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**IDENTIFICATION WHEAT GENOTYPES RESISTANT  
TO TAN SPOT *PYRENOPHORA TRITICI-REPENTIS***

**Abstract.** Intensified wheat production, changes in cultural practices including shifts from conventional tillage to reduced tillage practices, and wheat monoculture involving cultivation of susceptible cultivars has resulted in development of tan spot to epidemic proportions in Kazakhstan. *Pyrenophora tritici-repentis*, causal agent of tan spot on wheat. In recent years, there has been increasing distribution and harmfulness of *P. tritici-repentis* on wheat. The aim of the study was to identify and select wheat germplasm resistant to tan spot *P. tritici-repentis* using molecular markers. The results of field evaluation showed resistant reaction to tan spot in 76 wheat varieties (68%). Molecular screening of wheat germplasm was carried out based on the reaction to the fungal inoculum and to host-specific toxins (HST) produced by the *P. tritici-repentis*. The wheat germplasm insensitive to the toxins HST Ptr ToxA and Ptr ToxB was selected. As a result of molecular screening of 111 wheat genotypes using SSR marker *Xfcp623* linked to insensitivity gene to the selective toxin Ptr ToxA of tan spot, 31 carriers of effective *tsn1* gene were identified, which accounted for 27,9% of the genotypes studied. Ten samples of wheat (Jubileynaya 60, TOO11/TOOOO7, F3.71/TRM/VORONA/3/OC14, NANJTNG 82149 KAUZ, ECHA/LI115, Akmola 2, Kazakhstanskaya rannespelaya, Kazakhstanskaya 25, 428g/MK-122A and 190-Naz/GF55) are characterized with complex resistance to the races Ptr 1 and 5, as well as to 2 toxins (ToxA and ToxB) and to the *Septoria nodorum blotch* isolate SNB7k. 20 promising wheat lines resistant to tan spot were selected. These genotypes also showed a moderate and high level of field resistance and recommended to use in the breeding programs for resistance to tan spot.

**Key words:** wheat, tan spot, resistance genes, molecular markers.

**Introduction.** The Kazakhstan is one of the major wheat producers in the world. However, diseases and pests play an important role in yield reduction in Kazakhstan. Tan spot is one of the most harmful diseases of soft and hard wheat in many agricultural regions of the world including Kazakhstan. The causative agent of this disease is the homotallic ascomycete *P. tritici-repentis* (Died.) Drechsler; imperfect stage *Drechslera tritici-repentis* (Died.) Shoem. In Central Asia the disease was discovered in 1980s in Tajikistan and in recent years it has spread throughout Central Asia and Kazakhstan [1,2,3].

Five toxins (Ptr ToxA, ToxB, ToxC, and 2 toxins, united in a group Ptr ToxD) have been identified; three of them are well characterized while two are tentative. The *Tsn1* – Ptr ToxA, *Tsc2* – Ptr ToxB, and *Tsc1* – Ptr ToxC interactions have all been shown to play significant roles in the development of tan spot in common (hexaploid) wheat [4,5].

*P. tritici-repentis* isolates has been grouped in 8 races based on their ability to produce two distinct symptoms, necrosis and/or chlorosis on appropriate wheat differential [6]. Races 1 and 2 of *P. tritici-repentis* produce a host-selective toxin (HST), Ptr ToxA that induces necrosis symptoms [7]. Ptr ToxA is a well-characterized HST of *P. tritici-repentis* and the gene that encodes for Ptr ToxA production including the endogenous promoter has been cloned [8]. *Tsn1*, a single dominant gene that conditions sensitivity to Ptr ToxA on the long arm of chromosome 5B, has recently been cloned [9, 10]. Eight major genes for resistance to tan spot (*Tsr1-Tsr6*, *Tsr Har*, *TsrAri*) have been characterized and designated [11]. They located on chromosomes 2BS, 3A, 3BL, 3DS and 5BL.

