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IDENTIFICATION OF NEW SOURCES OF DISEASE RESISTANCE IN WHEAT

Abstract

Wheat breeding plays a pivotal role in ensuring food security, as wheat ranks among the most demanded and widely cultivated cereal crops globally. This article presents a comprehensive analysis of a collection of wheat breeding lines, utilizing agronomic, phytopathological parameters, and molecular-genetic screening. The main traits are described in detail, including days to heading (ranging from 21 to 221 days, predominantly mid-season lines), plant height (92–134 cm), and NDVI biomass index (51–72.5), with emphasis on promising lines exhibiting high NDVI values (>70). Evaluation for yellow rust resistance identified seven immune and five moderately susceptible lines; approximately 60% of the genotypes displayed immunity to the causal agent of *Pyrenophora tritici-repentis*. Resistance levels were classified according to the area under the disease progress curve (AUDPC): resistant (AUDPC <200), moderately resistant (200–400), and susceptible (>400) groups. Molecular screening revealed the presence of the recessive tsn1 allele, associated with resistance to PtrToxA, in 18 lines (52.94%). Correlation analysis indicated mostly weak associations between agronomic traits and disease resistance, except for expected strong positive correlations among parameters related to a single disease. Statistical analysis demonstrated considerable variability and the presence of outliers in most traits, underscoring the necessity for robust analytical methods. The findings highlight the effectiveness of integrating conventional and modern assessment approaches for selecting promising wheat lines in breeding programs.

Keywords: *wheat, tan spot, stripe rust, molecular markers, resistance genes*

Introduction

Wheat (Triticum aestivum L.) is a major cereal crop both globally and in Kazakhstan, where efforts to improve yield face significant challenges due to the continual evolution of disease pathogens. The emergence of new pests and diseases poses a persistent threat to food security, which is further aggravated by climate change - a factor that can trigger the appearance of novel pathogen races.

Crop diseases substantially impact both yield and quality of agricultural products worldwide [1]. Over the past decades, threats from diseases and pests have become increasingly severe within the context of global climate change, posing a significant challenge to food production. Obtaining information on the spatial distribution of diseases across large areas can help to ascertain the current status of infection, which is critical for accurately assessing yield losses [2, 3].

In Kazakhstan, protection against wheat rust epidemics relies largely on the cultivation of resistant varieties and timely fungicide application (i.e., before serious symptoms appear, which could otherwise result in greater economic losses). However, this approach may not always be economically feasible for farmers. Accurate identification of diseases in field conditions at their early onset, as well as during disease progression, is crucial for effective disease monitoring. Visual assessment of disease severity (such as estimating the proportion of infected plant tissue on leaves or across the entire sample) is frequently subjective [4–6] and requires substantial time and labor.

In recent years, considerable yield losses in Kazakhstan have been attributed to delayed detection -that is, insufficient monitoring of the development and spread of wheat diseases across cultivated areas [7, 8].

Stripe (yellow) rust represents a significant threat to food security in many countries worldwide. The disease is prevalent across much of North and South America, Europe, Eastern, Central, and Southern Asia, North Africa, and Australia. Climatic conditions in approximately 72% of global wheat cultivation areas are suitable for yellow rust development, and stable outbreaks are observed in about 42% of these regions. It is known that this disease occurs in more than 60 countries and is considered the most widespread wheat disease in Kazakhstan. Under conditions involving highly susceptible varieties and favorable weather, yellow rust can cause yield losses of up to 100%. In Kazakhstan, yellow rust is mainly found in the foothill and mountainous areas of the southern and southeastern regions, where winter wheat is predominantly grown under rainfed and irrigated conditions. The prevalence and severity of the disease fluctuate considerably, primarily depending on weather conditions in May and June, which correspond to the heading, flowering, and grain filling stages [9–11].

Tan spot is a relatively new disease of wheat, yet it is now widespread in many countries. It was first detected in the United States and Canada in the early 1940s, and by the 1980s–1990s, it had appeared in Western European countries. In eastern Canada, yellow leaf spot and septoria occur as a disease complex—the former dominating in drier areas, and the latter in regions with higher moisture. Yellow leaf spot is commonly observed on both winter and spring wheat in the southern, southeastern, and northern regions of Kazakhstan. The initial disease symptoms appear at the stem elongation stage of winter wheat; during heading, leaf infection on upper layers reaches 25–50%, and by the milky grain stage, disease incidence can reach 75–100%, leading to premature leaf desiccation.

