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ХАБАРШЫСЫ

ВЕСТНИК

НАЦИОНАЛЬНОЙ АКАДЕМИИ НАУК
РЕСПУБЛИКИ КАЗАХСТАН

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GENETIC VARIABILITY OF PERSPECTIVE BTREEDING MATERIAL OF SPRING BREAD WHEAT FOR RESISTANCE TO LEAF RUST IN RUSSIA AND KAZAKHSTAN

Abstract. Leaf rust, caused by *Puccinia triticina Erikss.*, is one of the major diseases of wheat in Russia and Kazakhstan. The resistance and genetic diversity of 61 spring wheat genotypes from Russia and 50 ones from Kazakhstan were studied. Field evaluation of Kazakhstani wheat material allowed to select 27 lines as resistant and 8 lines as moderate resistant to leaf rust. Molecular screening revealed 29 wheat lines characterized by the presence of *Lr* genes. As a result of phytopathological and molecular screening of Kazakhstani material, carriers of 2, 3, and 4 *Lr* genes were selected. The 92 % of Chelyabinsk' lines were characterized by high level of resistance to leaf rust both at the adult and seedling stages. Using molecular markers *Lr24, Lr9, Lr19, LrSp, Lr1, Lr3, Lr10, Lr26, Lr21* and *Lr34* genes separately or in different combinations has been revealed in Russian wheat lines. In the field conditions of the Southern Urals, isogenic lines with genes *Lr24, Lr25, Lr26, Lr28, Lr45, Lr47, Lr49, Lr51* and *Lr57* showed high resistance, and in lines with the genes *Lr17, Lr23, Lr29* and *Lr64* moderate resistance was observed. At the seedling stage all single pustule isolates were avirulent to Tc-lines with *Lr16, Lr19, Lr24, Lr28* and *Lr29* genes. In Kazakhstan virulence of *P. triticina* population collected in South-East and North-Kazakh regions was studied. Against the Almaty population *Lr9, Lr19, Lr24, Lr25* and *Lr28* genes with high efficacy, and gene *Lr45* with moderate efficacy were identified. All of the lines with the rest *Lr* genes were susceptible to the pathogen. The isogenic lines with genes *Lr19, Lr24, Lr25, Lr28, Lr36* and *Lr45* were characterized by high efficacy to the Kostanai *P. triticina* population. Virulence studies of *P. triticina* showed a similarity of pathogen structure on the Southern Urals of Russia and Northern Kazakhstan.

Key words: wheat, leaf rust, *Lr* genes, molecular markers, isolates, virulence.

Introduction. Leaf rust, caused by *Puccinia triticina Erikss.*, is one of the major diseases of wheat in Russia and Kazakhstan. Its harmfulness varies by year and region. The yield loss of genotypes may achieve 30-60 % depending on the environment and severity of infection [1]. The use of genetically resistant cultivars is considered to be the most effective, economic and environmentally safe method for disease control. The region of Central Asia is one of the world's most important producers of wheat, encompassing a production are of more than 15 million ha [2, 3]. Winter wheat cultivars are grown in the southern regions of the country, and spring wheats – in the Northern, Western and Eastern regions. Developing high yielding and leaf rust, stripe rust and stem rust resistant cultivars is an important objective of winter and spring wheat (*Triticum aestivum* L.) improvement programs in Central and West Asia [4-8]. Production of wheat in Kazakhstan is being constrained also by leaf spotting diseases, including tan spot, caused by *Pyrenophora tritici-repentis* [9-13] and common bunt, caused by *Tiletia caries* [14]. In the West Siberian and Ural regions of the Russian Federation, bordering Northern Kazakhstan, spring soft wheat (*Triticum aestivum*) is the leading grain crop. The development of resistant varieties, including leaf rust, is a priority in the breeding of this crop in Russia [15]. It was shown that there is one common population of *P. triticina* in the Urals and Western Siberia of Russia and Kazakhstan [16-18]. This should be taken into account when developing and locating cultivars with *Lr* genes in this vast territory. For successful control of leaf rust in a single epidemiological zone, information on the genetic diversity of promising new wheat material and monitoring of the virulence of pathogen populations in these areas needed. The present study aims to study the genetic diversity of leaf rust resistance sources in advanced spring bread wheat lines developed in Russia and Kazakhstan. The aim of this study was 1) to screen advanced wheat breeding lines for resistance to leaf rust, 2) to determine of *Lr*-genes by molecular markers and 3) to compare effectiveness of *Lr*-genes at the seedling and adult plant stages in Kazakhstan and Russian Southern Ural.

