Leaf rust resistance genes identification in the spring bread wheat breeding material of the Agricultural Research Institute for South-East Regions of Russia

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**Summary:** Leaf rust caused by *Puccinia triticina* is a common bread wheat disease in the Volga Region of Russia and breeding for this disease resistance is a priority for the Agricultural Research Institute for South-East Regions wheat program. Knowledge of the effective resistance genes present in the germplasm is relevant when selecting for effective and more durable resistance. *P. triticina* races with virulence to *Lr9*, *Lr19*, *Lr26* and with other different virulence combinations and molecular markers of *Lr* genes were used to determine which seedling resistance genes might be present in the 68 bread wheat lines and cultivars. Studies have shown that the effective protection against leaf rust widespread in the Volga Region spring bread wheat cultivars is controlled by *Lr6Ag* and *Lr6Agi*+*Lr19* genes. In addition, cultivars carry *Lr10*, *Lr19*, *Lr10+Lr26* genes. It was found that in the studied set of lines the leaf rust resistance is determined by the following *Lr*-genes and its combinations: 9, 10, 19, 26, 34, 37, 41, Satu, 6Ag. Moreover, usage frequency of *Lr19* is 89.5%, *Lr10* — 40.4%, *Lr26* — 31.6%, *Lr6Ag* — 21%, *Lr28* — 3.5%, *Lr34* — 3.5%, *Lr9* — 1.8%, *Lr37* — 1.8%, *LrSatu* — 1.8%. The frequency of two *Lr*-genes combinations is 45.7%, three — 21% and four *Lr*-genes — 5.3%. Mainly are used such *Lr*-genes combinations as: *Lr19+Lr26* and *Lr10+Lr19+Lr26* — 22.8%, *Lr19+Lr6Ag* — 7%. The four *Lr*-genes combinations has been included *Lr10+Lr26+Lr28+Lr6Ag* — 1.8%, *Lr1+Lr10+Lr26+Lr6Ag* — 1.8% and *Lr10+Lr19+Lr28+Lr6Ag* — 1.8%. In addition, the effective *Lr19* with non-identified *Lr*-genes from cultivar Saratovskaya 57 (L164) and *A. elongatum* (CI-7-57) combinations has been identified.

**Key words:** bread wheat, leaf rust, *Lr*-genes, molecular markers, resistance

**Introduction**

The best approach to control diseases such as leaf rust is genetic resistance based on effective resistance genes (Spanic et al., 2015). Unfortunately, many cultivars of winter and spring wheat do not contain effective race-specific resistance, and the breeding for non-racial specific resistance has not received sufficient development. Thus, due to its economic importance, resistance to leaf rust is a priority in the Agricultural Research Institute for South-East Regions (ARISER) breeding program. Because, currently, the bread wheat intraspecific genetic variability is unable to provide a sufficient protection degree against pathogens, the most promising in this regard are related wheat species, representatives of the genera *Aegilops*, *Secale*, *Agropyron*. In ARISER Laboratory of Genetic and Cytology during the period 1990—2017, the leaf rust resistant germplasm from such species as *T. durum* Desf., *A. elongatum*, *A. intermedium* Host, *A. speltoides* Tausch, *A. ventricosa* Tausch, *Secale cereale* L., triticale cv. Satu and also synthetics of CIMMYT breeding were used. As a result, set of introgressive lines resistant to leaf and stem rust were obtained. It should be noted that the main direction was the several *Lr*-genes in one genotype integrating to prolong the resistance effectiveness against the pathogen. Breeding and selection for leaf rust resistance in wheat cultivars can be facilitated by extensive genetic analyses using molecular markers that are linked or resistance specific (Kolmer et al., 2013).
Also gene postulations are possible because of gene-for-
gene specificity, where the infection types produced by
pathogen isolates on wheat cultivars under study are
compared to infection types produced by the same
isolates on the so-called differentials, often near isogenic
lines, each carrying known single resistance gene
(Pathan, Park 2007). But this method has a limitation
because if the sample carries two Le genes it is not
always possible to find the corresponding clone test.
For example, in the Volga region Lr19 and Lr26 genes are
inefficient in protecting wheat from leaf rust, despite their
combination efficacy (Lr19+Lr26). Accordingly, the clones
virulent to Lr19 and Lr26 are widely found in the pathogen
population, but there are none virulent to both. In this case
marker-assisted selection (MAS) combined with traditional
breeding techniques has become a valuable tool in
selection of individuals carrying genes, controlling the traits
of interest, such as disease resistance.