Genetic resistance remains the principal strategy for controlling wheat diseases. The identification of varieties exhibiting effective and durable resistance to rusts is a key objective in wheat breeding. Accordingly, the detection of resistance genes in modern wheat varieties and breeding lines, followed by the selection of optimal combinations of resistance genes, constitutes the critical first step toward the successful implementation of a breeding program [12, 13]. This study aims to identify sources of disease resistance and highly productive wheat genotypes under the conditions of the Almaty region.

Material and methods

The research strategy is based on an integrated approach that incorporates breeding, phytopathological, and molecular methods. The study focuses on promising winter wheat lines that are either currently cultivated or considered as candidates for new varieties under the conditions of Almaty region, Almalybak.

Phytopathological assessment of the severity of *Pyrenophora tritici-repentis* (tan spot) infection under field conditions is conducted by estimating the percentage of leaf area affected by tan spot. The evaluation is based on the Saari and Prescott scale (1975) [14], originally developed for septoria, as modified by O.Yu. Kremneva (2007) [15]. According to this scale, the following gradations of wheat leaf infection severity are used: 0% – very high resistance; 1–5% – high resistance; 6–20% – resistance; 21–30% – susceptibility; 31–50% – moderate susceptibility; 51–80% – high susceptibility; and 81–100% – very high susceptibility.

The Peterson scale was used to assess yellow rust. Evaluation of yellow rust symptoms was conducted by the CIMMYT-developed methodology, using five infection types (IT): 0 – immune; R – resistant; MR – moderately resistant; MS – moderately susceptible; and S – susceptible.

Molecular Screening Methods for tsn and Yr Resistance Genes in Wheat to Leaf Rust. Genomic DNA extraction was performed using the protocol described by Riede et al. (1996). DNA was isolated from 5-day-old wheat seedlings of each sample via the CTAB method [17]. DNA concentration was measured spectrophotometrically at 260 nm, and working solutions for PCR were adjusted to a final concentration of 20 ng/μl.

The PCR reaction mixture (25 μl total volume) consisted of 2.5 μl of genomic DNA, 1 μl of each primer (1 pM/μl) (SigmaAldrich, USA), 2.5 μl dNTP mix (2.5 mM each of dCTP, dGTP, dTTP,

and dATP) (ZAO Sileks, Russia), 2.5 µl MgCl2 (25 mM), 0.2 µl Taq polymerase (5 U/µl) (ZAO Sileks, Russia), 2.5 µl of 10X PCR buffer, and 12.8 µl ddH2O. PCR amplifications were carried out using a Mastercycler (Eppendorf, Germany). Amplification products were separated on a 2% agarose gel in TBE buffer (45 mM Tris-borate, 1 mM EDTA, pH 8) [18] with ethidium bromide added. A 100-bp DNA ladder (Fermentas, Lithuania) was used to estimate fragment sizes. Visualization of PCR products was performed using a gel documentation system (Gel Doc XR+, BIO-RAD, Hercules, USA).

Leaf samples from all test entries, including two reference cultivars, were genotyped using the SSR marker Xfcp623, which is specific for the detection of Tsn1 gene alleles. Primer sequences and PCR conditions followed the protocol described by Faris et al. (2010) [19]. The marker detects two alleles: a 380-bp amplicon corresponding to the dominant *Tsn1* (sensitivity) allele, and a null allele corresponding to the recessive *tsn1* allele (insensitivity to Ptr ToxA) [20]. The primer sequences for marker Xfcp623 (5′–3′) were: F – CTATTCGTAATCGTGCCTTCCG; R – CCTTCTCTCTCACCGCTATCTCATC.

Determination of Plant Biomass Index (NDVI – Normalized Difference Vegetative Index) was performed using a portable GreenSeeker device (Trimble Navigation Limited, USA). The NDVI index ranges from 0.00 to 1.0, with higher values indicating greater disease resistance [21]. The GreenSeeker sensor operates by emitting brief pulses of red and near-infrared light onto the plant canopy and subsequently measuring the amount of reflected radiation. Higher NDVI values are associated with increased productivity and resistance to diseases, as well as reduced nitrogen requirements.