Materials and methods. The study of resistance to leaf rust carried out in laboratory conditions at the seedling stage and in the field at the adult plant stage. Russian material included 61 advanced spring bread wheat lines, developed with the participation of donors carrying genetic material from *Aegilops speltoides, Ae. tauschii, Agropyron elongatum, Ag. intermedium*, and *Secale cereale*. This material developed in Chelyabinsk Research Institute of Agriculture (CARI). In addition, 40 isogenic wheat lines with *Lr* genes were included in field trials. All wheat tested in the field in 2019 in CARI under natural disease infection. The study of field resistance of 50 Kazakhstani wheat advanced spring wheat lines, developed in Scientific-Production Center of Grain Farming named after Barayev carried out during the 2018-2019 cropping seasons at the experimental station in v. Almalybak, Almaty region. Field leaf rust resistance of entries evaluated using the modified Cobb scale [19].

To assess the seedling resistance of the studied material in Kazakhstan the method of detached leaf segments preserved in water – benzimidazole solution was used (40 mg/L); virulence studies was performed using detached leaf method [20]. For inoculation, the combined Almaty and Kostanai populations *P. triticina* collected in 2019 were used. Before use, these populations were characterized by virulence. In Russia 10-days-old seedling were used for inoculation by urediniospores of each isolate *P. triticina*. To study leaf rust resistance, four test clones marked with virulence for the *Lr9, Lr19,* and *Lr26* genes, and the combined Chelyabinsk and Krasnodar populations were used. The virulence profile of this infectious material presented in table 1. Seedlings for their infection types to leaf rust according to Mains & Jackson (1926) were assessed [21].

Table1 – Characterization of the virulence of Russian clones and populations of *Puccinia triticina*

Populations and isolates	Origin	Virulence	Avirulence
		to Thatcher lines with *Lr* genes	
Test-clon 1 (K9)	Chelyabinsk reg., 2017	1, 2a, 2b, 2c, 3a, 3bg, 3ka, 9, 10, 11, 14a, 14b, 15, 16, 17, 18, 20, 30	19, 23, 24, 26, 28, 29, 44
Test-clon 2 (K19)	Tambov reg., 2016	1, 2a, 2b, 2c, 3a, 3bg, 3ka,10, 14a, 14b, 15, 17, 18, 19, 20, 30, 44	9, 11, 16, 23, 24, 26, 28, 29
Test-clon 3 (K26)	Krasnodar reg., 2017	1, 2a, 2b, 2c, 3a, 3bg, 3ka, 10, 11, 14a, 14b, 15, 17, 18, 20, 23, 26, 30, 44	9, 16, 19, 24, 28, 29
P_Kr	Krasnodar reg., 2018	1, 2b, 2c, 3a, 3bg, 3ka, 10, 11, 14a, 14b, 16, 17, 18, 23, 26, 30, 44	9, 2a, 15, 19, 20, 24, 28, 29
P_Chel	Krasnodar reg., 2018	1, 2a, 2b, 2c, 3a, 3bg, 3ka, 9, 10, 11, 14a, 14b, 15, 16, 17, 18, 20, 30	19, 23, 24, 26, 28, 29, 44

In Russia 10-day-old seedling were used for inoculation. Urediniospores of each isolate were inoculated on a differential host series consisting of 20 wheat single-gene near-isogenic lines known to possess resistance genes (*Lr*) 1, 2a, 2c, 3, 3bg, 3ka, 9, 10, 11,14a,14b, 15, 16, 17, 18, 19, 20, 24, 26, 28, 29, and 30 in a Thatcher genetic background. Additionally, lines with the *Lr28, Lr29, Lr44,* and *TcLr47* genes were included in the virulence analysis. To characterize the virulence of Kazakhstan populations, 32 Thatcher isogenic lines with the *Lr* genes were used.

DNA was extracted according to Dorokhov and Kloke (1997) [22]. The presence of molecular markers to resistance genes *Lr1* (WR003), *Lr3* (Xmwg798), *Lr9* (SCS5), *Lr10* (Fi.2245/Lr10-6/r2), *Lr19/Sr25* (SCS265), *Lr20/Sr15* (STS638), *Lr21* (Lr21F/R), *Lr24/Sr24* (Sr24#12), *Lr26/Sr31/Yr9/Pm8* (SCM9), *Lr28*(SCS421570), *Lr29*(Lr29F24), *Lr34/Sr57/Yr18* (csLV34), *Lr37/Sr38/Yr17* (Ventriup/LN2), *Lr41*(GDM35), *Lr47*(PS10), *Lr66*(LrSp) (S13), *Lr28* (Wmc 313), *Lr68* (csGS), *Lr19/Sr25* (PSY-E1), *Lr35/Sr39* (Sr39#50), *Lr37/Yr17/Sr38* (Ventriup/LN), *Lr39* (Xgwm 210) was determined. The amplification products were separated on 2%-agarose gels. Gels were visualized on Gel Documentation System (Gel Doc XR+, BIO-RAD, Hercules, USA) for documentation of allele types in cultivars.

