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 soft wheat from KarabAES, two varieties from AktAES (Ekada 113, Lin. 221/21g.) 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.

Keywords: 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 exports 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] including three not detected prior to 2013. Genotypic analysis of 20 isolates from 2013 and 2014 collections showed that the new races TTHST, TTKTK, and TTKBT belong to the Ug99 race group. International advanced breeding lines were evaluated against an isolate of TTKTT (Sr31, Sr24, and SrTmp virulence, Ethiopia [7]) with yield losses close to 100% on the most widely grown wheat cultivar, ‘Di-galu’. Sixty-four stem rust samples collected from the regions were analyzed. A meteorological model for airborne spore dispersal was used to identify which regions were most likely to have been infected from postulated sites of initial infection. Based on the analyses of 106 single-pustule isolates derived from these samples, four races of *Puccinia graminis* f. sp. *tritici* were identified: TKTTF, TTKSR, RRTTF, and JRQQC. Race TKTTF was found to be the primary cause of the epidemic in the southeastern zones of Bale and Arsi. Isolates of race TKTTF were first identified in samples collected in early October 2013 from West Arsi. It was the sole or predominant race in 31 samples collected from Bale and Arsi zones after the stem rust epidemic was established. Race TTKSK was recovered from 15 samples from Bale and Arsi zones at low frequencies. Genotyping indicated that isolates of race TKTTF belongs to a genetic lineage that is different from the Ug99 race group and is composed of two distinct genetic types. Results from evaluation of selected germplasm indicated that some cultivars and breeding lines resistant to the Ug99 race group are susceptible to race TKTTF. Appearance of race TKTTF and the ensuing epidemic underline the continuing threats and challenges posed by stem rust not only in East Africa but also to wider-scale wheat production.
genes that are characterized by a hypersensitive reaction upon infection [14]. Among them are Lr12, Lr13, Lr22u [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 Sr27 [22]. The Sr24 gene, derived from Thinopyrum ponticum, also confers resistance against Ug99 races and other stem races [23,24]. Resistance to stem rust in wheat, caused by Puccinia graminis f. sp. tritici, is based at least in part on the gene Sr31. During February 1999, high levels of stem rust infection were observed on entries in wheat (Triticum aestivum.

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

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

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

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 (KarabaAES), 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 x 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 GEL-QUANT gel documentation system (DNR Bio-Imaging Systen, Israel). The molecular weight of the fragments was assessed using 50bp, 100 bp and 1 kb DNA molecular weight markers «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-spe-
cific 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 genes.

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

<table>
<thead>
<tr>
<th>No</th>
<th>Cultivar and line names</th>
<th>Resistant genes of wheat cultivars to leaf and stem rust</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>( Lr10 )</td>
</tr>
<tr>
<td>1</td>
<td>TERTSIYA/3/SRN/… x CHELYABA YUBILEINAYA/…</td>
<td>+</td>
</tr>
<tr>
<td>2</td>
<td>TERTSIYA/3/SRN/… x CHELYABA YUBILEINAYA/4/…</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>TERTSIYA/3/SRN/AE.SQUARROSA(358)/… x CHELYABA YUBILEINAYA/…</td>
<td>+</td>
</tr>
<tr>
<td>4</td>
<td>LUTESCENS 210.99.10*2/4/… x TERTSIYA/3/SRN/…</td>
<td>+</td>
</tr>
<tr>
<td>5</td>
<td>LUTESCENS 210.99.10*2/… x LUTESCENS 307-97-23/…</td>
<td></td>
</tr>
<tr>
<td>6</td>
<td>LUTESCENS 210.99.10*2/… x LUTESCENS 307-97-23/…</td>
<td>+</td>
</tr>
<tr>
<td>7</td>
<td>LUTESCENS 210.99.10*2/… x LUTESCENS 307-97-…</td>
<td>+</td>
</tr>
<tr>
<td>8</td>
<td>LUTESCENS 210.99.10*2/… x LUTESCENS 307-97-23/11/CROC_1/…</td>
<td></td>
</tr>
<tr>
<td>9</td>
<td>LUTESCENS 210.99.10*2/4/… x LUTESCENS 307-97-23/11/CROC_1/…</td>
<td>+</td>
</tr>
<tr>
<td>10</td>
<td>LUTESCENS 210.99.10*… x LUTESCENS 307-97-23/11/CROC_1/…</td>
<td>+</td>
</tr>
<tr>
<td>11</td>
<td>LUTESCENS 210.99.10… x LUTESCENS 307-97-23/11/CROC_1/…</td>
<td>+</td>
</tr>
<tr>
<td>12</td>
<td>LUTESCENS 307-97-23/11/CROC_1/… x TERTSIYA/3/SRN/AE.SQUARROSA (358)/…</td>
<td>+</td>
</tr>
<tr>
<td>13</td>
<td>LUTESCENS 307-97-23/11/CROC_1/…</td>
<td>+</td>
</tr>
<tr>
<td>14</td>
<td>LUTESCENS 307-97-23/11/CROC_1/… x LUTESCENS 210.99.10*2/…</td>
<td>+</td>
</tr>
<tr>
<td>15</td>
<td>LUTESCENS 307-97-23/11/CROC_1/… x LUTESCENS 210.99.10…</td>
<td>+</td>
</tr>
<tr>
<td>16</td>
<td>LUTESCENS 307-97-23/11/CROC_1/… x LUTESCENS 210.99.10*2/…</td>
<td>+</td>
</tr>
<tr>
<td>17</td>
<td>LUTESCENS 307-97-23/11/CROC_1/… x LUTESCENS 210.99.10*2/…</td>
<td>+</td>
</tr>
</tbody>
</table>

