IRSTI 68.35.29 https://doi.org/10.52081/bkaku.2026.v77.i2.325

PRE-HARVEST SPROUTING AND SEED DORMANCY IN SPRING WHEAT COLLECTION: RELATIONSHIPS WITH YIELD COMPONENTS UNDER CONTRASTING ENVIRONMENTS IN KAZAKHSTAN

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Annotation. This study evaluated genetic variation in pre-harvest sprouting (PHS), seed dormancy, and yield-related traits in a diverse panel of 270 spring wheat accessions grown under two contrasting environments in Kazakhstan. Significant phenotypic variation was observed for agronomic traits, yield components, and PHS resistance, indicating substantial genetic diversity within the collection. Environmental conditions strongly influenced yield formation: spike productivity traits predominated in the Almaty region, whereas grain filling efficiency was the main determinant of yield in Kostanay. PHS exhibited wide variation among genotypes, with higher susceptibility observed in the northern environment. Nineteen genotypes showed stable resistance across both environments, representing valuable genetic resources for breeding. Notably, all resistant genotypes were characterized by red grain color, confirming the association between grain pigmentation and dormancy. Seed dormancy, assessed via germination index (GI), was significantly affected by environment and showed an inverse relationship with PHS. Correlation and multivariate analyses revealed weak negative relationships between PHS and yield components, suggesting that slightly reduce yield. Principal component analysis (PCA) and genotype-by-environment interaction (GGE) biplot analyses identified stable and high-performing genotypes, including CAWBIN-179, CAWBIN-222, and CAWBIN-385. These findings demonstrate the feasibility of combining high-yielding potential with PHS resistance in spring wheat breeding programs.

Keywords: *Triticum aestivum* L., pre-harvest sprouting, seed dormancy, plant adaptation, yield components.

Introduction. Pre-harvest sprouting (PHS) is a major constraint affecting wheat production worldwide, particularly in regions where rainfall and high humidity occur during the grain maturation period [1]. The premature germination of physiologically mature grains in the spike leads to substantial deterioration of grain quality, including increased α-amylase activity, reduced falling number, and impaired end-use properties such as baking quality [2-3]. As a consequence, PHS not only reduces grain market value but also limits its suitability for processing industries. In the context of ongoing climate change, the frequency of unpredictable precipitation events during the late stages of crop development has increased, making PHS an increasingly critical factor in wheat production systems [4].

Resistance to PHS is a complex trait governed by multiple genetic, physiological, and environmental factors [5-7]. To date, many genetic factors controlling these traits have been identified. For example, the transcription factor *Tamyb10* has been identified for grain color.

The *TaDFR* gene, which affects grain color, PHS resistance, and anthocyanin synthesis, is localized on chromosomes 3A, 3B, and 3B [8-10]. The *TaMFT* gene, a homolog of wheat *TaPHS1* associated with seed dormancy [11-12]. *TaMKK3-A*, formerly known as *Phs1*, located on chromosome 4A, is another key gene controlling seed dormancy [13]. Genes associated with seed dormancy *TaSdr*, *TaVp-1*, and *TaGASR34* were identified using a homology-based cloning approach, and corresponding functional markers were developed for them [14-16]. Among these, seed dormancy plays a central role in preventing premature germination under favorable moisture conditions [17]. Dormancy is primarily regulated by hormonal balance, particularly abscisic acid and gibberellins, and is influenced by both genetic background and environmental conditions during grain development [18-19]. However, the expression of dormancy is highly dynamic and can vary significantly across environments, making the evaluation of PHS resistance particularly challenging. This highlights the necessity of multi-environment testing to accurately assess genotype performance and stability.

In addition to its direct impact on grain quality, PHS may be associated with agronomic traits and yield components. Grain yield in wheat is a complex trait determined by several interrelated components, including the number of kernels per spike (NKS), thousand-kernel weight (TKW), and grain yield per unit area (YM2). These components are influenced by both genetic factors and environmental conditions and may contribute differently to yield formation under contrasting environments [20]. In particular, environmental variation can shift the relative importance of grain number versus grain weight, resulting in distinct yield formation strategies [21]. Understanding these relationships is essential for identifying genotypes that combine high yield potential with resistance to PHS.

To address these complexities, multivariate statistical approaches are widely used to analyze relationships among traits. Correlation analysis provides insight into pairwise relationships among variables, while principal component analysis (PCA) identifies major sources of variation and trait groupings [22]. Furthermore, genotype-plus-genotype-by-environment (GGE) biplot analysis is an effective tool for evaluating genotype performance and stability across environments, enabling the identification of both broadly and specifically adapted genotypes [23]. These approaches are particularly useful when analyzing large and diverse germplasm collections under contrasting environmental conditions.

Kazakhstan is an important region for wheat production, characterized by diverse climatic conditions, ranging from relatively dry, warm southeastern areas to cooler, more favorable northern regions. In 2023, prolonged rainfall led to severe PHS across approximately 2.7 million hectares in Kazakhstan, representing about 15% of the harvested area. Yield losses were particularly high in certain regions, reaching up to 20% in Kostanay and 60% in Karaganda [24]. Such environmental contrasts provide an excellent opportunity to study genotype performance, yield formation, and the expression of pre-harvest sprouting (PHS) under different conditions. To date, several studies in Kazakhstan have assessed PHS resistance in grain using biochemical approaches, analyzing α-amylase activity, molybdenum content, and abscisic acid (ABA) levels [25-26]. In addition, breeding programs have focused on developing high-yielding, high-quality bread wheat varieties with reduced susceptibility to PHS under the conditions of Western Kazakhstan [27]. However, comprehensive studies integrating PHS, seed dormancy, yield components, and multi-environment analysis in this region remain limited.

Therefore, the aim of this study was to evaluate the variation in pre-harvest sprouting and seed dormancy in a diverse collection of 270 spring wheat accessions and to investigate their relationships with agronomic traits and yield components under two contrasting environments in Kazakhstan. Specifically, the objectives were to 1) assess the level of PHS and germination index (GI), 2) analyze variation in plant adaptation and yield-related traits, 3) determine relationships among traits using correlation and principal component analysis, and 4) evaluate genotype performance and stability using GGE biplot analysis to identify genotypes combining high yield potential with resistance to pre-harvest sprouting.

Materials and Methods. *Plant material.* A collection of 270 spring bread wheat (*Triticum aestivum* L.) accessions was used in this study. The collection included: 1) 96 commercial and advanced cultivars from Kazakhstan and Russia, including 58 varieties officially approved for cultivation in Kazakhstan; 2) 84 breeding lines and 3 cultivars developed at the Alexandr Barayev Scientific-Production Center for Grain Farming (Shortandy, Akmola region); and 3) 84 cultivars and lines originating from Kazakhstan, Russia, USA, Canada, Mexico, Germany, and Australia, provided by the Research Institute of Biological Safety Problems (South Kazakhstan).

