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The influence of a translocation with the Lr19+Lr26 combination on grain productivity and bread-making quality in spring bread wheat.

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At the Agricultural Research Institute for the South-East Regions (ARISER), NILs based on the Saratov-bred spring bread wheat cultivar L503 and carrying translocations with the *Lr19+Lr26* combination, prospective lines were produced and studied. The data from 2005–11 indicate that the interaction of these translocations positively influences grain yield (Table 1). During this period, leaf rust epidemics were observed three times (2005, 2006, and 2008) and drought conditions four times (2007, 2009, 2010, and 2011). Grain productivity significantly increased in two leaf rust epidemics in lines with *Lr19+Lr26*, and twice under drought conditions. In the hard drought of 2010, spring bread wheat plants died. The main limiting factor for the use of T1BL·1RS translocations in wheat breeding is the influence on bread-making quality. The decrease of bread-making quality is coupled with genes for disease resistance and *Sec1*. In the NILs produced in the genetic background of cultivar L503, the presence of *Lr19+Lr26* translocations did not influence the grain protein content or gluten values. The increase in grain yield of lines containing *Lr19+Lr26*-translocations was not accompanied by decreased of grain protein content. Dough extensibility (P) and strength of flour (W) were not significantly lower in the NILs and perspective lines with *Lr19+Lr26* translocations compared with L503. Similar results were obtained for bread-making qualities. Loaf volume and porosity also were not significantly lower than L503 in the NILs and lines with *Lr19+Lr26* translocations (Table 2). Thus, the *Lr19+Lr26* translocations had positive effects on resistance to disease anddrought and grain productivity with good bread-making quality.

Table 1. Grain productivity, grain protein content, and gluten deformation index of L503 NILs and perspective lines of spring bread wheat with *Lr19+Lr26*.

NIL / line	Grain yield (kg/ha)	Grain protein content (%)	Gluten value	
			content (%)	strength
L503 (*Lr19*)	1,755 a	17.78	42.17	81
L503 (*Lr19+Lr26*)	2,096 bc	17.94	40.53	78
L503(*Lr19+Lr26*)//L505	2,301 c	17.79	39.32	81
LSD	47.79	NS	NS	NS

Table 2. Bread-making qualities of L503 NILs and perspective lines of spring bread wheat with *Lr19+Lr26* (dough extensibility = P and strength of flour = W).

NIL / line	Physical traits of dough			Bread-making qualities		
	P	P/L	W	loaf volume (cm^3)	porosity	crumb color
L503 (*Lr19*)	93.4	1.5	192	788	4.5	yellow
L503 (*Lr19+Lr26*)	84.6	1.4	166	760	4.4	yellow
L503(*Lr19+Lr26*)//L505	89.3	1.3	185	750	4.3	yellow
LSD	NS	NS	NS	NS	NS	

The agronomic performance of Lr19+Lr37 translocations in the set of NILs in the genetic background of the spring bread wheat cultivar Dobrynya.

S.N. Sibikeev and A.E. Druzhin .

We used a set of NILs in the genetic background of the spring bread wheat cultivar Dobrynya to associate positive agronomical traits of *Lr19* and *Lr37* translocations. The presence of both translocations in the NILs was confirmed with molecular markers; STS marker Gb Lr19 for the *Lr19* translocation and primers VENTRIUP and LN2 for the *Lr37* translocation (Gultyaeva EI et al. 2012). In the droughty conditions of 2011, NILs with *Lr19+Lr37* translocations were significant higher than Dobrynya for grain productivity. The NILs also surpassed Dobrynya in grain protein content, however, the results for gluten content and gluten strength were ambiguous. One line was higher than that of Dobrynya, and another line was equal to Dobrynya (Table 3). For dough extensibility (P) and strength of flour (W), NIL 118 was equal to and NIL 113 exceeded those of Dobrynya. Loaf volume and porosity were lower in the NILs with *Lr19+Lr37* translocations than in Dobrynya (Table 4). We conclude that translocations with the *Lr19+Lr37* combination improve drought resistance but do not depress bread-making properties.

