Leaf Rust Resistance in Common Wheat Varieties and Lines from the Collection of the Vavilov Plant Industry Institute Carrying Alien Genetic Material

A. S. Sadovaya^{*a*}, E. I. Gultyaeva^{*a*}, O. P. Mitrofanova^{*b*}, E. L. Shaidayuk^{*a*}, A. G. Hakimova^{*b*}, and E. V. Zuev^{*b*}

> ^aAll-Russia Institute of Plant Protection, St. Petersburg, Russia e-mail: gullena@rambler.ru
> ^bVavilov Institute of Plant Industry, St. Petersburg, Russia Received September 26, 2014; in final form, October 3, 2014

Abstract—Leaf rust resistance was estimated in 83 common wheat accessions carrying alien genetic material from the collection of the Vavilov Institute. Eight accessions with seedling resistance and 27 accessions with adult plant resistance were found. Analysis with molecular markers revealed genes highly and moderately efficient in Russia—Lr24, Lr39, Lr21, and Lr37—and a rye translocation 1AL.1RS. The accessions containing effective Lr genes are promising donors in Russian breeding programs. The lines raised with the use of T. timopheevii were heterogeneous for resistance. No molecular markers of the Lr50 gene known for this species were detected there. These lines demand further examination and selection.

Keywords: common wheat, leaf rust, resistance, molecular markers, *Lr* genes, alien genetic material **DOI:** 10.1134/S2079059715030144

INTRODUCTION

Leaf rust (the caused agent is Puccinia triticina Eriks.) is a common disease of wheat in all regions of Russia, which can lead to a significant loss of crops yield during epiphytoties. An environmentally safe method of protection against this disease is the cultivation of resistant varieties. The results of screening for the resistance to leaf rust of soft wheat varieties recommended for growing in Russia indicate demonstrable progress in breeding over the past ten years (Novozhylov et al., 1998; Gultyaeva et al., 2014a). There was a significant increase in the State Register of Selection Achievements of the Russian Federation of winter varieties with field resistance and spring ones with seedling resistance, while using molecular markers it was shown that many of them are protected by genes Lr19 and Lr9 (Gultyaeva et al., 2009b, 2014). The widespread cultivation of such varieties in Western Siberia, the Urals, and the Volga region led to the loss of their stability (Meshkova et al., 2008). In this respect, it is relevant to increase the diversity for Lrgenes in the domestic varieties of wheat and determine the strategy for their allocation in the regions.

To date, 67 Lr-genes were identified in wheat worldwide, more than 50% of which are alien (McIntosh et al., 2012). To identify most of them, molecular markers were developed that allow controlling the transfer of Lr-genes and significantly speeding up the creation of resistant varieties.

The wheat collection of the Vavilov Plant Industry Institute contains a large number of accessions obtained with the participation of different species of wheat, goatgrass, rye, and bluegrass, and were included in the collection over the years. These accessions may be of interest for breeding as sources of known effective alien Lr genes not previously used in Russia and those identified for the first time.

The purpose of this work is to characterize the varieties and lines of wheat from the collection of the Vavilov Plant Industry Institute, which carry foreign genetic material, for resistance to the leaf rust pathogen and identification of the Lr genes in them.

MATERIALS AND METHODS

The research material included 83 varieties and lines of wheat from the collection of the Vavilov Plant Industry Institute (41 winter and 42 spring types), obtained with the participation of *T. timopheevii* (Zhuk.) Zhuk. (2n = 4x = 28, GGAA), Aegilops tauschii Coss. (2n = 2x =14, *DD*), *Ae. speltoides* Tausch (2n = 2x = 14, SS), *Ae. ventricosa* Tausch ($2n = 4x = 28, D^vD^vN^vN^v$)), *Triticum timopheevii* ssp. *armeniacum* (= *Triticum araraticum* Jakubz.) (2n = 4x = 28, GGAA), *Thinopyrum ponticum* (= *Agropyron elongatum*), and the synthetic species *T. migushovae* Zhir. ($2n = 6x = 42, A^bA^bGGDD$). The synthetic species was created by E.G. Zhirov at the Krasnodar Agricultural Research Institute by

Test-						Тур	e of rea	ction i	n Tc <i>Lr</i> -	lines, j	points					
clone	1	2a	2b	2c	3a	3bg	3ka	9	14b	15	19	20	23	24	26	28
kLr9	3	3	3	3	3	3	3	3	3	3	0	3	Х	0-1	0	0
kLr19	3	3	3	3	3	3	3	0	3	3	3	3	3	1	0	0
k43	3	3	3	3	3	3	3	0	3	3	0	3	3	1-2	3	0
k18	0	0	3	3	3	3	3	0	3	3	0	0	3	0-1	3	0
kP19	3	0	0	3	3	3	3	0	3	3	0	0	1-2	0-1	3	0
k70	0	0	0	0	3	3	3	0	3	0	0	3	2-3	0-1	3	0
k60	3	3	3	3	0	0	0-1	0	3	3	0	3	3	0-1	0	0

Table 1. Type of response of test-clones of *P. triticina* when inoculating isogenic TcLr lines

crossing the natural hulless mutant *T. militinae* Zhuk. et Migusch., selected from the population of species *T. timopheevii*, with *Ae. tauschii* (Dorofeev et al., 1987).