Statistical analysis. The resistance behavior to leaf rust of all tested samples was evaluated using the Average Coefficient of Infection (ACI) and the Area Under the Disease Progress Curve (AUDPC). The Average Coefficient of Infection (ACI) was calculated following the methodology outlined by Saari and Wilcoxson (1974). AUDPC was calculated using the formula proposed by Wilcoxson et al. (1974). This approach enables a quantitative evaluation of disease progression over time, offering valuable insights into the resistance levels of various wheat genotypes.

$$AUDPC = \sum_{i=1}^{n-1} \left(\frac{yi + yi + 1}{2} X(ti + 1 - \text{ti}) \right)$$

where y_i is the average coefficient of infection for the i-th assessment yi_{+1} is the average coefficient of infection for the (i+1)-th assessment, $t_{i+1} - t_i$ is the number of days between the i-th and (i+1)-th assessments, and n is the total number of observations.

The susceptibility index (φ) is determined by dividing the Area Under the Disease Progress Curve (AUDPC) of a specific genotype by the AUDPC of a known susceptible control genotype. This ratio provides a quantitative assessment of how susceptible or resistant a particular genotype is in comparison to the susceptible control.

R-studio software was used to conduct a one-way analysis of variance (ANOVA) to evaluate the differences in productivity and resistance to leaf rust among genotypes and across years. Pearson correlation coefficients were calculated based on the mean values of the evaluated traits. PCA was conducted, and biplots were generated using R-studio software version R 3.5.3 (R Core Team, 2018).

Results

A comprehensive analysis of a collection of wheat breeding lines was conducted based on agronomic characteristics, phytopathological assessments, and the profile of resistance genes. Patterns in the distribution of key traits are described, with an in-depth characterization provided for groups of varieties and genotypes, as well as detailed individual profiles for the leading entries (Table 1).

For the trait "days to heading," the studied samples ranged from 21 to 221 days, with most lines classified as mid-season (213–219 days), which is optimal for the majority of continental regions. Plant heights ranged from 92 to 134 cm, with the majority falling within 105–118 cm. The maximum height (134 cm) was observed for line d.1770 Ramin × No.42 Almaly (Erythrospermum), and the

minimum (92 cm) for line d.845 (Erythrospermum). The biomass index, NDVI, among the studied lines ranged from 51 to 72.5. Four promising lines with high NDVI values (>70) were identified: Glenlea (71), d.1777 Darya × No.1724 (71), d.72 Tungysh × d.23 Brundage 96 (66.5), d.845... (69–72). Based on phytopathological assessment for yellow rust resistance, seven promising lines were identified with an immune response (IT=0), and five entries exhibited a moderately susceptible reaction (5–10MS). Assessment for resistance to *Pyrenophora tritici-repentis* showed that approximately 60% of the lines displayed an immune response to the pathogen.

The area under the disease progress curve (AUDPC) enabled the classification of the entries into three groups: (1) AUDPC <200, considered resistant (e.g., d.1770 Ramin, d.35-ICARDA, d.845, Glenlea, Salamouni, d.1777 Darya × 1724, among others); (2) AUDPC = 200–400, moderately resistant (e.g., F1 d.1031, some Lutescens entries); and (3) AUDPC >400, highly susceptible (e.g., d.36 Toma × Akmola, F8 Bermet, F6 Sanzar).

Results of molecular screening using the Xfcp623 marker identified the presence of the recessive tsn1 allele associated with resistance to PtrToxA toxin in 18 promising lines, representing 52.94% of the total genotypes analyzed. The tsn1 gene was predominantly found in accessions exhibiting high resistance to Pyrenophora tritici-repentis (see Table 1).

Figure 1 presents the results of boxplot analyses for the main agronomic and phytopathological parameters.