Table 2 – Phytopathological evaluation and molecular screening of advanced lines of wheat to leaf rust in Kazakhstan

Name of genotype	Field evaluation to leaf rust			*Lr28* 320 b.p.	*Lr68* 385 b.p.	*Lr19/ Sr25* 191b.p.	*Lr35/ Sr39* 250 b.p.	*Lr37/Yr17/ Sr38* 262 b.p.	*Lr39* 182 b.p.
	1-record	2-record	3-record						
304/14	0	0	0	+	–	–	+	–	–
351/12	0	0	0	–	–	+	–	+	–
39/14	0	0	0	–	–	+	–	–	–
64/15	0	0	0	+	+	+	–	–	–
297/13	10MS	10MS	30MS	–	–	–	–	–	–
385/12	0	0	0	+	–	–	+	+	+
29/13	0	10MR	20MS	–	–	–	–	–	–
125/14	0	0	10MS	+	–	–	+	–	–
319/14	0	0	5MR	+	–	–	+	+	–
189/14	0	0	10MS	+	–	–	–	–	–
206/14	20MS	20MS	40MS	–	–	–	–	–	–
89/14	0	0	10MS	–	–	–	+	+	–
129/12	0	0	0	–	–	–	+	+	+
348/13	10MS	20MS	20S	–	–	–	–	–	–
42/14	0	10MS	30MS	–	–	–	–	–	–
386/13	0	0	10MS	–	–	–	+	+	–
398/13	0	0	10MS	–	–	–	+	+	–
3/14	0	0	0	–	+	–	–	+	+
182/14	0	0	10MS	–	–	–	–	–	+
362/13	0	0	10MR	–	–	–	+	–	+
221/14	0	0	0	+	–	–	–	+	+
221/14	0	0	0	+	–	–	–	–	+
162/14	0	0	0	–	–	+	–	–	–
56/14	20MS	20MS	40MS	–	–	–	–	–	–
268/13	0	0	30S	–	–	–	–	–	–
320/12	0	0	20MS	–	–	–	–	–	–
89/13	20MS	30MS	50MS	–	–	–	–	–	–
339/13	0	0	0	–	+	–	–	–	+
186/14	5MR	10MS	20MS	–	–	–	–	–	–
25/13	0	0	0	–	+	+	–	–	+
100–11–17	0	0	5MR	–	–	–	–	–	+
94–11–19	0	0	0	–	–	–		–	–
365–12–1	0	0	5MR	–	–	–	–	–	–
399–12–3	0	0	0	–	–	–	+	–	–
399–12–7	0	0	0	–	–	–	–	–	–
116–10–4	0	0	0	–	–	–	+	–	+
211–10–10	0	0	0	–	–	–	+	–	+
211–10–12	0	0	0	–	–	–	+	–	–
239–10–15	0	0	0	–	–	–	–	–	–
239–10–17	0	0	0	–	–	–	–	+	+
239–10–18	0	0	0	–	–	–	–	–	+
66–10–6	0	0	10MR	–	–	–	–	–	–
66–10–12	0	0	0	–	–	–		–	–
56–10–13	0	0	5MR	–	–	–	–	+	+
56–10–15	0	0	0	–	–	–	–	–	–
366–13–5	0	0	0	–	–	–	+	+	+
151–13–6	0	0	10MR	–	–	–	–	–	–
149–12–15	0	0	0	–	–	–	–	–	–
353–12–22	0	0	10MR	–	–	–	–	–	–
206–11–3	0	0	0	–	–	–	–	–	–

Results. As a result of the field evaluation of leaf rust resistance in 50 Kazakhstani spring wheat advanced lines the group of immune samples included 27 wheat lines in which no symptoms of *P. triticina* disease were detected (table 2). A moderately resistant reaction (MR) was observed in 8 wheat lines (319/14, 362/13, 100-11-17, 365-12-1, 66-10-6, 56-10-13, 151-13-6 and 353-12-22).