Figure 1. Amplification products of leaf and stem rust resistant genes, where M – 100 bp marker; \( Lr10 – 310 \) bp; \( Lr13 – 120 \) bp; \( Lr16 – 180 \) bp; \( Lr19 – 130 \) bp; \( Lr34 – 150-229 \) bp; \( Lr39 – 190-280 \) bp; \( Sr24 – 500 \) bp; \( Sr26 – 207 \) bp; OK – negative control; \( M – 50 \) bp marker.
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) Shortandinskaya 125 x Lyutescens 86-91-94-1 (Шортандинская 125 х Лютеценс 86-91-94-1) +
28 Ilinskaya x Kazakhstanskaya 19 (Ильинская х 
Казахстанская 19) + + +
29 Omskaya 35 x Shortandinskaya (Омская 35 х 
Шортандинская улучшенная) + +
30 Omskaya 33 x Tselinnaya 24 (Омская 33 х 
Целинная 24) + +
31 Saratovskaya 51 x Aktyubinka (Саратовская 
51 х Актюбинка) +
32 Karabalykskaya 90 x Lyutescens 2/10-99 (Карабалыкская 90 х Лютеценс 2/10-99) + +
33 Karabalykskaya 4 x Karabalykskaya 90 (Карабалыкская 4 х 
Карабалыкская 90) + +
34 Karabalykskaya 7 x Sary-Arka (Карабалыкская 7 х 
Сары-Арка) + + +
35 Aktobe 39 (Актюбе 39) +
36 Stepnaya 2 (Степная 2) + +
37 Stepnaya 50 (Степная 50) + +
38 Ekada 113 (Экада 113) + + +
39 Karabalykskaya 90 x Lyutescens 2/10-99 (Карабалыкская 90 х Лютеценс 2/10-99) + +
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) +
Lr10 gene originated from Triticum aestivum L chromosome arm 1A [30]. Another rust-resistant gene Lr13, identified in “Manitou” Canadian wheat cultivar, is probably the most common and extensively spread gene over a large area [31]. 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 [32]. Nevertheless, Lr13 still demonstrates good resistance in field experiments in combination with other rust-resistant genes [14,33,34] caused by *Puccinia triticina* Eriks., is a common and widespread disease of wheat (*in Triticum aestivum* L...). Similarly, Lr19 shows high resistance in combination both at the seedling and adult plant stages [14].

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 [35,36] located in chromosome 3D, were designated Sr24 and Lr24. The gene in Agatha for resistance to *P. graminis tritici* was designated Sr25 and is linked with Lr19 in chromosome 7D. Both Agatha and Agatha possess additional genes for resistance to certain cultures of *P. graminis tritici*. Sr24 is considered a valuable source of resistance for wheat-breeding purposes, but Sr25 conferred an inadequate level of resistance to adult plants. A translocation from an A. elongatsum chromosome to wheat chromosome 6A, present in Australian cultivars Eagle, Kite and Jabiru, carries a third gene, Sr26, for stem rust resistance... DOIs:10.1071/AR9770037,10.0004-9409,journal Abbreviation:Aust. J. Agric. Res.,language:en,pages:37,source:DOI.org (Crossref). Sr26 was also derived from *Agropyron elongatum (Thinopyrum ponticum)* and was introduced to wheat chromosome 6A [23,37] where isolate from wheat Sr26 and Sr61
, with both genes independently introduced as alien chromosome introgressions from tall wheat grass (*in Thinopyrum ponticum*). Its continued resistance was confirmed towards *Pgt* pathotypes in combination with Sr2 and Sr24 resistance genes [37,38] initiated at the University of Sydney in 1919, have continued without interruption to the present day. The population structure of *Pgt* over the past 85 years has been strongly influenced by exotic introductions in 1925 (race 126). The relevance of this gene remains, as it keeps increasing in the wheat-growing area. However, from 1978 to 1985, pathotype 343-1,2,3,5,6 predominated in all regions. It is suggested that this pathotype was repeatedly derived from pathotype 326-1,2,3,5,6 at widely separated locations, and that these events facilitated its widespread increase. Another significant event was the specialization of P. *triticum* on triticale. Survey data suggest that pathotype 34-2,12, which rendered cultivar Coro susceptible, developed from pathotype 34-2, possibly during 1979. A second pathotype which attacked cultivar Satu (designated 34-2,12,13).

Lr16 was first reported in Canada and found in Selkirk variety [40]. As mentioned in the literature review, Lr16 was originated from wheat chromosome arm 2BS and assigned using microsatellite markers [41]. 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 [42].

The Lr34 gene is known to be present in lots of wheat cultivars and is described as a first-cloned gene that confers partial resistance to multiple pathogens [12]. Gene is positioned on the 7D chromosome [43]. 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 or alone (Table 2).

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 [44]. 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.

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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LITERATURE


25. Мынбаева Д.О., Жунусбаева Ж.К, Бегманова М.О,


REFERENCES


10. Rslayev A.S., Rslayev Sh.S. Principal approaches and achievements in studying race composition of wheat stem


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 исследовано 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 пятидесяти 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.

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

ПЦР-МАРКЕРЛЕРДІ ПАЙДАЛАНА ОТЫРЫП, ҚАЗАҚСТАНДЫҚ БИДАЙДЫҢ ЖАНА СОРТТАРЫҢ САБАҚ ЖӘНЕ ЖАПЫРАҚ ТАТТАРЫНА ТОЗІМДІЛІК ГЕНДЕРІНІҢ СКРИНИНГІ

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Кілттік сөздер: сабақ таты, жапырақ таты, бидай, Lr және Sr гендері, ПЦР маркерлер, ауылшаруашылық стационарлары.