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Research Article

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Identification of promising wheat lines resistant to tan spot (*Pyrenophora tritici-repentis*)

Wheat tan spot (yellow spot) is one of the most widespread and dangerous fungal diseases of wheat, caused by the phytopathogenic fungus *Pyrenophora tritici-repentis*. The aim of the study is to identify resistance to tan spot in promising wheat lines based on phenotypic indicators and molecular screening. A comprehensive assessment of wheat samples was carried out by the biomass index (NDVI), resistance to pathogens (PTR, AUDPC) and molecular markers. It was found that NDVI varies from 65 to 82, while high values (> 75) correlate with resistance (R^2 = 0.652), and low values (<70) — with susceptibility (S). Resistant samples (12 pcs., PTR = 5–10), including the Salamouni variety, and susceptible ones (7 samples, PTR = 15–35) were identified. As a result of molecular screening, PCR analysis of all studied genotypes showed the presence of the recessive gene tsn1 in 11 wheat genotypes (64.7 %). The integral indicator AUDPC (mean=70.8) demonstrated high variability (CV>50 %) and extreme values (up to 165). Statistical analysis confirmed the stability of NDVI (CV=6.5–6.7 %) and significant variability of PTR/AUDPC, reflecting mixed resistance. The results emphasize the need for an in-depth study of the relationship of molecular markers with resistance to tan spot.

Keywords: wheat, tan spot, resistance genes, molecular screening, resistance, NDVI, AUDPC.

Introduction

Wheat (*Triticum aestivum* L.) is one of the most important staple crops, with demand expected to increase to 330 kg per capita per year by 2050. Wheat production faces numerous threats, with an estimated 10–16 % of global wheat yields lost due to pests and diseases [1-2]. However, its productivity is significantly reduced by fungal pathogens such as brown rust (*Puccinia recondita*), yellow rust (P. *striiformis f. sp. tritici*), and tan spot (*Pyrenophora tritici-repentis*), which are among the most dangerous diseases capable of causing large-scale economic losses [3–8].

In Kazakhstan, control of leaf spot disease (tan spot) mainly relies on the use of resistant varieties and fungicide treatments. However, this approach, especially when chemical agents are applied untimely (before the appearance of critical symptoms), is often associated with high costs for farmers.

A key aspect of effective disease control is accurate diagnosis at early infection stages and monitoring of disease progression. Traditional methods, such as visual assessment of the affected tissue area, are subjective, labor-intensive, and require significant time.

A pressing issue for the Kazakh agricultural sector is the late detection of pathogens, which leads to substantial yield reductions due to insufficient disease spread control in the fields.

Tan spot is a relatively new wheat disease that is widespread in many countries. It was first detected in the 1940s in the USA and Canada, and during the 1980s–90s in Western European countries. In eastern Canada, tan spot and septoria occur together; the former in drier zones and the latter in more humid areas. Along with helminthosporium leaf blight, it is a widespread wheat disease in South Asian countries where wheat is grown in rice-wheat crop rotations. Its aggressiveness is promoted by cultivation of susceptible varieties and widespread adoption of zero-tillage technology. Tan spot is widespread on winter and spring wheat in the southern, southeastern, and northern regions of Kazakhstan. The first signs of the disease appeared during

stem elongation of winter wheat; at heading, leaf infection of the upper canopy was 25–50 %, increasing to 75–100 % at the milky ripeness stage, with premature leaf drying [9-10].

Three effector-dominant susceptibility gene interactions are known: ToxA-*Tsn1*, which causes necrotic symptoms, and ToxB-*Tsc2* and ToxC-*Tsc1*, both causing chlorosis. The *Tsn1*-ToxA interaction in leaf spot development depends on the host's genetic background, with the wheat gene *Tsn1* being the main factor determining susceptibility. Lamari et al. (2003) noted that this interaction follows a gene-for-gene inverse model. Genotypes lacking the *Tsn1* gene are insensitive to the toxin [11–14]. However, Adhikari et al. (2009) suggested that ToxA recognition via Tsn1 may activate key genes involved in the host's defense response and signaling pathways [14].

