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ANALYSIS OF LINKED LEAF AND STEM RUST RESISTANCE GENES IN WHEAT- RYE RECOMBINANT 'SELECTION 212'

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ABSTRACT

Correlated behaviour analysis of F_3 and BC_1F_2 families of crosses involving 'Selection 212', a rust resistant stock developed through exploitation of homoeologous recombination between wheat and rye chromosomes, demonstrated that a common recessive gene effective to leaf rust pathotypes 77-1, 77-3, 77-4 and 77-5 individually and a recessive gene conferring resistance to stem rust pathotype 40A in Sel. 212 are closely linked.

Key Words : Wheat, rye, leaf rust, stem rust, resistance, linkage.

A rust resistant wheat-rye recombinant 'Selection 212' was developed through exploitation of homoeologous recombination between wheat and rye chromosomes in the absence of chromosome 5B of variety Chinese Spring [1, 2]. Sel. 212, constituent parents (Sonalika, Chinese Spring and rye) and near-isogenic lines each carrying known gene for leaf or stem rust resistance, when tested with an array of leaf rust (*Puccinia recondita* f.sp. *tritici*) and stem rust (*P. graminis* f.sp. *tritici*) pathotypes at seedling stage led to the postulation that leaf and stem rust resistance gene(s) in Sel. 212 were different than designated genes [3]. Inheritance studies with selected pathotypes of leaf rust (77-1, 77-3, 77-4 and 77-5) and stem rust (40A and 122) revealed the presence of single recessive resistance gene to all the leaf rust pathotypes, as also a single recessive gene for resistance to stem rust pathotypes 40A and 122 [3]. The present investigation reports the detection of linkage between the leaf and stem rust resistance genes in Sel. 212.

MATERIALS AND METHODS

A set of 80 F_3 families of a cross Sel. 212 and Agra Local (AL) were tested with pathotypes 77-1, 77-3, 77-4 and 77-5 of leaf rust and pathotype 40A of stem rust and distributed into three classes viz., homozygous resistance, segregating and homozygous susceptible. Similarly 28 F_2 families of a backcross, (Sel. 212 × AL) × AL when tested with above listed pathotypes of leaf and stem rust were distributed into two classes viz., segregating and homozygous susceptible. The distribution of these F_3 and BC_1F_2 families against leaf rust pathotypes was compared with distribution against stem rust pathotype. Analysis of detection of linkage between genes for resistance operating against different pathotypes was carried out by using the procedure described by Mather [4]. The distribution of F_3 and BC_1F_2 families was set in a two-way contigent table. Chi-square test for goodness of fit was used to compare the observed ratio with the expected on the basis of Mendelian segregation. Deviation due to genes segregating for resistance to two pathotypes individually and deviation due to combined segregation of resistance genes detected linkage between genes operating against different pathotypes. Linkage was deduced by substracting the deviation due to individual gene segregation from the compound deviation due to joint segregation of genes.

RESULTS AND DISCUSSION

Correlated behaviour of F_3 families of the cross - Sel. 212 with Agra Local when tested with leaf rust pathotypes 77-1, 77-3, 77-4 and 77-5 and stem rust pathotype 40A at seedling stage is presented in Table 1. Chi-square value for distribution of F_3 families in the ratio of 1R : 2Seg : 1S against stem rust pathotype 40A was observed as 5.1 which was non-significant at 5% level of probability. Chi-square value for distribution of F_3 families against pathotype 77-1 was found to be 2.7 which was also non-significant ($P > 0.20$), showing that there is no deviation in the distribution of classes. Similar results were observed for the other pathotypes 77-3, 77-4 and 77-5. Chi-square values for independent segregation of two genes in the ratio of 1 : 2 : 1 : 2 : 4 : 2 : 1 : 2 : 1, was highly significant ($\chi^2 = 148.45$, $P < 0.001$). The Chi-square difference ($\chi^2 = 140.65$, $P < 0.001$) suggested tight linkage between leaf and stem rust resistance genes effective to pathotypes 77-1 and 40A respectively.

Inheritance studies [3] suggested the operation of same leaf rust resistance gene in Sel. 212 for providing resistance to each of the pathotypes 77-1, 77-3, 77-4 and 77-5. The F_3 families distribution with stem rust pathotype 40A when compared with F_3 families distribution against leaf rust pathotypes 77-3, 77-4 and 77-5 was highly significant with Chi-square linkage values of 135.0, 149.975 and 131.775 respectively, (all $P < 0.001$) which would suggest strong linkage between the stem rust resistance gene effective to pathotype 40A and the leaf rust resistance gene providing resistance to group 77 pathotypes of leaf rust.