The studied accessions were evaluated for resistance to leaf rust in the phase of seedlings and adult plants. Resistance in the seedling stage (the first leaf phase) were studied by the laboratory inoculation of leaf segments (Mikhailova et al., 2003) and infecting the intact plants. The type of response was taken into account on the eighth day after inoculation according to the scale of Mines and Jackson with the following score; 0, absence of symptoms or necrosis without pustules; 1, very small pustules surrounded by necrosis (R); 2, medium-sized pustules surrounded by necrosis or chlorosis (MR); 3, medium-sized pustules without necrosis (MS); 4, large pustules on one and the same leaf, chloroses, and necroses are present (M).

The resistance of adult plants was studied in 2013–2014 in the experimental field of the Vavilov Plant Industry Institute (St. Petersburg, Pushkin) under an artificial inoculation by spraying the experimental plots with a suspension of isolates from the north western population of the fungus *P. triticina*. The diseases severity of leaf rust was evaluated by the scale of Peterson et al. (Peterson et al., 1948), and the type of reaction by the scale of Mains and Jackson. During the growing season, several records were carried out: the first one after the first symptoms of the disease and the following ones every seven days. The main indicator of resistance consisted in the data of the last record, when there was the strongest manifestation of the disease (*Metody...*, 1988).

Identification of Lr genes was carried out using the phytopathological test and molecular markers. For the phytopathologic studies, seven isolates of leaf rust were selected. The characteristics of the fungal testclones for virulence to 16 isogenic TcLr lines are presented in Table 1. Isolate kLr9 was selected from the Omsk population in 2010, kLr19 from the Nizhny Novgorod population in 2012, k43 from the Omsk population in 2012, k18 from the Saratov population in 2011, kP19 from the Nizhny Novgorod population in 2011, k70 from the Tambov population in 2012, and k60 from the Kaliningrad population in 2012.

Using PCR markers, we identified 12 high and partially effective alien genes Lr9, Lr19, Lr21, Lr24, Lr28, Lr29, Lr35, Lr37, Lr39/41, Lr47, Lr50, and Lr66, as well as wheat-rye translocation 1BL.1RS (with genes Lr26/Sr31/Yr9/Pm8) and 1AL.1RS (Table 2). DNA extraction was carried out from the leaves of 7–10-day-old seedlings as described by Dorokhov and Cloquet (1997). DNA amplification was carried out according to the protocols shown in the literature (Table 2), modified when necessary. The amplified fragments were separated by electrophoresis in 1.5% agarose gel in a 1× TBE buffer, and the gels were stained with ethidium bromide and photographed under ultraviolet light.

RESULTS

The study of seedling resistance revealed eight accessions: Cutless (k-62517), KS90WGRC10 (k-62377), KS93U149 (k-62382), KS93U62 (k-63933), KS93U50 (k-63937), KS92WGRC22 (k-65156), KS96WGRC38 (k-65157), and KS96WGRC40 (k-65158), all from the United States, and immune to leaf rust throughout the growing season (Table 3). All the other studied accessions were characterized by varying degrees of susceptibility in the seedling stage and adult plant one.

By the results of the evaluation in the field conditions of the North West, variety Hadden (k-54855, United States), line IT-5 (k-50851, Russia), hybrid Cheyenne \times *T. timopheevii* (k-45678, Canada), and variety Brigadier (k-63322, France) were assigned to the highly resistant group (no disease symptoms). The group of resistant varieties comprised (lesion up to 5%) Vostorg (k-64584, Russia), which was marked with a moderately susceptible response type X (MS), as well as accessions with the susceptible type (a score of 3–4 (S)): Wisc. 245 (k-43577), ND600 (k-60781), and IL-1/ Chinese*2/*T. timopheevii* (k-45165), Allard 52-1-1-17-1 (k-49928), and KS86WGRC02 (k-62373), all from the United States; and AC Minto (k-62878, Canada), Alert (k-63901), and Beaufort (k-63920) from the