Figure 1 – Boxplots of AUDPC and agronomic traits of wheat genotypes

Table 2 presents an interpretation of the correlation matrix for the main variables included in the analysis: days to heading (DTH), plant height, NDVI average, mean yellow rust severity (YR-average), integrated yellow rust severity scale (AUDPC-Yr), mean septoria (tan spot) severity (PTR-average), and integrated septoria severity scale (AUDPC-Ptr). The DTH trait shows a weak positive correlation with plant height ($r \approx -0.011$); there are virtually no significant associations with NDVI average ($r = 0.037$), YR-average ($r = 0.057$), or AUDPC-Yr ($r = 0.058$). There is a weak negative correlation with tan spot severity (PTR-average, AUDPC-Ptr). Phytopathological assessment of yellow rust shows a perfect positive correlation with AUDPC-Yr ($r = 1$), as AUDPC reflects the overall intensity of yellow rust infection. There is also an almost complete positive correlation with AUDPC-Ptr ($r = 0.997$), which is expected since both parameters represent the degree of tan spot infection.

Таблица 1 – Breeding and genetic evaluation of promising wheat lines under the conditions of Almaty region

Sample name	Variety	Agronomic Traits					Phytopathological assessment against an infectious background							Presence of the gene
		Days to heading	Plant height	NDVI-1	NDVI-2	NDVI avg.	YR-1	YR-2	YR-3	PTR-1	PTR-2	PTR-3	AUDPC	
д.Сабина х д.74 Паллада/№57 Паллада	*Graecum*	216	100	71	58	64,5	40S	50S	50S	0	0	0	112	
д.1777 Дарья х №72 Тунгыш х д.133 Дарья/№68 Дарья	*Lutescens*	219	115	72	47	59,5	10MS	20MS	20MS	10	15	30	196	*tsn1*
д.1286 д.79 (ARDEAL/BOEMA//F135U2-1/5/ TX69A509-2//BBY2	*Barbarossa*	216	95	74	49	61,5	30MS	40S	40S	5	15	25	266	*tsn1*
д. №23х Купава х1774д. 23-ICARDA-IPBB-2013	*Erythroleucon*	215	108	73	57	65	20MS	30MS	30MS	0	0	0	182	*tsn1*
д. F_5 №20 х Уманка х 1773 д.22-ICARDA-IPBB-2013	*Erythroleucon*	216	113	75	52	63,5	30MS	40S	40S	5	10	20	224	
д.№23х Купава х1773 д.22-ICARDA-IPBB-2013	*Erytrospermum*	219	118	75	52	63,5	20MS	30MS	30MS	5	10	15	112	*tsn1*
д.179-КВ-ИББР-2012х д.1760 9-ICARDA-IPBB-2013	*Ferrugineum*	218	115	74	60	67	5MS	20MS	20MS	0	0	0	840	*tsn1*
д.1777 Дарья х №1724 $F_1$1581 х (д.807 F_4 (Наз х Уманка) х Алмалы) х Зимородок, №78 х д.42 Алмалы	*Graecum*	219	95	79	63	71	0	10MS	10MS	0	0	0	112	*tsn1*
д.1777 Дарья х №1737 F1д.1014 (д.99 F3(№ 25 Madsen x Cm.24) х Арап) х Brundage 96(APR) х д.23 Brundage 96 APR	*Erytrospermum*	219	107	78	65	71,5	10MS	20MS	20MS	0	0	0	112	*tsn1*
д.1772 Виза х №42 Алмалы х д.131Виза	*Velutinum*	213	112	78	63	70,5	5MS	20MS	20MS	0	0	0	805	*tsn1*
д. 35-ICARDA-IPBB-2013х д.Yr9	*Erythroleucon*	213	103	84	61	72,5	0	0	0	0	0	0	665	*tsn1*
д.845 F_5 № 23 х Купава х№1659д.1030Д620. F_4Улугбек хYr 4хМереке х197 Yr15	*Erythroleucon*	212	93	71	67	69	0	0	0	0	0	0	196	*tsn1*
д.845 F_5 № 23 х Купава х№1659д.1030Д620. F_4Улугбек хYr 4хМереке х197 Yr15	*Erytrospermum*	213	92	78	66	72	0	0	0	0	0	0	504	*tsn1*
д.1320 (д.113.338-К1-1//ANB/BUC/3/GS50A/4 /TREGO/JGR	*Milturum*	212	118	70	58	64	0	0	0	10	15	30	220	*tsn1*
д.867 F5 №23/Купава/22х д.74 Паллада	*Lutescens*	217	125	79	63	71	5MS	20MS	20MS	0	0	0	0	*tsn1*
д.89 Э-99 х №270 RL 6088(Sr40) х д.74Паллада	*Lutescens*	215	110	78	61	69,5	30MS	40S	40S	0	0	0	308	*tsn1*

