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SCREENING OF NEW WHEAT CULTIVARS ORIGINATING FROM KAZAKHSTAN FOR STEM AND LEAF RUST RESISTANCE GENES USING PCR MARKERS

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ABSTRACT

Leaf and stem rust that infect wheat lines are the most prevalent and damaging fungal diseases affecting the wheat production rates globally. One of the efficient and economically wise ways of controlling the disease progression is the breeding resistant wheat varieties. Use of molecular markers associated with resistance genes, might be useful for identifying the varieties, that carry the specific resistant genes. Sixty-four wheat cultivars and lines provided by domestic agricultural experimental stations were examined using DNA-markers for the presence of leaf (*Lr*) and stem (*Sr*) rust resistance genes. The reactions were carried out using eight pairs of different primers. Six *Lr* genes (*Lr10, Lr13, Lr16, Lr19* and *Lr39)* responsible for wheat resistance were detected using PCR. The molecular marker detection demonstrated the presence of a combination of several *Lr* genes, particularly *Lr16*, *Lr34* and *Lr39* in the fifteen spring wheat accessions. Six varieties in the nursery of spring soft wheat from KarabAES, two varieties from AktAES (Ekada 113, Lin. 225/21g.) and seven varieties from NorthKazAES (435/Lut 2, 659/12, 486/Lut 22, 23/07, Erith 42/12, 453 SP-2/19) carried the combination these three genes. In summary, the findings illustrate the usefulness of the investigated markers in detecting rust-resistant genes across various cultivars. These results can form a foundation for future research and is expected to be especially beneficial to breeders when choosing rust-resistant wheat varieties.

Keywords: stem rust, leaf rust, wheat, *Lr* and *Sr* genes, PCR-markers, agricultural experimental stations.

INTRODUCTION

Kazakhstan is considered one of the key regions with the highest wheat production rates in Central Asia. It was among the top ten countries that exported wheat between 2000 and 2016 [1]. Recent analysis has shown that Kazakhstan was the top 14th wheat producer reaching over 14 million tonnes of crop yield in 2020 [2]. Moreover, wheat production in Kazakhstan has a pivotal role in food security in Central Asia, as more than 70 % of the imported crops in these countries were from Kazakhstan [3]. However, the wheat production rates vary annually and can be low, which is limited by several factors, including unfavourable weather conditions (a short growing season with high temperatures in summer and limited water availability) and a lack of fertilizers [1]. But most importantly, it is the unsatisfactory phytosanitary condition of crops and the cultivation of wheat varieties susceptible to diseases.

Leaf rust (LR), caused by *Puccinia triticina Erics (Pt)*, is one of the frequently occurring fungal infections of wheat and is considered an important wheat disease globally and in Kazakhstan. Leaf rust infections are responsible for significant wheat yield losses of higher than 50% at even earlier stages and cover large geographical areas [4]. In Kazakhstan, leaf rust mainly occurred in the Northern, Eastern and Western regions of Kazakhstan. During 2001-2016 the incidents of leaf rust infection along with Septoria occurred eight times [5]. Another prevalent and dangerous rust disease that infects wheat is stem rust (SR) caused by *Puccinia graminis f.sp.tritici* (Pgt). Several epidemics were due to the outbreak of the stem rust pathogen, causing significant yield losses in Kenya [6], Ethiopia [7], North Kazakhstan [8], and Siberia [9, p. 2017–2018]. For instance, over one million hectares of land with wheat were affected by stem rust in the Northern part of Kazakhstan and the Omsk region of Russia [10,11].