The aim of this study was to determine the leaf rust
resistance genes presence in 57 wheat introgression lines
and 11 cultivars developed at the ARISER and to
postulate the known genes presence based on infection
type caused by well-characterized races of these
pathogens and using molecular markers.

Materials and Methods

Sixty-eight spring bread wheat lines and cultivars
(Table 1) developed at ARISER Russia and highly
resistant to P. triticina in the field were tested at the
seedling stage for infection types to postulate seedling
leaf rust resistance genes. Ten seedlings of each line
were grown in the pots with soil and were inoculated
withurediniospores suspension of single P. triticina race
when the first leaf had been fully expanded. Characteristics of using races to 27 isogenic lines are
presented in Table 2. All these 5 isolates had susceptible
infection type (3-4) to the Thatcher line with Lr1, Lr2b,
Lr2c, Lr3a, Lr3bg, Lr10, Lr11, Lr14a, Lr14b, Lr16,
Lr17, Lr18, Lr20, Lr21 and Lr30; and resistant type to the
Thatcher line with Lr24, Lr28, Lr29, Lr41 and Lr47. The main variation among races included virulence to TcLr9,
TcLr19 and TcLr26.

Plants were kept in 100 % humidity chamber
overnight and then maintained in the Versatile
Environmental Test Chamber MLR-352H (SANYO
Electric Co., Ltd., Japan) at 22° C. Infection types (IT)
were classified on 0-4 scale during 10-12 days after
inoculation on seedlings as described by E.B. Mains and
H.S. Jackson (1926), where 0 — no visible uredia; 0; —
hypersensitive flecks; 1 — small uredia with necrosis; 2 —
from small to medium sized uredia with green islands
surrounded by necrosis or chlorosis; 3 — medium sized
uredia with or without chlorosis; 4 — large uredia
without chlorosis; X — heterogeneous, similarly
distributed over the leaves. The plants with 0 to 2
infection types were classified as resistant, 3 to 4 and X
infection types as susceptible.

Leaf rust resistance genes (Lr) in wheat cultivars
and lines were also determined by molecular markers
WR03 (Lr1), SCS5 (Lr9), F1.2245/Lr106/r2 (Lr10),
SCS265 (Lr19), SIS638 (Lr20), Sr24f12, Sr24f50 (Lr24),
scm9 (Lr26), SCS421 (Lr28), Lr29F24 (Lr29),
CSLV34 (Lr34), Sr39=22 (Lr35), Ventripl/LN2 (Lr37),
GDM35 (Lr41), PS10 (Lr47) and S3-R16 (Lr60)
(http://maswheat.ucdavis.edu; Gupta et al., 2005, 2006;
Chenkuri et al., 2005; Qiu et al., 2007; Weng et al.,
2007; Marais et al., 2010). For Lr10, Lr26, Lr34 and
Lr37 genomic DNA was extracted from leaves of three
plants belonging to each wheat line using Dorokhov
and Kloke (1997). The PCR reactions were carried out
as proposed previously (Gultyaeva et al., 2009). The
amplified products were visible under UV light after
electrophoresis on 1.5% agarose gels containing
ethidium bromide.

Results

Resistance of 68 introgressive lines and cultivars to
leaf rust isolates at seedling plant stages is shown in
Table 1. Thirty five wheat samples had resistance
(IT=0) to all races used for multi-pathotype tests.
Accordingly, their resistance can be controlled by highly
effective Lr-genes, or their effective combinations.
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effective Lr-genes, or their effective combinations.
Using molecular markers, the combination of Lr19
and Lr26 genes was determined for lines №1, №13, №32-
33, №36 and №38. In lines №6, №19, №22, №34,
№40-41, №45-46, along with these genes, Lr10 was
determined, and in line №20 – Lr41-gene. The presence
of Lr41-gene in line №20 is probably due to the
presence of A. squarrosa (=A. tauschii Coss.) in pedigree.
In addition, a combination of Lr19+Lr41 genes was
determined in line №35. Effective Lr9 and Lr19 genes
combination is revealed in the line №18.