F_1д.1031Д628. F_4 (Наз х Обрий) Купава х Kalyansona (Yr2), №171 х д.48 Улугбек 600	*Lutescens*	216	105	77	63	70	10MS	30MS	30MS	0	0	0	110	
д.72Тунгыш х д.23 Brundage 96 APR	*Ferrugineum*	216	111	79	54	66,5	0	5MS	5MS	0	0	0	115	
д.23 Brundage 96 APR х №40 Наз х д.70 Мереке	*Lutescens*	214	700	76	60	68	30MS	40S	40S	0	0	0	182	
$F_3$587 Morocco х №41 Октябрина х д.46 Княжна	*Graecum*	218	96	79	61	70	20MS	40S	40S	0	0	0	224	
25-ICARDA-IPBB-2013 х д.588 MA F7 Бермет х RWKLDN 9	*Erytrospermum*	213	105	78	56	67	30MS	50S	50S	0	0	0	182	*tsn1*
U11AGEC-10 х д46 Княжна	*Erytrospermum*	219	110	77	62	69,5	20MS	40S	40S	10	25	15	182	
д.1770 Рамин х №42 Алмалы	*Erytrospermum*	219	101	76	55	65,5	0	0	0	0	0	0	84	
д.1770 Рамин х №42 Алмалы	*Erytrospermum*	215	134	75	48	61,5	30MS	40S	40S	0	0	0	196	
д.36 Тома х 57 Акмола	*Erytrospermum*	213	117	74	47	60,5	60S	60S	60S	10	20	30	182	
F_6 Санзар х Арап	*Erytrospermum*	215	101	72	47	59,5	60S	60S	60S	10	25	40	110	
F_6 Санзар х Арап	*Erytrospermum*	213	105	70	42	56	60S	60S	60S	0	0	0	56	
1060 д.5353[(CWARTN)Super KAUZ(Lr26,34)] х д.1017 F_7 (Yr 15 х Южная-12)	*Erytrospermum*	215	104	65	44	54,5	0	0	0	20	40	30	116	*tsn1*
587 Morocco х №31 Стекловидная24	*Graecum*	215	108	67	35	51	80S	80S	80S	10	30	30	155	
1138 д.906 F_5 (Алмалы х 29266) х д.5357(CWARTN) Pastor(Lr3,10,23+Sl.Rust.)	*Graecum*	215	107	68	41	54,5	80S	80S	80S	10	15	25	182	*tsn1*
F_8 Бермет х МК 3797	*Erytrospermum*	214	108	74	49	61,5	30MS	30MS	30MS	10	25	35	504	*tsn1*
F5Almaly x Umanka/1(Lr29-900bp-Lr29F18/R18)	*Erytrospermum*	215	112	71	48	59,5	90S	90S	90S	0	0	0	110	
F_5Parula 5355 x293 a.2006	*Ferrugineum*	221	112	79	60	69,5	0	0	0	10	15	15	0	
Glenlea	*Lutescens*	217	108	81	61	71	0	0	0	10	25	40	610	*Tsn1*
Salamouni	*Erytrospermum*	215	105	74	59	66,5	0	0	0	0	0	0	0	*tsn1*

Table 2 – Correlation matrix (Pearson)

Variables	ДДК	Высота растении	NDVI avg.	YR-average	AUDPC-Yr	PTR-average	AUDPC-Ptr
ДДК	**1**	-0,011	0,037	0,057	0,058	-0,035	-0,028
Высота растении	-0,011	**1**	0,071	0,103	0,107	-0,057	-0,060
NDVI avg.	0,037	0,071	**1**	-0,424	-0,418	-0,271	-0,278
YR-average	0,057	0,103	-0,424	**1**	1,000	-0,097	-0,096
AUDPC-Yr	0,058	0,107	-0,418	1,000	**1**	-0,103	-0,103
PTR-average	-0,035	-0,057	-0,271	-0,097	-0,103	**1**	0,997
AUDPC-Ptr	-0,028	-0,060	-0,278	-0,096	-0,103	0,997	**1**

