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RESEARCH ARTICLE

Evaluation of morpho-biological indicators of the winter wheat RIL population resistant to yellow rust

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Abstract

Yellow rust (*Puccinia striiformis* f. sp. *tritici*) is a critical threat to wheat production in Uzbekistan, often resulting in significant yield losses. Developing resilient varieties through recombinant inbred line (RIL) populations is essential to stabilise regional food security. This study evaluated the morpho-biological and agronomic performance of an F_8 RIL population (n = 100) derived from a cross between the resistant donor KR12-9010 and the high-yielding recurrent parent Jaykhun. The experiment was conducted during 2024–2025 at the Centre of Genomics and Bioinformatics, Tashkent (41°20' N, 69°18' E), using a randomised complete block design (RCBD) with three replicates. Plants were grown under an artificial infectious background created using a 1:300 ratio of *P. striiformis* urediniospores powder. Key observations included tillering, plant height, spike length, grain count per spike and grain weight per spike. Statistical analyses, including K-means clustering and analysis of variance (ANOVA), identified 43 "RIL_max" lines that were significantly superior to the recurrent parent Jaykhun. Notably, 26 elite lines surpassed the recipient in all evaluated traits and matched or exceeded the donor line KR12-9010, even under high disease pressure. These lines demonstrated successful introgression of resistance along with improved yield components. These findings provide advanced germplasm for wheat breeding programmes, offering a practical solution for sustainable production in rust-affected areas.

Keywords: morphological indicators; resistant genotypes; RIL population; wheat; yellow rust

Introduction

Wheat (*Triticum aestivum* L.) is one of the most important cereal crops in the world, serving as a primary food source for a large part of the global population (1). Wheat provides 18 % of the calories and 19 % of the protein required by humans (2). The annual increase in the global population leads to a significant increase in the demand for wheat and cereal crops. Despite this increasing demand for cereal crops, wheat production faces a number of potential constraints, which can be attributed to climate change and various abiotic and biotic factors (3).

The fungi that cause wheat rust are *Puccinia graminis* f. sp. *tritici*, *P. triticina*, *P. striiformis* f. sp. *tritici* and *Blumeria graminis* f. sp. *tritici*. Wheat yellow rust (*P. striiformis* f. sp. *tritici*) is widespread in temperate and arid regions of the world, including India, the United States of America (USA), China, Russia, Belarus, the Middle East, Pakistan and other Asian regions (4–6). Approximately 88 % of the world's wheat fields are affected by yellow rust. According to statistics, 5–6 million tons of wheat grain are lost annually due to yellow rust, with economic losses estimated at 979 million US dollars (7). While resistant wheat varieties can reduce yields by 10–70 %, in years of epidemic outbreaks, this can lead to 100 % yield losses (8, 9).

Wheat rust occurs every 3–5 years in many cool, temperate and humid countries around the world (10). In particular, China is one of the world's largest grain-producing countries, with an annual wheat yield of 128 million tonnes (11). Virulent strains of *P. striiformis* f. sp. *tritici* in wheat caused an average annual yield loss of 1.54 million tonnes in China from 2000–2018 (12). In the 2017 outbreak, wheat rust caused an average yield loss of more than 1.5 million tonnes, causing significant economic losses (13). Epidemics of yellow rust disease are frequent in Russia, mainly in the North Caucasus and cause significant yield losses (14). In recent years, the incidence of *P. striiformis* f. sp. *tritici* has been increasing in many regions of Russia. In particular, the disease is widespread in regions such as the North-West, West Siberia, Volga and Central Black Earth regions, significantly affecting the situation (15–18). Globally, approximately 43 million hectares of wheat-

growing area are susceptible to rust disease, of which 5.8 million hectares are in Pakistan (19, 20). The infected areas in Pakistan are mainly distributed in the northern foothills and mountainous areas of Balochistan, where the epidemic level is highest. The low yield of wheat cultivation in the country is mainly due to the widespread epidemic of yellow rust and the lack of resistance of wheat varieties (21, 22).

Recent fluctuations in Uzbekistan's air temperatures have accelerated the development of *P. striiformis* f. sp. *tritici* (Pst) populations. Research across Central Uzbekistan, the Fergana Valley, the Southern regions and Zarafshan indicates significant genetic similarity among local Pst genotypes (23). Consequently, extensive breeding efforts are underway to develop varieties and recombinant lines resistant to these specific regional races (24).

The objective of this study was to evaluate the morpho-biological traits of an F_8 RIL population under artificial yellow rust pressure and to identify elite lines that combine robust disease resistance with improved agronomic potential.

Materials and Methods

Plant materials

The experimental material consisted of 100 selected healthy recombinant inbred lines (RILs) at the F_8 generation. This population was developed through the pedigree method from a cross between the resistant donor genotype KR12-9010 and the high-yielding recurrent parent Jaykhun. Along with the RIL population, the parental genotypes and control varieties were included to evaluate comparative performance under disease pressure (Table 1).

Table 1. Samples used in the study

Sl. No.	Sample name	Characteristics	Source
1.	KR12-9010	Resistant to rust disease	SARI[a]
2.	Jaykhun (Zamin-1)	Moderate resistant to rust disease	SRIRA[b]
3.	RIL F_8 (KR 12-9010 × Jaykhun)	Resistant to rust disease	CGBASRUz[c]
4.	Morocco	Susceptible to rust disease	SRIPGR[d]

[a]Southern Agricultural Research Institute, Uzbekistan (SARI); [b]Scientific Research Institute of Rainfed Agriculture, Uzbekistan (SRIRA); [c]Center of Genomics and Bioinformatics, Academy of Sciences of the Republic of Uzbekistan (CGBASRUz); [d]Scientific Research Institute of Plant Genetic Resources, Uzbekistan (SRIPGR).