Molecular identification of carriers of *Lr* genes in wheat advanced lines was carried out. It was found that 29 wheat lines contain *Lr* genes (table 2). Twelve lines had 2 *Lr* genes. The lines 304/14 and 125/14 contains *Lr28* and *Lr35/Sr39* genes; the line 351/12 – *Lr19* and *Lr37/Yr17/Sr38* genes; the lines 89/14 and 386/13 – *Lr35/Sr39, Lr37/Yr17/Sr38* genes; the lines 362/13, 116–10–4 and 211–10–10 – *Lr35/Sr39* and *Lr39* genes; line 221/14 – *Lr28* and *Lr39* genes; the line 339/13 – *Lr68* and *Lr39* genes; the lines 239–10–17 and 56–10–13 – *Lr37/Yr17/Sr38* and *Lr39* genes. In 7 wheat lines, 3 *Lr* genes were detected: the line 64/15 contains *Lr28, Lr68*, and *Lr19/Sr25* genes; the line 319/14 – *Lr28, Lr35/Sr39* and *Lr37/Yr17/Sr38* genes; the line 129/12 – *Lr35/Sr39, Lr37/Yr17/Sr38* and *Lr39* genes; the line 3/14 – *Lr68, Lr37/Yr17/Sr3* and *Lr39* genes; line 221/14 – *Lr28, Lr37/Yr17/Sr38, Lr39* genes; the line 25/13 – *Lr68, Lr19/Sr25* and *Lr39* genes; the line 366–13–5 – *Lr35/Sr39, Lr37/Yr17/Sr38* and *Lr39* genes. Wheat line 385/12 characterized by the presence of 4 *Lr* genes (*Lr28, Lr35/Sr39, Lr37/Yr17/Sr38* and *Lr39*). As a result of phytopathological and molecular screening of Kazakhstani advanced lines, carriers of 2, 3, and 4 *Lr* genes of leaf rust resistance were selected.

In the field of the Chelyabinsk region, almost all the studied material was characterized by high level of resistance to rust leaf. Disease severity for other Thatcher isogenic lines varied from 10% to 70% (table 3).

Table 3 – Diseases severity and reaction type to leaf rust
of isogenic Thatcher (Tc) lines with *Lr* genes on the Russian Southern Ural in 2019

Tc–line with gene Lr	Disease severity (%) and reaction type	Tc–line with gene Lr	Disease severity (%) and reaction type	Tc–line with gene Lr	Disease severity (%) and reaction type
1	30 S	*15*	15 S	*32*	5 S
2a	5 S	*16*	20 S	*33*	30 S
2b	10 S	*17*	1 S	*34*	5 S
2c	30 S	*18*	20 S	*37*	30 S
3a	60 S	*19*	70 S	*38*	20 S
3ka	50 S	*20*	80 S	*45*	0
3bg	50 S	*21*	20 S	*47*	0
9	30 S	*22a*	1 S	*48*	5 S
10	5 S	*23*	1 S	*49*	0
11	70 S	*24*	0	*51*	0
12	10 S	*25*	0	*53*	0
13	10 S	*28*	0	*57*	0
14a	40 S	*29*	1 S	*64*	1 MR
14b	5 S				

A resistant type of reaction to leaf rust was observed in 92 % of advanced lines. The lines Lut. 26720, Lut. 26721 and Eritr. 26759 lines were susceptible to all clones and populations of *P. triticina*. The line Lut. 26534 showed a MR reaction when inoculated with a clone virulent to *Lr19* and S reaction to all other clones and populations of *P. triticina*. The line of Eritr. 26775 was susceptible to a clone virulent to *Lr26* and to the pathogen population from Chelyabinsk. The line Ferr. 26635 was struck by all clones and populations avirulent to *Lr9* and had a S reaction when infected with a virulent clone (K9) and the Chelyabinsk population, also virulent to *Lr9*, which suggests that it has this gene. All of the above lines have the adult plant resistance genes, or genes that have lost effectiveness, which individually are not effective, but with certain combinations can provide expression of resistance in the field.

Alien translocation from *Ag. elongatum* with highly effective seedling resistance genes to leaf (*Lr24*) and stem (*Sr24*) rust was detected in 7 breeding lines/ The genes *Lr19* and *Sr25* in the line Lut. 26706 were found. Translocation from *Ae. speltoides* (*LrSp)* was highly efficient for leaf and moderately effective for stem rust in 23 lines. Translocation from *Ae. umbellulata* (*Lr9*) was detected in 9 wheat lines.