The presented descriptive analysis of quantitative data summarizes the key statistical characteristics for seven variables: days to heading (DTH), plant height, mean NDVI, mean annual disease severity (Yr-average), AUDPC for mean annual disease severity (AUDPC-Yr), mean PTR value, and AUDPC for PTR (AUDPC-Ptr). All indicators contain 99 observations with no missing values, thereby ensuring the completeness of the dataset.

The value ranges differ substantially across variables. For example, DTH displays a wide spread from –42910 to 227, indicating the presence of extreme negative outliers. This is also reflected in the high skewness and kurtosis coefficients, denoting pronounced right-skewness and the presence of outliers. Plant height ranges from 75 to 700 cm, with a median of approximately 105 cm, and also exhibits marked positive skewness, indicating a large proportion of plants below the mean height and relatively few tall specimens (table 3).

The NDVI parameter has a narrower range (51 to 77) and relatively low variance, suggesting a more uniform distribution of this trait. Both the mean and median values for Yr-average and AUDPC-Yr show considerable dispersion, with high standard deviations and coefficients of variation, thus reflecting strong variability in disease manifestation among plants.

PTR-average and AUDPC-Ptr are characterized by high mean levels of variation, with median values nearly zero. This may reflect the underlying nature of the data—most plants possibly exhibited no disease symptoms, thereby shifting the distribution towards zero values.

High coefficients of variation and skewness for many variables indicate that the data are asymmetrically distributed and contain outliers, necessitating a cautious approach in subsequent statistical analyses and possibly the use of robust statistical methods. Meanwhile, the comparatively low variability observed for NDVI suggests that this parameter is a more reliable marker of mid-season plant status. Thus, the presented statistical indicators provide a comprehensive view of the distribution and variability of the key research parameters, highlighting the need to employ appropriate analytical methods that account for data heterogeneity and the presence of extreme values.

Table 3 – Descriptive statistics (Quantitative data)

Statistic	DTH	PH	NDVI avg.	*Yr*-average	AUDPC-*Yr*	PTR-average	AUDPC-Ptr
Nbr. of observations	99	99	99	99	99	99	99
Nbr. of missing values	0	0	0	0	0	0	0
Breakdown per subsample (%)	100	100	100	100	100	1001	100
Minimum	-42910,0	75,0	51,0	0,0	0,0	0,0	0,0
Maximum	227,0	700,0	77,0	93,3	1330,0	30,0	455,0
Freq. of minimum	1	1	1	31	31	57	57
Freq. of maximum	1	1	1	1	1	1	1
Range	43137,0	625,0	26,0	93,3	1330,0	30,0	455,0
1st Quartile	214,0	96,0	61,2	0,0	0,0	0,0	0,0
Median	216,0	105,0	65,5	13,3	196,0	0,0	0,0
3rd Quartile	218,5	114,0	69,0	34,62	504,0	18,3	262,5