One of the economical and sustainable methods of controlling plant diseases, and also supporting yield potential in cultivated crops is to select resistant varieties of wheat [12]. Therefore, genetic studies on leaf and stem rust-resistant genes are of particular importance. Up to now, more than 80 *Lr* genes for leaf resistance have been identified in wheat [13]. Some of them are active during all stages of wheat growth towards leaf rust and are described as all-stage resistance (ASR genes) also known as race-specific seedling resistance. Whereas, other genes are expressed at the adult plant stage and are known as race non-specific adult plant resistance (APR genes) [12,13]. Most resistance genes are race-specific *Lr* genes that are characterized by a hypersensitive reaction upon infection [14]. Among them are *Lr12, Lr13, Lr22a* [15], *Lr35, Lr37* [16], *Lr 48*, and *Lr 49* [17]. In contrast, non-race specific APR genes cause non-hypersensitive responses and are controlled by small-impact genes [18]. This type of resistance is associated with the durability and longevity of leaf rust resistance, which is characterized by slower infection frequency and longer latent period, less spore production. These genes include *Lr34*, *Lr46*, *Lr67* and *Lr68* [14]. However, it is important to note that not a single, but a combination of these genes can strengthen the resistance towards leaf rust [12]. Genes, associated with stem rust resistance are known as *Sr* genes and currently, there are more than 60 genes have been discovered [19]. Some are effective under certain temperature conditions, such as *Sr10* [20], and *Sr15* [21], some are resistant towards the races of Ug99 at high temperatures, such as *Sr21* [22]. The *Sr24* gene, derived from *Thinopyrum ponticum*, also confers resistance against Ug99 races and other stem races [23,24]. Similarly, the *Sr26* gene has the same source of derived plant and resistance against Ug99 races [23].

To date, numerous genes carrying resistance to stem and leaf rust have been identified. Currently, DNA-based molecular markers, associated with resistance genes have been

widely employed. This is useful for tracking, whether the wheat cultivars carry the specific resistant genes or not, using marker-assisted validation. In this study, we used several molecular markers, based on the literature review, that are linked to leaf and stem-resistant genes of wheat cultivars

MATERIALS AND METHODS

Plant material

The main source for research was spring wheat varieties of domestic origin. The analysis of genetic resistance comprised in total of sixty-four cultivars and lines from Karabalyk Agricultural Experimental Station (KarabAES), Aktobe Agricultural Experimental Station (AktAES) and North Kazakhstan Agricultural Experimental Station (NorthKazAES) to leaf and stem rust.

DNA Marker-associated molecular analysis of leaf and stem rust resistant genes of wheat

DNA isolation was performed using a commercial Plant DNA Isolation Kit (Magnetic Bead System) (Norgen Biotek Co. Thorold, ON, Canada) following the manufacturer's instructions. The quantity and the quality of the isolated DNA were checked on 1% agarose gel (Sigma-Aldrich, St. Louis, MI, USA) stained with ethidium bromide (TM MEDIA, India) in 1 × TBE buffer (Invitrogen, Waltham, MA, USA).

The selection of molecular markers associated with leaf and stem rust resistance genes was based on the literature sources (Table 1). The PCR reactions were carried out using 8 pairs of different primers. Each specific pair of primers has its own reaction conditions shown in Table 1. PCR was performed using a Mastercycler nexus cycler (Eppendorf, Germany) and 2720 Thermal Cycler (Applied Biosystems, USA). The amplified products were detected on 1.5% agarose gels (Invitrogen, Waltham, MA, USA) containing ethidium bromide (TM MEDIA, India) and the MINIBISPRO 16mm GELQUANT gel documenting system (DNR Bio-Imaging Systen, Israel). The molecular weight of the fragments was assessed using 50bp, 100 bp and 1 kb DNA molecular weight marker «GeneRuler DNA Ladder» (Thermo Fisher Scientific, Waltham, MA, USA).

RESULTS AND DISCUSSIONS

This study aimed to identify the cultivars and lines that carry specific genes of resistance towards leaf and stem rust, using previously selected gene-specific markers. Marker-specific molecular analysis for the resistance genes can provide an efficient approach for controlling diseases and help breeding plants, resistant to common wheat rust. We screened sixty-four cultivars and lines of domestic origin obtained from different local agricultural experimental stations (AES) for the presence of *Lr10, Lr13, Lr16, Lr19, Lr39*, *Sr24, and Sr26* genes (Table 1). The size of the amplified markers of the control cultivar is shown in Figure 1. Analysis of the closely linked markers for eight genes demonstrated, that they can be used for the detection of resistant genes.