Table 1. Correlated behaviour of F_3 families of the cross Sel. 212 × Agra Local when tested with stem rust pathotype 40A and leaf rust pathotypes 77-1, 77-3, 77-4 and 77-5 at seedling stage

		Pathotype 40A Number of families				$\chi^2_{1:2:1}$
		Res.	Seg.	Sus.	Total	
Pathotype 77-1	Res.	24	0	0	24	
	Seg.	1	41	0	42	2.7, 2df, $P > 0.20$
	Sus.	1	1	12	14	
	Total	26	42	12	80	
	$\chi^2_{1:2:1}$ = 5.1, 2df, $P > 0.05$					
	$\chi^2_{(Compound)1:2:1:2:4:2:1:2:1}$ = 148.4, 8df, $P < 0.001$					
	$\chi^2_{difference(Linkage)}$ = 140.65, 4df, $P < 0.001$					
Pathotype 77-3	Res.	23	0	0	23	
	Seg.	2	42	0	44	3.3, 2df, $P > 0.10$
	Sus.	1	0	12	13	
	Total	26	42	12	80	
	$\chi^2_{1:2:1}$ = 5.1, 2df, $P > 0.05$					
	$\chi^2_{(Compound)\ 1:2:1:2:4:2:1:2:1}$ = 143.5, 8df, $P < 0.001$					
	$\chi^2_{difference\ (Linkage)}$ = 135.0, 4df, $P < 0.001$					
Pathotype 77-4	Res.	25	0	0	25	
	Seg.	0	41	0	41	3.075, 2df, $P > 0.20$
	Sus.	1	1	12	14	
	Total	26	42	12	80	
	$\chi^2_{1:2:1}$ = 5.1, 2df, $P > 0.05$					
	$\chi^2_{(compound)\ 1:2:1:2:4:2:1:2:1}$ = 158.1, 8df, $P < 0.001$					
	$\chi^2_{difference\ (Linkage)}$ = 149.975, 4df, $P < 0.001$					
Pathotype 77-5	Res.	23	0	0	23	
	Seg.	2	41	0	43	2.475, 2df, $P > 0.20$
	Sus.	1	1	12	14	
	Total	26	42	12	80	
	$\chi^2_{1:2:1}$ = 5.1, 2df, $P > 0.05$					
	$\chi^2_{(Compound)1:2:1:2:4:2:1:2:1}$ = 139.3, 8df, $P < 0.001$					
	$\chi^2_{difference\ (linkage)}$ = 131.7, 4df, $P < 0.001$					

Table 2. Correlated behaviour of F_2 families of the backcross (Sel. 212 × AL) × AL when tested with stem rust pathotype 40A and leaf rust pathotypes 77-1, 77-3, 77-4 and 77-5 at seedling stage

		Pathotype 40 A Number of families			$\chi^2_{1:1}$
		Seg.	Sus.	Total	
Pathotype 77-1	Seg.	13	3	16	
	Sus.	2	10	12	0.571, 1df, P > 0.30
	Total	15	13	28	
	$\chi^2_{1:1} = 0.143$, 1df, $P > 0.70$				
	$\chi^2_{(\text{Compound})\ 1:1:1:1} = 12.28$, 3df, $P < 0.001$				
	$\chi^2_{\text{difference (Linkage)}} = 11.57$, 1df, $P < 0.001$				
Pathotype 77.3	Seg.	13	1	14	
	Sus.	2	12	14	0.000, 1df, P > 0.99
	Total	15	13	28	
	$\chi^2_{1:1} = 0.143$, 1df, $P > 0.70$				
	$\chi^2_{(\text{Compound})\ 1:1:1:1} = 17.42$, 3df, $P < 0.001$				
	$\chi^2_{\text{difference (Linkage)}} = 17.28$, 1df, $P < 0.001$				
Pathotype 77-4	Seg.	12	1	13	
	Sus.	3	12	15	0.143, 1df, P > 0.70
	Total	15	13	28	
	$\chi^2_{1:1} = 0.143$, 1df, $P > 0.70$				
	$\chi^2_{(\text{Compound})\ 1:1:1:1} = 14.57$, 3df, $P < 0.001$				
	$\chi^2_{\text{difference (Linkage)}} = 14.28$, 1df, $P < 0.001$				
Pathotype 77-5	Seg.	13	1	14	
	Sus.	2	12	14	0.000, 1df, P > 0.99
	Total	15	13	28	
	$\chi^2_{1:1} = 0.143$, 1df, $P > 0.70$				
	$\chi^2_{(\text{Compound})1:1:1:1} = 17.42$, 3df, $P < 0.001$				
	$\chi^2_{\text{difference (Linkage)}} = 17.28$, 1df, $P < 0.001$				

Correlated behaviour of F_2 families of the backcross (Sel. 212 × AL) × AL, when tested with leaf rust pathotypes 77-1, 77-3, 77-4 and 77-5 and stem rust pathotype 40A in seedlings is presented in Table 2. Twenty eight BC_1F_2 families when tested with individual pathotypes of leaf and stem rust exhibited distribution in the ratio of 1 Seg : 1 Sus. Significant Chi-square linkage values (11.572, 17.286, 14.285 and 17.286, all $P < 0.001$) were obtained when distribution of same set of BC_1F_2 families against pathotype 40A was compared with distribution against the pathotypes 77-1, 77-3, 77-4 and 77-5, respectively. These results concluded linkage between stem rust resistance gene effective to pathotype 40A and resistance gene operative for group 77 pathotypes of leaf rust.

These closely linked leaf and stem rust resistance genes, presumably derived from rye (*Secale cereale*), conferring resistance to the most virulent and predominant pathotype 77-5 of leaf rust and pathotype 40A of stem rust would greatly facilitate the incorporation of simultaneous resistance to both the rusts coupled with diversity in the future breeding programs.

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