Sum	-21723,0	11011,0	6433,5	2028,6	28994,0	806,6	11585,02
Mean	-219,4	111,2	64,9	20,4	292,8	8,1	117,0
Variance (n)	18596797,5	3673,8	29,7	489,7	98043,2	103,4	21645,6
Variance (n-1)	18786560,8	3711,3	30,0	494,7	99043,7	104,4	21866,5
Standard deviation (n)	4312,4	60,6	5,4	22,1	313,1	10,1	147,1
Standard deviation (n-1)	4334,3	60,9	5,4	22,2	314,7	10,2	147,8
Variation coefficient (n)	-19,6	0,5	0,08	1,08	1,06	1,24	1,25
Variation coefficient (n-1)	-19,7	0,5	0,08	1,08	1,07	1,252	1,26
Skewness (Pearson)	-9,79	9,24	-0,23	1,22	1,18	0,64	0,69
Skewness (Fisher)	-9,95	9,38	-0,23	1,24	1,20	0,65	0,70
Skewness (Bowley)	0,11	0,0	-0,09	0,23	0,22	1,0	1,0
Kurtosis (Pearson)	94,0	86,9	-0,2	1,1	1,02	-1,2	-1,1
Kurtosis (Fisher)	99,0	91,5	-0,2	1,2	1,1	-1,2	-1,1
Standard error of the mean	435,6	6,1	0,5	2,2	31,6	1,0	14,8
Lower bound on mean (95%)	-1083,8	99,0	63,8	16,0	230,1	6,1	87,5
Upper bound on mean (95%)	645,046	123,373	66,079	24,928	355,637	10,187	146,513
Standard error of the variance	2683794,4	530,1	4,2	70,6	14149,1	14,9	3123,7
Lower bound on variance (95%)	14464589,7	2857,5	23,1	380,9	76258,5	80,4	16836,0
Upper bound on variance (95%)	25393918,6	5016,6	40,6	668,7	133878,0	141,2	29557,1
nIQR	3,3	13,3	5,7	25,6	373,60	13,5	194,5
Qn	2,1	13,1	5,4	17,4	244,6	0,0	0,00

Conclusion

There is a growing trend toward disease management strategies that emphasize automated, non-destructive detection and quantitative assessment of plant diseases, enabling targeted intervention at specific field sites. In precision agriculture, the timely identification of crop diseases at different growth stages is crucial for effective management of both agricultural practices and economic outcomes. This study was conducted using an integrated approach, combining genetic-breeding and phytopathological methods. As a result, several promising, resistant lines exhibiting high productivity were identified under field conditions. The findings provide a comprehensive characterization of the wheat collection and demonstrate the effectiveness of integrating traditional agronomic and phytopathological assessments with molecular-genetic screening for selecting valuable germplasm in breeding programs.

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ӘР ТҮРЛІ АУРУЛАРҒА ТӨЗІМДІ БИДАЙДЫҢ ЖАҢА КӨЗДЕРІН ИДЕНТИФИКАЦИЯЛАУ

Аңдатпа

Бидай селекциясы азық-түлік қауіпсіздігін қамтамасыз етуде маңызды рөл атқарады, себебі бидай – әлемде ең кең тараған және ең сұранысқа ие дәнді дақылдардың бірі. Мақалада бидайдың селекциялық үлгілер коллекциясына агрономиялық, фитопатологиялық көрсеткіштер мен молекулалық-генетикалық скринингті қолдана отырып кешенді талдау жүргізілді. Негізгі белгілер жан-жақты сипатталды: масақтануға дейінгі күн саны (21–221 күн, негізінен орта мерзімді), өсімдіктің биіктігі (92–134 см), NDVI биомасса индексі (51–72,5), жоғары NDVI (>70) көрсеткен перспективті линиялары анықталды. Бидайдың сары тат ауруына төзімділігін бағалау нәтижесінде 7 иммунды және 5 орташа сезімтал желі анықталды, зерттелген үлгілердің шамамен 60%-ы пиренофороз қоздырғышына төзімді реакция көрсетті. Ауру дамуының ауданы бойынша (AUDPC) төзімділік деңгейлері топтастырылды: төзімді (AUDPC 400). Молекулалық скрининг барысында PtrToxA токсиніне төзімділікпен байланысқан рецессивті *tsn1* гені 18 үлгілерде (52,94%) анықталды. Корреляциялық талдау агрономиялық белгілер мен ауруларға төзімділік арасындағы байланыстардың әлсіз екенін, басқа аурудың көрсеткіштерінің арасында күтілетін жоғары оң корреляциялар барын көрсетті. Статистикалық талдау көпшілік көрсеткіштердің айтарлықтай өзгермелілігін және экстремалды мәндердің болуын айқындады, бұл деректерді тұрақты әдістермен талдау қажеттігін растайды. Алынған нәтижелер селекциялық бағдарламаларда бидайдың перспективалы формаларын іріктеу үшін дәстүрлі және заманауи бағалау әдістерін тиімді үйлестірудің маңыздылығын көрсетеді.

