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ACCUMULATION OF GENES FOR ENHACEMENT OF INCOMPLETE RESISTANCE TO *PUCCINIA RECONDITA TRITICI*

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Introduction

Results of breeding for the resistance altered according to possibilities, mostly connected with choice of the resistant parents (alien species, resistant varieties out of production and fortunately very often widespread varieties) (6). Pyramiding, or accumulating genes for the specific resistance was not successful because of practical reasons: how to select in progenies and to keep all genes from the initial parents? Transmission of genes from alien species, mostly causes expression of negative characteristics controlled by linked genes. Determination and transmission of genes in the interaction until now is most successful from the aspect of durability and long term protection level (4). Nowadays results suggest the more accurate way: combination of the parents with high level of incomplete resistance to increase that characteristics or to get the complete resistance to the present population of pathogen. It agrees with the most important point in breeding for the resistance: durability (2). High level of incomplete resistance is sufficient to avoid epidemics development of pathogens specially in semiarid regions (3).

This paper demonstrates the accumulation of genes which control this characteristics, by the testing of lines created from the progenies of the same combinations but partially in opposite direction from the future one.

Material and Methods

Lines from the progenies of complex crossings using the lines and varieties with different levels of incomplete resistance in field, and complete or incomplete resistance in the seedling stage under controlled conditions (Table 1) were studied for estimating the effect of gene accumulation.

Novosadska rana 2 was chosen as susceptible control widespread variety (sometimes it covers over 60 % of the area under the wheat in Yugoslavia), which had remarkable influence on the creating of the present *Puccinia recondita* population.

Tab. 1

Genealogies
series 1
**
(Loznička x Nova posavka) x Rana niska) x (NS 2853 x Zg-1-628-/77)
series 2
*
(Tobari 66 x Kavkaz) x (Nova banatka x NS 3143) x Rana niska) x (NS 2568/6 x MV 08/78)

Repeated estimation of the infection intensity according to Cobb scale (1963) in the comparative trials (1x5 m^2 in four replications) were the basis for AUDPC values counting (1) in 1993 and 1994, while maximal intensities were determined in 1991 and 1992.

Under the controlled conditions (15 °C day and 15 °C night, with constant relative humidity of the air of 60 %) the length of the latent period 50 and infection efficiency were estimated in the seedling stage (3). Inoculation was performed with the culture in the type of the race 77 which is virulent to all series of Lr genes except Lr 9, Lr 19 and Lr 24.

Results and Discussion

The lines from the same combination of the first series, expressed higher resistance level in the field conditions in comparison with those of the series two. In 1992 and 1993 these differences were not exposed because of inadequate conditions for development of *Puccinia recondita*. In 1994, 59 days from March to middle of June were rainy so the intensity of attack was stronger, material was differentiated according to the resistance. If we assume that mos susceptible lines in field conditions from series one (NS 2-2675, NS 2-2675/5) and two (NS 2-2742, NS 3160, NS 2-2740) carry only one gene for the resistance different than these in Novosadska rana 2, it is evident that the lines NS 2-2675/1, NS 2-2675/2, NS 2-2675/3, NS 2675/4 and NS 2-2741 carry at least two, and the line NS 2-2739 three additional genes (Tables 2 and 3). It is abvious that by interaction of these genes resistance is expressed in the field. As no parent line expressed such resistance in field, it is clear that we have new different (dependant of line) combinations of resistant genes. Hypersensitive reaction in the seedling stage was expressed from the interaction of genotypes NS 2-2675/3, NS 2-2675/4, NS 2739 and NS 2-2740. Lp 50 and infection efficiency values proved the higher differences between estimated lines in resistance combinations genes than can be concluded only according to field estimation data (Tab. 3). Because of insufficient number of applied isolates different according to the virulence, field susceptibility and seedling resistance of some parents, it is impossible to ascertain complete resistance from the combination of genes for the incomplete resistance (5).

Tab. 2: Infection intensities with *Puccinia recondita tritici* in 1991-1994

line/year and screening date	1994	1. 31.05. 2. 08.06. 3. 21.06.	1993	1. 01.06. 2. 07.06. 3. 14.06.	1992	1991
		1, 2, 3		1, 2, 3		
series 1						
*						
NS 2-2675		T, 5, 30		0, 0, T	0	0
NS 2-2675/1		0, 0, T		0, 0, T	0	0
NS 2-2675/2		0, 0, T		0, 0, T	0	0
NS 2-2675/3		0, T, T		0, 0, T	0	0
NS 2-2675/4		0, T, T		0, 0, T	0	0
NS 2-2675/5		0, T, 20		0, 0, T	0	0
series 2						
**						
NS 2-2738		0, T, 30		0, 0, T	0	T
NS 2-2739		T, 5, 5		0, 0, T	0	T
NS 2-3160		0, T, 30		0, 0, T	0	
NS 2-2740		0, T, 30		0, 0, T	0	0
NS 2-2741		T, 5, 20		0, 0, T	0	T
NS 2-2742		0, T, 40		0, 0, T	0	T
Novosadska Rana 2		5, 40, 80		T, T, T	20	35

Tab. 3: Characters of the incomplete resistance and AUDPC values in 1993 and 1994

line/parameter year	IT	LP 50	IF	AUDPC 1994	AUDPC 1993
NS 2-2675	4	9,1	5,6	254,5	3,5
NS 2-2675/1	4	10,0	3,0	7,5	3,5
NS 2-2675/2	4	10,3	6,0	7,5	3,5
NS 2-2675/3	;			17,5	3.5
NS 2-2675/4	0			17,5	3,5
NS 2-2675/5	4	8,3	3,5	141,0	3,5
NS 2-2738	4	8,5	4,0	206,0	3,5
NS 2-2739	;23	8,5	6,0	92,0	3,5
NS 2-3160	;			206,0	3,5
NS 2-2740	;			206,0	3,5
NS 2-2741	4	8,8	2,7	192,7	3,5
NS 2-2742	4			271,0	3,5

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