In the CIS countries, the pathogen in Moldova, Ukraine, Belarus, Central Asia and Kazakhstan was found [12]. There are a number of studies on the racial composition of *P. tritici-repentis* in Asia and Kazakhstan. The greatest diversity was observed in Azerbaijan, where races 1, 2, 3, 5, 7, and 8 were identified, and in Syria, where races 1, 3, 5, 7, and 8 were detected; the little variation was found in the virulence of isolates from Kazakhstan (race 1 and race 2) [1]. It has been revealed that race 1 is the most widespread race in Central Asia and Kazakhstan (87%), and races 2, 3 and 4 were minor [13]. It was found that races 1 and 2 dominate in the North Caucasus in Russia, and races 1 and 8 *P. tritici-repentis* dominate in Kazakhstan [14]. The results of previous studies indicate the possibility of identifying recessive alleles of genes resistant to *P. tritici-repentis* toxins using molecular markers [15,16]. Since Ptr ToxA toxin can be synthesized in races 1, 2, 7, and 8, and race 1 is widespread in Kazakhstan, the present study is dedicated to the search for gene carriers of resistance to Ptr ToxA toxin.

Currently, there is an increasing prevalence and increased damage of wheat by tan spot in Kazakhstan. The majority of commercial wheat cultivars currently grown in Kazakhstan are still susceptible to tan spot. The presence and activation of *P. tritici-repentis* requires the rapid development of new varieties resistant to disease. The relevance of such studies is due to the need to develop genetically diverse sources of resistance, donors and promising wheat lines that can be used in breeding of resistant varieties. The main objective of this study was the identification of wheat genotypes resistant to tan spot *P. tritici-repentis*.

**Materials and methods.** A collection of 111 common wheat germplasms, including elite lines and cultivars of wheat from Kazakhstan, Russia and CIMMYT evaluated for *P. tritici-repentis* resistance and were characterized using the molecular markers. The field experiments conducted at the Southeast Kazakhstan, Kazakh Research Institute of Agriculture and Plant Growing (KRIAPG), Almalybak (43°13'N, 76°36'E, and 789 masl), Almaty Reg., in the 2017-2018 crop seasons. The experiment conducted in a completely randomized design with three replications. The field evaluation of adult plants assessed three times according to the scale for appraising the foliar intensity of diseases [17] in the modification for tan spot [18]. The standard international wheat differentials included Glenlea and Salamouni cultivars, as well as 6B662 and 6B365 lines and used in the field and seedling tests.

Selection of resistant wheat genotypes based on germplasm screening against fungal inoculum and HST selective toxin of *P. tritici-repentis* was carried out on the basis of HST tests. The purified HST toxins provided by foreign collaborator, Dr. Ali S., University of South Dakota, USA. Toxins injected into wheat leaves. The presence or absence of necrosis / chlorosis symptoms on the infiltrated side of the leaf indicates sensitivity or insensitivity to HST.

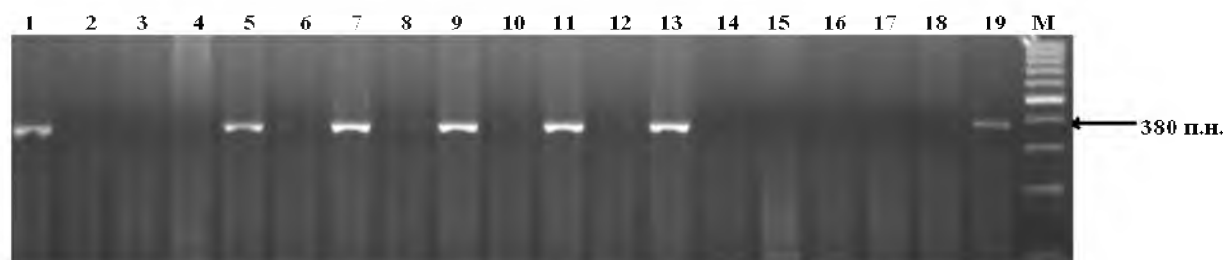
Genomic DNA extracted at two-leaf seedling stage for each individual plant using the CTAB method [19]. DNA concentration measured using a spectrophotometer SmartSpecTMPlus (Bio RAD). The DNA concentration for each sample was adjusted to 30 ng/μl. Samples were genotyped using the SSR marker *Xfcp623* designed to detect alleles of the *Tsn1* gene. The sequence of primers and PCR reaction conditions are given by [10]. The carriers of the *Tsn1* gene was also were detected using PCR protocol for SSR marker *Xfcp1* published at the WheatCAP website <http://maswheat.ucdavis.edu/protocols>]. The amplification products were separated on 2%-agarose gels, to determine the length of the amplification fragment 100 bp DNA Ladder (Ferments, Lithuania) was used. Gels were visualized on Gel Documentation System (Gel Doc XR+, BIO-RAD, Hercules, USA) for documentation of allele types in cultivars. Wheat entries 6B662 and Glenlea served as positive and negative controls, respectively.