Translocation from *S. sereale* (*Lr26, Sr31)* was identified in 6 lines. Translocation from *Ae. tauschii* with the APR genes *Lr21* and *Lr34* was identified in 10 lines. The *LrSp* gene is highly effective against leaf rust in the South Urals, although the *Lr9* and *Lr26* genes have lost their effectiveness. We have shown for the first time that in order to extend the useful life of these genes, their effective combination is of great importance. This is due to the fact that there are no isolates in the pathogen population that are simultaneously virulent to these two foreign genes [23]. Confirmation of this is a high level of field resistance of all lines with the *Lr26* + *Lr9* genes and the susceptibility of the line Ferr. 26635 and also the isogenic TcLr9 line. Cultivars with the *Lr26* gene susceptible in the Southern Urals, but the line Erit. 26762 with *Lr26*, had a high level of resistance in the field and laboratory conditions. The *Lr26* gene cannot ensure its resistance to leaf rust. This fact suggests the presence of additional gene (s) in this wheat line. At the lines Lut. 26729 and Lut. 26721 identified ineffective *Lr3* gene. At the line Eritr. 26759 – *Lr1* and *Lr10*; at the lines Eritr. 26760, Eritr. 26775 – *Lr10*; at the line Lut. 26765 – *Lr3* and *Lr26* genes identified. The study the virulence of the South Ural *P. triticina* population showed that all isolates studied were avirulent to Tc–lines with gene *Lr16, Lr19, Lr24, Lr28* and *Lr29* and virulent to *Lr1, Lr3a, Lr3bg, Lr3ka, Lr14a, Lr14b, Lr17* and *Lr18*. Virulence frequencies to other TcLr–line varied 10 to 30%.

In Kazakhstan virulence of *P. triticina* population collected in Almaty (South–East) and North–Kazakh (North) region of Kazakhstan was studied. Against the Almaty population genes *Lr9, Lr19, Lr24, Lr25* and *Lr28* with high efficacy (reaction type 0, 1 and ;), and gene *Lr45* with moderate efficacy were identified. Tc–lines with genes *Lr17* and *Lr18* had a moderate susceptible type reaction X, and all the rest of the lines were susceptible to the pathogen. The Kostanai population differed in virulence from the Almaty population. The lines with genes *Lr19, Lr24, Lr25, Lr28, Lr36* and *Lr45* were characterized by high efficacy in relation to the Kostanai population. Tc–lines with *Lr23, Lr29* and *Lr32* genes had a moderate susceptible type reaction X, and all other lines were highly susceptible to *P. triticina* (type 3–4).

Thus, different efficacy of the *Lr9* and *Lr36* genes with respect to the south and north Kazakhstan populations of *P. triticina* were revealed. Russian populations from Chelyabinsk were close in virulence to North Kazakhstan P. triticina populations.

Discussion. As a result of the studies, seedling and adult plant resistance to leaf rust in advanced spring bread wheat lines and their diversity in *Lr* genes were characterized. A study of the diversity of Russian lines revealed effective *Lr* genes (*Lr24, LrSp*) individually and in combination with ineffective *Lr* genes; an effective combination of the *Lr9* + *Lr26* genes has been revealed. The *Lr9* and *Lr26* genes separately in the South Urals lost their effectiveness.

Identified earlier in the Chelyabinsk advanced lines with *Lr24* and *Lr21* genes were not found in commercial wheat cultivars. In Russia cultivars French (Kanyuk) and German (KVS Akvilon) cultivars with *Lr24* and *Lr21* genes and in Kazakhstan Aina cultivar with the *Lr24* gene are recommended for industrial cultivation [24]. The cultivation of varieties with the *Lr24* gene shows different duration of its resistance: from 5 years to 20 years [25]. The *Lr9* and *Lr19* genes identified in the lines from Chelyabinsk belong to the group widely distributed in Russian cultivars [24, 26]. A positive example is the combination of the *Lr19* (or *Lr9*) genes with the ineffective *Lr26* gene or with *Lr37* APR gene [26, 15]. Most Russian and Kazakhstani isolates of *P. triticina*, are virulent to Tc–lines with the *Lr9* or *Lr19*, *Lr1, Lr3,* and *Lr10* genes [15, 24]. The *Lr21* gene detected in a number of lines is new for Russian and Kazakhstan wheat cultivars and belongs to the partially effective group.