Integrated plant disease management requires combining multiple strategies for effective disease control. For tan spot, using resistant wheat varieties is the best option for sustainable disease management. Host resistance is also the most cost-effective and environmentally safe method to combat the disease. Therefore, breeding resistant wheat varieties should be a primary goal in managing tan spot, including assessing the susceptibility of embryonic tissue to the disease.

The aim of this study is to identify tan spot resistance in promising wheat lines based on disease phenotypes and molecular screening. The results will provide valuable knowledge to regional wheat breeders and phytopathologists involved in developing tan spot management strategies.

Experimental

Seventeen promising wheat lines grown in the Almaty region were used as research material. These wheat samples were tested for brown rust in laboratory studies at both the seedling stage and on mature plants under field conditions. The differential varieties Glenlea and Salamouni were used as controls for the negative and positive Tsn1 gene, which controls resistance to wheat yellow spot.

The studies were conducted during the 2024 growing season at the experimental site of the Kazakh Research Institute of Agriculture and Crop Production (KAZNIIzIR), Almalybak village, Almaty region (N43°14'210"; E076°41'282"). The experiment was designed as a completely randomized block design with three replications. All plots were surrounded by one-meter-wide strips planted with the highly susceptible Morocco variety. The size of each individual plot was 3 m² (3 m by 7 rows at 15 cm spacing). All recommended cultivation methods for commercial fields were applied, including fertilization, irrigation, and other management practices.

During the study period, weather conditions were favorable for the development of brown rust (http://weatherarchive.ru as of April 22, 2024). The amount of precipitation exceeded the norm, which increased environmental humidity and facilitated effective infection of plants with *Pyrenophora tritici-repentis* spores.

Phytopathological assessment of adult plants for yellow spot, including type and severity of infection, was recorded and evaluated on leaves in late May and early June, when the plots were at the maturation and milk-wax ripeness stages, respectively. For phytopathological evaluation of tan spot severity caused by *P. tritici-repentis*, the percentage of leaf area affected by yellow spot was assessed using the Saari and Prescott scale [15], originally developed for septoria and modified by O.Yu. Kremneva [16]. This leaf infection severity scale for wheat uses the following gradations: 0 % — very high resistance; 1–5 % — high resistance; 6–20 % — resistance; 21–30 % — susceptibility; 31–50 % — susceptibility; 51–80 % — high susceptibility; 81–100 % — very high susceptibility.

The area under disease progress curve (AUDP) was also assessed in the field, calculated using the formula by Wilcoxson et al. [17]:

$$S = 1/2S(x1+x2)\,(t1-t2) + \ldots.\,(xn-1+xn)\,(tn-tn-1)$$

where,

S — area under disease progress curve;

x1 — disease intensity at the first assessment, %;

x2 — disease intensity at the second assessment, %;

xn — disease intensity at the last assessment, %;

(t1-t2) — number of days between the first and second assessments;

(tn-tn-1) — number of days between the last and penultimate assessments.

Molecular Screening Methods for the Tsn1 Gene Conferring Wheat Resistance to Leaf Spot. Genomic DNA extraction was performed according to the method proposed by Riede et al. [18]. DNA was isolated

from 5-day-old wheat seedlings for each individual sample using the CTAB method. DNA concentration was measured spectrophotometrically at a wavelength of 260 nm. DNA concentration in the working PCR solution was adjusted to 20 ng/µl. The PCR reaction mixture (25 µl) contained 2.5 µl genomic DNA, 1 µl of each primer (1 pM/µl) (SigmaAldrich, USA), 2.5 µl dNTP mix (2.5 mM dCTP, dGTP, dTTP, and dATP) (ZAO "Sileks", Russia), 2.5 µl MgCl2 (25 mM), 0.2 µl Taq polymerase (5 units/µl) (ZAO "Sileks", Russia), 2.5 µl 10X PCR buffer, and 12.8 µl ddH2O. PCR amplification was carried out on a Mastercycler amplifier (Eppendorf, Germany). Amplification products were separated on a 2 % agarose gel in TBE buffer (45 mM Tris-borate, 1 mM EDTA, pH 8) with ethidium bromide. A 100-bp DNA ladder marker (Fermentas, Lithuania) was used to determine fragment sizes. Results were visualized using a gel documentation system (Gel Doc XR+, BIO-RAD, Hercules, USA) [18].