Experimental design

The study was conducted from October 2024 to June 2025 in the experimental fields of the special seed production facility of the Centre of Genomics and Bioinformatics in the Tashkent region, Uzbekistan. This field is located 0.5 km northeast of Tashkent (41°20' N, 69°18' E), in the upper reaches of the Chirchik River, at an altitude of 398 m above sea level. The soil of the experimental field is typical grey soil with low humus content and is classified as medium loam in terms of mechanical composition. Laboratory analysis of research samples was conducted at the Department of Personal Study of Agricultural Crops.

The trial was laid out in a randomized complete block design (RCBD). Each genotype was sown in a 1 × 5 m plot with three replications and a density of 400–500 plants per m^2. To ensure a uniform artificial infectious background, the susceptible control variety Morocco was planted every 10 rows as a spreader and a misting system maintained humidity levels above 75 % during the inoculation period.

The tillering period of wheat (from the beginning of tillering to heading) usually depends on the variety, climatic conditions and cultivation practices. Usually, an air temperature in the range of 15–20 °C is considered favourable for wheat tillering. It is also influenced by day length, humidity (timely watering) and the level of mineral fertiliser supply.

Tillering analysis of the research samples was conducted in the second decade of March. In this analysis, 10 plants from each family were selected and their tillering indicators were recorded. The collected data were subjected to one-way analysis of variance (ANOVA).

Artificial inoculation and disease assessment

To create an artificial infectious background in studies of stripe rust of wheat, uredinospores of the fungus *P. striiformis* f. sp. *tritici* were used. Rust spores collected from the regions of Tashkent, Jizzakh, Samarkand and Kashkadarya were propagated by infecting the wheat variety Morocco.

Field and laboratory experiments were conducted to assess the resistance of the research samples to yellow rust. In the field experiments, the infectious background was created by mixing *P. striiformis* f. sp. *tritici* spores at a ratio of 1:300 (1 g of spores with 300 g powder) and adding 100 µL of Tween 20 to 1 L of distilled water. The mixture was sprayed on plants along the borders and between the rows during the first 10 days of December under an average air temperature of 10 °C and humidity above 70–75 % (25). The process included the precise application of *P. striiformis* f. sp. *tritici* urediniospores, followed by strict humidity management to ensure optimal spore germination and fungal development under field conditions.

Phenotypic trait evaluation and data collection

Field evaluations commenced immediately following seedling emergence. During the vegetative period, the following morpho-biological and agronomic indicators were monitored: vegetative traits, including germination rate, tillering capacity and leaf/stem morphology; and maturity and architecture traits, including early ripening characteristics, plant height (stem length) and spike shape. Following physiological maturity, detailed laboratory analyses were conducted to evaluate yield components. For these assessments, 10 representative spikes (ears) were harvested from each RIL family. Each spike was examined individually for technical quality parameters, including spike length (cm), number of grains per spike and grain weight per spike (g). The raw data obtained from these individual measurements were summarised to determine the mean values for each characteristic per genotype across the three replicates.

Statistical analysis

Preliminary analyses of phenotypic and genotypic data were performed using Microsoft® Office Excel. Quantitative and qualitative traits were statistically analysed using the NCSS 2017 software package, employing statistical methods such as descriptive statistics, analysis of variance (ANOVA), Tukey-Kramer test, Kruskal-Wallis test and K-means cluster analysis.

Results and Discussion

Cluster analysis and genetic diversity

The evaluation of the F_8 RIL population under an artificial yellow rust infectious background revealed significant phenotypic diversity. The 100 lines were divided into three distinct groups using K-means cluster analysis based on their agronomic performance ($p \leq 0.05$). These groups were identified as J_KR_129010_RIL_max (43 families), RIL_mean (36 families) and RIL_min (21 families) (Fig. 1). The RIL_max group represents the successful introgression of resistance from the donor KR12-9010 while recovering or improving the high-yielding characteristics of the recurrent parent Jaykhun.

Analysis of tillering during the second decade of March revealed significant variation in developmental rates. The RIL_max group achieved a mean tillering number of 9.33, which is superior to both the recurrent parent Jaykhun (7.32) and the susceptible control Morocco (8.12) (Table 2). Tukey-Kramer test results confirmed that these differences were statistically significant ($p < 0.001$), suggesting that the introgressed genomic regions from the donor KR12-9010 enhanced the vegetative vigour of the RILs (Table 3). The Kruskal-Wallis test further validated these findings, with a high test statistic (z = 6.03) indicating robust median differences (Table 4 & Fig. 2).

Plant height and architecture

For wheat varieties in Uzbekistan, a medium height (90–110 cm) is preferred to balance biomass production with lodging resistance. The RIL_max cluster averaged 93.68 cm, statistically similar to the resistant donor KR12-9010 (94.92 cm), while the parent Jaykhun was significantly shorter at 61.36 cm (Table 5 and 6). This architecture allows for higher photosynthetic capacity and easier mechanical harvesting (Table 7 & Fig. 3).