It was found that 29 Kazakh wheat lines contain *Lr* genes for leaf rust resistance. As a result of phytopathological evaluation and molecular screening of Kazakhstani advanced breeding material, carriers of 2, 3, and 4 *Lr* genes of leaf rust resistance were selected. An earlier study leaf rust resistance in Kazakhstan, allowed to rank the spring wheat cultivars by level of seedling resistance. It was shown that the North Kazakhstan population of *P. triticina* was characterized by high virulence: 97 % were susceptible and only 4 % were resistant to the pathogen. The latter include cultivars Aktobe 39, Astana and Albidum 31 [27]. Among the 30 wheat entries, the genes *Lr10* and *Lr37* in three (L–1090, Krasnovodapadskaya 210 and Madsen) and *Lr19* and *Lr68* in cultivars (Pallada and Yegemen) were found [5]. The most valuable donor of leaf rust resistance was the line Almaly/Obriy with three identified *Lr* genes (*Lr34/Yr18, Lr37/Sr38/Yr17* and *Lr68*) [28].

A population analysis of the virulence of leaf rust *P. triticina* of wheat indicated a similarity of their structure in the Southern Urals of Russia and Northern Kazakhstan. The information obtained should be taken into account when locating genetically protected cultivars in these regions. The study and development of new cultivars should be carried out taking into account their resistance not only to local pathogen populations prevailing in a particular region, but also to those races that may appear in the population due to possible airborne drift from neighboring regions.

Conclusion. For successful control of leaf rust in a single epidemiological zone (Urals and Western Siberia of Russia, Kazakhstan), the genetic diversity of promising new breeding wheat material and monitoring of the virulence of pathogen populations in these areas was carried out. As a result of this study the genetic diversity of leaf rust resistance sources in advanced spring bread wheat lines developed in Russia and Kazakhstan was revealed. A population analysis of the virulence of leaf rust *P. triticina* of wheat indicated a similarity of their structure in the Southern Urals of Russia and Northern Kazakhstan.

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РЕСЕЙ МЕН ҚАЗАҚСТАНДА ҚОҢЫР ТАТҚА ТӨЗІМДІГІ БОЙЫНША ЖАЗДЫҚ ЖҰМСАҚ БИДАЙДЫҢ ПЕРСПЕКТИВТІ СЕЛЕКЦИЯЛЫҚ МАТЕРИАЛДАРЫНЫҢ ГЕНЕТИКАЛЫҚ АЛУАН ТҮРЛІЛІГІ

Аннотация. Қоңыр тат қоздырушысы *Puccinia triticina* Erikss – Қазақстан мен Ресейдегі бидайдың негізгі ауруларының бірі. Оның зияндылығы жыл мен бидай өсірілетін аймаққа байланысты өзгереді. Орта мен инфекцияның таралуына байланысты генотиптердің өнімділігінің шығыны 30–60 %-ға жетуі мүмкін. Генетикалық төзімді сорттарды қолдану – аурумен күресідің ең эффективті, үнемді және экологиялық жағынан қауіпсіз тәсілі. Қоңыр татпен нәтижелі күресу үшін Челябинск ауылшаруашылық ғылыми-зерттеу институтының 61 жаздық бидай генотиптері мен Бараев атындағы ауылшаруашылық ғылыми-өндірістік орталығының 50 генотипінің генетикалық алуан түрлілігі мен төзімділігі екі елде де зерттелді. Қазақстанда фитопатологиялық скрининг негізінде дала жағдайында бидай перспективті линияларынан қоңыр татқа 27 төзімді линия мен 8 орташа төзімді линия іріктеліп алынды. Қазақстандық перспективті линиялардың молекулалық скринингі қоңыр татқа төзімділік *Lr* гендері бар 29 бидай линиясын анықтауға мүмкіндік берді. Екі төзімділік *Lr* гендері бар 12 линия анықталынды: 304/14 және 125/14 линияларында *Lr28* бен *Lr35/Sr39* гендері; 351/12 линиясында – *Lr19* және *Lr37*/*Yr17*/Sr38; 89/14 және 386/13 линияларында – *Lr35/Sr39, Lr37/Yr17/Sr38;* 362/13, 116–10–4 және 211–10–10 линияларында – *Lr35/Sr39* бен *Lr39;* 221/14 линиясында – *Lr28, Lr39*; 339/13 линиясында – *Lr68, Lr39*; 239–10–17 мен 56–10–13 линияларында – *Lr37/Yr17/Sr38, Lr39* гендері идентификацияланды. Үш *Lr* гендері бар бидайдың 7 линиясы анықталды: 64/15 линиясында – *Lr28, Lr68* және *Lr19/Sr25;* 319/14 линиясында – *Lr28*, *Lr35/Sr39, Lr37/Yr17/Sr38;* 129/12 линиясында – *Lr35/Sr39*, *Lr37/Yr17/Sr38* және *Lr39*; 3/14 – *Lr68, Lr37/Yr17/Sr3* және *Lr39*; 221/14 линиясында – *Lr28, Lr37/Yr17/Sr38, Lr39*; 25/13 лияниясында – *Lr68, Lr19/Sr25* және *Lr39*; 366–13–5 линиясында –*Lr35/Sr39, Lr37/Yr17/Sr38* және *Lr39* гендері идентификацияланды. 4 *Lr* гендері бар бидайдың 385/12 линиясы идентификацияланды: *Lr28, Lr35/Sr39, Lr37/Yr17/Sr38* және *Lr39*. Бидайдың қазақстандық перспективті селекция материалдарының молекулалық скринингі мен фитопатологиялық бағалауы нәтижесінде қоңыр татқа 2, 3, 4 төзімділік *Lr* гендері бар тасымалдаушылар таңдалып алынды. Зерттелген Челябнскінің селекциялық материалдарының 92 % линиялары өсімдіктің өскін және ересек сатысында да қоңыр татқа жоғары төзімділігімен ерекшеленді. Молекулалық маркерлерді қолданып, бидайдың ресейлік линияларынан *Lr24, Lr9, Lr19, LrSp, Lr1, Lr3, Lr10, Lr26, Lr21* және *Lr34* гендері жеке немесе әртүрлі комбинацияларда анықталынды.