Field experiments and trait evaluation. Field trials were conducted during the 2024 growing season at two contrasting locations in Kazakhstan: the Kazakh Research Institute of Agriculture and Plant Growing (KRIAPI, Almaty region, southeastern Kazakhstan) and the Karabalyk Agricultural Experimental Station (KAES, Kostanay region, northern Kazakhstan). The experiment was established using a randomized plot arrangement with two replications at each location. Plants were grown in experimental plots with 15 cm row spacing and 5 cm spacing between plants within rows. Standard agronomic practices were applied throughout the growing season [28]. Mean values of agronomic traits were calculated from harvested data across both environments. The climate conditions recorded during the trials are shown in Table 1.

Table 1 – Location, environment, and weather data at two regions in Kazakhstan

Site / Region	KRIAPI, Almaty region	KAES, Kostanay region
Latitude / Longitude	43°21′ / 76°53′	53.45 / 62.03
Altitude, m	740	189
Soil type	Light chestnut (humus 2.0-2.5%)	Black soil (humus 4.5-5.0%)
Conditions	Rainfed	Rainfed
Year	2024	2024
Annual rainfall, mm	383.6	251.7
Mean temperature, °C	19.7	18.5
Max temperature, °C	24.5	22.8
Min temperature, °C	13.5	10.7

The evaluated traits were grouped into two categories: 1) Plant adaptation traits: heading date (HD), seed maturation date (SMD), vegetation period (VP), and plant height (PH); 2) Yield components: spike length (SL), number of kernels per spike (NKS), thousand kernel weight (TKW), kernel width (KW), kernel length (KL) and grain yield per m^2 (YM2).

Assessment of pre-harvest sprouting. Resistance to PHS was evaluated using standard laboratory approaches. Spikes were collected at the wax ripeness stage from both experimental locations. To assess resistance to PHS, or germination index (GI), two common methods were used, described in the works of Yiwen et al. (2022), Liu et al. (2021), and Walker-Simmons et al. (1988) [5, 29,30]: measuring grain germination in the spike in a climate chamber and calculating the GI in Petri dishes. The percentage of sprouted grains (PHS, %) and germination index (GI, %) were used as indicators of sprouting susceptibility.

Statistical analysis. Analysis of variance (ANOVA) was performed to assess the effects of genotype (G), environment (region, R), and the genotype × environment interaction (G×R) on all traits studied. Pearson correlation analysis was conducted to evaluate relationships among agronomic traits, yield components, and PHS-related parameters.

Statistical analyses, including Pearson’s correlation coefficients, boxplot visualization, ANOVA, GGE biplot, and PCA, were conducted using the R statistical environment [31].

Results and discussion. *Variation of agronomic traits and yield formation of wheat collection.* The distribution of agronomic traits showed significant variability among the 270 spring wheat accessions evaluated in two contrasting environments, indicating high phenotypic diversity within the studied germplasm (Figure 1).

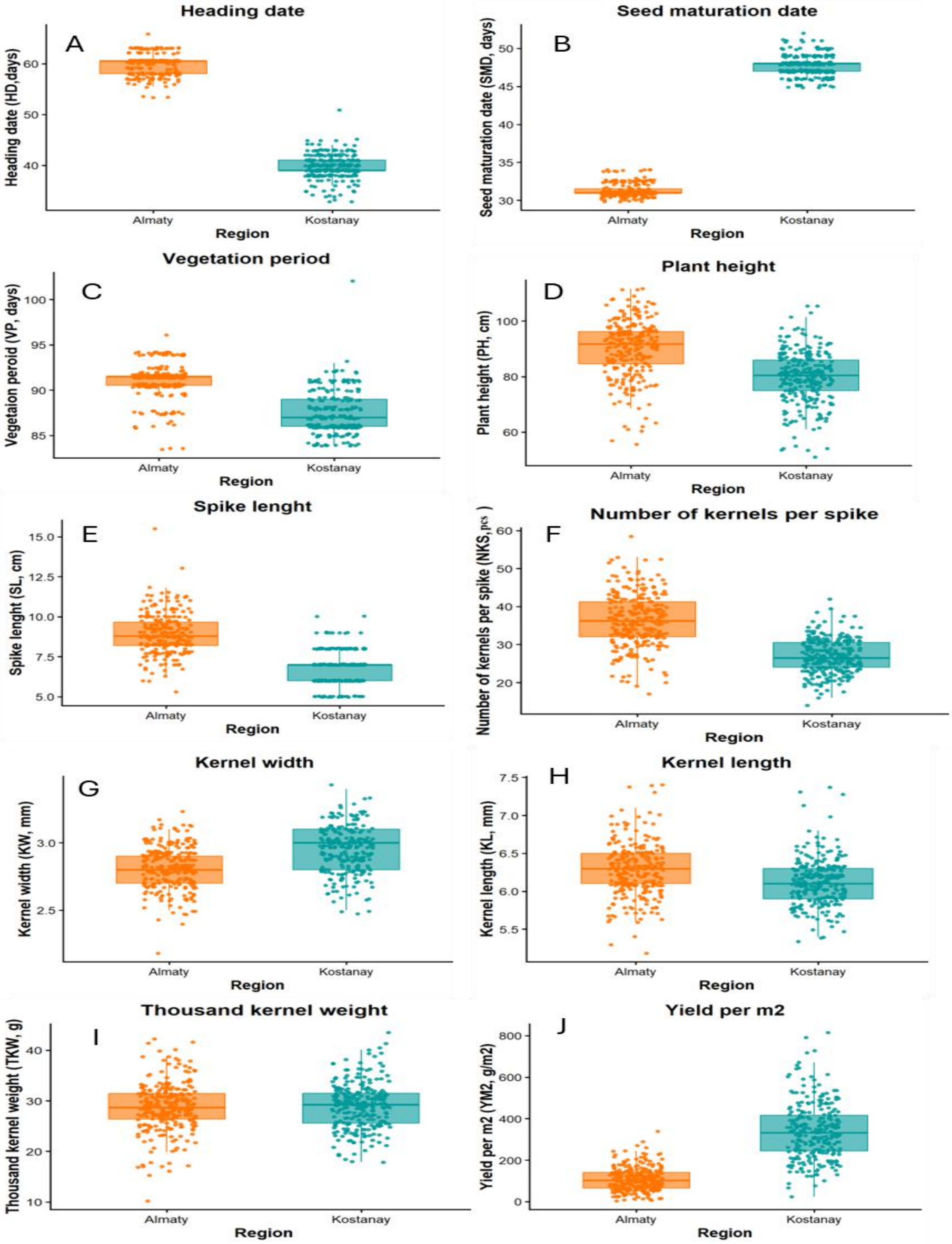


Figure 1 – Distribution of agronomic traits among 270 spring wheat accessions evaluated in two regions of Kazakhstan