**Results.** The results of field evaluation the resistance of 111 genotypes of wheat to tan spot showed, that immune and resistant (0 - 10%) were 76 varieties (68%) of the total number of wheat entries. The immune type of reaction to tan spot demonstrated 16 varieties of wheat, including Princes, Koks, Opaks 18, Odesskaya 120, Pyrotiks-50, Polovchanka, Raminal, Rasad, Sanzar 8, Taza, Tyniysh, Umanka, Sharora and Erythrospermum 78. The most susceptible varieties were Azharly, Basar, Batyr, Bulava, Bezostaya 1, Kyzylbidai, Lutescens 9 and others. Thus, the results of the field evaluation of tan spot allowed to rank the material studied on the level of resistance. Immune and resistant reaction type to tan spot showed 76 wheat cultivars.

In previous studies, we used markers *Xfcp1*, *Xfcp393*, *Xfcp394* and *Xfcp620*. Our results using these markers enabled the screening of a large number of wheat accessions for resistance to the Ptr ToxA [15, 16]. However, the repeatability and matching molecular data and phytopathological evaluations was not

always complete. With further development of PCR, we found, that the most adequate for the identification of carriers of resistance to tan spot is a molecular marker *Xfcp623* [20,21,22]. This functional marker was developed by Faris et al., 2013 as a result of mapping, sequencing and cloning of the *Tsn1* locus (intron 5). From a practical point of view this marker is the most effective and reliable [4].

In this regard, to identify genes *Tsn1* and *tsn1* in the studied wheat material the SSR marker *Xfcp623* was used. As an example, the results of the PCR amplification products, when the *Xfcp623* primers were tested on 17 wheat genotypes, are shown in the figure. Marker *Xfcp623* formed fragment size 380 bp, which is associated with a dominant allele *Tsn1* sensitive to ToxA *P. tritici-repentis*.



DNA amplification profile for of wheat cultivars and lines obtained with diagnostic marker *Xfcp623* linked to the *Tsn1* gene sensitive to Ptr ToxA. 1–Kazakhstanskaya 4, 2–Kazakhstanskaya 19, 3–Omskaya 28, 4–Omskaya 35, 5–Zhalyln, 6–Kargaly 9, 7–Karaspan, 8–Akmola 3, 9–Severyanka, 10–Albidum 31, 11–BR35/BR14, 12–CEP80111/VEE, 13–ALTAR 84/AE, 14–TPAP#1/OPATA, 15–CROC 1AE, 16–TALHUENJNJA, 17–Kenzhegaly, 18–Salamouni (the insensitive control for toxin Ptr ToxA, carrier of recessive gene *tsn1*), 19–Glenlea (negative control), M – marker for molecular weight (Gene Ruler 100 bp DNA Ladder)

As shown in figure, 6 out of 17 samples (Kazakhstanskaya 4, Zhalyln, Karaspan, Severyanka, BR35/BR14, ALTAR 84/A) had polymorphic band identical to molecular marker *Xfcp623*, linked the dominant *Tsn1* allele conferring toxin Ptr ToxA sensitivity. Ten entries including Kazakhstanskaya 19, Omskaya 28, Omskaya 35, Kargaly 9, Akmola 3, Albidum 31, CEP80111/VEE, TPAP#1/OPATA, CROC 1AE, TALHUENJNJA, and Kenzhegaly showed null-allele, linked the recessive *tsn1* allele conferring toxin Ptr ToxA insensitivity. Thus, of the 17 analyzed promising wheat lines 10 wheat genotypes insensitive to the ToxA toxin of *P. tritici-repentis* were identified.