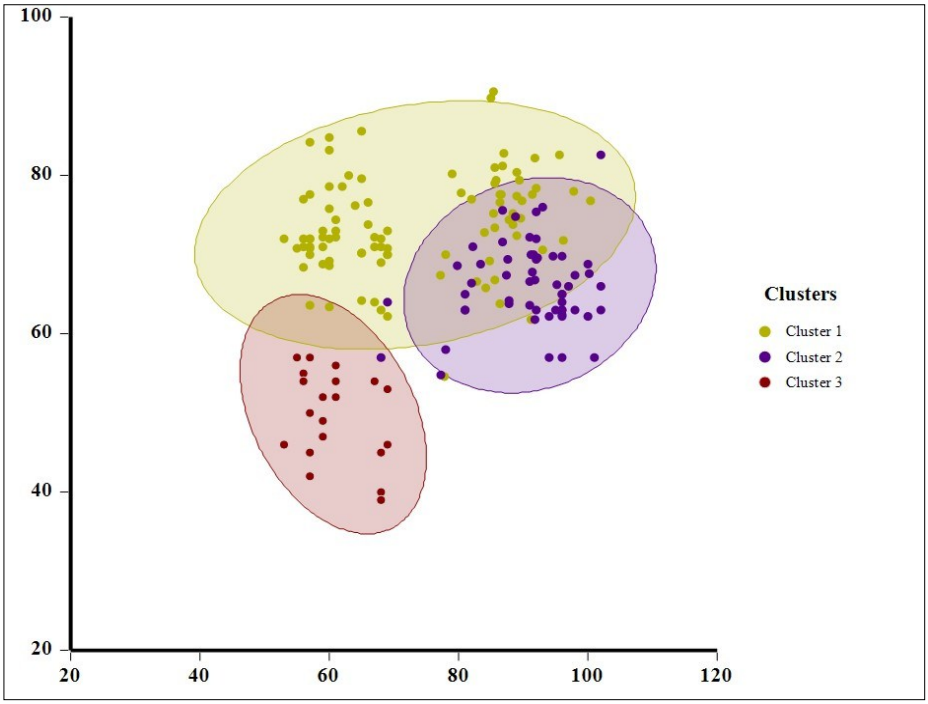

Fig. 1. K-means cluster analysis of agronomic indicators in the population line ($p \leq 0.05$).

Table 2. Analysis of descriptive statistics data on the tillering number of the studied samples

Sample name	Mean	Effect	Median	Mean difference (%)	Standard deviation	Standard error √(MSE/ni)
J_KR_129010_RIL_max	9.331	1.233325	9.3	0.000	0.44978	0.1725
J_KR_129010_RIL_mean	7.977	- 0.125387	7.95	- 14.53729	0.15578	0.1758
J_KR_129010_RIL_min	6.838	- 1.257827	6.9	- 26.7	0.45436	0.1494
Jaykhun	7.32	- 0.776762	7	- 21.5434	1.18039	0.149
KR12_9010	9	0.9032837	9	- 3.5369	1.44337	0.1793
Morocco	8.12	0.0232374	8	- 12.9689	1.12989	0.1694

Table 3. Tukey-Kramer test analysis of tillering number among the studied genotypes (differences among all samples and confidence intervals of *p* -values)

Sample name	Mean	Simult.C.I.	Lower 95.0 % difference	Mean simult.C.I.	*p* -value
J_KR_129010_RIL_max	9.330041	-	-	-	-
J_KR_129010_RIL_mean	7.971367	0.6469778	1.358674	2.070369	0.001
J_KR_129010_RIL_min	6.838889	1.831732	2.491152	3.150572	0.00001
Jaykhun	7.32	1.291131	2.010041	2.728952	0.0001
KR12_9010	9	-0.3888693	0.3300411	1.048952	0.77387
Morocco	8.12	0.4911307	1.210041	1.928952	0.01

Table 4. Kruskal-Wallis test analysis of the tillering number of the research genotypes

Sample name	J_KR_129010_RIL_max	J_KR_129010_RIL_mean	J_KR_129010_RIL_min	Jaykhun	KR12_9010	Morocco
J_KR_129010_RIL_max	0	3.9319**	8.4005**	6.0356**	1.6583	3.6579**
J_KR_129010_RIL_mean	3.9319**	0	4.112**	2.1236*	2.2138*	0.2323
J_KR_129010_RIL_min	8.4005**	4.112**	0	1.7802	6.4469**	4.3151**
Jaykhun	6.0356**	2.1236*	1.7802	0	4.2955**	2.3332*
KR12_9010	1.6583	2.2138*	6.4469**	4.2955**	0	1.9623*
Morocco	3.6579**	0.2323	4.3151**	2.3332*	1.9623*	0