The Normalized Difference Vegetative Index (NDVI) was measured using a portable Green Seeker device (Trimble Navigation Limited, USA). NDVI ranges from 0.00 to 1.0; the higher the value, the greater the resistance to diseases.

Results and Discussion

Climatic conditions during the 2024 growing season at the experimental site of the Kazakh Research Institute of Agriculture and Crop Production (Almalybak village, Almaty region) were generally favorable for the development and progression of foliar fungal diseases, including tan spot caused by *Pyrenophora tritici-repentis*. According to meteorological data obtained from the regional weather archive (weatherarchive.ru), the study period was characterized by increased precipitation compared to the long-term average, particularly during the critical stages of wheat growth.

Excess rainfall contributed to elevated air and canopy humidity, creating optimal conditions for spore germination, infection, and subsequent disease spread. Moderate temperatures combined with frequent precipitation events enhanced leaf wetness duration, which is a key factor promoting successful penetration and colonization of host tissues by *P. tritici-repentis*. These environmental conditions facilitated effective natural infection pressure in the field, ensuring reliable differentiation of wheat genotypes based on their disease responses. Overall, the prevailing climatic conditions during the 2024 growing season provided a suitable background for the evaluation of tan spot severity and allowed for an accurate assessment of resistance levels under field conditions with high disease pressure.

A comprehensive assessment of 19 wheat accessions (including promising lines CP_1–CP_17 and control varieties Glenlea and Salamouni) was conducted across four key parameters: plant biomass index (NDVI), field resistance to pathogens (PTR, AUDPC), and the presence of the PTR resistance gene. The results revealed significant relationships for breeding. According to the research results, the NDVI biomass index, which reflects the photosynthetic activity of plants, ranged from 65 to 82 (Tab. 1). The highest values were demonstrated by: CP_4_2024 (80), CP_11_2024 (80), CP_12_2024 (82) — these accessions are distinguished by an optimal physiological state, which is typical of stress-resistant plants. The lowest NDVI values were recorded for the promising CP_15_2024 line (65), with low values associated with severe disease pressure or exposure to abiotic stressors (e.g., drought). A positive correlation (R2 = 0.652) was identified: high NDVI values (>75) were associated with resistance (R), while low NDVI values (<70) were associated with susceptibility (S).

Table 1

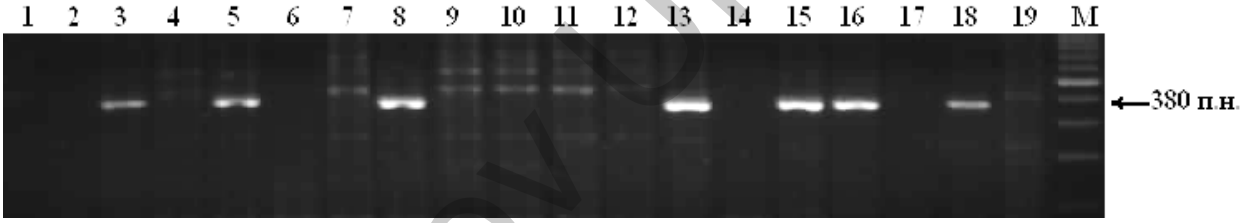
Results of a comprehensive study of promising wheat lines

№	Code of line	NDVI	Phytopathological evaluation to PTR	AUDPC	Molecular screening	
1	CP_1_2024	75	5	55	null	*tsn1*
2	CP_2_2024	78	10	65	null	*tsn1*
3	CP_3_2024	74	25	105	380	*Tsn1*
4	CP_4_2024	80	10	50	null	*tsn1*
5	CP_5_2024	70	25	110	380	*Tsn1*
6	CP_6_2024	72	10	60	null	*tsn1*
7	CP_7_2024	81	5	30	null	*tsn1*
8	CP_8_2024	70	15	70	380	*Tsn1*
9	CP_9_2024	73	10	35	null	*tsn1*

Continuation of Table 1

№	Code of line	NDVI	Phytopathological evaluation to PTR	AUDPC	Molecular screening	
10	CP_10_2024	75	10	40	null	*tsn1*
11	CP_11_2024	80	5	50	null	*tsn1*
12	CP_12_2024	82	5	55	null	*tsn1*
13	CP_13_2024	68	25	120	380	*Tsn1*
14	CP_14_2024	71	10	65	null	*tsn1*
15	CP_15_2024	65	25	135	380	*Tsn1*
16	CP_16_2024	68	25	70	380	*Tsn1*
17	CP_17_2024	75	10	40	null	*tsn1*
18	Glenlea	69	35	165	380	*Tsn1*
19	Salamouni	77	5	25	null	*tsn1*