Table 3. Grain productivity, grain protein content, and gluten deformation index of Dobrynya NILs and perspective lines of spring bread wheat with *Lr19+Lr37*.

NIL / line	Grain yield (kg/ha)	Grain protein content (%)	Gluten value	
			content (%)	strength
Dobrynya (*Lr19*)	2,695 a	14.98	37.4	80
NIL 113 Dobrynya (*Lr19+Lr37*)	2,864 b	15.75	35.4	68
NIL 118 Dobrynya (*Lr19+Lr37*)	3,156 c	16.10	40.0	78
LSD	153			

Table 4. Bread-making qualities of Dobrynya NILs and perspective lines of spring bread wheat with *Lr19+Lr37* (dough extensibility = P and strength of flour = W).

NIL / line	Physical traits of dough			Bread-making qualities		
	P	P/L	W	loaf volume (cm^3)	porosity	crumb color
Dobrynya (*Lr19*)	108	1.9	249	810	5.0	yellow
NIL 113 Dobrynya (*Lr19+Lr37*)	156	2.7	366	700	4.5	yellow
NIL 118 Dobrynya (*Lr19+Lr37*)	110	1.7	249	710	5.0	yellow

Resistance screening to a local population of leaf rust among species and relatives of bread wheat.

S.N. Sibikeev, A.E. Druzhin, T.D. Golubeva, and T.V. Kalintseva.

Screening for resistance to a local population of leaf rust among 25 species and relatives of bread wheat gave the following results: 14 lines from 10 species/relatives of bread wheat and one triticale cultivar, Satu, were resistant. Temperature sensitivity for resistance to leaf rust was found in *T. turgidum* and *T. petropavloskyi* in 2006. With the purpose of enlarging the gene pool of bread wheat for *Lr* genes, hybrids were obtained between the spring bread wheat cultivars Saratovskaya 68, Saratovskaya 70, Saratovskaya 73, and Saratovskaya 74 and lines of the resistant species.

Evaluating spring bread wheat cultivars for resistance to tan spot (Pyrenophora tritici-repentis (Died.) Drechsler.) in 2011.

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Tan spot, caused by the ascomycete fungus *Pyrenophora tritici-repentis*, is one of the most serious foliar diseases of wheat. The average yield loss caused by this pathogen is 5–10%, but in epipdemic years, losses can be up to 30%.

Moreover, tan spot also causes significant losses in grain quality by grain shriveling, red smudge, and black point. In recent years, this disease more often appear in the plantings of spring bread wheat in the Lower Volga Region of the Russian Federation. To screen for resistance to this pathogen, we evaluated 140 introgression lines of spring bread wheat in a nursery. Among the lines, 35 were resistant (% infection = 0) to the local tan spot population. NIL L400R, with a *Thinopyrum intermedium* 6Agi (6D) substitution was more resistant to tan spot than its sib lines L400S that lack 6Agi (Table 5). The combination of translocations T7DS·7DL-7Ae#1L (*T. elongatum*) and T6BS·6BL-6U#1L (*Ae. umbellulata*) and T7DS-7DL-7Ae#1L and 4BS·4BL-2R#1L (*S. cereale*) increase the resistance of the spring bread wheat lines to the tan spot, however, the combination T7DS·7DL-7Ae#1L and T1BL·1R#1S significantly increased susceptibility. NILs with a combination of T7DS·7DL-7Ae#1L and T3DS·3DL-3Ae#1L (*T. elongatum*) did not significantly differ on the extent of damage with respect to the cultivar (Table 5).

Table 5. The reaction of cultivars and NILs of spring bread wheat to *Pyrenophora tritici-repentis*.