Gene, translocat- translocat- billedPrimersNucleotide sequence (5-3) L^9 Aegilops umbellulutaSCS5FTGCGCCCTTCAAAGGAAG L^9 Aegilops umbellulutaSCS5FTGCGCCCTTCAAAGGAAG L^9 Aegilops umbellulutaSCS35FGGCGGATAAGCAGAGGAGGAGG L^19 Aegilops umbellulutaSCS35FGGCGGATAAGCAGAGTGTG L^21 Aegilops umbellulutaSCS35FGGCGGATAAGCAGAGTGTG L^21 Aegilops tauschiiL.21FCGCGGATAAGCAGGAGGTGTG L^24 Aegilops tauschiiL.21FCGCGGATAAGCAGGAGGTGG L^24 Aegilops speltoidesSCS35FGATAGCAGGAGAGTGGACAGGAGG L^29 Aegilops speltoidesSCS31FACAGGAAATGAGCAGCAGG L^29 Aegilops speltoidesSCS31FACAGGAAATGAGCACACAG L^29 Aegilops speltoidesSCS31FACAGGAAAGCATCACCACAG L^29 Aegilops speltoidesSCS31FACAGGAAAGCATCACACAG L^29 Aegilops speltoidesSCS31FACAGGAAAACGACACACAG L^29 Aegilops speltoidesSCS31FACAGGAAAACGACACACAG L^29 Aegilops speltoidesBCD260F1GAAGTTAAAAGAACTCACACACAG L^39 Aegilops ventricosaL.29F24FGTGACTCAGGCAAACAGCACACACACACACACACACACAC						
Aegilops umbellulataSCS5F SCS5RAgropyron elongatumSCS265FAgropyron elongatumSCS265FAgropyron elongatumSCS265FAgropyron elongatumLr21FAgropyron elongatumSCS73FAgropyron elongatumSCS73FAgropyron elongatumSCS73FAgropyron elongatumSCS73FAgropyron elongatumLr29F24 FAgropyron elongatumLr29F24 FAgrops speltoidesSr39R3Agrops speltoidesSr33R3Agrops speltoidesPS10RAgrilops speltoidesPS10RAgrilops speltoidesSS10LAgrilops speltoidesSS10LAgrilops speltoidesSS10LAgrilops speltoidesS10RAgrilops speltoidesS13RAgrilops speltoidesS13RAgrilops speltoidesS13RAgrilops speltoidesS13RAgrilops sp	Gene, transloca- tion	Source species	Primers	Nucleotide sequence (5'-3')	Amplicon size, bp	Literary source
Agropyron elongatumSCS265FAgropyron elongatumSCS265RAegilops tauschii $Lr21F$ Lr21F $Lr21F$ Agropyron elongatumSr24#12FSr24#12FSr24#12FAgropyron elongatumSCS73FAgropyron elongatumSCS73FAgropyron elongatumSCS421FAgropyron elongatum $Lr29F24 F$ Agropyron elongatum $Lr29F24 F$ Agrilops speltoides $SF332 F$ Agrilops speltoides $S10R$ Agrilops speltoides $S13R$ Agrilops speltoides $SCM9F$ Agrilops speltoides $SCM9F$ Agrilops speltoides $SCM9F$ Agrilops speltoides $S13R$	Lr-9	Aegilops umbellulata	SCS5F SCS5R	TGCGCCCTTCAAAGGAAG TGCGCCCTTCTGAACTGTAT	550	Gupta et al., 2005
Aegilops tauschii Lr21F Aegilops tauschii Lr21F Agropyron elongatum Sr24#12F Agropyron elongatum SCS73F SCS73F SCS73F Agropyron elongatum SCS73F Agropyron elongatum SCS73F Agropyron elongatum SCS73F Aegilops speltoides SCS421F Agropyron elongatum Lr29F24 F Lr29F24 F Lr29F24 F Agropyron elongatum Lr29F24 F Agropyron elon	Lrl9	Agropyron elongatum	SCS265F SCS265R	GGCGGATAAGCAGAGCAGAG GGCGGATAAGTGGGTTATGG	512	Gupta et al., 2006
Agropyron elongatumSr24#12F Sr24#12LAgropyron elongatumSCS73F SCS73RAgropyron elongatumSCS73F SCS421LAgropyron elongatumLr29F24 F Lr29F24 LAgilops speltoidesSr39F2 Sr39R3Aegilops speltoidesBCD260F1 35R2And Agilops speltoidesSr39F2 Sr39R3Aegilops speltoidesSr39F2 Sr39R3Argilops speltoidesBCD260F1 35R2And Agilops speltoidesSr39F2 Sr39R3Argilops speltoidesSr39F2 Sr39R3And Agilops speltoidesNeutriup CDM35-R BCD260F1Argilops speltoidesNeutriup SIRSArgilops speltoidesS10R SIRSArgilops speltoidesS13R S13RArgilops speltoidesS13R S13RIRS/Secale cerealeScongFSCM9F	Lr21	Aegilops tauschii	Lr21F Lr21R	CGCTTTTACCGAGATTGGTC TCTGGTATCTCACGAAGCCTT	699	http://maswheat.ucdavis.edu/protocols/ Lr21/index.htm
Agropyron euorgaumSCS73FAegilops speltoidesSCS421FScS73RSCS421LAegilops speltoidesSCS421LAgropyron elongatumLr29F24 LAgropyron elongatumLr29F24 LAgrilops speltoidesSr39R3Aegilops speltoidesSr39R3Aegilops speltoidesSr39R3Aegilops speltoidesNentriupAegilops speltoidesNentriupArgilops speltoidesNentriupArgilops speltoidesSr39R3Argilops speltoidesNentriupArgilops speltoidesPS10RArgilops speltoidesPS10RArgilops speltoidesPS10LArgilops speltoidesPS10RArgilops speltoidesPS10LArgilops speltoidesPS10LArgilops speltoidesPS10LIRS/Secale cerealeIRS/Secale cerealeSCM9FSCM9F	<i>PC</i> 1		Sr24#12F Sr24#12L	CACCCGTGACATGCTCGTA AACAGGAAATGAGCAACGATGT	500	Mago et al., 2005