Оңтүстік Оралдың далалық жағдайында *Lr24, Lr25, Lr26, Lr28, Lr45, Lr47, Lr49, Lr51, Lr57* (зақымдалу деңгейі 0) гендері бар изогенді линиялар жоғары төзімділік танытты, ал *Lr17, Lr23, Lr29* және *Lr64* гендері бар линияларда орташа төзімділік байқалды (зақымдалу деңгейі 5 %-ға кем). Өскін сатысында барлық монопустулалық изоляттар *Lr16, Lr19, Lr24, Lr28* және *Lr29* гендері бар Тс линияларға авирулетті болды. Қазақстанның Алматы (Оңтүстік-шығыс) және Солтүстік Қазақстан (солтүстік) облыстарынан жиналған *P. triticina* популяциясының вируленттілігі зерттелді. Алматылық популяция қоздырушысына жоғары эффективті (реакция типі 0, 1 және;) *Lr9, Lr19, Lr24, Lr25* және *Lr28* гендері мен орташа эффективті *Lr45* гендері идентификацияланды. Қалған *Lr* гендері бар барлық линиялар патогенге төзімсіз болды. *Lr19, Lr24, Lr25, Lr28, Lr36* және *Lr45* гендері бар изогенді линиялар қостанайлық *P. triticina* популяциясына жоғары эффективтілігімен ерекшеленді. Бидайдың *P. triticina* қоңыр татының вируленттілігінің популяциялық анализі Ресейдің Оңтүстік Орал мен Қазақстанның Солтүстігіндегі олардың құрлымының ұқсастығын көрсетті. Алынған мәліметтер осы аймақта генетикалық қорғалған сорттарды орналастыруда ескерілуі қажет. Жаңа сорттарды шығару мен зерттеу кезінде белгілі бір аймақта тек жергілікті патогеннің популяциясына төзімділігін есепке алумен ғана жүргізілмеуі керек, сонымен қатар көршілес аймақтардан ауа арқылы таралуы мүмкін популяцияларға төзімділігін де ескеру қажет.

Түйін сөздер: бидай, қоңыр тат, *Lr* гендері, молекулалық маркерлер, изоляттар, вируленттілік.

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ГЕНЕТИЧЕСКОЕ РАЗНООБРАЗИЕ ПЕРСПЕКТИВНОГО СЕЛЕКЦИОННОГО МАТЕРИАЛА ЯРОВОЙ МЯГКОЙ ПШЕНИЦЫ ПО УСТОЙЧИВОСТИ К БУРОЙ РЖАВЧИНЕ В РОССИИ И КАЗАХСТАНЕ