According to the molecular screening, the use of gene-specific markers showed the presence of a combination of several *Lr* genes, particularly *Lr16*, *Lr34* and *Lr39* in the fifteen spring wheat accessions (Table 2). The table below illustrates, that six varieties in the nursery of spring soft wheat from KarabAES, two varieties from AktAES (Ekada 113, Lin. 225/21g.) and seven varieties from NorthKazAES (435/Lut 2, 659/12, 486/Lut 22, 23/07, Erith 42/12, 453 SP-2/19) carried the combination of above-mentioned three gen es.

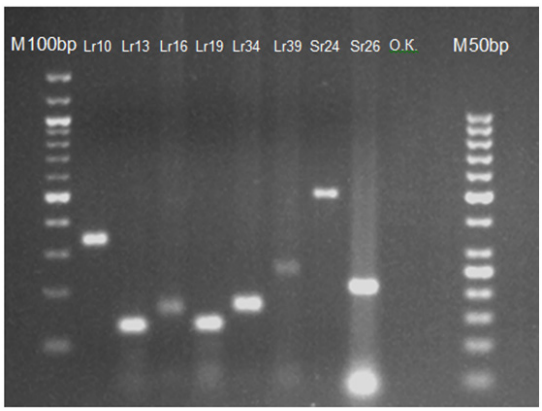

Figure 1. Amplification products of leaf and stem rust resistant genes, where M – 100 bp marker; *Lr10* – 310 bp.; *Lr13* – 120 b.p.; *Lr16* – 180 b.p.; *Lr19* – 130 b.p.; *Lr34* – 150-229 b.p.; *Lr39* – 190-280 b.p.; *Sr24* – 500 b.p.; *Sr26* – 207 b.p.; OK – negative control; M – 50 bp marker.

Table 1. DNA markers, associated with resistant genes against leaf and stem rust

Lr gene	PCR conditions (temperature and time)	Size of amplified product (bp)	References
Lr10	94°C – 5 min, 40 cycles (94°C – 20 sec; 60°C – 1 min ; 72°C – 1,30 min); 72°C – 7 min	310	[25,26]
Lr13	94°C –2,5 min, 40 cycles (94°C –1,5 min; 55°C –1,5 min 72°C –1,5 min); 72°C –10 min	120	[27]
Lr16	94°C – 3 min, 40 cycles (94°C – 1 min; 55°C – 1 min; 72°C –2 min) 72°C –10 min	180	[26]
Lr19	94°C – 3 min; 40 cycles (94°C – 1 min; 58°C – 1 min; 72°C – 2 min); 72°C – 10 min	130	[26]
Lr34	94°C – 5 min; 40 cycles; (94°C – 40 sec; 58°C – 30 sec; 72°C – 1 min); 72°C – 7 min	150-229	[28]
Lr39	94°C –2,5 min; 40 cycles (94°C –1,5 min; 55°C –1,5 min; 72°C –1,5 min); 72°C –10 min	190-280	[26,29]
Sr24	94°C –5 min; 35 cycles; (94°C –1 min; 62°C –1 min; 72°C –2 min); 72°C –10 min	500	[23]
Sr26	94°C –3 min; 35 cycles (94°C –1 min; 60°C –1 min; 72°C –2 min); 72°C –10 min	207	[23]

Table 2. Molecular screening of resistant wheat cultivars and lines to diseases using DNA markers