As a result of molecular screening of total 111 wheat genotypes using SSR marker *Xfcp623*, 31 carriers of *tsn1* gene accounted for 27,93% of the samples studied were identified. It should be noted that the phytopathological evaluation of wheat samples in which the genes for resistance to tan spot toxins were found, showed a high and moderate degree of field resistance (5-15%) to diseases. The association between resistance to tan spot and the presence of a toxin toxicity gene ToxA, *tsn1* was noted. The correspondence between phenotypic and molecular analyzes was 95-98%.

Molecular screening of wheat germplasm and screening based on the reaction to the fungal inoculum and to HST toxins allowed selecting of wheat genotypes resistant to leaf spot diseases based. As an example, the table shows the 10 most resistant and the 10 most sensitive genotypes to the the 2 races and toxins of *P. tritici-repentis* (Ptr), and to the race of *S. nodorum* blotch (SNB7k). In the table the results of PCR to identify genes for resistance to toxin Ptr Tox A, as well as the response to fungal inoculum: race 1 of Ptr, toxin HST ToxA, race 5 of Ptr, toxin HST ToxV, race of Septoria SNB7k has shown.

In PCR using SSR marker *Xfcp1* first 10 genotypes formed DNA fragment of 374 bp which is associated with the presence of the recessive allele *tsn1*, insensitive to Ptr ToxA, and the next 10 wheat samples formed fragment of 402 bp, typical for dominant allele *Tsn1*, susceptible to Ptr ToxA. Thus, the complex resistance to two races of Ptr (1 and 5), two toxins (HST ToxA and HST ToxB) and the race of Septoria SNB7k were found in Kazakhstani commercial varieties (Yubileynaya 60, Jubileynaya 60, Akmola 2, Kazakhstanskaya rannespelaya, Kazakhstanskaya 25), as well as in developed in our laboratory advanced lines (428g/MK-122A and 190-Naz/GF55), and aslso lines from CIMMYT (TOO11/TOOOO7, F3.71/TRM/ VORONA/3/OC14, NANJTNG 82149 KAUZ and ECHA/LI115). Using the technology of selection for HST-toxins and marker assisted selection, a new wheat material adapted for Kazakhstan, resistant to the aggressive toxins of LSD, was selected.

Selection of disease resistant wheat genotypes based on germplasm screening using inoculum of fungi and HST toxins

Name of entry	Marker <i>Xfep1</i>		Reaction to inoculum of Ptr				
	I	S	Race 1	HST ToxA	Race 5	HST ToxB	SNB7k
Jubileynaya 60	374 II.H.	–	1	I	1	I	1
TOO11/TOOOO7	374 II.H.	–	1	I	2	I	1
F3.71/TRM/VORONA/3/OC14	374 II.H.	–	1	I	2	I	1
NANJTNG 82149 KAUZ	374 II.H.	–	1	I	2	I	2
ECHA/LI115	374 II.H.	–	1	I	2	I	2
Akmola 2	374 II.H.	–	3	I	2	I	2
Kazakhstanskaya rannepelaya	374 II.H.	–	1	I	2	I	2
Kazakhstanskaya 25	374 II.H.	–	2	I	1	I	3
428g/MK-122A	374 II.H.	–	1	I	1	I	1
190-Naz/GF55	374 II.H.	–	1	I	1	I	1
Bogarnaya 56	–	402 II.H.	4	S	2	I	4
Bulava	–	402 II.H.	4	S	2	I	5
Mereke75	–	402 II.H.	4	S	1	I	5
Nureke	–	402 II.H.	4	S	2	I	4
Steklovinaya 24	–	402 II.H.	3	S	2	I	4
Saratovskaya 42	–	402 II.H.	5	S	2	I	4
Farabi	–	402 II.H.	4	S	2	I	4
Karlygash	–	402 II.H.	4	S	3	I	2
Gozgon	–	402 II.H.	4	S	1	I	5
Kysylbiday	–	402 II.H.	4	S	2	I	2