Genes Lr10 and Lr19 were revealed in the high-
resistant introgressive lines №26, №48, №55-56, and
Lr19 gene in the lines №3, №12, №15, №31 and №42.
Their resistance to all used races predicts the additional
genesis presence beyond Lr19 gene, since other lines
carrying Lr10+Lr19, demonstrated a susceptible
character (Table 1). In line №3, according to its pedigree,
the additional gene may be Lr25. Genes from durum
wheat Lr164 (Saratovskaya 57) in line №15 may be
additional. In lines №42, №48 and №55 gene Lr6Ag
originates from cultivars Belyanka, Favorit and lines
Multi 6R, accordingly. Line №31 has a source of Lr24
gene in its lineage, but this gene has not been identified.
Probably, the resistance of this line can be provided by
an additional unknown or just a new gene. Furthermore,
additional or new resistance genes to leaf
rust can be found in lines №26 and №56, in the first
one originates from A. elongatum (CI-7-57 2n=70), and
in the second one originates from the Australian Sr35
gene source.

Lr1 and Lr19 genes and LrSp gene originates from
A. speltoides were revealed in line №10. The LrSp gene is
Table 1. Characteristic of bread wheat breeding lines and cultivars for resistance to leaf rust

<table>
<thead>
<tr>
<th>№</th>
<th>Pedigree</th>
<th>Lr genes</th>
<th>Infection type to races</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Lr19 Lr26</td>
<td>R1 R2 R3 R4 R5</td>
</tr>
<tr>
<td>1</td>
<td>L2032*6//Comod87</td>
<td></td>
<td>0 0 0 0 0</td>
</tr>
<tr>
<td>2</td>
<td>Dobrunya*5/Tc L9</td>
<td>Lr10 Lr19</td>
<td>0 3 0 0 0</td>
</tr>
<tr>
<td>3</td>
<td>Dobrunya*4/Tc L25</td>
<td>Lr10</td>
<td>0 3 0 0 0</td>
</tr>
<tr>
<td>4</td>
<td>Dobrunya*5//Milan/Prinia L653</td>
<td>Lr19</td>
<td>0 3-4 0 0 0</td>
</tr>
<tr>
<td>5</td>
<td>Dobrunya*5//Milan/Prinia L654</td>
<td>Lr19</td>
<td>0 3-4 0 0 0</td>
</tr>
<tr>
<td>6</td>
<td>L503 Lr19 Lr26</td>
<td>Lr10 Lr19 Lr26</td>
<td>0 0 0 0 0</td>
</tr>
<tr>
<td>7</td>
<td>Saratovskaya55/Ag. el 66//Saratovskaya 29</td>
<td></td>
<td>0 3-4 0 0 0</td>
</tr>
<tr>
<td>8</td>
<td>S55/Ag.el*4//S29/3//L1015 Lr10 Lr19 Lr26</td>
<td>Lr19</td>
<td>0 3-4 0 0 0</td>
</tr>
<tr>
<td>9</td>
<td>L505<em>2//L505</em>2//Cuckoo line L195</td>
<td>Lr5b</td>
<td>0 0 0 0 0</td>
</tr>
<tr>
<td>10</td>
<td>L505/L505//L583//Cuckoo line L195</td>
<td>Lr1 Lr19 Lr5p</td>
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</tr>
<tr>
<td>11</td>
<td>S55*7/T dic-s//L2032</td>
<td>Lr10</td>
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</tr>
<tr>
<td>12</td>
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<td>0 0 0 0 0</td>
</tr>
<tr>
<td>13</td>
<td>L2032*5//Seci82</td>
<td>Lr19 Lr26</td>
<td>0 0 0 0 0</td>
</tr>
<tr>
<td>14</td>
<td>L505*2//Croc/Ae.squar(224)//Yaco</td>
<td>Lr19 Lr34</td>
<td>0 3-4 0 0 0</td>
</tr>
<tr>
<td>15</td>
<td>L505*2//T dic-s//Saratovskyzolotistaya 1.164//S55</td>
<td>Lr19</td>
<td>0 2 0 0 0</td>
</tr>
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<td>16</td>
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<td>Lr19</td>
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<td>18</td>
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<td>Lr10 Lr19 Lr26</td>
<td>0 0 0 0 0</td>
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<tr>
<td>19</td>