No	Cultivar and line names	Resistant genes of wheat cultivars to leaf and stem rust							
		Lr 10	*Lr 13*	*Lr 16*	*Lr 19*	*Lr 34*	*Lr 39*	*Sr 24*	*Sr 26*
1	2	3	4	5	6	7	8	9	10
1	TERTSIYA/3/SRN/… x CHELYABA YUBILEINAYA/…			+			+		
2	TERTSIYA/3/SRN/… x CHELYABA YUBILEINAYA/4/…						+		
3	TERTSIYA/3/SRN/AE.SQUARROSA(358)//… x CHELYABA YUBILEINAYA/…			+			+		
4	LUTESCENS 210.99.10*2/4/… x TERTSIYA/3/SRN/ …			+					
5	LUTESCENS210.99.10*2/…x LUTESCENS 307-97-23/ …			+			+		
6	LUTESCENS 210.99.10*2/… x LUTESCENS 307-97-23/…			+			+		
7	LUTESCENS 210.99.10*2/… x LUTESCENS 307-97-….			+			+		
8	LUTESCENS 210.99.10*2/… x LUTESCENS 307-97-23/11/CROC_1/….			+		+	+		
9	LUTESCENS 210.99.10*2/4/ x LUTESCENS 307-97-23/11/CROC_1/ …			+		+	+		
10	LUTESCENS 210.99.10*… x LUTESCENS 307-97-23/11/CROC_1/ …			+					
11	LUTESCENS 210.99.10… x LUTESCENS 307-97-23/11/CROC_1/…						+		
12	LUTESCENS 307-97-23/11/CROC_1/…. x TERTSIYA/3/SRN/AE.SQUARROSA (358)//…					+	+		
13	LUTESCENS 307-97-23/11/CROC_1/…			+		+	+		
14	LUTESCENS 307-97-23/11/CROC_1/… x LUTESCENS210.99.10*2/..			+			+		
15	LUTESCENS 307-97-23/11/CROC_1/… x LUTESCENS210.99.10…			+			+		
16	LUTESCENS 307-97-23/11/CROC_1/… x LUTESCENS210.99.10*2/…			+			+		
17	LUTESCENS 307-97-23/11/CROC_1/… x LUTESCENS210.99.10*2/…			+			+		
18	Aina (Айна)						+		
19	Fantasiya (Фантазия)			+		+	+		
20	CHELYABAYUBILEINAYA/4/BETTY/3/…x TERTSIYA*2/3/EMB16/…			+			+		
21	LUTESCENS 30-94/3/…			+		+	+		
22	LUTESCENS290-99-7/…			+			+		
23	BELYANKA/4/…						+		
24	OMSKAYA35/GRANITE/3/...						+		
25	ALBIDUM29/ZLATA/5/…			+			+		
26	WS - Stru 133001s7					+			
27	Lada x Karabalykskaya (Лада х Карабалыкская 90)						+		
28	Shortandinskaya 125 x Lyutescens 86-91-94-1 (Шортандинская 125 х Лютесценс 86-91-94-1)			+					
29	Ilinskaya x Kazakhstanskaya 19 (Ильинская х Казахстанская 19)			+		+	+		
30	Omskaya 35 x Shortandinskaya (Омская 35 х Шортандинская улучшенная)			+			+		
31	Omskaya 33 x Tselinnaya 24 (Омская 33 х Целинная 24)			+			+		
32	Saratovskaya 51 x Aktyubinka (Саратовская 51 х Актюбинка)			+					
33	Karabalykskaya 90 x Lyutescens 2/10-99 (Карабалыкская 90 х Лютесценс 2/10-99)			+			+		
34	Karabalykskaya 4 x Karabalykskaya 90) Карабалыкская 4 х Карабалыкская 90			+			+		
35	Karabalykskaya 7 x Sary-Arka (Карабалыкская 7 х Сары-Арка)			+		+	+		
36	Aktobe 39 (Актюбе 39)			+					
37	Stepnaya 2 (Степная 2)			+			+		
38	Stepnaya 50 (Степная 50)			+			+		
39	Ekada 113 (Экада 113)			+		+	+		
40	Dinastiya (Династия)			+			+		
41	Stepnaya 53 (Степная 53)						+		
42	Stepnaya 75 (Степная 75)						+		
43	Lin.P-1413m (Лин. Р-1413м)					+	+		
44	Lin.P-1415m (Лин. Р-1415м)					+	+		
45	Lin. 201/21g (Лин. 201/21г.)						+		

46	Lin.205/21g (Лин. 205/21г.)					+	+		
47	Lin.225/21g (Лин. 225/21г.)			+		+	+		
48	Erit 255 (Эрит 255)						+		
49	435/Lyut 2 (435/Лют 2)			+		+	+		
50	659/12			+		+	+		
51	486/Lyut 22 (486/Лют 22)			+		+	+		
52	63/Lyut 37 (63/Лют 37)					+	+		
53	23/07			+		+	+		
54	218/10			+			+		
55	Erit 42/12 (Эрит 42/12)			+		+	+		
56	Lyut 13/12 (Лют 13/12)			+			+		
57	384/06-1			+			+		
58	134 SP-21/19 (134 СП-21/19)			+			+		
59	189 SP-21/19 (189 СП-2/19)			+			+		
60	316 SP-21/19 (316 СП-2/19)			+			+		
61	435 SP-21/19 (435 СП-2/19)			+			+		
62	450 SP-21/19 (450 СП-2/19)			+			+		
63	453 SP-21/19 (453 СП-2/19)			+		+	+		
64	73/07			+		+	+		