Note: HD – heading date (days), SMD – seed maturation date (days), PH – plant height (cm), SL – spike length (cm), NKS – number of kernels per spike, KW – kernel width (mm), KL – kernel length (mm), TKW – thousand kernel weight (g), YM2 – yield per m² (g m²)

Traits related to plant development, including HD, SMD, VP, and PH, as well as yield components such as SL, NKS, TKW, KW, KL, and YM2, exhibited wide ranges (Figure 1). A clear regional differentiation was observed, reflecting the strong influence of environmental conditions on plant growth and productivity. In the KRIAPI (Almaty region), genotypes demonstrated a longer plant developmental stage, with HD reaching 59.8 ± 0.12 days compared to 39.7 ± 0.14 days in KAES (Kostanay region), while SMD ranged from 31.3 ± 0.05 to 47.6 ± 0.08 days. Similarly, plant height was greater in the Almaty region (90.1 ± 0.63 cm vs. 79.9 ± 0.56 cm), followed by higher values of SL (8.9 ± 0.08 cm vs. 6.7 ± 0.06 cm) and NKS (36.4 ± 0.43 vs. 26.9 ± 0.27 pcs).

In contrast, grain yield per m² was significantly higher in the Kostanay region (338.7 ± 8.19 g/m² vs. 108.4 ± 3.43 g/m²), indicating that this environment is more favorable for efficient grain filling and yield realization. Kernel traits also showed environment-specific patterns, with higher kernel width (3.0 ± 0.01 mm) observed in the Kostanay region, indicating differences in grain development processes (Figure 1).

Pre-harvest sprouting and seed dormancy. Pre-harvest sprouting (PHS) showed substantial variation among genotypes, with mean values of 55.2 ± 1.47% in the KRIAPI (Almaty region) and 60.2 ± 1.37% in KAES (Kostanay) (Figure 2A). The higher PHS levels observed in the Kostanay region indicate that environmental conditions there were more favorable for sprouting, likely due to differences in temperature and moisture during grain maturation.

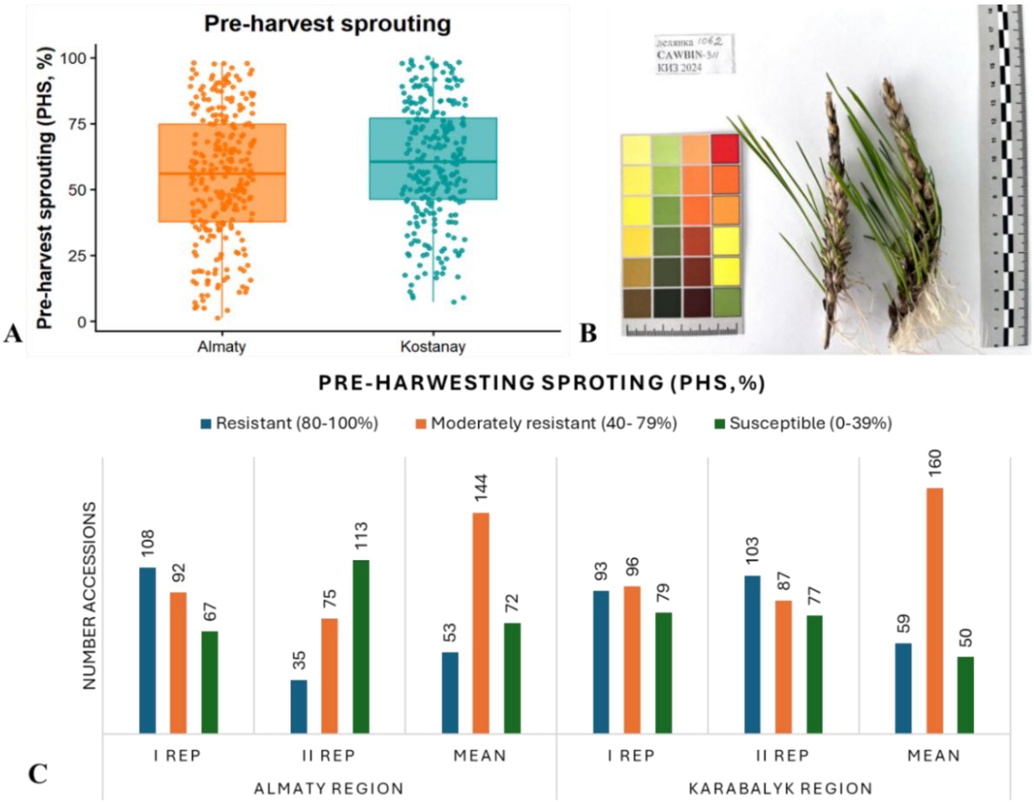


Figure 2 – Distribution of pre-harvest sprouting (PHS, %) among 270 spring wheat accessions evaluated in two regions of Kazakhstan (Almaty and Kostanay) Note: A – distribution of PHS values across genotypes; B – example of spike germination under controlled conditions in a climate chamber; C – classification of genotypes into three categories based on PHS levels.

A total of 53 resistant genotypes were identified in the Almaty region, and 59 in the Kostanay region, confirming the availability of genetic variation for PHS resistance (Figure

2B, C). Importantly, 19 genotypes exhibited stable resistance across both environments, highlighting their robustness under contrasting conditions. These genotypes included CAWBIN-246, CAWBIN-254, CAWBIN-259, CAWBIN-263, CAWBIN-272, CAWBIN-273, CAWBIN-279, CAWBIN-285, CAWBIN-298, CAWBIN-325, CAWBIN-346, CAWBIN-351, CAWBIN-363, CAWBIN-367, CAWBIN-376, CAWBIN-385, CAWBIN-387, CAWBIN-408, and CAWBIN-430. Among these, three genotypes originated from Russia and Germany, while the majority (16 genotypes) were developed in Kazakhstan, including accessions from the Barayev Scientific and Practical Center for Farming and genotypes included in the State Register of Breeding Achievements. Notably, all 19 genotypes that exhibited stable resistance to pre-harvest sprouting across both environments were characterized by red grain color, suggesting a strong association between grain pigmentation and sprouting resistance. The germination index (GI), used as an indirect indicator of seed dormancy, also showed considerable variation among genotypes across both regions (Figure 3A, B). GI values ranged from 90.6 ± 0.41% in the KRIAPI (Almaty region) to 93.55 ± 0.22% in the KAES (Kostanay region) (Figure 3A).