Aegilops speltoidesSCS421FAegilops speltoidesSCS421LAgropyron elongatumLr29F24 LAgropyron elongatumLr29F24 LSr39F2Sr39F3Aegilops speltoidesBCD260F1Aegilops speltoidesBCD260F1Aegilops ventricosaNentriupAnd the state speltoidesBCD260F1Aegilops speltoidesBCD260F1Aegilops speltoidesBCD260F1Aegilops speltoidesCDM35-LAegilops speltoidesCDM35-LAegilops speltoidesPS10LAegilops speltoidesPS10LAegilops speltoidesBCD382-FAegilops speltoidesS13RAegilops speltoidesS13RIRS/Secale cerealeSecale cerealeSCM9F	17.74	Agropyron etongutum	SCS73F SCS73R	TCGTCCAGATCAGAATGTG CTCGT GATTAGCAGTGAG	719	Cherukuri et al., 2003; Prabhu et al., 2004
Agropyron elongatumLr29F24 FAgropyron elongatumLr29F24 LAgilops speltoidesSr39F2Aegilops speltoidesSr39F3Aegilops speltoidesSr206F1Agilops ventricosaUentriupArgilops ventricosaLN2Aegilops speltoidesSFR2Aegilops ventricosaLN2Aegilops speltoidesCDM35-LAegilops speltoidesSF10LAegilops speltoidesPS10RSsp. armeniacumWMS382-FAegilops speltoidesS13RAegilops speltoidesS13RSsp. armeniacumWMS382-FMS382-FWMS382-FMS382-FS13RIRS/Secale cerealeScM9FSCM9F	Lr28	Aegilops speltoides	SCS421F SCS421L	ACAAGGTAAGTCTCCACCCA AGTCGACCGAGATTTTAACC	570	Cherukuri et al., 2005
Aegilops speltoidesSr39F2 Sr39R3Aegilops speltoidesBCD260F1 35R2Aegilops ventricosaWentriup LN2 $Aegilops ventricosa$ LN2 GDM35-L GDM35-R 41)Aegilops tauschiiGDM35-L GDM35-R PS10R $Aegilops speltoides$ PS10R PS10R $Aegilops speltoides$ PS10R S10R $Aegilops speltoides$ PS10R S10R $Aegilops speltoides$ PS10R S10R $Aegilops speltoides$ PS10R S13R-L $Aegilops speltoides$ S13R S13R $Aegilops speltoides$ SCM9FIRS/Secale cerealeSCM9RSCM9R	Lr29	Agropyron elongatum	Lr29F24 F Lr29F24 L	GTGACCTCAGGCAATGCACACAGT GTGACCTCAGAACCGATGTCCATC	006	Procunier et al., 1995
Aegilops spenotues BCD260F1 Aegilops ventricosa Wentriup Aegilops ventricosa Ventriup Argilops ventricosa Ventriup Argilops ventricosa Ventriup Argilops speltoides PS10R Aegilops speltoides PS10L Argilops speltoides PS10L Argilops speltoides PS10L Argilops speltoides PS10L Argilops speltoides PS10L Inspire SSP. armeniacum WMS382-F WMS382-F Argilops speltoides I6-S13F 16- IRS/ Secale cereale SCM9F	1	Lacitors endived	Sr39F2 Sr39R3	AGAGAGAGTAGAAGAGCT AGAGAGAGAGCATCCACC	006	Gold et al., 1999
Aegilops ventricosa Ventriup LN2 41) Aegilops tauschii GDM35-L 61) Aegilops tauschii GDM35-R 7 Aegilops speltoides PS10R 7 Filtum timopheevii PS10L 8 Ssp. armeniacum WMS382-F 9 Aegilops speltoides B13R1-R 18 Aegilops speltoides S13R 18 Secale cereale SCM9F	0017	samonade edonizar	BCD260F1 35R2	GAAGTTAAAGAGGTCTTGAC TTTTGAGAATCAGTCATCAC	931	Seyfarth et al., 1999
41) Aegilops tauschii GDM35-L Aegilops speltoides PS10R Triticum timopheevii GDM87-L Ssp. armeniacum WMS382-F Aegilops speltoides I6-S13F 16- IRS/ Secale cereale SCM9F	Lr37	Aegilops ventricosa	Ventriup LN2	AGGGGCTACTGACCAAGGCT T GCAGCTACAGCAGTATGTACACAAAA	259	Helguera et al., 2003
Aegilops speltoides PS10R Aegilops speltoides PS10L Triticum timopheevii GDM87-L Ssp. armeniacum WMS382-F WMS382-F WMS382-F Aegilops speltoides 16-S13F 16- IRS/ Secale cereale SCM9F	Lr39 (=Lr41)	Aegilops tauschii	GDM35-L GDM35-R	CCTGCTCTGCCCTAGATACG ATGTGAATGTGATGCATGCA	190	http://maswheat.ucdavis.edu/protocols/ Lr39/index.htm
Initicum timopheevii GDM87-L Triticum timopheevii GDM87-R ssp. armeniacum WMS382-F WMS382-F WMS382-R Aegilops speltoides 16-S13F 16- 1RS/ Secale cereale SCM9F 1RS/ Secale cereale SCM9R	Lr47	Aegilops speltoides	PS10R PS10L	GCTGATGACCCTGACCGGT TCTTCATGCCCGGTCGGGT	282	Helguera et al., 2000
ssp. armeniacum WMS382-F Aegilops speltoides 16-S13F 16- 1RS/ Secale cereale SCM9F	1 "SU	Triticum timopheevii	GDM87-L GDM87-R	AATAATGTGGCAGACAGTCTTGG CCAAGCCCCAATCTCTCTCT	139	http://maswheat.ucdavis.edu/protocols/
Aegilops speltoides 16-S13F 16- S13R IRS/ Secale cereale SCM9F	0017	ssp. armeniacum	WMS382-F WMS382-R	GTCAGATAACGCCGTCCAAT CTACGTGCACCATTTTG	110	Lr50/index.htm
/ Secale cereale SCM9F SCM9R	Lr66	Aegilops speltoides	16-S13F 16- S13R	GGTGAACGCTAAACCCAGGTAACC CAACCTGGGAAGATGCTGAG	695	Marais et al., 2009
	1BL.1RS/ 1AL.1RS	Secale cereale	SCM9F SCM9R	TGACAACCC CCTTTCCCTCGT TCATCGACGCTAAGGAGGACCC	207/228	Wèng et al., 2007