Based on the phytopathological evaluation (PTR), resistant (R) accessions were identified: 12 accessions with damage scores of 5–10 (CP_1_2024, CP_2_2024, CP_4_2024, CP_6_2024, CP_7_2024, CP_9_2024, CP_10_2024, CP_11_2024, CP_12_2024, CP_14_2024, CP_17_2024 and the control cultivar Salamouni). Seven accessions with scores of 15–35 were classified as susceptible (S). The Glenlea cultivar had the highest score (35), confirming its status as a control cultivar for susceptibility. Molecular screening using PCR analysis of all studied genotypes revealed the presence of the recessive tsn1 gene in 11 wheat genotypes (64.7 %) and the presence of the dominant Tsn1 gene, which is resistant to the PTR ToxA toxin. Six samples (35.3 %) were found to contain DNA fragments of 380 bp (Fig. 1). Of the 19 wheat samples studied, six samples were found to contain 380 bp, and these genotypes are sensitive to the PtrToxA toxin.



1-CP_1_2024, 2- CP_2_2024, 3- CP_3_2024, 4- CP_4_2024, 5- CP_5_2024, 6- CP_6_2024, 7- CP_7_2024, 8- CP_8_2024, 9- CP_9_2024, 10- CP_10_2024, 11- CP_11_2024, 12- CP_12_2024, 13- CP_13_2024, 14- CP_14_2024, 15- CP_15_2024, 16- CP_16_2024, 17- CP_17_2024, 18- Glenlea (sensitive to toxin PtrToxA), 19- Salamouni (insensitive to the toxin PtrToxA)

Figure 1. Products of wheat DNA amplification using primers to the *Xfcp623* locus associated with the *Tsn1/tsn1* resistance gene

Table 2 presents the complete descriptive statistics of the studied promising wheat lines. Descriptive statistical analyses were performed for four key traits: normalized difference vegetation index (NDVI), tan spot severity (PTR), area under the disease progress curve (AUDPC), and molecular screening results. A total of 19 observations were included for each variable, with no missing values, ensuring complete datasets for all statistical evaluations.

NDVI values ranged from 65.0 to 82.0, with a mean of 73.84 and a median of 74.0, indicating relatively high and stable canopy greenness across the tested genotypes. The low coefficient of variation (CV = 6.5 %) and narrow interquartile range reflected limited dispersion and a high degree of uniformity among genotypes. The distribution of NDVI values was approximately symmetrical, as indicated by near-zero skewness (Pearson = 0.07) and negative kurtosis (Pearson = −1.02), suggesting a slightly flattened distribution relative to normality.

Tan spot severity (PTR) showed a much wider range, varying from 5.0 to 35.0, with a mean of 14.21 and a median of 10.0. The relatively high coefficient of variation (CV = 63.8 %) reflected substantial variability in disease response among genotypes. Positive skewness (Pearson = 0.76) indicated a right-tailed dis-

tribution, with a greater frequency of genotypes exhibiting low to moderate disease severity and fewer highly susceptible entries.

AUDPC values ranged from 25.0 to 165.0, with a mean of 70.79 and a median of 60.0, confirming pronounced differences in disease progression over time. The coefficient of variation (CV = 52.9 %) indicated considerable heterogeneity in resistance levels. The distribution was positively skewed (Pearson skewness = 1.03), suggesting that most genotypes exhibited relatively low AUDPC values, while a limited number showed strong disease development. The slightly positive kurtosis (Pearson = 0.13) reflected moderate peakedness of the distribution.

Molecular screening data were binary (0/1) and ranged from 0 to 1, with a mean value of 0.37, indicating that 36.8 % of the evaluated genotypes carried the targeted molecular marker(s). The distribution was characterized by a high coefficient of variation (CV = 130.9 %), which is typical for binary traits. The median value of 0.0 confirmed that the majority of genotypes lacked the marker, while positive skewness reflected the lower frequency of marker-positive entries.

