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Genetic Analysis and Resistance Profiling of Wheat Stripe Rust in Egyptian Cultivars

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Abstract: Six Egyptian bread wheat (*Triticum aestivum* L.) cultivars were evaluated at the Kafr El-Hamam Agricultural Research Station, Sharqia Governorate, Egypt, during the 2024 and 2025 growing seasons to assess their response to stripe rust under artificial inoculation. The study aimed to detect and introgress the yellow rust resistance gene *Yr15* into six parental cultivars; Giza-171, Gemmeiza-11, Sids-12, Misr-1, Misr-2, and Sids-14 and their corresponding F_1 and F_2 hybrids. The cultivars displayed variable reactions to stripe rust, with Giza-171 and Sids-14 exhibiting slow-rusting characteristics, whereas Gemmeiza-11, Sids-12, Misr-1, and Misr-2 showed rapid disease progression. The area under the disease progress curve (AUDPC) closely reflected disease severity across genotypes. *Yr15* was not detected in any of the parental cultivars. Segregation patterns observed in the F_2 populations of crosses with *Yr15* confirmed its absence in all tested cultivars. Broad-sense heritability exceeded 98%, indicating strong genetic control and the feasibility of selecting resistant plants as early as the F_2 generation; however, delayed selection is preferable due to the considerable dominance effects influencing resistance expression. Yield-related traits showed superior mean values in the F_2 populations compared with their respective parents, reflecting favorable recombination. These findings underscore the need for breeders to diversify resistance sources rather than relying solely on complete or race-specific resistance genes, thereby strengthening long-term resilience against stripe rust.

Key words: Wheat, *Triticum aestivum*, stripe rust, *Puccinia striiformis*, disease resistance, heritability, breeding populations.

1. Introduction

Wheat (*Triticum aestivum* L.) remains one of the most essential cereal crops worldwide, serving as a primary source of calories and protein for large populations across developing and developed countries (Curtis 2002). The increasing global demand for wheat, together with climate variability and the continual emergence of new pathogen races, poses a major challenge to ensuring sustainable wheat production. In Egypt, wheat is considered a strategic crop where production is frequently threatened by biotic stresses, particularly stripe rust, which has historically caused severe epidemics and significant yield losses **(Omara *et al.*, 2021 and Shahin *et al.*, 2024)**. Stripe rust, caused by *Puccinia striiformis* f. sp. *tritici* (Pst), is one of the most destructive diseases of wheat and is capable of reducing grain yield by 10–70% depending on the cultivar and epidemic conditions **(Roelfs *et al.*, 1992; Omara *et al.*, 2016; Omara *et al.*, 2022b and Mabrouk *et al.*, 2022)**. The pathogen thrives under cool and humid environments and produces new virulent races capable of overcoming previously effective resistance genes **(Line ad Chen, 1995)**. Because chemical control is costly and environmentally undesirable, genetic resistance is widely regarded as the most sustainable approach for managing the disease **(McIntosh *et al.*, 1995 and Omara *et al.*, 2021)**.

In Egypt, wheat stripe rust reached epidemic levels several times, including the widespread outbreak in 1967 on cultivar Giza-144, in 1995 on all cultivars such as Giza-163, Giza-164, Giza-166, Sakha-69, Sakha-92, and all Sids lines, and again in 1997 on all cultivars except Sakha-61. Subsequent epidemics occurred in 2015 on Sakha-93 and in 2019 on Sids-12, Gemmiza-11, and Shandweel-1. These epidemics affected numerous bread-wheat cultivars, including Giza-144, Giza-150, Gemmeiza-1, Sakha-8, Giza-163, Sakha-69, Sids-1, Sids-12, Sids-13, Gemmeiza-7, and Gemmeiza-11. These findings were reported by **Abd El-Hak *et al*. (1972), El-Daoudi *et al*. (1996), Abu El-Naga *et al*. (1997)**, in addition to unpublished data.