The classification of genotypes into dormancy categories revealed distinct patterns. In the Almaty region, 134 genotypes demonstrated strong dormancy, 85 moderate, and 49 weak, whereas in the Kostanay region, the number of strongly dormant genotypes decreased (80), and moderately dormant genotypes increased (114). This shift suggests that environmental conditions influence the expression of dormancy, likely through physiological processes regulating hormone balance and seed maturation (Figure 3C).

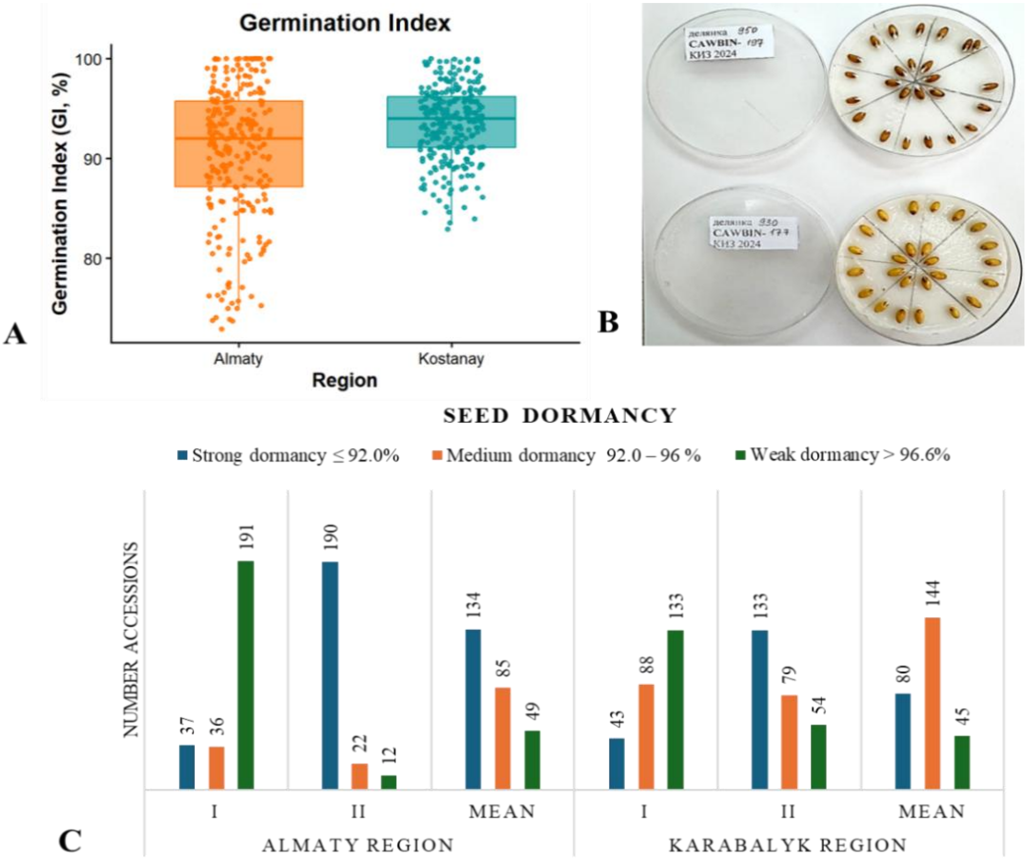


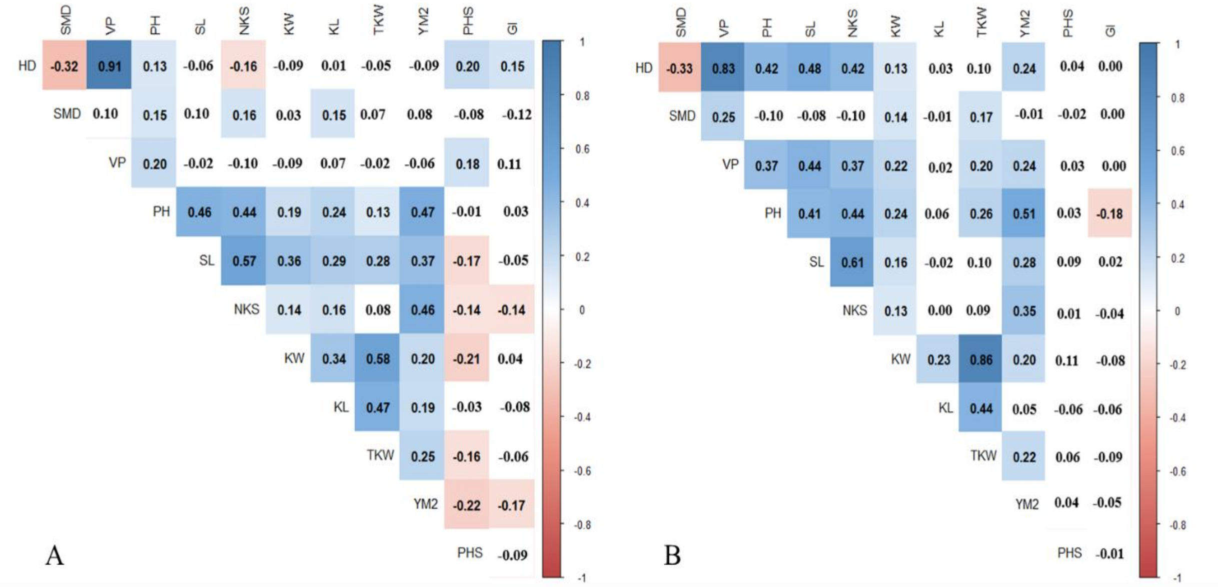
Figure 3 – Distribution of germination index (GI, %) as an indicator of seed dormancy among 270 spring wheat accessions evaluated in two regions of Kazakhstan

Note: A – distribution of GI values across genotypes; B – representative examples of seed germination in Petri dishes; C – comparison of selected genotypes based on seed dormancy and related traits

A total of 45 genotypes consistently exhibited moderate dormancy across both environments. Among these, CAWBIN-385 was particularly notable for combining moderate dormancy with resistance to PHS. This combination is of high practical value, as it indicates the presence of genotypes that can maintain resistance while ensuring adequate germination.

Trait relationships and environmental effects. The Pearson correlation analysis revealed distinct patterns of relationships among agronomic traits, yield components, and pre-harvest sprouting (PHS)-related parameters in the two studied environments (Figure 4).