Table 2. PCR markers used to identify alien Lr genes

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VIR catalog	Accession name	Origin	Alien species in pedigree	Type	Type of reaction of seedlings when inoculated with test-clones	ion of { with	in of seedlings wl with test-clones	gs when	l inocu	lated	Disease in the field of r	Disease development in the field (%) and type of reaction	Identified <i>Lr</i> genes and transloca-	Information on the availability of <i>Lr</i> genes
по.)	kLr9	kLr19	k43	k18	kP19	k70	k60	2013	2014	tions	by GRIS***
						<u>S</u>	Spring wheat	leat						
62517	Cutless	United States	Ae. tauschii	Я	R	R	R	R	R	R	0	0	Lr21	Lr21
60781	ND600	:	:	S	R	R	S	R	S	R	1S	1S		Lr21
54855	Hadden	:	T. timopheevii	S	S	S	S	S	S	S	0	0		Lr13
50851	Line IT-5	Russia	:	MS	MS	S	S	MR	MS	R	0	0		
50847	Line IT-1	:	:	S	S	S	S	S	S	S	$0, 5S^{**}$	$0, 5S^{**}$		LrTt1LrTt2
50852	Line IT-6	:	:	MR	S	S	R	R	R	R	$0, 5S^{**}$	0		
50857	Line IT-13a	:	:	S	S	S	S	S	S	S	$0, 1S^{**}$	$0, 1S^{**}$		
50858	Line IT-15	:	:	S	R	MS	S	S	S	MS	0	$0, 1S^{**}$		
50849	Line IT-3	:	2	S	s	S	S	S	S	S	1MR	1–5MR, 10–15MR**		LrTt1LrTt2
50853	Line IT-7	:	2	MR	MR	S	Я	Я	×	S	0, 5S**	0, 5S, 20–30S**		
50850	Line IT-4	:	2	S	S	S	S	S	S	S	$0, 70S^{**}$	0.50-70S**		
50854	Line IT-8	:	:	S	MS	S	S	S	S	S	10S	0.30–50S**		
61518	Line 36	Estonia	2	R	К	S	Я	Я	S	Я	0, 5S, 30–40S**	$0, 10S, 30-40S^{**}$		
62878	AC Minto	Canada	Ae. tauschii	R	MR	R	MR	R	R	MR	1S	5S		Lr11 Lr13 Lr22a
65264	I	Mexico	:	S	S	S	R	R	S	S	5S	SS		
43577	Wise. 245	United States	T. timopheevii	S		S	S	S	S	S	0, 1S	5S		Lr12
45165	IL-1/Chinese*2/ T. timopheevii	Canada	•	S	К	S	R	S	S	S	5S	5MS		
49928	Allard 52-1-1-17- 1	United States	•	S	S	S	S	S	S	S	5S	5S		Lr12
43091	Blue A	Canada	Ag. elongatum	S	S	S	R	S	S	S	10MS	30M		

