

Genetics of wheat Somaclones Resistance to *Bipolaris sorokiniana* Shoem.

L. G. TYRYSHKIN and N. A. TYRYSHKINA-SHISHELOVA*

Vavilov All-Russian Institute of Plant Industry (VIR), 190000 St.-Petersburg, Russia

*Tel.: +7 812 466 4704, Fax: +7 812 113 7094, E-mail: tyr@na8418.spb.edu

Abstract

Genetics of resistance to common root rot and dark brown leaf spot blotch (both caused by *Bipolaris sorokiniana* Shoem.) was studied in wheat somaclonal lines, obtained in calluses culture of samples 181-5 and Vera. Four different approaches were used: linear analysis of resistance in generations of segregating somaclonal lines, hybridological analysis, study of resistance components, study of possible durability of resistance. Results showed, that resistance to both diseases is likely controlled by polygenic systems with additive actions of minor genes. Different lines possess non-identical genetic systems for resistance. Several lines kept their initial level of resistance to spot blotch after 5 cycles of the pathogen artificial population reproduction.

Keywords: wheat; somaclonal variability; genetics of resistance; dark brown leaf spot blotch; common root rot; *Bipolaris sorokiniana*

INTRODUCTION

Bipolaris sorokiniana Shoem. is a wide spread pathogen of cereal causing dark brown leaf spot blotch and common root rot being the most severe in barley and wheat. Evaluation of Vavilov All-Russian Institute of Plant Industry World collection wheat samples showed that most genotypes including that described as possessing any resistance are susceptible to the diseases in seedling stage (TYRYSHKIN & SHEVCHENKO 1994; TYRYSHKIN & SHISHELOVA 2001a).

Significant somaclonal variability was found for these traits in early generations of plants obtained in *in vitro* cultures of 6 spring wheat samples; analysis of segregation in R_3 of resistant R_2 lines showed possible polygenic control of resistance (TYRYSHKIN 1997). All lines of susceptible varieties lost their resistance in $R_{3,4}$ and that of moderately resistant initial genotypes (181-5 and Vera) were resistant or segregating for resistance in R_6 ; analysis of F_2 from crosses of resistant R_8 lines with susceptible varieties indicated possible oligogenic

control of resistance to 2 diseases (TYRYSHKIN *et al.* 2000). The purpose of the work is to determine genetic control of resistance in somaclonal lines of late generations with use of 4 different approaches.

MATERIALS AND METHODS

Seedling resistance to leaf spot blotch and common root rot were studied in R_7 lines, obtained as progeny of single seeds of R_6 families early identified as highly resistant, F_3 from crosses of stable resistant R_8 lines with susceptible varieties, F_2 from crosses between resistant R_8 lines.

All lines resistant to dark brown leaf spot blotch are progeny of somaclonal variants of sample 181-5, that resistant to common root rot are progeny of somaclonal variants of 181-5 and cv. Vera (TYRYSHKIN *et al.* 2000). Lines with first number 709 are that of Vera, all others in this study – are lines of initial sample 181-5; lines with the same first numbers are progeny of one regenerated plant.

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To study resistance to dark brown leaf spot blotch leaf segments of wheat seedlings placed on cotton wool wetted with water were sprayed with water suspension of the pathogen conidia of aggressive strain T (30 000 c/ml). After 3 days type of reaction was scored according 0–6 scale, where 0 – absence of the disease symptoms, 6–100% of leaf surface diseased. To study mechanisms of resistance: (a) leaf segments were sprayed with conidia suspension (15 000c/ml) and after 3 days number of spots was counted, (b) drops of the suspension (0.05 ml) were placed on leaves and after 3 days size of spots was measured (mm). To estimate development of common root rot the modified “roll” method was used. Roots of plants grown in rolls of paper (2–4 days after seed germination) were inoculated by spraying with strain T conidia suspension (60 000 c/ml). Disease rating on roots and coleoptiles was scored at 10–13 days after inoculation according to 0–6 scale: 0 – no symptoms, 6 – plant death (TYRYSHKIN & SOLOVIEVA 2001).

Possible durability of resistance to spot blotch was determined with original method (TYRYSHKIN & VORONKOVA 1997). Leaf segments of samples under study were infected with artificial pathogen population (mixture of 40 independent isolates), after symptoms of the disease appearance leaves were dried and placed on cotton wool wetted with lactose solution (20 g/l). Conidia formed after 3–4 days were used to infect leaves of the same sample (1 cycle of reinoculation). After 5 cycles fungi was isolated from leaves on semiselective media (TYRYSHKIN *et al.* 1984) and multiplied on Chapec’s media. Levels of resistance to initial and resulted populations were compared.