Developing resistant wheat genotypes is a key approach for managing stripe rust, but it requires understanding pathogen diversity, race distribution, and the effectiveness of resistance genes **(Mabrouk *et al*., 2022 and Omara *et al*., 2022b)**. Genetic resistance remains the most economical and reliable method for reducing yield losses **(Pink 2002)**. Through coordinated breeding efforts in Egypt, several high-yielding and yellow-rust-resistant cultivars such as Giza-171, Sids-14, Misr-3, and Misr-4 have been recently developed. Breeders have traditionally relied on hypersensitive resistance (HR) genes, yet the emergence of new virulent races highlights the need to identify effective resistance genes within parental germplasm to develop stronger, more durable resistant lines **(Hamada *et al*., 2015; Abd El-Majeed *et al*., 2017; Abd El-Majeed *et al*., 2018; Omara *et al*., 2021 and Kumber *et al*., 2022)**. Identifying yellow rust resistance genes also ensures the strategic combination of diverse genes, preventing the release of cultivars with similar genetic backgrounds **(Kolmer 1996).**

Plant disease resistance is generally divided into quantitative resistance, which involves multiple genes or QTLs and provides partial resistance, and qualitative resistance, which depends on a single major gene and confers resistance to specific pathogens (**Kaur & Bariana, 2010**). Durable resistance is largely associated with quantitative resistance, as it slows the development and expression of wheat leaf rust. In contrast, qualitative resistance tends to be less stable over time. Although individual rust resistance genes often have only a low to moderate effect, combining four or five genes can result in strong and effective resistance **(Singh *et al*., 2000)**. Pathologists and wheat breeders continue to focus on improving wheat yield by enhancing genetic resistance particularly adult plant resistance—to rust diseases **(Omara *et al*., 2021)**. As a result, considerable emphasis has been placed on developing cultivars that possess long-lasting or slow-rusting resistance, achieved through the quantitative inheritance of multiple genes **(Parlevliet 1975; Kaur & Bariana 2010; Omara *et al*., 2021)**. Stripe rust remains a major threat to many Egyptian commercial wheat cultivars, often causing severe infections and significant yield losses, especially in the northern regions. Therefore, genetic pyramiding is essential for establishing sustainable yellow rust resistance in Egypt **(Atia *et al*., 2021)**. Accordingly, this study aimed to introgress the yellow rust resistance gene *Yr15* into six Egyptian wheat cultivars through genetic analysis to enhance disease resistance and agronomic performance in the resulting hybrids.

2. Materials and Methods

2.1. Plant Materials

Six Egyptian bread wheat cultivars; Giza-171, Gemmeiza-11, Sids-12, Misr-1, Misr-2, and Sids-14 along with the monogenic line carrying the *Yr15* resistance gene (Table 1), were used in this study. All cultivars were obtained from the Wheat Research Department, Field Crops Research Institute, Agricultural Research Center (ARC), Giza.

2.2. Experimental Site and Seasons

Field evaluations were conducted at the experimental farm of Kafr El-Hamam Agricultural Research Station, Sharqia Governorate, during the 2024 and 2025 growing seasons.

2.3. Experimental Design and Plot Layout

The experiment was arranged in a randomized complete block design (RCBD) with three replicates. Each plot consisted of four rows, 3 m in length, spaced 30 cm apart, with 5 g of seeds sown per row.

2.4. Disease Nursery and Inoculation

The highly susceptible variety Morocco was planted as a spreader belt surrounding all experimental plots to serve as a field nursery for yellow rust. Artificial inoculation was performed using a mixture of urediniospores of the most virulent stripe rust races, obtained from the Sakha stripe rust greenhouse, Wheat Pathology Research Department, Plant Pathology Research Institute, ARC. Urediniospores were mixed with talcum powder at a 1:20 (v/v) ratio following the method of **Tervet and Cassel (1951).**

Table (1). Six wheat cultivars and *Yr15* used in this study with their pedigree

No.	Cultivars	Pedigree
1	Giza171	Sakha93/Gemmeiza9 S 6-1GZ-2GZ-2GZ-0S
2	Gemmeiza11	BOW"S"**/KVZ''S''**//**7C**/SERI82**/3/**GIZA168/SKHA61
3	Sids12	Buc//7c**/ald/**5**/maya74/**on//1160-147**/3/**bb**/gll/**4/chat"s'"
4	Misr1	OASIS**/SKAUZ**//**4*BCN/**3/2*PASTOR
5	Misr2	SKAUZ/BAV92
6	Sids14	Bow"s"***/Vee''s''//Bow's'/***Tsi***/3/***BANI SUEF 1 SD293-1SD-2SD-4SD-0SD
7	*Yr15*	IRAGI