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VIR catalog no. Accession name 62377 KS90WGRC10 62382 KS93U149 63933 KS93U62 63933 KS93U62 63937 KS93U62 63937 KS93U62 63937 KS96WGRC40 65157 KS96WGRC38 65158 Brigadier 65157 Brigadier 65158 Brigadier 65157 Brigadier 65158 Brigadier 65157 Brigadier	Origin United States "	Alien species in pedigree <i>Ae. tauschii</i> <i>Ae. tauschii</i> <i>Ag. elongatum</i> <i>Ae. tauschii</i> <i>Ae. tauschii</i> <i>Ae. tauschii</i> <i>Ae. tauschii</i> <i>armeniacum</i>	KL ¹⁹	Type when i R R R R R R R R R R R R R R R R R R R	Type of reaction of seedlings when inoculated with test-clones Lr19 k43 k18 kP19 k70 Winter wheat R	of reaction of oculated with (43 k18 1 Winter wheat R R R R R R	f seedlii h test-c k P19 R R R R R R R	R R R R R R R R R R R R R R R R R R R	R R R R	Disease development in the field $(\%)$ and type of reaction 2013 2014 - 0 0 0 0 0 0 0 0 0 0 0	velopment eld (%) f reaction 2014 0	Identified <i>Lr</i> genes and trans- locations	Information on the availability of <i>Lr</i> genes by GRIS***
62.377 KS90WGRC10 62.382 KS93U149 62.382 KS93U62 63.937 KS93U62 63.156 KS92WGRC 20 65.156 KS92WGRC 20 65.157 KS96WGRC 40 65.157 KS96WGRC 38 63.322 Brigadier 63.322 Brigadier 63.322 Brigadier 63.322 Brigadier 63.323 Brigadier 64.308 @Флилт 64.584 @Востолг		m vii ss		kLr19 R R R R R R R	k43 Winte R R R R R R	k18 srwhea R R R R R R R	kP19 t R R R R R	k70 R R R R	k60 R R R R R	2013 - 0 0 0	2014 0	locations	GRIS***
62377 KS90WGRC10 62382 KS93U149 63933 KS93U62 63937 KS93U62 63156 KS92WGRC22 65156 KS92WGRC22 65157 KS96WGRC38 65157 KS96WGRC38 65157 KS96WGRC38 65157 KS96WGRC38 65157 KS96WGRC38 65157 Chevenne× 63322 Brigadier 63328 G. Chevenne× 7. <i>timopheevii</i>) 64308 @Флинт		um vii ss	~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	~ ~ ~ ~ ~ ~ ~ ~ ~	Winte R R R R	R R R R R R R R R R R R R R R R R R R	¹ ~ ~ ~ ~ ~ ~ ~ ~	~ ~ ~ ~ ~ ~ ~ ~	~ ~ ~ ~ ~ ~ ~	0 0 0 0	0		
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		vii ss	X X X X	~ ~ ~ ~ ~	R R	<u>к</u> к к	х х	2 2 2	R R	0 0	0	Lr24, Lr39	Lr24 Lr39
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	" France	vii ss	К	a	R		¥	4	К	0	I	1AL.1RS	Lr39
	France	•		4	MR	R	R	К	MR	I	0	1AL.1RS	Lr41 Lr50 1AL. IRS
		Ae. ventricosa	К	Я	Я	S	S	S	К	0	I	1BL.1RS (<i>Lr26</i>) <i>Lr37</i>	Lr13 Lr26 Lr37
	Canada	T. timopheevii	S	S	S	S	S	S	S	0	I		
	Russia	T. migushovae	S	S	S	S	S	S	S	15	0		
	:	2	R	R	R	S	S	S	R	1S	5MR	IBL.IRS (<i>Lr26</i>)	
63901 Alert	United Kingdom	Ae. ventricosa	R	S	R	R	S	R	I	0	5S	Lr37	
63920 Beaufort	2	2	×	Я	К	S	S	R	Я	0	5S	IBL.IRS (<i>Lr26</i>) <i>Lr37</i>	Lr1 Lr26 Lr37
62373 KS86WGRC02	United States	Ae. tauschii	S	S	S	S	R	S	R	5S	I	Lr21	Lr21 Lr 41
63300 Arche	France	Ae. ventricosa	К	R	S	S	S	S	S	1S	10S	Lr37	Lr13 Lr37
63031 Steele	United States	Ae. tauschii	S	S	S	R	К	×	S	10S	15S		Lr2a, Lr10 Lr21
62811 Centurion	France	Ae. ventricosa	S	S	S	S	S	S	S	5S	20S	Lr37	

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Table 3. (Contd.)

LEAF RUST RESISTANCE IN COMMON WHEAT VARIETIES AND LINES

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United Kingdom. Accessions Archer (k-63300, France) and Steele (k-63031, United States) were characterized by moderate resistance (disease development 15%, response type S). Moderate susceptibility (disease development of 20-30%) was detected in the winter variety Centurion (k-62811, France) and the wheat-bluegrass substituted wheat line Blue A (k-43091, Canada), where it had a lower response type (M).

The high heterogeneity for resistance to leaf rust was observed in eight introgressive lines, created at the Vavilov Plant Industry Institute by N.A. Skurygina (1984) with the use of T. timopheevii, and line 36 (k-61518) from Estonia. These lines contained both plants without symptoms of the disease and plants infected to varying degrees (Table 3). In 2013-2014, the maximum development of the disease was not more than 5% in the infected plants of lines IT-1 (k-50847), IT-6 (k-50852), IT-13a (k-50857), and IT-15 (k-50858); up to 10-15% in line IT-3 (k-50849), which, in contrast to other lines, was characterized by moderate resistance of the reaction type (2); the disease development did not exceed 40% in lines 36 and IT-7 (k-50853) and 70% in lines IT-4 (k-50850) and IT-8 (k-50854) (Table 3).

All the other accessions studied under field conditions showed high susceptibility to leaf rust. Disease development of 50-60% characterized accessions KS86WGRC05 (k-62375) and KS86WGRC07 (k-62376) from the United States and PPG 64 (k-40230, Russia); 70-80%, Wb.58633 (k-45164, Canada), Dipka (k-60340, the Republic of South Africa), Amidon (k-62515, United States), and Fleischman 481 (k-43231, Hungary), as well as wheat-bluegrass hybrids created in Russia and Germany: PPG 599 (k-38289), PPG 1 (k-40229), PPG 54/49 (k-40697), PPG 60/49 (k-40859), PPG 59/49 (k-40860), PPG 56/49 (k-40870), PPG 55/49 (k-40871), PPG 29 (k-48704), PPG 5 (k-54691), PPG 113 (k-58539), PPG 115 (k-58540); 90-100%, Timstein (k-38498), Bledsoe (k-44405), Idaed 59C (k-44456), Idaed 59B, (k-45670), Molly (k-63555), KS86WGRC04 (k-62374), KS89WGRC03 (k-62715), KS89WGRC06 (k-63875), and U1865-1-4-1 (k-63938), all from the United States; Wb.60414 (k-45162) and Pewter (k-49440, k-45182) from Canada; N43 (k-47033, Brazil); South Africa 43 (k-45295) and Gouritz (k-64137) from the Republic of South Africa; 690 F4 Sel.D.l. (k-49432, Kenya); Titan (k-58433, Australia); UH 96 (k-60551, Czechoslovakia until 1992); Livanjka (k-60991, Yugoslavia until 1990); and Gartus 598 (k-59398), Saratovskaya 73 (k-64556), Zhirovka (k-63377), L-500 (k-62903), line IT-2 (k-50848), line IT-11a (k-50855), line IL-6 (k-60773), PPG 186 (k-40231), and PPG 347 (k-58541), all from Russia.