Phenological traits showed strong associations, particularly between HD and VP, with a high positive correlation observed in both regions (r = 0.91 in Almaty and r = 0.83 in Kostanay), indicating a consistent relationship between developmental timing traits. In both regions, strong positive correlations were observed among yield-related traits. In the Almaty region (Figure 4A), SL showed a positive correlation with PH and TKW, while KW was strongly associated with KL. Similarly, in the Kostanay region (Figure 4B), strong positive relationships were observed between KW and KL, and between SL and PH. Correlations involving PHS and GI were generally weak or negligible in both regions. In Almaty, PHS showed slight negative correlations with YM2 (r = −0.22) and TKW (r = −0.16), whereas in Kostanay, correlations between PHS and most traits were near zero. GI also showed weak associations with most traits in both environments (Figure 4).



A

	SMD	VP	PH	SL	NKS	KW	KL	TKW	YM2	PHS	GI
HD	-0.32	0.91	0.13	-0.06	-0.16	-0.09	0.01	-0.05	-0.09	0.20	0.15
SMD		0.10	0.15	0.10	0.16	0.03	0.15	0.07	0.08	-0.08	-0.12
VP			0.20	-0.02	-0.10	-0.09	0.07	-0.02	-0.06	0.18	0.11
PH				0.46	0.44	0.19	0.24	0.13	0.47	-0.01	0.03
SL					0.57	0.36	0.29	0.28	0.37	-0.17	-0.05
NKS						0.14	0.16	0.08	0.46	-0.14	-0.14
KW							0.34	0.58	0.20	-0.21	0.04
KL								0.47	0.19	-0.03	-0.08
TKW									0.25	-0.16	-0.06
YM2										-0.22	-0.17
PHS											-0.09

B

	SMD	VP	PH	SL	NKS	KW	KL	TKW	YM2	PHS	GI
HD	-0.33	0.83	0.42	0.48	0.42	0.13	0.03	0.10	0.24	0.04	0.00
SMD		0.25	-0.10	-0.08	-0.10	0.14	-0.01	0.17	-0.01	-0.02	0.00
VP			0.37	0.44	0.37	0.22	0.02	0.20	0.24	0.03	0.00
PH				0.41	0.44	0.24	0.06	0.26	0.51	0.03	-0.18
SL					0.61	0.16	-0.02	0.10	0.28	0.09	0.02
NKS						0.13	0.00	0.09	0.35	0.01	-0.04
KW							0.23	0.86	0.20	0.11	-0.08
KL								0.44	0.05	-0.06	-0.06
TKW									0.22	0.06	-0.09
YM2										0.04	-0.05
PHS											-0.01

Figure 4 – Pearson correlation matrix among agronomic traits, yield components, and pre-harvest sprouting-related traits in 270 spring wheat accessions grown in two regions of Kazakhstan: A – Almaty region, B – Kostanay region

Note: HD – heading date (days), SMD – seed maturation date (days), PH – plant height (cm), SL – spikes length (cm), NKS – number of kernels per spike (pcs), TKW – thousand kernels weight (g), YM2 – yield per m^2 (g/m^2), KW – kernel width (mm), KL – kernel length (mm), GI – germination index (%), PHS – pre-harvest sprouting (%) Correlations with $P < 0.05$ are highlighted in color. The color indicates a positive (blue) or negative (red) correlation.

The analysis of variance (ANOVA) revealed that genotype (G), environment (region, R), and their interaction (G×R) had significant effects on most of the studied traits (Table 2). Genotype had a highly significant effect ($P < 0.001$) on all major agronomic traits, including PH, SL, NKS, KW, KL and YM2. This indicates substantial genetic variability within the studied collection. The environmental effect (region) was also highly significant for most traits. Particularly strong effects were observed for SL, YM2, PH, and NKS, indicating a pronounced influence of environmental conditions on plant development and yield formation. In contrast, the effect of region on TKW was not significant. For PHS, genotype (P = 0.018) and environment (P = 0.007) effects were significant, whereas interaction was not (P = 0.95). For GI, only the environmental effect was significant (P < 0.001) (Table 2).

Table 2 – Analysis of variance (ANOVA) for agronomic traits, yield components, and pre-harvest sprouting parameters in 270 spring wheat accessions evaluated in two regions of Kazakhstan

Plant height (PH, cm)						
1	**2**	**3**	**4**	**5**	**6**	**7**
Factor	Df	Sum Sq	Mean Sq	F-value	Pr(>F)	P-value
Genotype (G)	268	55388	207	5.624	<2e-16	***
Region (R)	1	25563	25563	695.626	<2e-16	***
G:R	264	36896	140	3.803	<2e-16	***
Spike length (SL, cm)						
Factor	Df	Sum Sq	Mean Sq	F value	Pr(>F)	P-value
Genotype (G)	268	884	3.3	7.644	<2e-16	***
Region (R)	1	1202.9	1202.9	2787.612	<2e-16	***
G:R	264	371.9	1.4	3.264	<2e-16	***
Number of kernels per spike (NKS, pcs),						
Factor	Df	Sum Sq	Mean Sq	F value	Pr(>F)	P-value
Genotype (G)	268	17607	66	2.47	< 2e-16	***
Region (R)	1	22494	22494	845.707	< 2e-16	***
G:R	264	14939	57	2.127	4.52E-13	***
Thousand kernel weight (TKW, g)						
Factor	Df	Sum Sq	Mean Sq	F value	Pr(>F)	P-value
Genotype (G)	268	11695	43.64	1.432	0.00054	***
Region (R)	1	11	10.92	0.358	0.54969	
G:R	258	8604	33.35	1.094	0.20802	
Kernel width (KW, mm)						
Factor	Df	Sum Sq	Mean Sq	F value	Pr(>F)	P-value
Genotype (G)	268	12.642	0.047	1.746	1.95E-07	***
Region (R)	1	3.561	3.561	131.79	< 2e-16	***
G:R	258	8.851	0.034	1.27	0.016	*
Kernel length (KL, mm)						
Factor	Df	Sum Sq	Mean Sq	F value	Pr(>F)	P-value
Genotype (G)	268	63.05	0.235	2.607	< 2e-16	***
Region (R)	1	5.35	5.354	59.327	1.03E-13	***
G:R	258	28.08	0.109	1.206	0.0464	*
Yield per m2 (YM2, g/m2)						
Factor	Df	Sum Sq	Mean Sq	F-value	Pr(>F)	P-value
Genotype (G)	268	5991435	22356	3.075	<2e-16	***
Region (R)	1	14315071	14315071	1968.941	<2e-16	***
G:R	267	5283655	19789	2.722	<2e-16	***
Pre-harvest sprouting (PHS, %)						
Factor	Df	Sum Sq	Mean Sq	F value	Pr(>F)	P-value
Genotype (G)	268	325655	1215	1.249	0.01811	*
Region (R)	1	7042	7042	7.238	0.00738	**
G:R	267	217265	814	0.836	0.94858	
Germination Index (GI, %)						
Factor	Df	Sum Sq	Mean Sq	F value	Pr(>F)	P-value