2.5. Disease assessment

Disease severity (DS) was assessed four times at 10-day intervals based on the percentage of leaf area affected by rust pustules. Infection responses were classified as immune, resistant, moderately resistant, moderately susceptible, or susceptible (S). These data were used to determine final rust severity (FRS) and to calculate the area under the disease progress curve (AUDPC) following the method of **Pandey *et al.* (1989).**

2.6. Hybridization and production of F_1 generations

Six bread wheat cultivars; Giza-171, Gemmeiza-11, Sids-12, Misr-1, Misr-2, and Sids-14 were crossed with the *Yr15* monogenic line, which served as the male parent, at the Kafr El-Hamam Agricultural Research Station, Sharqia Governorate. Seeds from each hybrid combination were planted in single 2-m rows with 30 cm inter-row and 10 cm intra-row spacing. A randomized complete block design (RCBD) was used to ensure uniform production of F_1 seeds for subsequent genetic analysis.

2.7. Evaluation of F$_1$ and F$_2$ populations

F$_1$ and F$_2$ seeds derived from each cross were sown in field plots consisting of 15 rows, each 3 m in length and spaced 30 cm apart. To ensure uniform disease pressure, the highly susceptible cultivar Morocco was planted as a border around each plot. Artificial inoculation was applied at the tillering stage using a previously prepared mixture of urediniospores and talcum powder (1:20, v*/v)* **(Tervet and Cassel 1951).** Disease severity was recorded for F$_1$ and F$_2$ plants at the onset of visible symptoms. F$_2$ individuals were classified into six severity classes. Severity levels of 0–10%, 11–20%, and 21–30% were considered low-severity phenotypes, whereas 31–40%, 41–50%, and 51–60% represented high-severity phenotypes, facilitating the distinction between resistant and susceptible segregants **(Peterson *et al*., 1948 and Roelfs *et al*., 1992)**.

2.8. Genetic segregation and statistical analysis

Segregation patterns in the F$_2$ populations were evaluated to determine the mode of inheritance of *Yr15*-mediated resistance. The agreement between observed and expected segregation ratios was evaluated using the chi-square (χ^2) test, following the method described by **Steel and Torrie (1960).** This analysis enabled the verification of Mendelian segregation and the assessment of gene action contributing to stripe rust resistance in the studied populations.

2.9. Frequency distribution and genetic analysis of disease severity

The frequency distribution of yellow rust severity was analyzed for the parental lines and the F$_1$ and F$_2$ populations under field conditions. Chi-square analysis was applied to test the goodness of fit between observed phenotypic classes and the expected segregation ratios. Gene action and dominance effects were examined to estimate the minimum number of genes involved in resistance. The degree of dominance in the F$_1$ and F$_2$ generations was calculated using the following formula.$h_1 = (X\ F_1 - X\ MP)/D$ and $h_2 = 2(X\ F_2 - XMP)/D$ **(Wright 1968 and Remero and Fery 1973).**

Where:

D = ($\bar{X}$ h$_p$ – $\bar{X}$ MP).

$\bar{X}$ F$_1$ and $\bar{X}$ F$_{2=}$ Mean values of the F$_1$ and F$_2$.

$\bar{X}$ h$_{p\,=}$ High parent values.

$\bar{X}$ MP = Mid-parent value.

The significance of dominance estimates (h$_1$ and h$_2$) was evaluated by comparing the F$_1$ and F$_2$ means with the mid-parent value using a t-test. Broad-sense heritability was estimated based on variance components following the method described by **Lush (1949).**

2.10. Yield components

Yield-related traits, including plant height, number of spikes per plant, number of kernels per plant, 100-kernel weight (g), and grain yield per plant (g), were evaluated in the F$_2$ populations of six crosses (*Yr15* × Giza 171, *Yr15* × Gemmeiza 11, *Yr15* × Sids 12, *Yr15* × Misr 1, *Yr15* × Misr 2, and *Yr15* × Sids 14). Differences between parental lines were assessed using a t-test. Phenotypic, genotypic, and environmental variances were estimated based on data from the parental lines and their F$_1$ and F$_2$ generations. An F-ratio test was conducted to determine whether the F2 variance significantly exceeded the corresponding environmental variance.