Regular Test: Medians are significantly different if *z*-value > 1.9600

Bonferroni Test: Medians are significantly different if *z*-value > 2.9352

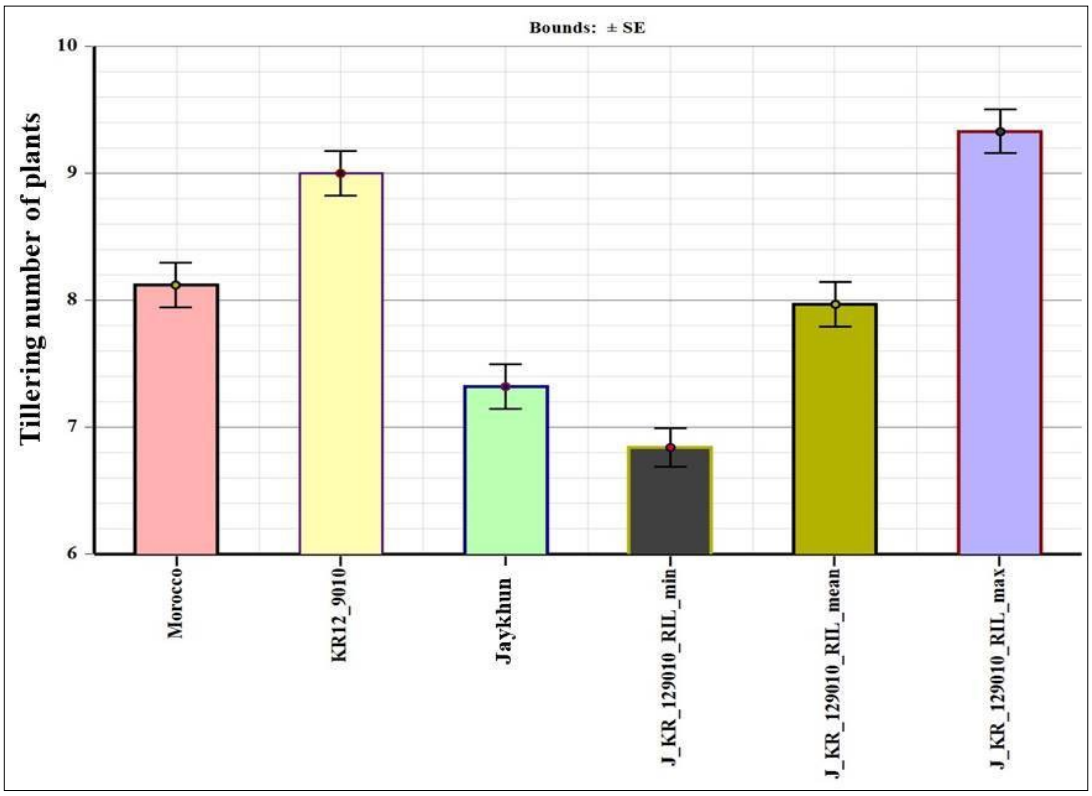

Fig. 2. One-way analysis of covariance (ANCOVA) of tillering performance in the wheat RIL population and parental and control genotypes.

Table 5. Analysis of descriptive statistical data on the plant height of the research samples

Sample name	Mean	Effect	Median	Mean difference (%)	Standard deviation	Standard error √(MSE/ni)
J_KR_129010_RIL_max	93.683	13.3771	92	0.000	3.102267	0.8363
J_KR_129010_RIL_mean	87.863	7.55116	87.8	-6.461	1.132021	0.8735
J_KR_129010_RIL_min	82.3675	2.05613	83.1	-12.07	3.135346	0.8381
Jaykhun	61.36	-18.956	60	-34.502	3.067029	0.8194
KR12_9010	94.92	14.6038	96	1.32	5.964618	0.8407
Morocco	61.68	-18.636	59	-34.16	5.69883	0.807

Table 6. Tukey-Kramer test analysis of plant height among the studied genotypes (difference between all samples and confidence intervals of *p* -value)

Sample name	Mean	Lower 95.0 % simult.C.I.	Mean difference	Upper 95.0 % simult.C.I.	*p* -value
J_KR_129010_RIL_max	93.68333	-	-	-	-
J_KR_129010_RIL_mean	87.86364	2.320115	5.819697	9.319279	0.001
J_KR_129010_RIL_min	82.36875	7.891925	11.31458	14.73724	0.0001
Jaykhun	61.36	28,93507	32.32333	35.71159	0.00001
KR12_9010	94.92	-4.624926	– 1.236667	2.151592	0.89977
Morocco	61.68	28.61507	32.00333	35.39159	0.00001

Table 7. Kruskal-Wallis test analysis of plant height among the studied genotypes

Sample name	J_KR_129010_RIL_max	J_KR_129010_RIL_mean	J_KR_129010_RIL_min	Jaykhun	KR12_9010	Morocco
J_KR_129010_RIL_max	0	2,246*	4.2767**	7.5473**	0.3823	7.594**
J_KR_129010_RIL_mean	2.246*	0	1.9367	5.1103**	2.6415*	5.156**
J_KR_129010_RIL_min	4.2767**	1.9367	0	3,2272**	4.7024**	3.2739**
Jaykhun	7.5473**	5.1103**	3.2272**	0	8.0118**	0.0472
KR12_9010	0.3823	2.6415*	4.7024**	8.0118**	0	8.0589**
Morocco	7.594**	5.156**	3.2739**	0.0472	8.0589**	0