Note: Ptr – tan spot, SNB – Septoria, HST ToxA and ToxB – tan spot toxins, SNB7k – race od Septoria; I – insensitivity, S – sensitivity to toxins.

**Discussion.** ToxA toxin is synthesized by races 1, 2, 7, and 8, and the ToxB toxin is synthesized by races 2, 7, and 8 [23]. Previous studies have shown that races 1 and 8 are widespread in Kazakhstan [14]. The comparative analysis of phenotypic and molecular data on the presence or absence of resistance genes and expression of resistance to disease in the field was carried out. Sensitivity to the toxin Ptr ToxA produced by isolates of race 1 (nec+chl-), controlled by one dominant gene *Tsn1*, located on the long arm of chromosome 5B [10]. It is assumed that the sensitivity to the toxin Ptr ToxA and susceptibility to necrosis of the fungus is controlled by the same gene [24]. The *Tsn1* gene responsible for sensitivity to the protein components of plant toxins, Ptr ToxA, produced by the fungus *P. tritici-repentis*; this toxin is one of the main factors associated with the development of *P. tritici-repentis* in susceptible wheat genotypes [25].

In this regard, the present study was aimed at assessing varieties and promising lines of wheat from Kazakhstan and abroad for resistance to race 1 and race 5 and sensitivity to toxins Ptr ToxA and Ptr ToxB *P. tritici-repentis*. The results of field evaluation showed resistant reaction to tan spot in 76 wheat varieties (68%); almost the same results were obtained in previous study [21]. Results molecular screening for resistance to tan spot obtained in this study contradict the previous data related to field evaluation to tan spot in Kazakhstan and in South Russia that showed a low level of resistance among most commercial wheat cultivars [26]. Based on our results, it is important to carry out breeding for resistance to most common races of pathogen.

For successful selection of immunity, international cooperation with CIMMYT is of great importance. Our studies have shown that varieties resistant to tan spot must be developed using a variety of germplasm. Broad based tan spot resistance sources from the CIMMYT may contribute to the resistance observed in our study and can be utilized to develop cultivars with broad-genetic base durable resistance to wheat tan spot.

**Conclusion.** Results of field phytopathological screening of 111 commercial wheat varieties tan spot allowed ranking the studied material according to the level of resistance. The immune and resistant type of reaction to tan spot showed 76 varieties of wheat. As a result of molecular screening of 111 wheat genotypes using SSR marker linked to insensitivity genes to the HST Ptr ToxA, 31 carriers of effective *tsn1* gene were identified, which accounted for 27,9% of the 111 samples studied. Based on the results of molecular screening and the study of the reaction of wheat samples to the inoculum and to the toxins of diseases, 10 disease-resistant lines have been identified. These genotypes also showed a moderate and high level of field resistance and recommended to use in the breeding programs for resistance to tan spot. The results of study are used in wheat breeding programs for tan spot resistance with the Marker Assisted Selection.

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#### ПИРЕНОФОРОЗГА *PYRENOPHORA TRITICI-REPENTIS* ТӨЗІМДІ БИДАЙ ГЕНОТИПТЕРІН ИДЕНТИФИКАЦИЯЛАУ

**Аннотация.** Бидай өндірісінің қарқынды дамуы, тәжірибие алаңында бидай өндірісінің өзгерістері, дәстүрлі топырақты өңдеуден минималды тәжірибиеге өту және төзімсіз бидай сорттарының монокультура ретінде өсіру пиренофороздың дамуының эпидемия көлеміне әкелін соқтырады. Пиренофороз дүниежүзінің көптеген ауылшаруашылық аймақтары мен Қазақстанның жұмсақ және қатты бидайының аса қауіпті ауруларының бірі болып табылады. Пиренофороздың қоздырушысы *Pyrenophora tritici-repentis*. Соңғы жылдары бидайда *P. tritici-repentis*-тің дамуы мен қауіптілігі бақылануда. Қазіргі таңда бес токсин (Ptr ToxA, ToxB, ToxC және 2 токсин, Ptr ToxD тобына біріктірілген) идентификацияланған.