Table 2

Results of descriptive statistics for the studied promising wheat lines

Statistic	NDVI	PTR	AUDPC	Molecular screening
Nbr. of observations	19	19	19	19
Nbr. of missing values	0	0	0	0
Obs. without missing data	19	19	19	19
Sum of weights	19	19	19	19
Breakdown per subsample (%)	100,000	100,000	100,000	100,000
Minimum	65,000	5,000	25,000	0,000
Maximum	82,000	35,000	165,000	1,000
Freq. of minimum	1	5	1	12
Freq. of maximum	1	1	1	7
Range	17,000	30,000	140,000	1,000
1st Quartile	70,000	7,500	45,000	0,000
Median	74,000	10,000	60,000	0,000
3rd Quartile	77,500	25,000	87,500	1,000
Sum	1403,000	270,000	1345,000	7,000
Mean	73,842	14,211	70,789	0,368
Variance (n)	22,975	82,271	1400,693	0,233
Variance (n-1)	24,251	86,842	1478,509	0,246
Standard deviation (n)	4,793	9,070	37,426	0,482
Standard deviation (n-1)	4,925	9,319	38,451	0,496
Variation coefficient (n)	0,065	0,638	0,529	1,309
Variation coefficient (n-1)	0,067	0,656	0,543	1,345
Skewness (Pearson)	0,066	0,764	1,029	0,546
Skewness (Fisher)	0,072	0,831	1,119	0,593
Skewness (Bowley)	-0,067	0,714	0,294	1,000
Kurtosis (Pearson)	-1,022	-0,724	0,125	-1,702
Kurtosis (Fisher)	-0,955	-0,561	0,562	-1,856
Standard error of the mean	1,130	2,138	8,821	0,114
Lower boundon mean (95 %)	71,469	9,719	52,257	0,130
Upper boundon mean (95 %)	76,216	18,702	89,322	0,607
Standard error of the variance	8,084	28,947	492,836	0,082
Lower boundon variance (95 %)	13,846	49,583	844,155	0,140
Upper boundon variance (95 %)	53,036	189,917	3233,383	0,537

Continuation of Table 2

Statistic	NDVI	PTR	AUDPC	Molecular screening
Mean absolute deviation	4,061	7,950	29,584	0,465
Median absolute deviation	4,000	5,000	20,000	0,000
Geometric mean	73,686	11,572	62,228	-
Geometric standard deviation	1,069	1,942	1,678	-
Harmonic mean	73,531	9,523	55,122	-
nIQR	5,560	12,973	31,505	0,741
Qn	6,178	10,297	30,890	0,000

For all traits, 95 % confidence intervals for the mean were calculated, providing reliable estimates of central tendency under field conditions. Overall, the statistical analysis demonstrated low variability for NDVI, moderate to high variability for disease-related traits (PTR and AUDPC), and high heterogeneity in molecular screening results, allowing robust differentiation of wheat genotypes based on physiological performance, disease resistance, and genetic background.

Figure 2 presents Box plot visualizations of the studied parameters in the promising wheat lines. The obtained data emphasize the need for deeper investigation of the relationships between molecular markers and disease resistance.