Regular Test: Medians are significantly different if *z*-value > 1.9600

Bonferroni Test: Medians are significantly different if *z*-value > 2.9352

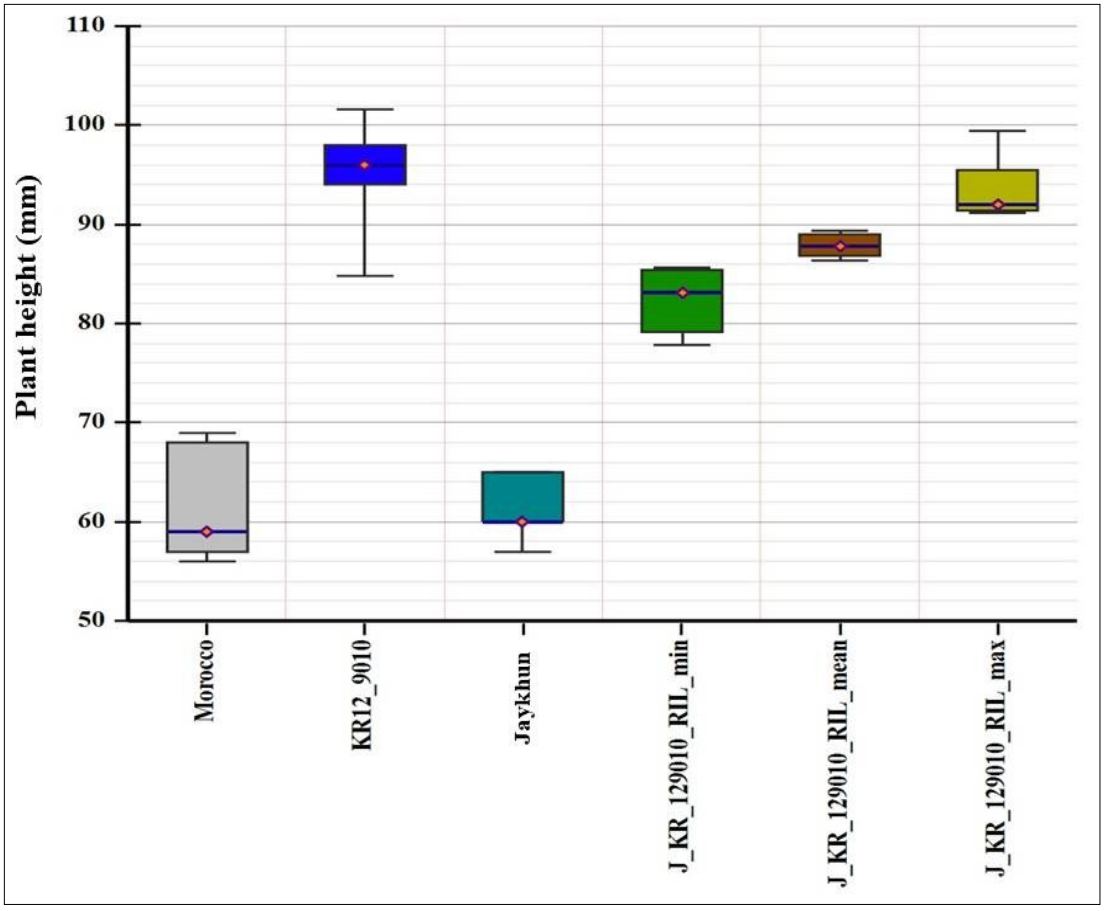

Fig. 3. One-way analysis of variance (ANOVA) of plant height in the wheat RIL population and parental and control genotypes.

Spike productivity and sink capacity

Spike length

The RIL_max group averaged 13.44 cm, significantly outperforming the recurrent parent Jaykhun (11.35 cm) and the control Morocco (8.9 cm) (Table 8, 9 & Fig. 4).

Grains per spike

One of the most significant improvements was observed in grain count. The RIL_max lines reached 80.34 grains, compared to 62.51 in Jaykhun (Table 10). Fig. 5 illustrates transgressive segregation, where several RILs exhibited higher grain counts than even the resistant donor.

The Kruskal-Wallis analysis confirms the high statistical significance of the grain count differences between the clusters (Table 11). Specifically, the z-value of 8.65 between the RIL_max group and Jaykhun demonstrates that the increased sink capacity is not due to chance but is a robust genetic characteristic of the selected elite lines.

Table 8. Tukey-Kramer test analysis of spike length among the studied genotypes (difference between all samples and confidence interval of *p* -value)

Sample name	Mean	Simult.C.I.	Lower 95.0 % difference	Mean simult.C.I.	*p* -value
J_KR_129010_RIL_max	13.446	-	-	-	-
J_KR_129010_RIL_mean	12.786	0.30176	0.6601	1.0183	0.01
J_KR_129010_RIL_min	12.06	1.0678	1.3863	1.7046	0.001
Jaykhun	11.35	1.73208	2.0943	2.456	0.0001
KR12_9010	13.24	-0.1555	0.2067	0.5688	0.57334
Morocco	8.9	4.1594	4.5463	4.9330	0.00001

Table 9. Kruskal-Wallis test analysis of spike length among the studied genotypes

Sample name	J_KR_129010_RIL_max	J_KR_129010_RIL_mean	J_KR_129010_RIL_min	Jaykhun	KR12_9010	Morocco
J_KR_129010_RIL_max	0	3.3932**	7.1691**	8.37**	0.9987	9,7199**
J_KR_129010_RIL_mean	3.3932**	0	3.151**	4.75**	2.2467*	6.3031**
J_KR_129010_RIL_min	7.1691**	3.151**	0	2.162*	5.6041**	4.0062**
Jaykhun	8.3487**	4.7574**	2.1625*	0	6.9363**	1.8071
KR12_9010	0.9987	2.2467*	5.6041**	6.94**	0	8.3467**
Morocco	9.7199**	6.3031**	4.0062**	1.8071	8.3467**	0