Кілт сөздер: бидай, сарыдақ, сары тат, молекулалық маркерлер, төзімді гендер

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ИДЕНТИФИКАЦИЯ НОВЫХ ИСТОЧНИКОВ УСТОЙЧИВОСТИ ПШЕНИЦЫ УСТОЙЧИВЫХ К РАЗЛИЧНЫМ БОЛЕЗНЯМ

Аннотация

Селекция пшеницы играет ключевую роль в обеспечении продовольственной безопасности, поскольку пшеница является одной из самых востребованных и широко выращиваемых зерновых культур в мире. В статье проведён комплексный анализ коллекции селекционных образцов пшеницы с использованием агрономических, фитопатологических показателей и молекулярно-генетического скрининга. Детально охарактеризованы основные признаки: дни до колошения (21–221 дней, преимущественно среднеспелые), высота растений (92–134 см), индекс биомассы NDVI (51–72,5) с выделением перспективных линий с высоким NDVI (>70). Оценка устойчивости к желтой ржавчине выявила 7 иммунных и 5 умеренно восприимчивых линий, около 60% образцов проявили иммунитет к возбудителю пиренофороза. Сгруппированы уровни устойчивости по площади под кривой развития болезни (AUDPC): устойчивые (AUDPC <200), среднеустойчивые (200–400), восприимчивые

(>400). Молекулярный скрининг выявил рецессивный аллель tsn1, ассоциированный с устойчивостью к PtrToxA, у 18 линий (52,94%). Корреляционный анализ показал преимущественно слабые связи между агрономическими признаками и устойчивостью к болезням, кроме ожидаемых сильных положительных корреляций между параметрами одного заболевания. Статистический анализ демонстрирует значительную вариабельность и наличие выбросов среди большинства показателей, что требует использования устойчивых методов анализа. Результаты подчеркивают эффективность сочетания традиционных и современных методов оценки для отбора перспективных форм пшеницы в селекционных программах.

Ключевые слова: пшеница, желтоватая пятнистость, желтая ржавчина, молекулярные маркеры, гены устойчивости

Authors' contributions

K.M.: Conceptualization; Data curation; Formal analysis; Investigation; Methodology; ; Roles/Writing – original draft; and Writing – review & editing; **K.A.:** Conceptualization; Data curation; Formal analysis; Investigation; Methodology; ; Roles/Writing – original draft; and Writing – review & editing; **K.Zh.:** Resources; Software; Supervision; Validation; Visualization; Roles/Writing – original draft; and Writing – review & editing; **B.A.:** Resources; Software; Supervision; Validation; Visualization; Roles/Writing – original draft; and Writing – review & editing; **B.K.:** Resources; Software; Supervision; Validation; Visualization; Roles/Writing – original draft; and Writing – review & editing; **K.N.:** Resources; Software; Supervision; Validation; Visualization; Roles/Writing – original draft; and Writing – review & editing.

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АЛМАТЫ ОБЛЫСЫ ЖАҒДАЙЫНДА ЖАЗДЫҚ ҚАТТЫ БИДАЙДЫҢ КӘДІМГІ ТАМЫР ШІРІГІ АУРУЫНА (BIPOLARIS SOROKINIANA) АГРОТЕХНОЛОГИЯЛЫҚ ЖӘНЕ БИОТИКАЛЫҚ ФАКТОРЛАРДЫҢ ӘСЕРІН БАҒАЛАУ

Аңдатпа

Бұл зерттеу Қазақстанның әртүрлі топырақ-климаттық жағдайларында жаздық қатты бидайдың кәдімгі тамыр шірігіне шалдығуына әсер ететін факторларды кешенді түрде талдауға арналған. Жұмыста фитопатологиялық бағалаудың заманауи әдістері, соның ішінде далалық, зертханалық және молекулалық-генетикалық зерттеулерқолданылды. Далалық тәжірибелер 2024 жылы екі өңірде (Алматы және Ақтөбе облыстарында) үш факторлы схема бойынша жүргізілді: өсімдік дамуының фазалары, жұқтыру фоны (фунгицидті, инфекциялық, табиғи) және 14 бидай сорты мен желілері. Зерттеу жаздық қатты бидайдың кәдімгі тамыр шірігіне шалдығу деңгейіне арналған.