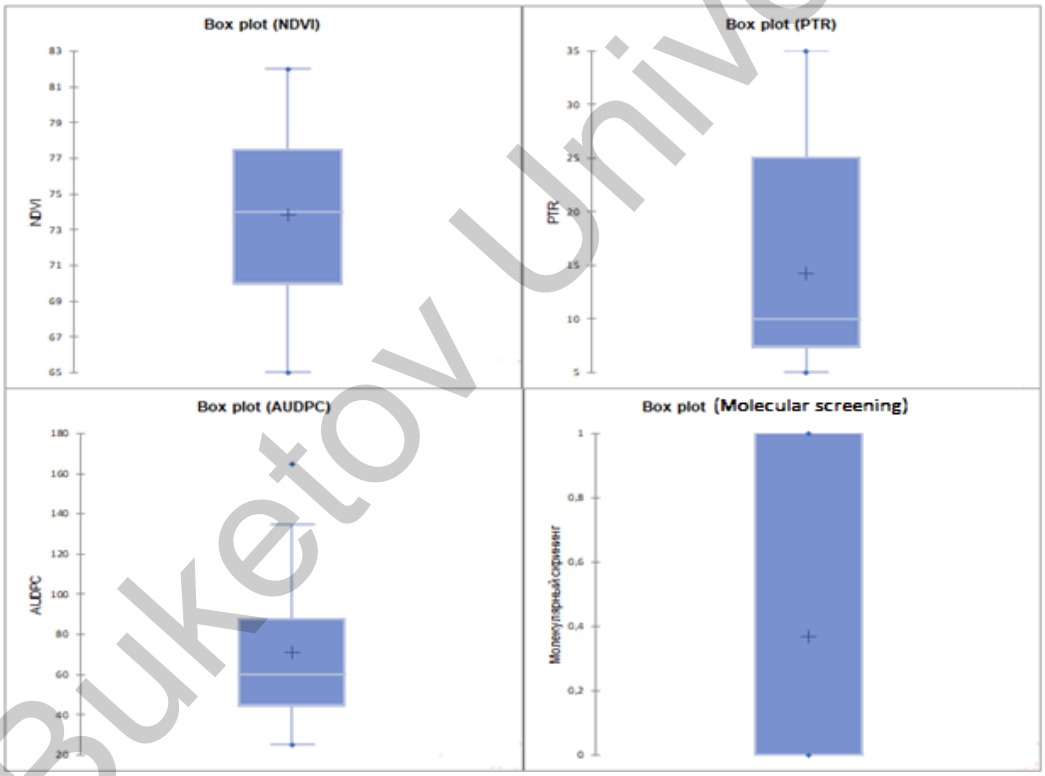


Figure 2. Box plot diagram of the studied promising wheat lines

Box plot visualizations illustrating the distribution of NDVI, tan spot severity (PTR), AUDPC, and molecular screening results among the studied promising wheat lines. The box plots display the median, interquartile range, and minimum–maximum values for each trait, highlighting differences in variability and distribution patterns. NDVI values show a relatively narrow dispersion, indicating stable physiological performance across most genotypes, whereas PTR and AUDPC exhibit wider variability, reflecting contrasting levels of disease response and progression. Molecular screening data demonstrate a binary distribution corresponding to the presence or absence of the *Tsn1/tsn1* alleles. Overall, the box plot analysis emphasizes heterogeneity among wheat genotypes and underscores the importance of integrating phenotypic and molecular data to better understand the genetic basis of resistance to *Pyrenophora tritici-repentis*.

Conclusion

The results of this study confirm that the climatic conditions of the 2024 growing season provided a reliable and informative background for evaluating wheat resistance to tan spot caused by *Pyrenophora tritici-repentis*. Elevated precipitation and moderate temperatures ensured high natural infection pressure, allowing clear differentiation of genotypes based on physiological performance, disease severity, and genetic composition. Integrated analysis of NDVI, phytopathological traits (PTR and AUDPC), and molecular screening revealed substantial variability among the 19 studied wheat accessions. NDVI values showed low variability and strong association with disease response, confirming NDVI as a reliable indicator of plant health under disease pressure. A positive relationship between NDVI and resistance ($R^2 = 0.652$) demonstrated that genotypes with higher biomass stability exhibited reduced disease severity and slower disease progression. Phytopathological assessments identified twelve resistant accessions with low PTR and AUDPC values, while seven accessions were classified as susceptible. The cultivar Glenlea consistently exhibited the highest disease severity, validating its role as a susceptible control, whereas Salamouni confirmed its resistance under field conditions. Molecular screening revealed that 35.3 % of genotypes carried the dominant *Tsn1* allele associated with sensitivity to PtrToxA, while 64.7 % carried the recessive *tsn1* allele. In general, the presence of *tsn1* corresponded to reduced disease severity; however, inconsistencies between molecular and phenotypic data highlight the quantitative nature of tan spot resistance and the involvement of additional resistance loci. Overall, the combined use of NDVI-based phenotyping, disease progression metrics, and molecular markers enabled robust identification of promising wheat lines with enhanced resistance to tan spot. These genotypes represent valuable breeding material for developing cultivars with improved and durable resistance under the agro-climatic conditions of southeastern Kazakhstan.

Conflict of interest

The authors declare no conflict of interest.