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<td>Lr19 Lr34</td>
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<tr>
<td>20</td>
<td>Belyanka//Altar84/Ae.squar(224)//Pgo 4//C68//L481//16</td>
<td>Lr10 Lr19</td>
<td>0 3-4 0 0 0</td>
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<tr>
<td>21</td>
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<tr>
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<td>0 0 0 0 0</td>
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<tr>
<td>23</td>
<td>Dobrunya*6//Agis181 (1.426//16)</td>
<td>Lr10</td>
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<tr>
<td>24</td>
<td>Dobrunya<em>2/L503</em>2//L583//Cuckoo line L195</td>
<td>Lr19 Lr41</td>
<td>0 3 0 0 0</td>
</tr>
<tr>
<td>25</td>
<td>S55/Ag.el*5//S29 (Age-7D)</td>
<td>Lr10 Lr19 Lr26</td>
<td>0 0 0 0 0</td>
</tr>
<tr>
<td>26</td>
<td>C55/Ag.el*5//C29 (Age-7D)</td>
<td>Lr10 Lr19</td>
<td>0 0 0 0 0</td>
</tr>
<tr>
<td>27</td>
<td>S70*4/3/ C55//Agis181 (224)//Yaco</td>
<td>Lr10 Lr19</td>
<td>0 0 0 0 0</td>
</tr>
<tr>
<td>28</td>
<td>L505 Lr10 Lr19 Lr26</td>
<td>Lr10 Lr10 Lr26</td>
<td>0 0 0 0 0</td>
</tr>
<tr>
<td>29</td>
<td>Dobrunya*6//Agis181 (1.426//16)</td>
<td>Lr10</td>
<td>0 0 0 0 0</td>
</tr>
<tr>
<td>30</td>
<td>Dobrunya*6//Agis181 (1.426//16)</td>
<td>Lr10</td>
<td>0 0 0 0 0</td>
</tr>
<tr>
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<td>Dobrunya*6//Agis181 (1.426//16)</td>
<td>Lr10</td>
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<td>Lr10</td>
<td>0 0 0 0 0</td>
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<td>33</td>
<td>Dobrunya*6//Agis181 (1.426//16)</td>
<td>Lr10</td>
<td>0 0 0 0 0</td>
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<tr>
<td>34</td>
<td>Dobrunya*6//Agis181 (1.426//16)</td>
<td>Lr10</td>
<td>0 0 0 0 0</td>
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<tr>
<td>35</td>
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<td>Lr10</td>
<td>0 0 0 0 0</td>
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<tr>
<td>36</td>
<td>Dobrunya*6//Agis181 (1.426//16)</td>
<td>Lr10</td>
<td>0 0 0 0 0</td>
</tr>
<tr>
<td>37</td>
<td>Dobrunya*6//Agis181 (1.426//16)</td>
<td>Lr10</td>
<td>0 0 0 0 0</td>
</tr>
<tr>
<td>38</td>
<td>Dobrunya*6//Agis181 (1.426//16)</td>
<td>Lr10</td>
<td>0 0 0 0 0</td>
</tr>
<tr>
<td>39</td>
<td>Dobrunya*6//Agis181 (1.426//16)</td>
<td>Lr10</td>
<td>0 0 0 0 0</td>
</tr>
</tbody>
</table>
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<table>
<thead>
<tr>
<th>Races</th>
<th>Virulence to Lr genes</th>
<th>Avirulence to Lr genes</th>
</tr>
</thead>
<tbody>
<tr>
<td>R1</td>
<td>1,2a,2b,2c,3a,3b,3g,3ka,9,10,11,14a,14b,15,16,17,18,20,21,30</td>
<td>19, 23, 24, 26, 28, 29, 41, 47</td>
</tr>
<tr>
<td>R2</td>
<td>1,2a,2b,2c,3a,3b,3g,3ka,10,11,14a,14b,15,16,17,18,19,20,21,30</td>
<td>9, 23, 24, 26, 28, 29, 41, 47</td>
</tr>
<tr>
<td>R3</td>
<td>1,2a,2b,2c,3a,3b,3g,3ka,10,11,14a,14b,15,16,17,18,20,21,26,30</td>
<td>9, 19, 23, 24, 28, 29, 41</td>
</tr>
<tr>
<td>R4</td>
<td>1,2a,2b,2c,3a,3b,3g,3ka,10,11,14a,14b,15,16,17,18,20,21,30</td>
<td>9, 19, 23, 24, 26, 28, 29, 41, 47</td>
</tr>
<tr>
<td>R5</td>
<td>1,2a,2b,2c,3a,3b,3g,3ka,10,11,14a,14b,16,17,18,20,21,26,30</td>
<td>2a, 9, 15, 19, 23, 24, 28, 29, 41</td>
</tr>
</tbody>
</table>

