independence showed that the genes governing resistance to the two races are different (Table 2). Tests on the near isogenic lines having *Sr*1, *Sr*5, *Sr*6, *Sr*7a, *Sr*7b, *Sr*8, *Sr*9a, *Sr*9b, *Sr*10, *Sr*11, *Sr*13, *Sr*14 and *Sr*16 from the 'Marquis' background showed that lines carrying *Sr*6 and *Sr*9b are effective to race 15C. In F2 of the cross between lines *Sr*6 and E5008, segregants susceptible to 15C were observed, suggesting the absence of *Sr*6 in E5008. However, the absence of segregation in F2 progeny of the cross between line carrying *Sr*9b and E5008 indicated the operation of *Sr*9b in E5008 for resistance to race 15C. Race 122 is avirulent on line with *Sr*8 producing 22-IT. From F2 of the cross *Sr*8 – Mq × E5008, 185 seedlings were tested against race 122. Segregation was observed which indicated the absence of *Sr*8 in E5008.

Table 1. Segregation of F2 seedlings of the cross E5008 × 'Agra Local' when tested with races 15C and 122

Race	Number of seedlings			Expected ratio	X^2	P lies between
	Res.	Sus.	Total			
15C	201	72	273	3R:1S	0.283	0.50-0.70
122	115	176	291	7R:9S	2.112	0.10-0.20

Analysis of E6160

F1 seedlings of the cross E6160 × 'Agra Local' exhibited near immunity (0; IT) with race 15C, and high resistance (0;–1 IT with race 122. For both races, resistance was dominant.

Table 2. Correlated behaviour of the lines derived from the F2 of the backcross E5008 × 'Agra Local' when tested with races 122 and 15C

E5008 × 'Agra Local'[2]	Race 122 Number of families			Total (Race 15C)	Expected (1:1)	X^2 df1	P lies between
	Seg. 1R:3S	Seg. 7R:9S	Sus.				
Race 15C							
Seg.	13	6	8	27	22.50	1.800	0.10-0.20
Sus.	12	3	3	18	22.50		
Total (Race 122)	25	9	11	45			
Expected (2:1:1)	22.50	11.25	11.25				
	X^2 df2	0.734			P	0.30-0.50	
X^2 df2 for independence			1.266		P	0.50-0.70	

The results of the F2 and F2 backcross families are given in Tables 3 and 4.

The F2 segregation indicates the operation of one dominant and one recessive gene governing resistance to race 15C. These results were confirmed in F2 backcross families where the data agree with the expected 3 segregating families: 1 susceptible family ratio. Segregating families were of two distinct types: some families segregating for 0; IT and others for 0;–1 IT. This indicates that two distinct genes determining 0; and 0; –1 types of reaction respectively are operating for resistance to race 15C.

In order to find out if the resistance genes of E6160 against 15C were identical to *Sr*6 and *Sr*9b, two of the genes found effective against 15C, the F2 of the cross *Sr*6 – Mq × E6160 was tested and observed to segregate for susceptibility, indicating the absence of *Sr*6. The involvement of *Sr*9b in E6160 was deduced indirectly from absence of segregation in a large F2 population and in F3 progenies of the cross E5008 × E6160 in tests against 15 C. The recessive gene for resistance against 15C in E5008 is possibly a new gene as yet not described.

F2 seedling segregation against race 122 was 3 resistant: 1 susceptible, suggesting the presence of one dominant gene for resistance. This conclusion finds support from data of backcross families (Table 4). Among the resistant segregants, those with 2 IT were characteristically conspicuous. On the *Sr*8 – Mq, race 122 produces 2 IT. There was reason to suggest, therefore, that the resistance of E6160 may be due to *Sr*8. However, segregation for susceptibility was observed among 243 F2 seedlings of cross *Sr*8 – Mq × E6160 when tested with race 122. It is, therefore, concluded that the gene for resistance to race 122 in E6160 is not *Sr*8 and is likely to be a new gene. Correlated behaviour of common backcross families tested against the two races suggests that the genes conferring resistance to race 15C and 122 are independent (Table 4). The resistance in E5008 to race 15C is governed by a single dominant gene. This dominant gene, as discussed earlier, is identical with the dominant gene for resistance in E6160.