Lr10 gene originated from *Triticum aestivum* L chromosome arm 1A [30]. *Lr10* is among the most common genes found in European and Russian wheat genotypes [31–33]. In the present study, the results of the molecular analysis did not detect the known *Lr* genes, such as *Lr10* and *Lr19* in the provided experimental samples. Similarly, the molecular marker evaluation of the spring wheat obtained from Southern Kazakhstan and Omsk regions did not reveal these genes [34]. However, the molecular screening of wheat samples in the different study showed the presence of the *Lr10* gene only in two Kazakh genotypes (Yegmen and Dinara) and the *Lr19* gene in one sample from Russia [35]. According to some studies, *Lr10* lost its efficacy and the virulence of the leaf rust pathogen for this gene was common in many regions [36,37]. *Lr19* gene along with *Lr9*, *Lr25* and *Lr29* is still effective against the population of leaf rust pathogen in different regions of Kazakhstan [38]. Moreover, low virulence of these particular genes has been noticed in Iran, demonstrating its effectiveness against the wheat leaf rust pathogen population [39]. The retained efficacy of the *Lr19* gene might be suggested for use in wheat breeding programs for enhancing leaf rust resistance in cultivated wheat varieties. It was hypothesized that the absence of the known *Lr* genes resistant to leaf rust might be safeguarded with the presence of additional *Lr* genes or multiple minor genes within their genetic makeup, protecting the plant [34].

Another rust-resistant gene *Lr13*, identified in the "Manitou" Canadian wheat cultivar, is probably the most common and extensively spread gene over a large area [37]. Its importance is defined by the rendering of durable adult plant resistance, however, there has been little discussion about its ineffectiveness towards rust in several countries [40]. Molecular analysis of the presence of *Lr13* in our studied samples did not reveal this gene. However, in a similar study, the DNA marker analysis of the lines from Kazakhstan showed its presence [41]. Nevertheless, *Lr13* still demonstrates good resistance in field experiments in combination with other rust-resistant genes [14,42,43].

Sr24, closely linked to leaf rust resistance *Lr24* gene, was first originally identified from *Agropyron elongatum* and located on the 3DL chromosome. Lines, containing *Sr24* might be an effective source for breeding stem rust disease-resistant cultivars [44,45]. *Sr26* was also derived from *Agropyron elongatum* (*Thinopyrum ponticum*) and was introduced to wheat chromosome 6A [23,46]. Its continued resistance was confirmed towards *Pgt* pathotypes in combination with *Sr2* and *Sr24* resistance genes [46,47]. The relevance of this gene remains, as it has been showing its effectiveness since 1969 [48, p. 1969–1985]. As can be seen from Table 2, the molecular markers specific to *Sr24* and *Sr26* did not reveal these genes in the studied cultivars. Both genes are known to be effective against the highly virulent and aggressive race UG99 [49]. Even though this virulent race is predominantly established in Eastern African regions, there is a huge concern about the possible dispersal and migration of this race to other parts of the world [50]. Furthermore, the subsequent announcement of the UG99 race occurrence in Iran (2008) held huge concern from Russian scientists about the distribution of the race through the Caucasus or the Caspian Sea due to the movement of air masses [51,52]. The UG99 pathotypes have not been found in Kazakhstan, however, the risk of the occurrence is also possible due to the above-mentioned reasons. Therefore, it might be reasonable to incorporate these genes when breeding the wheat cultivars as protective measures.

Lr16 was first reported in Canada and found in the Selkirk variety [53]. As mentioned in the literature review, *Lr16* was originated from wheat chromosome arm 2BS and assigned using microsatellite markers [54]. This gene confers resistance at the seedling stage. In the present study, the *Lr16* gene in combination with *Lr34* was found in twelve wheat lines and four cultivars. It seems to be consistent with other research, which found that a combination of these two genes exhibited better resistance in wheat lines, than the lines with *Lr16* or *Lr34* alone [55].