1	2	3	4	5	6	7
Genotype (G)	268	14176	52.9	0.566	1	
Region (R)	1	2572	2572.4	27.542	2.32E-07	***
G:R	266	13182	49.6	0.531	1	
Note: P – values are provided with significance level indicated by the asterisks; * P < 0.05, ** P < 0.01, *** P < 0.001						

Multivariate analysis of genotype performance. Principal component analysis (PCA) revealed a clear separation of genotypes according to the two environments studied (Figure 5). The first principal component (PC1) accounted for 40.5% of the total variation, while the second component (PC2) accounted for 17.3%, together explaining 57.8% of the overall variability. Genotypes from the Almaty region were predominantly distributed on the negative side of PC1, whereas those from the Kostanay region were on the positive side, indicating strong environmental differentiation. The PCA biplot showed that traits associated with plant development and spike productivity, including HD, VP, PH, SL, and NKS, were grouped towards the Almaty region. In contrast, yield-related traits such as YM2, KW, and SMD were associated with the Kostanay region. TKW and KL were positioned along the vertical axis (PC2), indicating their contribution to variation independent of regional separation. PHS and GI were clustered near the origin of the biplot, suggesting weaker associations with the main axes of variation and limited contribution to the differentiation between environments.

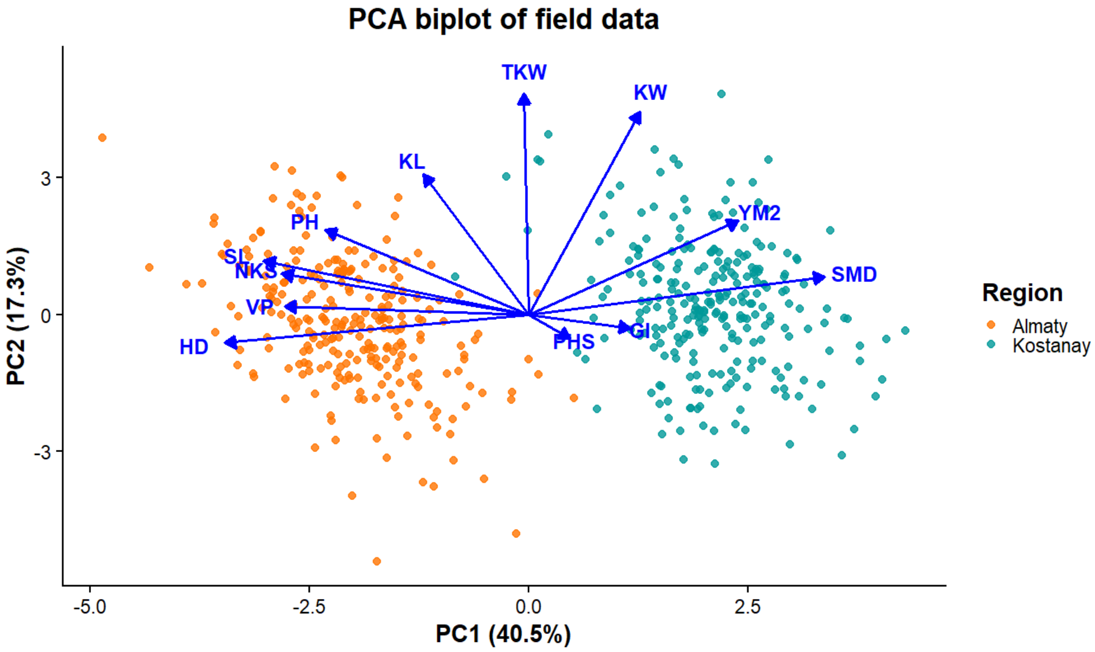


Figure 5 – Principal component analysis (PCA) biplot of all studied traits showing the distribution of 270 spring wheat accessions across two regions (Almaty and Kostanay)

The GGE biplot further demonstrated genotype stability and adaptability (Figure 6). With PC1 explaining 85.3% of the variation, most genotypes clustered near the origin, indicating stable performance across environments. However, several genotypes showed specific adaptation, reflecting genotype × environment interactions. Genotypes such as CAWBIN-179 and CAWBIN-222 combined high-yield performance with stability, making them particularly valuable for breeding programs.

The identification of top-performing genotypes revealed clear differences between environments (Table 3). In the Almaty region, yield formation was primarily associated with spike productivity, with CAWBIN-179 showing the highest NKS (58.5 pcs).

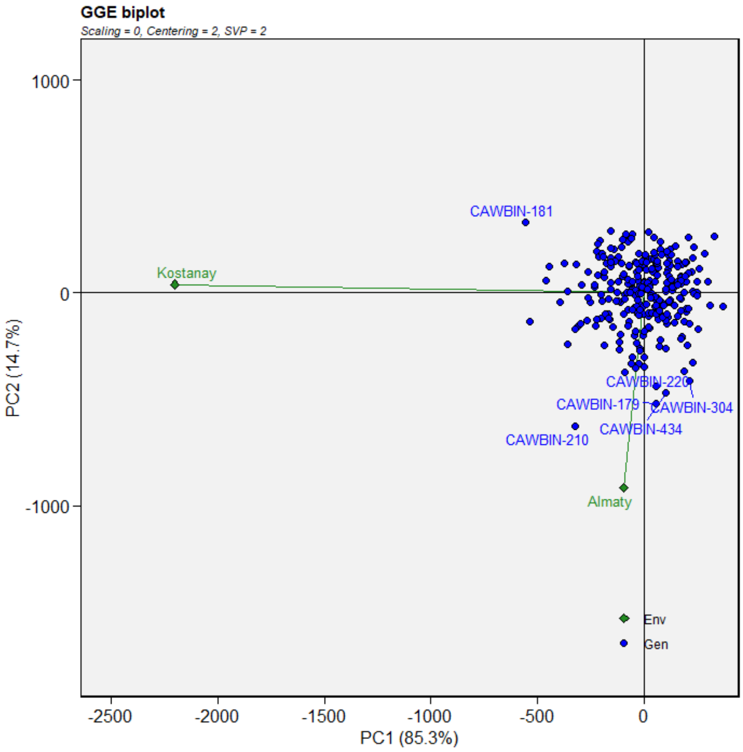


Figure 6 – GGE biplot showing genotype performance and stability for grain yield (YM2) across two environments (Almaty and Kostanay)

In contrast, in the Kostanay region, yield was driven by grain filling, with CAWBIN-181 achieving the highest yield (815.5 g/m²). The presence of genotypes that perform well across environments, such as CAWBIN-179 and CAWBIN-222, highlights the potential to develop broadly adapted cultivars. At the same time, environment-specific genotypes may be useful for targeted breeding programs.