Cultivar / NIL	Translocation	% infection
L 400 R	6Agi (6D)	5
L 400 S	—	30
L 503	T7DS·7DL-7Ae#1L	0
L 503 (*Lr26+Lr19*)	T7DS·7DL-7Ae#1L	0
L 503 (*Lr26+Lr19*)	T7DS·7DL-7Ae#1L + T1BL·1R#1S	5–10
L 505//L503 (*Lr26+Lr19*)	T7DS·7DL-7Ae#1L + T1BL·1R#1S	5
Dobrynya	T7DS·7DL-7Ae#1L	30
Dobrynya (*Lr19+Lr9*)	T7DS·7DL-7Ae#1L + T6BS·6BL-6U#1L	3
Dobrynya (*Lr19+Lr24*)	T7DS·7DL-7Ae#1L +T3DS·3DL-3Ae#1L	30
Dobrynya (*Lr19+Lr25*)	T7DS·7DL-7Ae#1L + 4BS·4BL-2R#1L	10

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The microclonal propagation of sterile triticale plants.

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Applying biotechnology to crop improvement induces nonconventional plant breeding methodology. In biotechnology and plant breeding, preserving and propagating sterile plants, undoubled haploids, and remote hybrids for future use is important. The most frequent explant sources for morphogenetic callus induction in cereals are mature and immature embryos. To establish tissue culture systems in sterile plants, it is necessary to select the explant source.

Wheat–triticale hybrids (three genotypes) and haploids (nine genotypes) were grown in a phythotron. Somatic embryogenesis was used to produce the largest number of plantlets. Segments of immature inflorescence 2–3 cm and completely covered by leaves served as explants to establish callus cultures. A solid MS nutrient medium, supplemented with 2 mg/L 2,4-D and 2% sucrose was optimum for callus induction. Callus cultures were grown in the dark, with subculturing on fresh culture medium every 3–4 weeks. The subsequent elimination of 2,4-D from the culture medium and the addition of IAA (1 mg/L) allowed for embryogenesis. Centers of morphogenesis were milky white, compact, and modulary. The start of regeneration was observed within 7–10 days. The frequency of callus induction ranged from 76.5 to 84.0% and the frequency of morphogenetic callus was from 39.1 to 46.6%.

The microclonal propagation of sterile triticale sterile was elaborated using segments of immature inflorescence as source of totipotent cultures. Embryogenic callus and plant regeneration were formed. This technology allows one to obtain clones of each genotype in an unlimited amount for use in breeding work.

Identification of leaf rust resistance genes of lines of soft spring and winter wheats.

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Leaf rust resistance genes were identified in 14 introgressed lines of soft wheat carrying noncompensating translocations from *Aegilops speltoides*, *Triticum turgidum* subsps. *dicoccum* and *persicum*, and wheat cultivars from the collection of the All-Russian Institute of Plant Breeding using phytopathological and molecular methods.

After molecular screening of wheat cultivars, we discovered three with gene *Lr9* and one with *Lr19* (Table 6, p. 197). The identification of *Lr9* used SCAR marker SCS5 (Gupta et al. 2005). A characteristic 550-bp fragment was found among breeding lines 6 and 7, Clez Alta, and a control line Tc *Lr9*. The results from the molecular screening of these species correspond with the phytopathological test. Gene *Lr9* in line 11 is unidentified despite the fact that it was used when the line was created. In addition to leaf rust resistance, this line also has mildew resistance from *T. turgidum* subsp. *persicum*.

Table 6. Leaf rust (*Lr*) genes identified using DNA markers.