Аннотация. Бурая ржавчина, возбудитель *Puccinia triticina* Erikss., является одним из основных заболеваний пшеницы в России и Казахстане. Его вредность варьирует в зависимости от года и региона возделывания пшеницы. Потеря урожайности генотипов может достигать 30–60% в зависимости от среды и тяжести инфекции. Использование генетически устойчивых сортов считается наиболее эффективным, экономичным и экологически безопасным методом борьбы с болезнями. Для успешной борьбы с бурой ржавчиной в обеих странах была изучена устойчивость и генетическое разнообразие 61 генотипа яровой пшеницы Челябинского научно-исследовательского института сельского хозяйства и 50 генотипов Научно-производственного центра зернового хозяйства имени Бараева. В Казахстане на основе фитопатологического скрининга в полевых условиях перспективных линий селекции пшеницы отобрано 27 устойчивых линий пшеницы и 8 умеренно устойчивых линий к бурой ржавчине. Молекулярный скрининг казахстанских перспективных линий позволил выявить 29 линий пшеницы, характеризующихся наличием *Lr* генов устойчивости к бурой ржавчине. У 12 линий выявлено по 2 *Lr* гена устойчивости: у линий 304/14 и 125/14 идентифицированы гены Lr28 и Lr35/Sr39; у линии 351/12 – *Lr19* и *Lr37*/*Yr17*/Sr38; у линий 89/14 и 386/13 – *Lr35/Sr39, Lr37/Yr17/Sr38*; у линий 362/13, 116–10–4 и 211–10–10 – *Lr35/Sr39* и *Lr39*; у линии 221/14 – *Lr28, Lr39*; у линии 339/13 – *Lr68, Lr39*; у линий 239–10–17 и 56–10–13 – *Lr37/Yr17/Sr38, Lr39*. В 7 линиях пшеницы выявлено по 3 *Lr* гена: у линии 64/15 – *Lr28, Lr68* и *Lr19/Sr25*; у линии 319/14 – *Lr28*, *Lr35/Sr39, Lr37/Yr17/Sr38*; у линии 129/12 – *Lr35/Sr39*, *Lr37/Yr17/Sr38* и *Lr39*; у линии 3/14 – *Lr68, Lr37/Yr17/Sr3* и *Lr39*; у линии 221/14 – *Lr28, Lr37/Yr17/Sr38, Lr39*; у линии 25/13 – *Lr68, Lr19/Sr25* и *Lr39*); у линии 366–13–5 –*Lr35/Sr39, Lr37/Yr17/Sr38* и *Lr39*. Идентифицирована линия пшеницы 385/12 с 4–мя *Lr* генами: *Lr28, Lr35/Sr39, Lr37/Yr17/Sr38* и *Lr39*. В результате фитопатологической оценки и молекулярного скрининга перспективного казахстанского селекционного материала пшеницы были отобраны носители 2–х, 3–х и 4–х *Lr* генов устойчивости к бурой ржавчине. Из изученного челябинского селекционного материала 92% линий характеризовались высоким уровнем устойчивости к листовой ржавчине как на стадии взрослого растения, так и на стадии проростков. В российских линиях пшеницы с использованием молекулярных маркеров были выявлены гены *Lr24, Lr9, Lr19, LrSp, Lr1, Lr3, Lr10, Lr26, Lr21* и *Lr34* по отдельности или в различных комбинациях. В полевых условиях Южного Урала высокую устойчивость проявили изогенные линии с генами *Lr24, Lr25, Lr26, Lr28, Lr45, Lr47, Lr49, Lr51, Lr57* (степень поражения 0), а в линиях с генами *Lr17, Lr23, Lr29* и *Lr64* наблюдали умеренную устойчивость (степень поражения менее 5%). На стадии проростков все монопустульные изоляты были авирулентны к Тс–линиям с генами *Lr16, Lr19, Lr24, Lr28* и *Lr29*. В Казахстане изучена вирулентность популяции *P. triticina,* собранной в Алматинской (Юго-Восток) и Северо-казахстанской (Север) областях Казахстана. Идентифицированы высокоэффективные (тип реакции 0, 1 и;) против алматинской популяции возбудителя гены *Lr9, Lr19, Lr24, Lr25* и *Lr28*, а также ген *Lr45*, характеризовавшийся умеренной эффективностью. Все линии с остальными Lr генами были восприимчивы к патогену. Изогенные линии с генами *Lr19, Lr24, Lr25, Lr28, Lr36* и *Lr45* характеризовались высокой эффективностью по отношению к костанайской популяции *P. triticina.* Популяционный анализ вирулентности бурой ржавчины пшеницы *P. triticina* показал сходство их структуры на Южном Урале России и в Северном Казахстане. Полученная информация должна учитываться при размещении генетически защищенных сортов в этих регионах. Изучение и разработка новых сортов должны проводиться с учетом их устойчивости не только к местным популяциям патогенов, преобладающим в конкретном регионе, но и к тем расам, которые могут появиться в популяции из–за возможного переноса по воздуху из соседних регионов.

Ключевые слова: пшеница, бурая ржавчина, *Lr* гены, молекулярные маркеры, изоляты, вирулентность

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