The *Lr34* gene is known to be present in lots of wheat cultivars and is described as a first-cloned gene that confers par-

tial resistance to multiple pathogens [12]. Gene is positioned on the 7D chromosome [56]. *Lr34* has resistance in adult plant stages, however, under certain conditions, it can confer resistance in seedling stages too. It is also worth mentioning, that in combination with other leaf rust-resistant genes, it can demonstrate a synergetic effect [28]. As expected, *Lr34* was identified in twenty-two wheat samples in combination (*Lr34*, *Lr39* and *Lr16*) or alone (Table 2). These results of the current study are in keeping with recent molecular screening of domestic wheat accessions, where *Lr34* was found at high frequency with an occurrence of 22.8%. According to their results, the combination of *Lr37, Lr34* and *Lr68* genes demonstrated the highest efficiency and lowest susceptibility to leaf rust [57]. In contrast, a different study has found the *Lr34* gene in combination with *Lr1* and *Lr26* in their studied Kazakh cultivars [35]. The resistance of the *Lr34* gene is no longer effective in Russia, however, it is used in combination with other genes to provide a durable resistance of the cultivars [58]. *Lr39* has been derived from *Aegilops tauschii* and mapped to chromosome 2DS. The combination of several resistance genes may enhance the durable resistance to leaf rust. It was suggested that *Lr39* exhibits improved resistance to leaf rust when combined with other resistant genes [59]. In this study, the *Lr39* gene was present in forty-three lines and fifteen cultivars in combination with either *Lr16* or *Lr34* alone, or both.

The effectiveness of resistance genes towards the pathogen population can vary between regions and show different results due to several factors. It might be due to genetic diversity and variability of the pathogen, environmental conditions (temperature, humidity etc.) or the continuous use of the same resistance genes that lead to the virulence of the pathogen and the diminishment of the gene's efficacy. Nevertheless, this combination of results provides some support for proving the occurrence of adult plant and seedling resistance genes in our local cultivars and lines. This outlines that the use of genes selected with DNA markers is of particular importance for wheat resistance breeding in Kazakhstan.

CONCLUSION

In the present study, we examined sixty-four cultivars and lines from KarabAES, AktAES and NorthKazAES and characterized leaf and stem rust resistance genes using specific molecular markers. We examined the presence of eight *Sr* and *Lr* resistance genes, including *Lr10*, *Lr13*, *Lr16*, *Lr19*, *Lr34*, *Lr39*, *Sr24* and *Sr26* in the analyzed samples. Molecular screening showed a total of fifteen spring wheat accessions that carried a combination of several *Lr*-genes (*Lr16*, *Lr34* and *Lr39*) of resistance. Of these, six varieties in the nursery of spring soft wheat from KarabAES, two from AktAES (Ekada 113, Lin. 225/21g.), seven from NorthKazAES (435/Lut 2, 659/12, 486/Lut 22, 23/07, Erit 42/12, 453 SP-2 /19). To conclude, the results demonstrate the usefulness of the examined markers for the identification of rust-resistance genes in different cultivars, which may serve as a base for future studies and should prove to be particularly valuable to breeders in selecting wheat-resistant varieties.

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СКРИНИНГ НОВЫХ СОРТОВ ПШЕНИЦЫ КАЗАХСТАНСКОГО ПРОИСХОЖДЕНИЯ НА НАЛИЧИЕ ГЕНОВ УСТОЙЧИВОСТИ К СТЕБЛЕВОЙ И ЛИСТОВОЙ РЖАВЧИНЕ С ИСПОЛЬЗОВАНИЕМ ПЦР-МАРКЕРОВ