RESULTS AND DISCUSSION

In progeny of almost all 12 R₆ families resistant to spot blotch and 9 – resistant to root rot, resistant, segregating for resistance and susceptible R₇ lines were identified (TYRYSHKIN & SHISHELOVA

Table 1. Segregation for resistance to *B. sorokiniana* in F₃ from crosses between wheat somaclonal lines and susceptible varieties

Cross	Genetic control of resistance according to analysis of F ₂	Phenotypes ratios R:RS:S*		χ^2
		expected	observed	
Resistance to dark brown leaf spot blotch				
Luba × 817,7	2 recessive genes	7:8:1	1:22:8	32.32 **
Luba × 819,2,7	2 recessive genes	7:8:1	3:24:8	279
Luba × 873,6	2 complementary genes	1:8:7	4:24:26	2.69
Moskovskaja 35 × 871,1,5	2 complementary genes	1:8:7	2:18:12	0.83
Moskovskaja 35 × 819,3,6	1 dominant gene	1:2:1	3:26:6	113.65
819,12,9 × Luba	2 recessive genes	7:8:1	2:12:9	9.07
817,18 × Saratovskaja	1 recessive gene	1:2:1	0:8:25	520.84
Resistance to common root rot				
709,13,9,1,2 × Luba	2 complementary genes	1:8:7	9 :49: 37	1.22**
709,13,9,2,3 × Luba	2 complementary genes	1:8:7	1: 16: 14	13.72
709,13,9,1,3 × Luba	2 complementary genes	1:8:7	5:31: 18	5.40
709,13,9,2,6 × Luba	2 complementary genes	1:8:7	4:12:20	3.78
Moskovskaja 35 × 709,9,9,1	2 complementary genes	1: 8:7	0:9:28	8.11
Moskovskaja 35 × 709,9,9,6	2 complementary genes	1:8:7	0:11:36	13.15
900,4,12,1,5 × Luba	2 complementary genes	1:8:7	2:34:18	2.14
900,4,12,22,1 × Luba	2 complementary genes	1:8:7	2:22:38	7.88
900,4,12,1,2 × Luba	2 complementary genes	1:8:7	0:13:43	20.34
900,14,5 × Moskovskaja 35	1 dominant gene	1:2:1	20:50:11	6.45

*R = resistant, RS = segregating for resistance, S = susceptible F₃ families

** $\chi^2 t = 5.99$, $P = 0.05$

Table 2. Disease rating of dark brown leaf spot blotch on leaves of wheat somaclonal lines and varieties after inoculation with different inoculums of *B. sorokiniana*

Sample	Disease score after inoculation with		
	strain T	initial population	5 th subpopulation
871,2,2,6	2	0–1	5
883,2,18	2	3–4	0–1
818,11,8,1	2	2	2
877,1,8	2	2–3	1–2
873,1,10,1	2	2	2
904,1,7,1	2	2	1
873,5,5,3,2	2–3	1–2	1–2
819,3,6,13,7	2	1–2	4
819,3,6,13,8	1	1	2
181-5	3–4	3–4	3–4

2001b). We suppose that segregation for resistance in late generations of somaclonal variants can be explained by: (a) constant reversion of mutations to susceptibility, (b) polygenic control of the traits with additive action of many minor genes, (c) incomplete penetration of resistance. Last hypothesis is of little possibility because of presence of non-segregating R_6 and R_7 lines. Identification of resistant R_7 lines without segregation in next generations may be result of their homozygosity for minor genes or stabilizing of mutations for major genes. Analysis of F_2 from crosses of lines with susceptible varieties showed that resistance can be controlled by 1–2 genes (TYRYSHKIN *et al.* 2000). Only for 5 combinations (2 – for resistance to spot blotch and 3 – to root rot) from 17 studied data on F_3 are not in contradiction with that on F_2 (Table 1). In 12 lines resistance can not be controlled by less than 3–4 genes acting additively indicating occasional coincidence of F_2 data with expected at oligogenic control of the trait. Lines with possible digenic control of resistance to common root rot (709,13,9,1,3; 709,13,9,2,6; 900,4,12,1,5) are progeny of R_7 lines for which another R_8 lines obviously can not have oligogenic resistance; thus these R_7 lines possessed more than 2 genes for resistance. For 2 lines 873,6 and 871,1,5 resistance to spot blotch possibly is controlled by two complementary recessive genes; at least for last line it must be result of stabilizing of mutations for the trait. For 3 between-lines crosses of lines resistant

to root rot and 6 – to spot blotch susceptible plants were found in F_2 proving different genetic control of resistance in lines of the same initial variety.

Analysis of components of resistance to dark brown leaf spot blotch revealed significant differences between lines and initial variety in average number of spots on leaves and in average spot. Lines 819,3,6,15; 819,7,7,3; 819,3,6,4 differ significantly from another for 1 of 2 components under study indicating different genetic control of resistance in different lines – progeny of the same regenerated plants.

Assessment of R_8 lines for resistance to artificial population of the pathogen and to subpopulations after 5 cycle of reproduction on resistant lines showed differential interaction line \times inoculum (Table 2). Evident lost or lowering of resistance level as result of pathogen adaptation was observed for two lines – 871,2,2,6 and 819,3,6,13,8. These two fact proved conclusion on difference in genetic systems of somaclonal lines.

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