Table 2. Characteristic of Puccinia triticina races used in multi pathotype tests

- The low-efficiency Lr10 gene was detected in the highly resistant lines №11 and №58. In the line №29 the combination of inefficient genes Lr1, Lr10 and Lr26 was revealed, in line №21 – Lr10 and Lr26. Undoubtedly, these genes can play a role in these lines resistance strengthening, but lines' №11 and №29 resistance is ensured the most likely by the presence of additional new or unidentified genes from T. dicoccoides, in line №58 – from triticale Satu (LrSatu), in the line №21 – from cultivar Belyanka (Lr6Ag), since the Lr41 gene from A. tauschii hasn’t been identified in this line.

- The high resistance of cultivars Favorit (№67) and Voevoda (№68) is provided by the gene Lr6Ag (Sibikeev et al., 2017), an effective marker for which is not provided. Genes Lr10, Lr26 and Lr28 were specified in line №28 and genes Lr10 and Lr28 – in line №30. At the same time, the amplicon size in the TcLr28 line was slightly lower than that of these two lines. It was shown that the SCS421 marker was not strictly specific for this gene (Serfling et al., 2011). Lr28 gene was transferred to bread wheat from Ae. speltoides (McIntosh et al., 1995). Donors A. speltoides in pedigree of these lines are absent so this marker presence in lines №28 and №30 may be a false positive result indication. In line №28, according to its pedigree, it can be expected Lr6Ag gene presence from cultivar Belyanka, in line №30 from the Agis181 line having the genetic material from A. intermedium (Badayeva E.D., unpublished data).

- Along with highly resistant lines and cultivars, 24 lines were identified in the studied collection, which were resistant to all races used, except R2 race which was virulent to TcLr19 (Table 1). According to the multi-pathogen test, Lr19 gene presence can be assumed in these samples. These lines also performed the yellow color of the flour, i.e. a feature linked to Lr19 gene presence. There were cultivars Dobrunya, L503, L505, carrying this gene in the most lines pedigree. Using the marker SCS265, Lr19 gene presence was confirmed in the introgressive lines №2, №4-5, №7-8, №14, №16-17, №23, №24, №25, №27, №37, №39, №43, №47, №49-50, №52-54, №57 and cultivar Dobrynia (№66). In most of the studied lines, Lr19 gene with other ineffective Lr-genes combination was determined, and these actions were not observed in the phytopathological test seedling stage. Their presence in the lines genotypes practically did not affect the reaction type under test clone R2 inoculation in the seedling phase. Partial resistance Lr34 gene was identified in line №14 which effect appeared in the adult wheat plants phase. The inefficient Lr10 gene, which is widely distributed in ARISER cultivars, has been identified in the lines №2, №24-25, №27, №39,
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leaf rust having the widespread in Volga Region of leaf rust epiphytotics are observed on average once identified in line №51, probably transferred from cultivar Milan or Prinia. However, resistance cleavage in this line was observed after inoculation by isolates virulent to Lr19 (R2).

Cultivars Prohorovka and Yugo-Vostochnaya 2 were susceptible to clones virulent to Lr26, indicating that they possessed this gene. This fact was also confirmed using scm9 marker. Along with this one, Lr40 gene was identified in these cultivars. Cultivars Saratovskaya 55, Saratovskaya 68, Saratovskaya 70 and Albidum 32 were susceptible by all used test isolates, and the cultivar Saratovskaya 73 performed a variation in resistance. Ineffective Lr10 gene was revealed in Saratovskaya 68 and Saratovskaya 73 cultivars, which had a wide representation in ARISER selection cultivars.