Зерттеудің мақсаты – молекулалық әдістерді қолданып, *P. tritici-repentis* пиренофорозға төзімді бидай гермоплазмаларын анықтау және іріктеу. Дала жағдайында бағалау нәтижесінде бидайдың 76 сорты (68 %) пиренофорозға төзімді реакция танытты. Пиренофорозға 16 бидай сорты иммунды реакция типін көрсетті, олар Princes, Коксу, Опакс 18, Одесская 120, Пиротрикс-50, Половчанка, Раминал, Расад, Санзар 8, Таза, Тунгыш, Уманка, Шарора және Эритроспермум 78. Ажарлы, Басар, Батыр, Булава, Безостая 1, Кызылбидай, Лютеценс 9 және басқада сорттар ауруға төзімсіз болды. *P. tritici-repentis* продуцирлейтін, (HST) ие қожайынның спецификалық токсини мен саңырауқұлақ инокулятының реакция негізінде бидайдың ұрықтық плазмасының молекулалық скринингі жүргізілді. HST Ptr ToxA мен Ptr ToxB токсиндеріне төзімді бидай гермоплазмасы іріктелінді. Пиренофороздың Ptr ToxA селективті токсиніне төзімді генмен байланысқан SSR типті *Xfcp623* маркерлері қолданылып, бидайдың 111 генотипіне молекулалық скрининг жүргізу нәтижесінде, эффективті *tsn1* генінің 31 тасымалдаушысы идентификацияланды, ол зерттелген генотип-тердің 27,9% құрады. Токсиндерге төзімділік гендері бар бидай үлгілерін фитопатологиялық бағалау нәтижесінде ауруға дала жағдайында орташа және жоғары (5-15 %) төзімділік танытты. Ауруға төзімділік пен ToxA токсиніне төзімді *tsn1* генінің арасындағы байланыс анықталынды. Молекулалық және фенотиптік анализдердің арасындағы сәйкестілік 95-98 % құрады.

SSR-типті *Xfcp1* маркерін қолданып ПЦР анализ жүргізу нәтижесінде Ptr ToxA-ға төзімді *tsn1* рецессивті генімен байланысқан көлемі 374 ж.н. құрайтын ДНК фрагменттері бар 10 генотип анықталынды, сонымен қатар Ptr ToxA-ға төзімсіз көлемі 402 ж.н. құрайтын *Tsn1* доминантты гені бар бидайдың 10 үлгісі идентификацияланды.

Бидайдың 10 үлгісі (Юбилейная 60, TOO11/TOOOO7, F3.71/TRM/ VORONA/3/ OC14, NANJTNG 82149 KAUZ, ECHA/LI115, Акмола 2, Казахстанская раннеспелая, Казахстанская 25, 428g/МК-122А и 190-Naz/GF55) раса 1 мен 5-ке, сонымен қатар 2 токсинге (ToxA мен ToxB) және *Septoria nodorum blotch* SNB7k изолятына кешенді төзімділігімен сипатталды. Зерттеу нәтижесінде, пиренофорозға төзімді, бидайдың перспективті линиялары таңдалынды. Бұл генотиптер дала жағдайында да орташа және жоғары төзімділік танытты және пиренофорозға төзімділік селекция бағдарламаларында қолдануға ұсынылды.