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АННОТАЦИЯ

Листовая и стеблевая ржавчина являются наиболее распространенными и вредоносными грибковыми заболеваниями, которые существенно влияют на уровень производства пшеницы во всем мире. Одним из эффективных и экономически целесообразных способов контроля развития этих болезней является селекция устойчивых сортов пшеницы. Использование молекулярных маркеров, связанных с генами устойчивости, может быть полезным для идентификации сортов, несущих конкретные гены устойчивости. В данном исследовании было исследованы 64 сорта и линии пшеницы, предоставленные отечественными сельскохозяйственными опытными станциями. Скрининг на наличие генов устойчивости к листовой (*Lr*) и стеблевой (*Sr*) ржавчине проведен с помощью 8 пар ДНК-маркеров. Шесть генов устойчивости к листовой ржавчине (*Lr10, Lr13, Lr16*, *Lr19* и *Lr39*) были выявлены методом ПЦР. Использование молекулярных маркеров показало наличие комбинации нескольких генов *Lr*, в частности *Lr16*, *Lr34* и *Lr39*, у пятнадцати образцов яровой пшеницы. Шесть сортов в питомнике яровой мягкой пшеницы от КарабСХОС, два сорта от АктСХОС (Экада 113, лин. 225/21г.) и семь сортов от СевКазСХОС (435/Лют 2, 659/12, 486/Лут 22, 23/07, Эрит 42/12, 453 СП-2/19) несли комбинацию этих трех генов. Таким образом, полученные результаты иллюстрируют полезность исследованных маркеров для обнаружения генов устойчивости к ржавчине у различных сортов. Данные результаты могут стать основой для будущих исследований и, как ожидается, могло быть особенно полезно селекционерам при выборе устойчивых к ржавчине сортов пшеницы.

Ключевые слова: стеблевая ржавчина, бурая ржавчина, пшеница, гены *Lr* и *Sr*, ПЦР-маркеры, сельскохозяйственные опытные станции.

ПТР-МАРКЕРЛЕРДІ ПАЙДАЛАНА ОТЫРЫП, ҚАЗАҚСТАНДЫҚ БИДАЙДЫҢ ЖАҢА СОРТТАРЫН САБАҚ ЖӘНЕ ЖАПЫРАҚ ТАТТАРЫНА ТӨЗІМДІЛІК ГЕНДЕРІНІҢ СКРИНИНГІ

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ТҮЙІН

Бидайдың жапырақ және сабақ таты аурулары бидай өндірісіне кері әсер тигізетін кең таралған және зиянды саңырауқұлақ ауруларының бірі. Бұл аурулардың дамуын тежейтін тиімді әдістерінің бірі – бидайдың төзімді сорттарын өндірісте пайдалану. Төзімділік гендерімен байланысты молекулалық маркерлерді пайдалану белгілі бір төзімділік гендері бар сорттарды анықтау үшін пайдалы болуы мүмкін. Бұл зерттеуде отандық ауылшаруашылық тәжірибе станциялары ұсынған 64 бидай сорттары мен линияар зерттелді. Жапырақ (*Lr*) және сабақ (*Sr*) таты ауруларына төзімділік гендерінің скринингі 8 жұп ДНҚ маркері арқылы жүзеге асырылды. ПТР әдісімен жапырақ татына төзімділіктің алты гені (*Lr10, Lr13, Lr16, Lr19* және *Lr39*) анықталды. Молекулалық маркерлерді қолдану арқылы жаздық бидайдың он бес сортүлгісінде *Lr16, Lr34* және *Lr39* төзімділік гендер комбинациясы анықталды. Зерттеу нәтижесінде жаздық жұмсақ бидай питомнигіндегі алты сорт КарабАТС, екі сорт АктАТС (Экада 113, лин. 225/21г.) және СевказАТС жеті сортүлгісінде (435/Лют 2, 659/12, 486/Лут 22, 23/07, Эрит 42/12, 453 СП-2/19) аталған төзімділік гендер комбинациясы анықталды. Осылайша, зерттелген маркерлердің әртүрлі сорттардың тат түрлеріне төзімділік гендерін анықтау үшін тиімділігін көрсетеді. Алынған нәтижелеріді болашақ зерттеулерге негіз бола алады. Сонымен қатар, тат түрлеріне төзімді бидай сорттарын шығаруда селекционерлерге пайдалы болады деп күтілуде.

Кілттік сөздер: сабақ таты, жапырақ таты, бидай, *Lr* және *Sr* гендері, ПТР маркерлер, ауылшаруашылық тәжірибе станциялары.