Importantly, the combined analysis of yield traits, PHS resistance, and seed dormancy suggests that it is possible to identify genotypes that balance productivity and stress resistance. In particular, genotypes with moderate seed dormancy and stable PHS resistance represent the most promising candidates for breeding programs aimed at improving wheat resilience under changing climatic conditions.

Table 3 – Top-performing spring wheat accessions based on yield components (NKS, TKW, YM2) in two regions of Kazakhstan

Kazakh Research Institute of Agriculture and Plant Growing (Almaty region)					
1	**2**	**3**	**4**	**5**	**6**
Accessions	NKS, pcs	Accessions	TKW, g	Accessions	YM2,g/m^2
CAWBIN-	58.5	CAWBIN-177	42.2	CAWBIN-210	338.8
CAWBIN-	53.0	CAWBIN-176	41.6	CAWBIN-179	288.7
CAWBIN-	52.5	CAWBIN-172	41.4	CAWBIN-434	269.8
CAWBIN-	52.3	CAWBIN-243	40.1	CAWBIN-220	259.6
CAWBIN-	52.3	CAWBIN-170	39.8	CAWBIN-304	244.9
CAWBIN-	51.5	CAWBIN-433	38.7	CAWBIN-433	242.8
CAWBIN-	50.3	CAWBIN-219	38.7	CAWBIN-204	232.4
CAWBIN-	49.3	CAWBIN-363	38.4	CAWBIN-305	230.7
CAWBIN-	49.0	CAWBIN-185	38.0	CAWBIN-404	229.5
CAWBIN-	48.7	CAWBIN-240	38.0	CAWBIN-332	227.2

1	2	3	4	5	6
Kaz 4	30.5	Kaz 4	29.4	Kaz 4	140.8
Min*	17.00	Min*	10.20	Min*	6.2
Max*	58.5	Max*	42.2	Max*	338.8
Mean ±SE*	36.3+0.43	Mean ±SE*	28.6+0.29	Mean ±SE*	108.3+3.43
Karabalyk Agricultural Experimental Station (Kostanay region)					
Accessions	NKS, pcs	Accessions	TKW, g	Accessions	YM2,g/m^2
CAWBIN-	42.0	CAWBIN-410	43.5	CAWBIN-181	815.5
CAWBIN-	39.5	CAWBIN-432	41.3	CAWBIN-217	791.0
CAWBIN-	38.5	CAWBIN-217	40.5	CAWBIN-188	728.0
CAWBIN-	37.5	CAWBIN-179	40.1	CAWBIN-278	717.5
CAWBIN-	37.5	CAWBIN-172	39.4	CAWBIN-218	672.0
CAWBIN-	36.0	CAWBIN-218	39.3	CAWBIN-440	658.0
CAWBIN-	36.0	CAWBIN-229	38.8	CAWBIN-212	644.0
CAWBIN-	36.0	CAWBIN-391	38.1	CAWBIN-339	640.5
CAWBIN-	35.0	CAWBIN-207	37.5	CAWBIN-222	612.5
CAWBIN-	34.5	CAWBIN-414	37.4	CAWBIN-279	612.5
Aina	33.0	Aina	40.1	Aina	283.5
Min*	14.00	Min*	17.93	Min*	24.50
Max*	42.00	Max*	43.48	Max*	815.50
Mean ±SE*	26.90+0.27	Mean ±SE*	28.95+0.28	Mean ±SE*	338.65+8.19

The results of this study clearly demonstrate that both genetic factors and environmental conditions play a decisive role in determining agronomic traits, yield formation, and resistance to PHS in spring wheat. The strong differentiation observed between the Almaty and Kostanay regions confirms that environmental conditions significantly influence plant development and productivity (Figure 1), which is consistent with previous studies emphasizing the importance of genotype × environment interactions in wheat [32-33].

The contrasting patterns of yield formation observed in the two environments indicate the presence of different adaptive strategies. In the Almaty region, higher values of spike-related traits (SL and NKS) suggest that yield formation is primarily determined by sink capacity, i.e., the potential number of kernels (Figure 1). In contrast, the significantly higher yield observed in the Kostanay region indicates that yield formation is more dependent on grain filling efficiency and assimilate partitioning (Figure 1). Similar shifts between sink- and source-limited yield formation have been reported in wheat under varying environmental conditions [34]. PHS exhibited substantial variation among genotypes, confirming its complex genetic architecture (Figure 2) [6-7]. The identification of 19 genotypes with stable resistance across environments is particularly important, as stability is a key requirement for breeding. Notably, all resistant genotypes had red grain color, consistent with previous findings that red-grained wheat is generally associated with greater dormancy and improved resistance to sprouting [35]. This relationship is often explained by the genetic linkage between grain color genes and loci controlling seed dormancy [36]. Seed dormancy is widely recognized as the primary physiological mechanism underlying resistance to PHS [19]. In the present study, dormancy was assessed indirectly using the GI, which revealed differences between environments (Figure 3). The higher GI values observed in the Kostanay region indicate reduced dormancy, which corresponds well with the higher PHS levels recorded in this environment (Figure 3). This confirms the inverse relationship between dormancy and sprouting susceptibility.

A particularly important finding of this study is the identification of genotypes with moderate dormancy as the most promising for breeding. While strong dormancy effectively prevents premature germination, it may adversely affect germination uniformity and field emergence, both of which are critical for crop establishment. Conversely, weak dormancy increases susceptibility to PHS (Figure 3). Therefore, moderate dormancy represents an optimal balance between protection against sprouting and the maintenance of agronomic performance, as reported in previous studies [37].

The correlation analysis provides further insight into trait relationships. The strong positive correlations among yield components indicate coordinated development of structural and grain traits, which is essential for yield formation. In contrast, the weak correlations between PHS, GI, and yield traits suggest that resistance to sprouting is largely independent of productivity (Figure 4). This is a highly important finding from a breeding perspective, as it indicates that improving PHS resistance is unlikely to result in yield penalties. Similar conclusions have been reported in previous studies [35]. The ANOVA results further support these conclusions by showing that yield-related traits are strongly influenced by genotype × environment interactions, whereas PHS showed no significant interaction effect (Table 2). This suggests that resistance to PHS is relatively stable across environments and is primarily genetically controlled. In contrast, the strong environmental effect on GI indicates that dormancy expression is sensitive to environmental conditions during seed development, highlighting the importance of multi-environment testing [38]. Multivariate analyses (PCA and GGE biplot) provided an integrated view of genotype performance. The clear separation of environments in PCA confirms the strong environmental influence on trait expression, while the positioning of PHS and GI near the origin indicates their weak association with major yield components (Figure 5). The GGE biplot further identified genotypes with stable performance across environments, which are particularly valuable for breeding programs (Figure 6).