#	Description	*Lr9*	*Lr10*	*Lr19*	*Lr20*	*Lr26 iag95*	*Lr26 SCM9*	*Lr34*	*Lr35*	*Lr37*
1	Saratovskaya 29/*T. persicum*//*T. dicoccum*				+				+	
2	Saratovskaya 55//*T. dicoccum*/*Ae. speltoides*								+	
3	Saratovskaya 55// *T. dicoccum*/ *Ae. speltoides*		+						+	
4	Saratovskaya 29//*T. persicum*/3/ *T. dicoccum*/*Ae. speltoides*								+	
5	Saratovskaya 29// *T. dicoccum*/*Ae. speltoides*								+	
6	Saratovskaya 29/*T. persicum*//*Lr9*	+								
7	Saratovskaya 29/*T. persicum*/*Lr9*	+								
8	Saratovskaya 29/*T. persicum*//*T. dicoccum*/*Ae. speltoides*								+	
9	Saratovskaya 55//*T. dicoccum*/*Ae. speltoides*								+	
10	Saratovskaya 55//*T. dicoccum*/*Ae. speltoides*								+	
11	Saratovskaya 29/*T. persicum*//*Lr9*								+	
12	Saratovskaya 29/*T. persicum*// *T. dicoccum*/*Ae. speltoides*								+	
13	Saratovskaya 55//*T. dicoccum*/*Ae. speltoides*								+	
14	Saratovskaya 29/*T. persicum*// *T. dicoccum*/*Ae. speltoides*								+	
15	Clez Alta	+								
16	K-34612			+						
17	W464//VEE/KOEL/3/PEG//MRL/BUC		+			+	+	+		
18	CROC-1/*Ae. tauschii* (205)//KAUZ/3/ATTILA					+	+			

A characteristic 130-bp fragment was found in sample 16 with the help of STS marker Gb *Lr19* (Prins et al. 2001). A 487-bp fragment was discovered in lines 1–5 and 8–14 with the help of marker Sr39#22 for gene *Lr35*. Gene *Lr35* is located on the short arm of chromosome 2B and is situated in the same translocation with seedling gene *Sr39*, which defends against *Puccinia graminis* race Ug99 (TTKS) (Singh et al. 2008). Diploid *Ae. speltoides* is the source of this translocation.

When marker PS10 for gene *Lr47* from *Ae. speltoides* was being applied its carriers were not discovered. Although gene *Lr35* has the potential for leaf rust resistance, examples of its application have not been given in the literature to date (McIntosh et al. 1995; Mago et al. 2009; Serfling et al. 2011). A good example of introgressing *Lr*/*Sr* genes from *Ae. speltoides* in Russia is the set of amphidiploid lines ((*T. dicoccum* x *Ae. speltoides*)*5//Saratovskaya 29) created at the ARJPB (Odintsova et al. 1991). These lines were widely used in many selection centres in the USSR, including SRJA of South-East. Thus, the existence of the given translocation in lines 1–5 and 8–14 is logical. Their resistance to

race *P. graminis* Ug99+*Lr24* (TTKST) (Sibikeev et al. 2011) is important to characteristics of these lines. Leaf and stem rust resistance, possibly caused by Lr and Sr cohesion, supports the existence of *Lr35*/*Sr39* genes in lines 1–5 and 8–14.

Although *Lr10* was identified with the primers F 12245 and *Lr10*-6/r2 (Schachermayr et al. 1997), an amplicon with a molecular weight of 310 bp was discovered in lines 3 and 17.

Using the primers STS638-L and STS638-R for gene *Lr20* (Neu et al. 2002), a marker of 540 bp was found in line 1 and in the control Thatcher with *Lr20;* line 1 includes wild *T. persicum* and *T. dicoccum* in the pedigree. Today, *Lr20* has lost its efficiency practically everywhere (McIntosh et al. 1995; Khan et al. 2005).

To identify gene *Lr26*, two markers, SCM9 (Mago et al. 2002) and iag95 (Weng et al. 2007), were used. A characteristic 207-bp component of SCM9 and an ~1,000-bp iag95 marker were identified in lines 17 and 18, which corresponds to their gender lines.

By applying phytopathological and molecular methods and also analyzing pedigrees, we discovered *Lr* genes and their combinations in 14 introgressive lines and in four soft spring wheats. These results are very important for programs that use the application of certain *Lr* genes and their combinations in practical selection.

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