Regular Test: Medians are significantly different if *z*-value > 1.9600

Bonferroni Test: Medians are significantly different if *z*-value > 2.9352

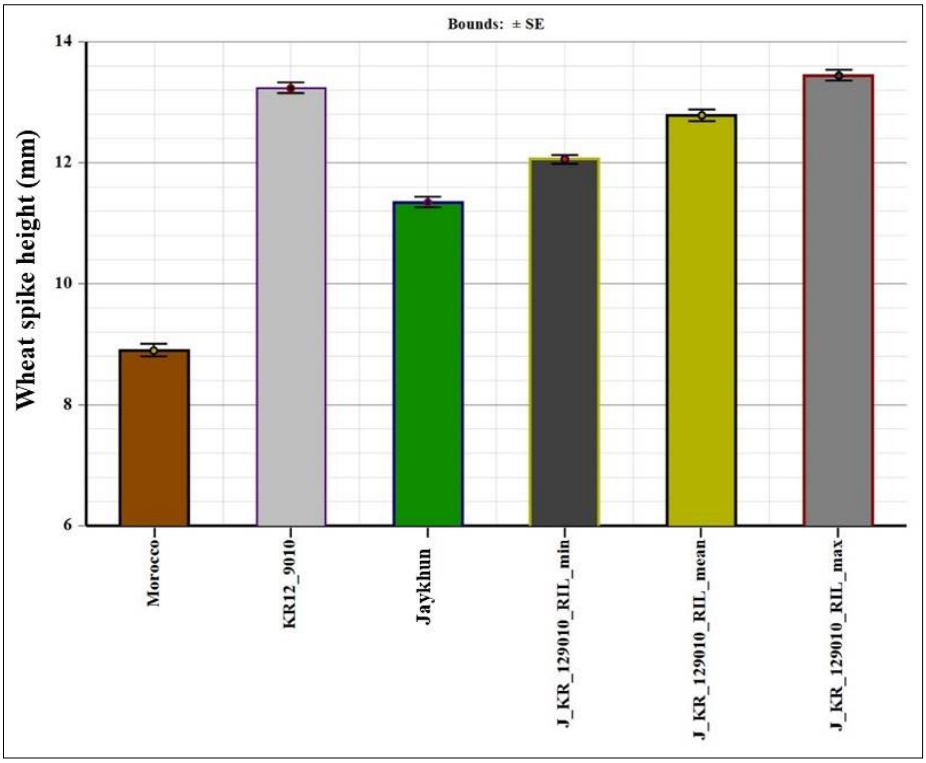

Fig. 4. One-way analysis of covariance (ANCOVA) for spike length in the wheat RIL population and parental and control genotypes.

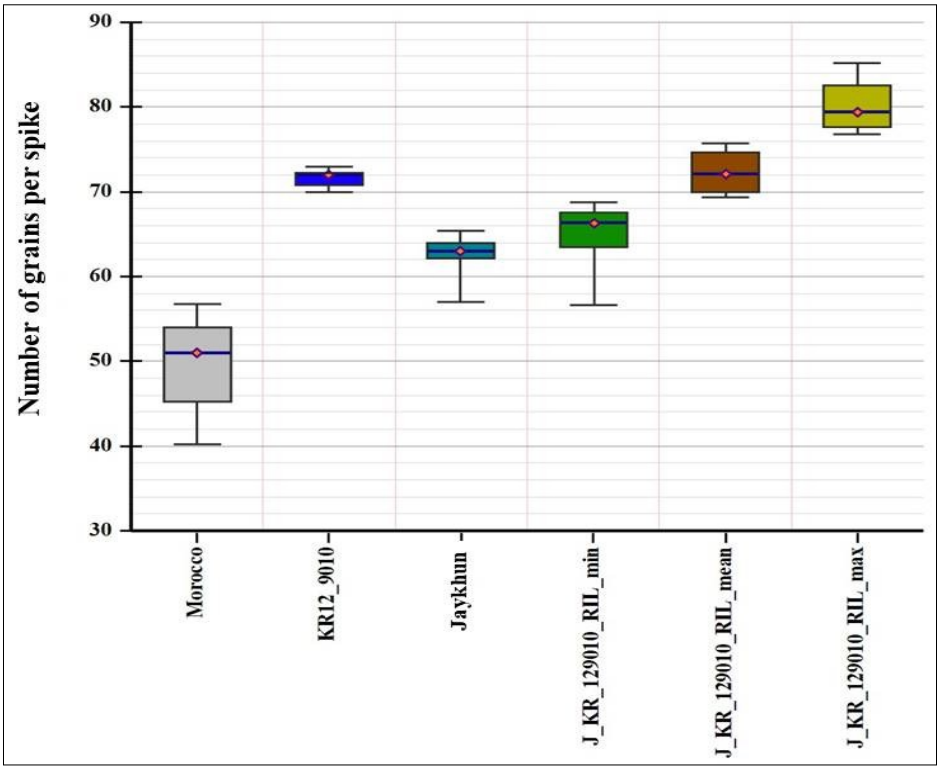

Fig. 5. One-way analysis of variance (ANOVA) for the number of grains per spike in the wheat RIL population and parental and control genotypes.

Table 10. Tukey-Kramer test analysis of the number of grains per spike among the studied genotypes (difference between all samples and confidence interval of *p* -value)

Sample name	Mean	Simult.C.I.	Lower 95.0 % difference	Mean simult.C.I.	*p* -value
J_KR_129010_RIL_max	80.34118	-	-	-	-
J_KR_129010_RIL_mean	72.34706	5.599401	7.994118	10.38883	0.001
J_KR_129010_RIL_min	64.7125	13.19683	15.62868	18.06052	0.0001
Jaykhun	62.512	15.22785	17.82918	20.4305	0.00001
KR12_9010	71.6368	6.103049	8.704376	11.3057	0.001
Morocco	49.55	28.00877	30.79118	33.57359	0.0000001

Table 11. Kruskal-Wallis test analysis of the number of grains per spike among the studied genotypes