A limitation of the present study is that genotype × environment interaction was evaluated using only two locations during a single growing season. Although the selected sites represent contrasting agroecological zones of Kazakhstan, the relatively limited number of environments may not fully capture the range of environmental variability encountered in wheat production. Therefore, additional multi-environment and multi-year trials are required to provide a more comprehensive assessment of genotype stability, adaptability, and environmental responsiveness.

Overall, the results demonstrate that it is possible to combine high yield potential, stability, and resistance to pre-harvest sprouting within a single genotype. In particular, genotypes exhibiting moderate dormancy and stable resistance, such as CAWBIN-385, represent promising candidates for breeding programs aimed at improving wheat resilience under changing climatic conditions.

Conclusion. This study provides strong evidence that pre-harvest sprouting resistance, seed dormancy, and yield-related traits can be effectively integrated in spring wheat. The substantial genetic variation observed, along with the identification of stable genotypes across contrasting environments, highlights the potential for developing resilient cultivars adapted to diverse conditions. Importantly, the weak relationships between PHS and yield components suggest that improving sprouting resistance is unlikely to result in yield penalties. The identification of genotypes with moderate dormancy as optimal further emphasizes the importance of balancing resistance and agronomic performance. The consistent performance of genotypes such as CAWBIN-179, CAWBIN-222, and CAWBIN-385 demonstrates their value as promising breeding material. These findings are particularly relevant under climate change scenarios, where increased rainfall variability elevates the risk of PHS. Overall, this study provides important insights into the genetic and environmental regulation of PHS and offers practical guidance for breeding high-yielding and resilient wheat varieties.

Funding. This research has been funded by the Science Committee of the Ministry of Science and Higher Education of the Republic of Kazakhstan for 2024-2026 (Grant No. AP22785823 «Identification of DNA markers and genes associated with the "pre-harvest sprouting" in the collection of bread wheat Triticum aestivum L.»)

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КӨКТЕМГІ БИДАЙ КОЛЛЕКЦИЯСЫНДАҒЫ ТАМЫРДА ӨНУ ЖӘНЕ ТҰҚЫМНЫҢ ТЫНЫШТЫҒЫ: ҚАЗАҚСТАННЫҢ ӘРТҮРЛІ ЖАҒДАЙЛАРЫНДА ӨНІМДІЛІК КОМПОНЕНТТЕРІМЕН БАЙЛАНЫСЫ

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Аңдатпа. Бұл зерттеуде Қазақстанның екі түрлі экологиялық жағдайында өсірілген жаздық бидайдың 270 үлгісінен тұратын коллекцияда тамырда өну (ТӨ), тұқымның тыныштығы және өнімділікке байланысты белгілердің генетикалық әртүрлілігі бағаланды. Агрономиялық белгілер, өнім компоненттері және ТӨ төзімділігі бойынша айтарлықтай фенотиптік өзгергіштік анықталды, бұл коллекциядағы генетикалық әртүрліліктің жоғары екенін көрсетеді. Қоршаған орта жағдайлары өнім қалыптасуына айтарлықтай әсер етті:

Алматы өңірінде масақ өнімділігі басым болса, Қостанай өңірінде дәннің толысу тиімділігі негізгі фактор болды. Тамырда өну генотиптер арасында кең ауқымда өзгерді, солтүстік ортада жоғары сезімталдық байқалды. Он тоғыз генотип екі ортада да тұрақты төзімділік көрсетті, бұл оларды селекция үшін құнды генетикалық ресурс етеді. Барлық төзімді генотиптердің қызыл дәнді болуы дән пигментациясы мен тұқымның тыныштығы арасындағы байланысты растайды. Тұқымның тыныштығы өну индексі (ӨИ) арқылы бағаланып, қоршаған ортаға тәуелді екені және ТӨ-пен кері байланыста болатыны анықталды. Корреляциялық және көпөлшемді талдау нәтижелері ТӨ пен өнім компоненттері арасында әлсіз теріс байланыс бар екенін көрсетті, яғни өнімділіктің аздап төмендеуіне әкелуі мүмкін. Негізгі координаттар әдісі және генотип-қоршаған орта өзара әрекеттесуі талдаулары тұрақты әрі жоғары өнімді генотиптерді (CAWBIN-179, CAWBIN-222, CAWBIN-385) анықтады. Бұл нәтижелер жаздық бидай селекциясында жоғары өнімділік пен ТӨ төзімділігін біріктіруге болатынын көрсетеді.

Тірек сөздер: *Triticum aestivum* L., тамырда өну, тұқымның тыныштығы, өсімдік бейімделуі, өнімділік компоненттері.

ПРОРАСТАНИЕ НА КОРНЮ И ПОКОЙ СЕМЯН В КОЛЛЕКЦИИ ЯРОВОЙ ПШЕНИЦЫ: ВЗАИМОСВЯЗЬ С КОМПОНЕНТАМИ УРОЖАЙНОСТИ В КОНТРАСТНЫХ УСЛОВИЯХ КАЗАХСТАНА

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Аннотация: В данном исследовании оценивалось генетическое разнообразие по признакам прорастания на корню (ПНК), физиологический покоя семян и компонентам урожайности в разнообразной панели из 270 образцов яровой пшеницы, выращенных в двух контрастных условиях Казахстана. Выявлена значительная фенотипическая вариабельность по агрономическим признакам, компонентам урожайности и устойчивости к ПНК, что указывает на высокое генетическое разнообразие коллекции. Условия среды существенно влияли на формирование урожая: в Алматинской области преобладали признаки продуктивности колоса, тогда как в Костанайской области основным фактором урожайности была эффективность налива зерна. Прорастание зерна в колосе сильно варьировало между генотипами, при этом более высокая восприимчивость наблюдалась в северных условиях. Девятнадцать генотипов продемонстрировали стабильную устойчивость в обоих регионах, представляя ценные генетические ресурсы для селекции. Примечательно, что все устойчивые генотипы характеризовались красной окраской зерна, что подтверждает связь между пигментацией зерна и покоем семян. Покой семян, оцененный по индексу прорастания (ИП), значительно зависел от условий среды и имел обратную связь с ПНК. Корреляционный и многомерный анализы выявили слабую отрицательную связь между ПНК и компонентами урожайности, что указывает на возможное незначительное снижение урожайности. Метод главных координат и взаимодействия генотип-среда позволили выявить стабильные и высокопродуктивные генотипы, включая CAWBIN-179, CAWBIN-222 и CAWBIN-385. Полученные результаты демонстрируют возможность сочетания высокой урожайности и устойчивости к ПНК в селекционных программах яровой пшеницы.

Ключевые слова: *Triticum aestivum* L., прорастание на корню, покой семян, признаки адаптации растений, компоненты урожайности.