With the use of test-clones, it was revealed that the studied accessions of common wheat do not have partially effective alien genes Lr9 and Lr19; at the same time, it was demonstrated that the winter varieties Vostorg, Brigadier, and Beaufort have gene Lr26.

Molecular genetic screening of introgression accessions did not find markers of genes Lr9, Lr19, Lr29, Lr35, Lr47, Lr50, and Lr66. Marker GDM35 of gene Lr39 was revealed in lines KS90WGRC10 and KS93U62; markers Sr24#12 and SCS73 of gene Lr24 were revealed in lines KS93U149, KS93U62, KS93U50, and KS92WGRC22; marker Lr21F/R of gene Lr21 were revealed in accessions KS86WGRC02 and Cutless; and marker Ventriup/LN2 of gene Lr37 was found in varieties Brigadier, Alert, Beauford, Arche, and Centurion. The amplification the product size of 207 bp obtained using marker SCM9 and indicating the presence of 1BL.1RS with gene Lr26 was observed in the Brigadier, Vostorg, and Beaufort varieties, and a size of 228 bp (translocation 1AL.1RS) in lines KS90WGRC10, KS93U149, KS93U62, KS93U50, KS92WGRC22, KS96WGRC40, and KS96WGRC38. Line Blue A was revealed to have an amplification product obtained using marker SCS421 of gene Lr28, which was slightly different in size from the control line.

DISCUSSION

In modern times, the most effective genes in all regions of Russia are Lr24, Lr28, Lr29, Lr39 (= Lr41) and Lr47, but none of them has been identified in recommended for growing varieties (Gultyaeva et al., 2009a, b, 2014a; Zhemchuzhina and Kurkova, 2010). The studied accessions in the collection revealed carriers of genes Lr24 and Lr39 individually and in combination (Table 3).

An accession of *Ae. tauschii* TA2460 was the source of gene *Lr39* for lines KS90WGRC10 and KS93U62, and North American winter varieties TAM200 and Century were the source of bluegrass gene *Lr24* for KS93U149, KS93U62, KS93U50, and KS92WGRC22. In turn, the latter gene was obtained from variety Amigo as part of the chromosomal segment of bluegrass 3Ae#1L. Wheat-rye translocation T1AL.1RS was transferred from variety Amigo into all the lines mentioned above, as well as lines KS96WGRC40 and KS96WGRC38 (Jiang et al., 1994). It should be noted that the marker of gene *Lr39* was not detected in line KS93U149, although the same accession of *Ae. tauschii* TA2460 was one of its parent forms.

Gene Lr39 was found mostly in the North American varieties, and variety Thunderbolt was the first whose genotype was introduced with this gene. This variety was grown in large areas in several states, and in 2002 virulent isolates were first marked (http://maswheat. ucdavis.edu/protocols/Lr39/index.htm). Gene Lr24is widespread in wheat varieties of the North American and Australian breeding; however, due to the nonoptimal areas occupied by varieties with this gene, it has lost some of its effectiveness in these countries (McIntosh et al, 1995). So far, it remains effective in Western Europe and Russia (Mesterházy et al., 2000; Zhemchuzhina and Kurkova, 2010; Tyryshkin et al., 2014; Gultyaeva et al., 2014b). In wheat-bluegrass substituted line Blue A, in which a pair of chromosomes 4D is replaced by 4Ael (Zeven, 1991), a DNA fragment was identified slightly different in size from the marker of gene Lr28 originating from Ae. speltoides. In 2013–2014, in the field conditions, the lesion of this line varied from 10 to 30% with response type X, and line TcLr28 was immune (0%). In the phase of seedlings, most isolates of P. triticina were avirulent on leaves of line TcLr28 but virulent in line Blue A, which confirms the lack of gene Lr28 in it.

The group of genes characterized as partially effective in Russia are Lr9, Lr19, Lr25, Lr27 + Lr31, Lr36, Lr38, Lr42, Lr45, Lr49, and Lr50. The virulence of pathogen strains to lines with genes Lr25, Lr36, Lr38, Lr42, Lr45, Lr49, and Lr50 occurs sporadically, at different times and in different regions, and does not exceed 15%. Virulence to tester lines TcLr19 and TcLr9 is observed in those regions with high concentration of varieties—carriers of genes Lr9 and Lr19 (Meshkova et al., 2008). The phytopathological tests and molecular markers did not reveal accessions with these genes in the studied set. According to the pedigree, the accession of KS96WGRC38 may have gene Lr50 whose donor could have been the accession TA895 of wild Ararat wheat T. araraticum (Brown-Guedira et al., 1999). However, the use of SSR-markers GDM87 and WMS382 did not confirm the presence of this gene in KS96WGRC38. Gene Lr50 is characterized as partially effective in North America and is mainly used in breeding in pyramiding with other Lr-genes (http://maswheat.ucdavis.edu/protocols/ Lr50/index.htm).