Studies have shown the effective protection against leaf rust having the widespread in Volga Region of Russia spring bread wheat cultivars is controlled only by Lr6Ag and Lr6Ag+Lr19 genes. In addition, cultivars carry Lr-genes – Lr10, Lr19, Lr10+Lr26. It was found that in the studied ARISER breeding set of lines the leaf rust resistance is determined by the combinations following Lr-genes: 9, 10, 19, 26, 34, 37, 41, Satu, 6Ag.

Discussion

In the Volga region P. triticina is the most severe parasite on both winter and spring bread wheat. The leaf rust epiphytotics are observed on average once every three to four years. In such years, the wheat harvest is reduced up to 20–30% or more, protein and gluten content in the grain is significantly reduced as well. The analysis of the pathogen epiphytotic chronology shows that in the Volga region the damage from leaf rust has become stronger in recent times than in the first half of the 20th century. The following factors are the main to favor the epiphytotics development. First of all, these are structural changes in wheat acreage. Until 1960s wheat in the Volga region was represented only by spring bread and spring durum wheat, the conditions for maintaining the local P. triticina inoculums were unfavorably time-limited (April-August). Currently, the share of spring durum wheat in total wheat crops is less than 10%, spring bread wheat is no more than 25%, but winter bread wheat is more than 65%. Thus, at present moment from spring until late autumn the leaf rust inoculum propagated on live plants both winter and spring wheat. In addition, in the Volga region, there is no wide diversity of cultivars with various resistance genes to leaf rust. For example, in 1960s and 1970 winter bread wheat cultivars Mironovskaya 808 and Bezostaya 1 entered the fields, which carried gene Lr3, and then there were spring bread wheat cultivars, which also contained a single from Lr-genes – Saratovskaya 46 (Lr14), Ershovskaya 32 (Lr23). In the early 1990s through Volga and the Urals regions there was a rapid widespread of L503, L505 and Samsar cultivars containing the Lr19 gene from A. elongatum. After reaching these cultivars the "critical" plantings area (about 100 thousand hectares), the first pustules of P. triticina were found in fields, in Saratov and Orenburg regions simultaneously (Sibikeev et al., 1996). Lr19-gene usage quickly changed P. triticina population structure. To the end of 20th century in Volga region among the studied 28 Lr-genes already 22 were overcome by pathogen, only Lr9 and Lr24 showed high efficiency (Sibikeev et al., 2007). Wheat rust resistance genetics information in Volga regions is widely available (Cultyaeva et al., 2012, Sibikeev et al., 2017). Based on the available information and present research it could be concluded that ARISER wheat leaf rust resistance is based on Lr19, Lr26, Lr6Ag and Lr10. Cultivars L503, L505, Dobrynna have the genes Lr9+Lr19, Belyanka, Favorite, Voevodka – Lr6Ag, Lebedushka – Lr6Ag+Lr19 (Sibikeev et al., 2017). Leaf rust epiphytotics in 2016–2017 vegetation period in Saratov region showed only Belyanka, Favorite, Voevodka and Lebedushka with genes Lr6Ag, and Lr6Ag+Lr19 having high-efficiency resistance to the pathogen. Breeding and genetic programs for production bread wheat cultivars resistant to leaf rust are impossible without pathogen and its virulent properties study. Studies have shown that many races are generally present in the P. triticina population in Low Volga region and their relative frequencies may change significantly from one year to another (Ivanova et al., 2011). Races with new virulence combinations often overcome cultivars resistance a few years after release. In connection with the above, it is necessary to have and produce a sufficient number of effective genes of resistance to leaf rust and their combinations to provide a diversity of cultivars for them. Our study showed the following diversity and frequency of Lr-genes usage: Lr19 – 89.5%, Lr10 – 40.4%, Lr26 – 31.6%, Lr6Ag – 21%, Lr28? – 3.5%, Lr41 – 3.5%, Lr9 – 1.8%, Lr34 – 1.8%, Lr27 – 1.8%, Lr5αt – 1.8%. The frequency of two Lr-genes combinations is 45.7%, three – 21% and four Lr-genes – 5.3%. Mainly used are such Lr-genes combinations as: Lr19+Lr26 and Lr10+Lr19+Lr26 – 22.8%, Lr19+Lr6Ag – 7%. Into the four Lr-genes combinations has been included Lr10+Lr26+Lr28?+Lr6Ag – 1.8%, Lr1+Lr10+Lr26+Lr6Ag – 1.8% and Lr10+Lr19+Lr28?+Lr6Ag – 1.8%. In addition, the effective combination of Lr19 with non-identified Lr-genes from durum wheat cultivar Saratovskaya 57 (L164) and A. elongatum (2n=70 Cl-7-57) combinations has been detected. The different countries planting bread wheat have different situation for the diversity of genes for resistance to leaf rust in cultivars and primary breeding material. A study in China in 2015 of 84 bread
wheat cultivars by test the virulence of 12 races of *P. triticina* and 8 molecular markers of *Lr* genes showed that twelve *Lr* genes, including *Lr3, Lr5, (Lr3Lh), (Lr3Kd), Lr11, Lr13, Lr14a, Lr16, Lr26, Lr27, Lr30 and Lr31 were postulated to be present either singly or in combinations. *Lr5* and *Lr26* were detected most often in the tested cultivars, with frequencies of 51.2 and 38.1%, respectively. No wheat *Lr* genes were detected in 16 cultivars, and 4 cultivars may carry unknown *Lr* genes (Xiao-li Ren et al., 2015). In China in 2018, 35 cultivars were tested by 16 *Pt*-races and 15 *Lr* genes molecular markers. Seedlings of 20 tested wheat cultivars showed high resistance phenotype compared to at least one *Pt* race. Only three *Lr* genes (*Lr10* and *Lr26*) were identified in some of the tested cultivars. Five cultivars including Lianshang 66, Hemai 9735, Luyuan 301, Majai 17, and Taishan 027 showed typical APR reaction in the field. These results indicate that the diversity of known *Lr* genes in the tested wheat cultivars is relative low (Li J et al., 2018). In the Egypt in 2014 the similar study showed ten genes, *Lr13, Lr19, Lr24, Lr26, Lr34, Lr35, Lr36, Lr37, Lr39*, and *Lr46*, were detected in fifteen wheat cultivars. The most frequently occurring gene in Egyptian wheat cultivars were *Lr13, Lr24, Lr34, and Lr36* identified in all the cultivated species, followed by *Lr26* and *Lr35* (93%), *Lr39* (66%), *Lr37* (53%), and *Lr46* (26.6%) of the cultivars, and finally *Lr19* was present in 33.3% of cultivars. It is concluded that there was a good variation in *Lr* genes carried by wheat cultivars commercially grown in Egypt (Imbay et al., 2014).