Sample name	J_KR_129010_RIL_max	J_KR_129010_RIL_mean	J_KR_129010_RIL_min	Jaykhun	KR12_9010	Morocco
J_KR_129010_RIL_max	0	3.7631**	8.1343**	8.66**	3.7153**	10.259**
J_KR_129010_RIL_mean	3.7631**	0	4.4286**	5.19**	0.2511	7.0207**
J_KR_129010_RIL_min	8.1343**	4.4286**	0	1.0401	3.8385**	3.1142**
Jaykhun	8.6581**	5.1939**	1.0401	0	4.604**	2.035*
KR12_9010	3.7153**	0.2511	3.8385**	4.60**	0	6.3742**
Morocco	10.2594**	7.0207**	3.1142**	2.035*	6.3742**	0

Regular Test: Medians are significantly different if *z*-value > 1.9600

Bonferroni Test: Medians are significantly different if *z*-value > 2.9352

Grain weight and correlation analysis

Grain weight per spike is a primary determinant of yield potential, particularly when plants are subjected to biotic stress such as yellow rust. The evaluation of the F_8 (KR12-9010 × Jaykhun) RIL population showed that the J_KR_129010_RIL_max group achieved a mean grain weight of 4.13 g (Table 12). This represents a significant improvement over the recurrent parent Jaykhun (2.64 g) and the susceptible control Morocco (2.16 g) (Table 12).

While the statistical means are detailed in Table 12, the phenotypic distribution illustrated in Fig. 6 reveals the presence of transgressive segregants within the RIL_max cluster. Several elite lines exceeded the donor parent KR12-9010 (3.16 g), indicating a successful combination of high sink capacity from the donor and the adaptive background of Jaykhun. The Kruskal-Wallis test confirmed the robustness of these findings, with a *z*-value of 10.28 between the RIL_max group and the Morocco control (Table 13). These 26 high-performing families demonstrate superior grain-filling efficiency, making them primary candidates for further regional stability trials (Fig. 6).

The superior performance of the RIL_max cluster can be attributed to the synergistic relationship between morphological architecture and disease resilience. The increased plant height and significantly longer spikes observed in these lines (Fig. 3 and 4) suggest a higher sink capacity, which allowed for greater accumulation of photoassimilates. While yellow rust (*P. striiformis* f. sp. *tritici*) typically reduces yield by depleting the plant's energy during the grain-filling stage, the RIL_max lines maintained high grain weight per spike (mean 4.13 g), indicating that the introgression of resistance genes from KR12_9010 prevented the pathogen from disrupting the vascular transport of nutrients. This biological efficiency confirms that these lines successfully combined the “stay-green” potential of the resistant donor with the high-yielding architecture of the parent Jaykhun.

In recent years, shifting climate patterns, specifically fluctuations in temperature and increased humidity, have significantly impacted disease management and crop productivity, influencing both host resistance and pathogen adaptation (26). Given these vulnerabilities, evaluating the genetic diversity and resistance characteristics of wheat germplasm is critical for ensuring yield stability across diverse environments (27, 28). While the Jaykhun variety has historically been a high-yielding staple in the State Register of Uzbekistan, the emergence of new physiological races of yellow rust has compromised its resistance. This study demonstrates that by hybridising Jaykhun with the resistant donor KR12-9010, it is possible to develop high-yielding RILs that maintain productivity. Rigorous evaluation under artificial inoculation with urediniospores allowed for the successful identification of elite lines that combine the established agronomic excellence of Jaykhun with robust, climate-resilient resistance.

Statistical analysis of the F_8 (KR_129010 × Jaykhun) RIL population indicates that the 43 families within the J_KR_129010_RIL_max cluster achieved optimal values across all morpho-biological and agronomic traits. Notably, these RILs demonstrated transgressive segregation, where several lines were equal to the donor KR12-9010 for height and resistance, yet superior in grain number and spike length. Consequently, these 43 families represent the most promising genetic material for advancing regional wheat productivity under disease pressure.

The technical execution of the artificial inoculation and the resulting phenotypic health of the selected RILs are visually summarised in Fig. 7. Fig. 7A shows the application of *P. striiformis* f. sp. *tritici* urediniospores to the RIL population and parental genotypes. The maintenance of strict humidity levels (Fig. 7B) ensured a uniform infectious background, allowing for the clear identification and comparative evaluation of the J_KR_129010_RIL_max lines. These elite lines remained productive and maintained high leaf health despite high disease pressure, whereas the Morocco control exhibited characteristic yellow rust symptoms and severe chlorosis (Fig. 7C).

Table 12. Tukey-Kramer test analysis of grain weight per spike among the studied genotypes (difference between all samples and confidence interval of *p* -value)

Sample name	Mean	Lower 95.0 % simult.C.I.	Mean difference	Upper 95.0 % simult.C.I.	*p* -value
J_KR_129010_RIL_max	4.1355	-	-	-	-
J_KR_129010_RIL_mean	3.6442	0.3346	0.49134	0.6481	0.01
J_KR_129010_RIL_min	3.1734	0.8078	0.96211	1.1165	0.001
Jaykhun	2.6498	1.3181	1.48571	1.6534	0.00001
KR12_9010	3.1632	0.8047	0.97230	1.1399	0.001
Morocco	2.1615	1.7947	1.97396	2.1533	0.000001