Table 3. Segregation of F2 seedlings of the cross E6160 × 'Agra Local' when tested with races 15C and 122.

Race	Number of seedlings			Expected	X^2	P lies
	Res.	Sus.	Total	ratio		between
15C	207	39	246	13R:3S	1.345	0.20-0.30
122	133	50	183	3R:1S	0.463	0.70-0.80

Discussion

In the variety E5008, the dominant gene for resistance against race 15C has been identified to be *Sr*9b. This gene has probably evolved into E5008 from 'Frontana' which

Table 4. Correlated behaviour of the lines derived from the F2 of the backcross (E6160 × Agra Local) when tested with races 15C and 122.

E6160 × 'Agra Local'[2]	Race 15C						
	Number of families			Total (Race 122)	Expected (1:1)	X^2 df1	P lies between
	Seg. 3R:1S and 13R:3S	Seg. 1R:3S	Sus.				
Race 122							
Seg. (3R:1S)	17	4	3	24	25		
						0.080	0.70-0.80
Sus.	10	8	8	26	25		
Total (Race 15C)	27	12	11	50			
Expected (2:1:1)	25	12.5	12.5				
	X^2 df2	0.360			P	0.80-0.90	
X^2 df2 for independence				5.159	P	0.05-0.10	

is a parent of E5008 and possesses *Sr*9b (Knott and Shen 1961). Against race 122, one of the two recessive genes imparting resistance is probably *Sr*12. The other gene does not bear any similarity to any known gene. This conclusion is based on the following observations:

(i) The chromosomes of E5008 carrying genes for resistance are 1D and 3B (Sawhney, unpublished data). On chromosome 1D, *Sr*18 has been located (Sears et al. 1957; Baker et al. 1970); *Sr*18 is the gene for resistance in the variety 'Hope'. Since race 122 is virulent on 'Hope', the operation of *Sr*18 in E5008 is excluded. The reported genes on 3B are *Sr*2, *Sr*3 and *Sr*12. *Sr*2 and *Sr*3 are genes for adult plant resistance (Sears et al. 1957; Campbell and McGinnis 1958; Knott 1968). *Sr*12 is a seedling resistance gene and is known to be present in 'Thatcher', which is a progenitor of E5008. Race 122 produces only low infection on 'Thatcher' and on *Sr*-12-Mq. It is therefore, likely that *Sr*12 operates in E5008 for its resistance against race 122. A firm conclusion in this regard can only be had when F2 of the Cross *Sr*12 × E5008 is tested against race 122. This cross was not available in the present investigation.

(ii) *Sr*8 is the other known gene effective against race 122. This gene is located on chromosome 6A (Sears et al. 1957); 6A does not carry any gene for resistance to race 122 (Sawhney, unpublished data). Moreover the cross *Sr*8 mq × E5008 segregates for susceptibility to race 122.

In the variety E6160, two genes, one dominant and one recessive, operate for resistance against race 15C. The observation that cross E6160 × E5008 does not segregate either in F2 or in F3 progenies, suggests that the two varieties carry at least one common gene for resistance. This common gene could be *Sr*9b which has been identified in E5008 and is effective against this race. The other effective gene against 15C, *Sr*6, is not involved in the resistance of E6160, since the cross *Sr*6 × E6160 segregates for susceptibility in the F2. Thus, one of the two genes for resistance against race 15C, the recessive one, seems to be a hitherto undesignated gene.

The dominant gene for resistance against race 122 in E6160, again, is a gene not described so far. Monosomic analysis has located this gene on chromosome 7B (Joshi unpublished data). This gene is not *Sr*17, the gene located on 7B by McIntosh et al. (1967), because varieties 'Spica' and 'Renown' carrying *Sr*17 are susceptible to race 122.

Our observation of two kinds of segregants in F2 of the cross E6160 × 'Agra Local', those with parental low IT (0;–1) of E6160 and those with 2 IT suggests that in addition to the newly identified gene, modifier gene(s) also is /are present in E6160. The finding of Joshi (Unpublished data) suggesting minor gene for resistance against race 122 on chromosome 7D supports this conclusion.

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