**Conclusion**

The studied breeding lines will be used in breeding programs in Volga region of Russia to expand the genetic diversity of wheat varieties by using alien genes.

**References**


Identifikacija gena za otpornost na lisnu rđu u jarom oplemenjivačkom materijalu hlebne pšenice u Poljoprivrednom istraživačkom institutu za jugoistočne oblasti u Rusiji

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Sažetak: Lisna rđa hlebne pšenice koju prouzrokuje Puccinia triticina je često oboljenje u oblasti Volge u Rusiji, a oplemenjivanje na otpornost na ovog patogena je prioritetni zadatak programa pšenice u Poljoprivrednom istraživačkom institutu za jugoistočne oblasti. Poznavanje efektivnih gena za otpornost koje su prisutne u germplazmi je važno pri oplemenjivanju na efektivnu i dugotrajnu otpornost. Korišćene su rase P. triticina sa virulentnošću na Lr9, Lr19, Lr26 i sa drugim kombinacijama različitih virulentnosti i molekularni markeri Lr gena u cilju određivanja prisutnosti gena za otpornost u 68 linija i sorti hlebne pšenice. Rezultati pokazuju da se efikasna zaštita od lisne rđe široko rasprostranjena u jarim sortama hlebne pšenice u oblasti Volge kontroluje genima Lr6-Ag i Lr6-Ag+Lr19. Pored toga, sorte nose i gene Lr10, Lr19, Lr10+Lr26. U analiziranoj grupi linija, otpornost na lisnu rđu je određena sledećim Lr-genima i njihovim kombinacijama: 9, 10, 19, 26, 34, 37, 41, Satu, 6Ag. Identifikovan je efikasan Lr19 sa neidentifikovanim Lr-genima iz sorte Saratovskaya 57 (L164) i A. elongatum (CI-7-57) kombinacijama.

Ključne reči: hlebna pšenica, lisna rđa, Lr-geni, molekularni markeri, otpornost

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