**Түйін сөздер:** бидай, пиренофороз, төзімділік гендері, молекулалық маркерлер.

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### ИДЕНТИФИКАЦИЯ ГЕНОТИПОВ ПШЕНИЦЫ, УСТОЙЧИВЫХ К ПИРЕНОФОРОЗУ *PYRENOPHORA TRITICI-REPENTIS*

**Аннотация.** Интенсивное производство пшеницы, изменения в практике возделывания пшеницы, включающие переход от традиционной обработки к минимальной обработке почвы, и монокультура пшеницы, включающая возделывание восприимчивых сортов, способствуют развитию пиренофороза до масштабов эпидемии. Пиренофороз является одним из самых вредных заболеваний мягкой и твердой пшеницы во многих сельскохозяйственных регионах мира, включая Казахстан. *Pyrenophora tritici-repentis* – возбудитель пиренофороза пшеницы. В последние годы наблюдается рост распространения и вредоносности *P. tritici-repentis* на пшенице. К настоящему времени идентифицировано пять токсинов (Ptr ToxA, ToxB, ToxC и 2 токسينа, объединенных в группу Ptr ToxD).

Целью исследования было выявление и отбор гермоплазмы пшеницы, устойчивой к пиренофорозу *P. tritici-repentis*, с использованием молекулярных маркеров. Результаты полевой оценки показали устойчивую реакцию к пиренофорозу у 76 сортов пшеницы (68%). Иммунный тип реакции к пиренофорозу показали 16 сортов пшеницы, в том числе Princes, Коксу, Опакс 18, Одесская 120, Пиротрикс-50, Половчанка, Раминал, Расад, Санзар 8, Таза, Тунгыш, Уманка, Шарора и Эритроспермум 78. Наиболее восприимчивыми оказались сорта Ажарлы, Басар, Батыр, Булава, Безостая 1, Кызылбидай, Лютеценс 9 и другие. Молекулярный скрининг гермоплазма пшеницы проводился на основе реакции к инокулуму гриба и специфические для хозяина токсины (HST), производимые *P. tritici-repentis*. Отобрана гермоплазма пшеницы, нечувствительная к токсинам HST Ptr ToxA и Ptr ToxB. В результате молекулярного скрининга 111 генотипов пшеницы с использованием SSR маркера *Xfcp623*, сцепленного с геном нечувствительности к селективному токсину Ptr ToxA пиренофороза, был идентифицирован 31 носитель эффективного гена *tsn1*, что составило 27,9% от числа изученных генотипов. Фитопатологическая оценка образцов пшеницы, в которых были обнаружены гены устойчивости к токсинам, показала высокую и умеренную степень полевой устойчивости (5-15%) к болезням. Была отмечена связь между устойчивостью к болезни и наличием нечувствительного к токсину ToxA гена *tsn1*. Соответствие между фенотипическим и молекулярным анализами составило 95-98%.

В результате ПЦР анализа с использованием SSR-маркера *Xfcp1* 10 генотипов формировали ДНК фрагмент размером 374 п.н., что указывает на наличие рецессивного гена *tsn1* нечувствительного к Ptr ToxA. Десять образцов пшеницы формировали фрагмент размером 402 п.н., характерный для доминантного гена *Tsn1*, чувствительного к Ptr ToxA. Выявлено десять образцов пшеницы (Юбилейная 60, ТОО11/ТОООО7, F3.71/TRM/ VORONA/3/ OC14, NANJTNG 82149 KAUZ, ЕЧА/Л1115, Акмола 2, Казахстанская раннеспелая, Казахстанская 25, 428g/МК-122А и 190-Naz/GF55), которые характеризовались комплексной устойчивостью к расам 1 и 5, к 2 токсинам (ToxA и ToxB), а также к изоляту *Septoria nodorum blotch* SNB7k. Таким образом, в результате исследований отобраны перспективные линии пшеницы, устойчивые к пиренофорозу. Эти генотипы также показали умеренный и высокий уровень полевой устойчивости и рекомендованы для использования в программах селекции на устойчивость к пиренофорозу.

**Ключевые слова:** пшеница, пиренофороз, гены устойчивости, молекулярные маркеры.

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