Author contribution

The manuscript was written through contributions of all authors. All authors have given approval to the final version of the manuscript. CRediT: **Raimbekova B.T.** — Conceptualization; Data curation; Formal analysis; Investigation; Methodology; Writing original draft; editing; **Anuarova L.E.** — data curation, investigation, formal analysis, methodology; **Kyrbasova E.A.** — resources, software, supervision, visualization; **Imanova E.M**. — resources, validation, visualization; **Sartayeva A.A.** — supervision, validation, original draft writing; **Doszhanova A.S**. — investigation, data curation.

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Пиренофорозға төзімді (*Pyrenophora tritici-repentis*) перспективті бидай линияларын сәйкестендіру

Бидай пиренофорозы (сары дақ) *Pyrenophora tritici-repentis* фитопатогенді саңырауқұлағы қоздыратын кең таралған және қауіпті ауруларының бірі. Зерттеудің мақсаты — фенотиптік көрсеткіштер мен молекулалық скрининг негізінде перспективті бидай линияларының пиренофорозға төзімділігін анықтау. Бидай үлгілерін кешенді бағалау биомасса индексі (NDVI), патогенге төзімділік (PTR, AUDPC) және молекулалық маркерлер негізінде жүргізілді. NDVI 65-тен 82-ге дейін өзгеретіні анықталды, яғни жоғары мәндер (>75) қарсылықпен (R^2=0,652), ал төмен мәндер (<70) — сезімталдықпен (S). Төзімді үлгілер (12 дана, PTR=5–10), оның ішінде Salamouni сорты және төзімсіз үлгілер (7 үлгі, PTR=15–35) айқындалды. Молекулярлық скрининг нәтижесінде барлық зерттелген генотиптердің ПТР талдауы бидайдың 11 генотипінде (64,7 %) рецессивті *tsn1* генінің болуын көрсетті. Интегралды AUDPC индексі (орташа = 70,8) жоғары өзгергіштік (CV>50 %) және экстремалды мәндерді (165-ке дейін) көрсетті. Статистикалық талдау NDVI тұрақтылығын (CV=6,5–6,7 %) және аралас қарсылықты көрсететін PTR/AUDPC айтарлықтай өзгермелілігін растады. Нәтижелер тотығу дақтарына төзімділікпен молекулалық маркерлердің байланысын одан әрі зерттеу қажеттілігін көрсетеді.

Кілт сөздер: бидай, пиренофороз, төзімділік гендер, молекулалық скрининг, төзімділік, NDVI, AUDPC

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Идентификация перспективных линий пшеницы устойчивых к пиренофорозу (*Pyrenophora tritici-repentis*)

Пиренофороз пшеницы (желтая пятнистость) — одно из наиболее распространённых и опасных грибковых заболеваний пшеницы, вызываемое фитопатогенным грибом *Pyrenophora tritici-repentis*. Целью исследования является идентификация устойчивости к пиренофорозу перспективных линий пшеницы на основе фенотипических показателей и молекулярного скрининга. Проведена комплексная оценка образцов пшеницы по индексу биомассы (NDVI), устойчивости к патогенам (PTR, AUDPC) и молекулярным маркерам. Установлено, что NDVI варьирует от 65 до 82, при этом высокие значения (>75)

коррелируют с устойчивостью (R^2=0,652), а низкие (<70) — с восприимчивостью (S). Выделены устойчивые образцы (12 шт., PTR=5–10), включая сорт Salamouni, и восприимчивые (7 образцов, PTR=15–35). В результате молекулярного скрининга ПЦР-анализ всех исследованных генотипов показал наличие рецессивного гена *tsn1* у 11 генотипов пшеницы (64,7 %). Интегральный показатель AUDPC (среднее=70,8) продемонстрировал высокую вариабельность (CV>50 %) и экстремальные значения (до 165). Статистический анализ подтвердил стабильность NDVI (CV=6,5–6,7 %) и значительную изменчивость PTR/AUDPC, отражающую смешанную устойчивость. Результаты подчеркивают необходимость углубленного изучения связи молекулярных маркеров с устойчивостью к пиренофорозу.

Ключевые слова: пшеница, пиренофороз, гены устойчивости, молекулярный скрининг, устойчивость, NDVI, AUDPC

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