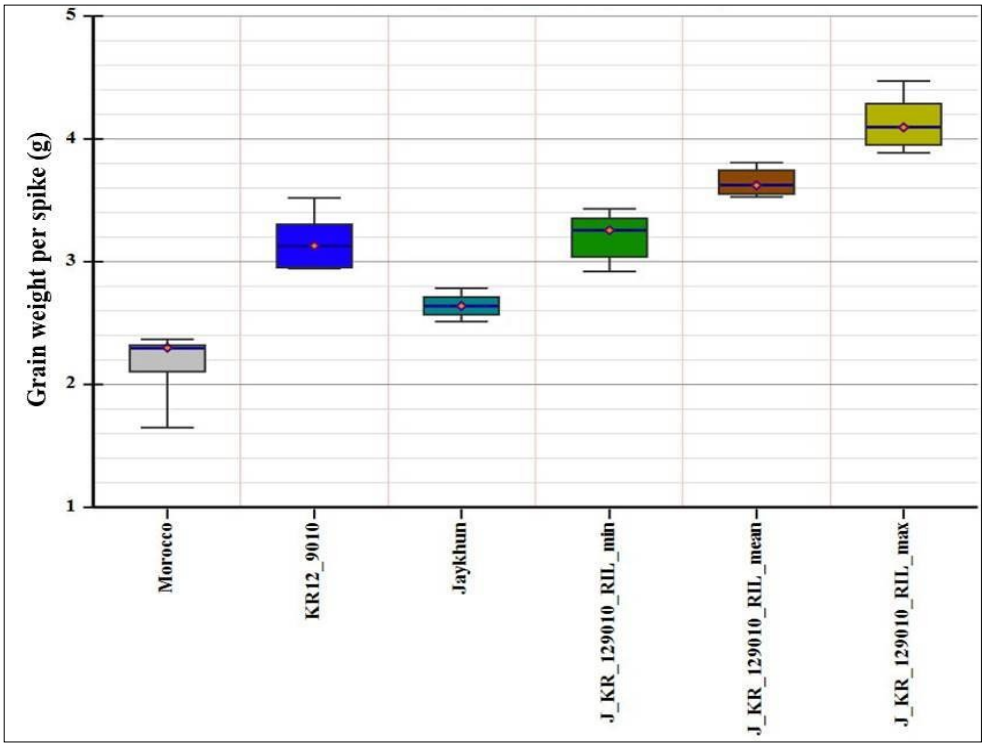

Fig. 6. One-way analysis of covariance (ANCOVA) of grain weight per spike in the wheat RIL population and parental and control genotypes.

Fig. 7. Artificial inoculation and field evaluation process. (A) Application of *Puccinia striiformis* f. sp. *tritici* urediniospores to the RIL population and parental genotypes; (B) Maintaining high humidity/moisture conditions to facilitate spore germination and fungal development; (C) Comparative field evaluation of resistance levels between the resistant RIL_max lines and susceptible control.

Table 13. Kruskal-Wallis test analysis of grain weight per spike among the studied genotypes

Sample name	J_KR_129010_RIL_max	J_KR_129010_RIL_mean	J_KR_129010_RIL_min	Jaykhun	KR12_9010	Morocco
J_KR_129010_RIL_max	0	2.8462*	6.5433**	9.1500**	6.1128**	10.282**
J_KR_129010_RIL_mean	2.8462*	0	3.5972**	6.408	3.4072**	7.7058**
J_KR_129010_RIL_min	6.5433**	3.5972**	0	3.1295	0.0892	4.6505**
Jaykhun	9.1530**	6.4080**	3.1295**	0	2.8319*	1.6201
KR12_9010	6.1128**	3.4072**	0.0892	2.8319	0	4.2900**
Morocco	10.2821	7.7058**	4.6505**	1.6201	4.2900**	0

* **Pairwise (unadjusted) test:** If the *z*-value > 1.9600, the medians are significantly different

Bonferroni test: If the *z*-value > 2.9352, the medians are significantly different

The superior performance of the RIL_max group is attributed to the successful introgression of resistance from KR12_9010 without yield drag. The positive correlation between increased plant height and spike length provided the necessary sink capacity to maintain high grain weights even under fungal pressure. This confirms the recovery of the Jaykhun agronomic background while enhancing rust resistance.

While these results are promising, a limitation of the current study is the evaluation at a single site; future research should involve multi-environmental trials to confirm the stability of these traits across diverse agro-climatic zones in Uzbekistan.

Conclusion

The F_8 (KR12-9010 × Jaykhun) RIL population was evaluated under an artificial infectious background of yellow rust urediniospores to identify high-yielding, resistant genotypes. This research successfully identified 26 elite wheat lines that combine the high yield potential of the Jaykhun variety with the durable yellow rust resistance of KR12-9010. The biological success of this RIL_max group stems from a favourable correlation between morphological traits and disease resilience, ensuring stable grain weight (mean 4.13 g) even under high pressure from *P. striiformis* f. sp. *tritici*.

These 26 elite families, which comply with regional breeding standards, will be submitted to the State Variety Testing Department for registration as new commercial varieties. While these lines represent a critical resource for enhancing food security in Uzbekistan amidst fluctuating climate conditions, further multi-environmental trials are necessary to confirm the stability of these traits across different agro-climatic zones.

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Authors' contributions

JKN conducted the laboratory and field experiments, collected the data, performed statistical analysis and wrote the manuscript. NNK, ISN, UAB, AKM, MMK, RIM, MAJ, VSK, NRR, SIM, YAM, IEB and BKR participated in the experiments and in the revision of the manuscript. ZTB revised and approved the final manuscript. All authors read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest: The authors declare that they have no conflict of interest.

Ethical issues: None

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