All of the above identified Lr genes belong to the seedling group whose effect is manifested in all phases of wheat ontogeny starting with the first leaf. Genes Lr21 and Lr37, identified in some accessions of the studied set, refer to the resistance genes of adult plants; their effect was observed in the later stages of ontogeny, such as after booting. According to the Catalogue of Gene Symbols for Wheat (McIntosh et al., 2012), this group also includes genes Lr12, Lr13, Lr22a, Lr22b, Lr34, Lr35, Lr46, Lr48, and Lr67.

Gene Lr21 belongs to the group of highly efficient genes in the United States and Canada (McIntosh et al., 1995). In Western Europe, the disease severity on line TcLr21 varied from 0 to 100% depending on the year and country (Mesterházy et al., 2000; Hanzalová et al., 2008). In the seedling stage, gene Lr21 was described as inefficient in Russian populations of P. triticina (Gultyaeva et al., 2009a, b; Zhemchuzhina and Kurkova, 2010), but in adult plant stage in the North West in the period from 2002 to 2014, line TcLr21 was moderately resistant (lesion from 5 to 30%), as well as line KS89WGRC07 previously described as a donor of gene Lr40 (in the present period Lr40 =Lr21) (McIntosh et al., 1995). Using a molecular marker, it was seen that both this line and variety Cutless have gene Lr21, but it was not found in Steele and

ND 600. According to the information base Genetic Resources Information System for Wheat and Triticale, ND 600 is a synonymous name of variety Cutless, while in the collection of wheat of the Vavilov Plant Industry Institute these accessions have different numbers. For resistance to leaf rust, their differences were revealed both in the phase of seedlings and adult plants. Variety Cutless refers to the immune group throughout the growing season, and ND 600 turned out to be heterogeneous when inoculated with clones in the phase of seedlings, while in the field conditions its leaves were observed with individual fungal pustules (growth of 1%). This accession was created using an almost isogenic line of the Thatcher RL-6043 variety, the source of gene Lr21 (McIntosh et al., 1995), which was confirmed only for the Cutless variety.

Until recently, gene Lr37 was a highly efficient gene for the resistance of adult plants worldwide (McIntosh et al, 1995). Virulence to it was first described in Australia in 2002. To date, this gene has lost its efficiency in Western Europe, due to massive cultivation of varieties carrying it (Serfling et al., 2011). In Russia, disease severity of line TcLr37 varies in the regions. In the North West, it varies depending on the year from 5 to 30%. Varieties of winter Brigadier, Alert, Beaufort, Arche, and Centurion wheat, containing this gene, were infected from 5 to 20%, which is probably due to the presence of additional Lrgenes in their genotypes (Table 3).

Of some interest for breeding may be a series of IT lines, obtained at the Vavilov Plant Industry Institute in 1970 by crossing common wheat with the *T. timopheevii* species and described as resistant to leaf rust (Skurygina, 1984). The performance of many lines was noted in this analysis (Table 3). According to Skurygina (1984), all these lines have two dominant genes, LrTt1 and LrTt2, and additionally, according to R.A. McIntosh, gene Lr18 (Skurygina, 1989). Field estimation of the lines in the North West region in 2013–2014 showed that most of the lines are heterogeneous for resistance. Of these, it is necessary to select resistant plants and use the molecular and cytological methods to identify resistance genes in them.

Using a universal marker SCM9, which exposes translocations 1BL.1RS from variety Kavkaz and 1AL.1RS from variety Amigo, accessions carrying these translocations were found (Table 3). The massive use of gene Lr26 in the selection at the end of the 1960s and the subsequent breeding of varieties homogeneous for this gene over large areas led to the formation of a powerful selective background for the accumulation of virulent clones. Currently, clones of the fungus, virulent to gene Lr26, are widespread in all regions of Russia. Nevertheless, it should be noted that translocation 1BL.1RS carries (except for resistance genes) genes that increase the grain yield and drought tolerance by increasing the root mass (Kim et al., 2004). In this respect, breeders are seeking efficient combinations of gene Lr26 with other Lr genes. One good example is the use of combination Lr19 + 26 (Sibikeev et al., 2011).

Despite the fact that no known Lr genes were found in translocation 1AL. 1RS, varieties carrying it are characterized by a certain level of resistance (Weng et al., 2007). This is confirmed in the present analysis—the majority of accessions with this translocation were resistant. Among the zoned varieties, translocation 1AL.1RS was found only in variety Bogdanka.

Thus, as a result of the given screening for resistance to leaf rust, we identified accessions—carriers of alien genes which can be used in domestic breeding. However, it is necessary to develop a scientifically reasoned strategy for their allocation in the Russian regions, so as not to reproduce the situation that occurred with genes Lr19 and Lr9.

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