3. Results

3.1. Development of yellow rust disease in wheat cultivars and *Yr15* at the adult plant stage

The yellow rust severity was assessed across all examined cultivars (Giza 171, Misr 1, Misr 2, Sids 12, Sids 14, and Gemmeiza 11), as well as *Yr15*, following artificial inoculation for yellow rust during 2024 and 2025 growing seasons (Fig. 1). Significant differences in disease severity percentages were observed among the evaluated cultivars. The Gemmeiza 11 and Sids 12 cultivars exhibited faster disease progression than the other cultivars. It was also noted that the least affected variety was Giza 171 and that the resistance gene *Yr15* has not been affected yet. By comparing AUDPC, it was noted that the most affected varieties were Gemmeiza-11 and Sids-12, with values ranging from 1416.5 to 1583.0. The least affected variety was Giza-171, with values ranging from 103.0 to 142.0. The severity of the disease was greater in the first season (2024) than in the second season (2025) (Fig.1).

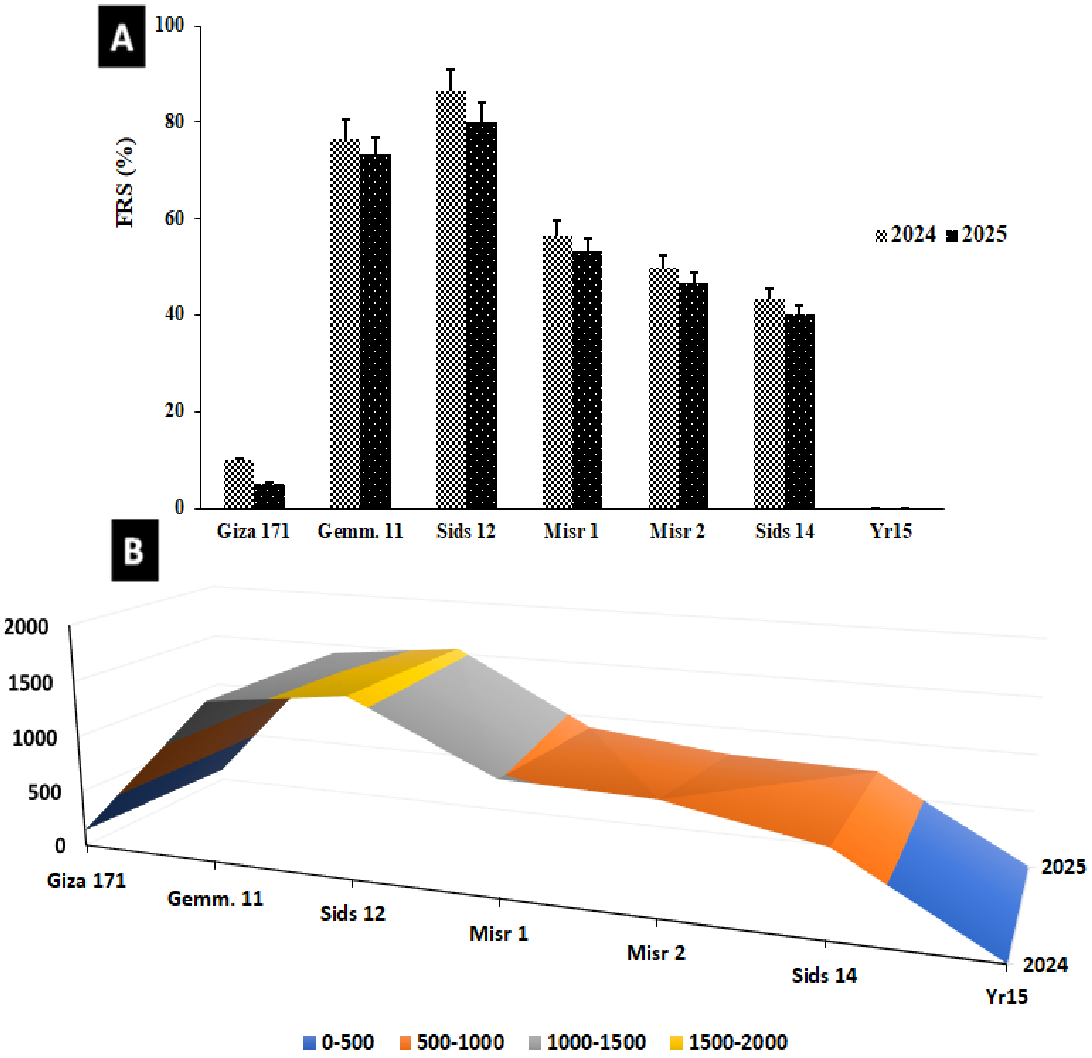

Fig. (1). (A) Final rust severity (FRS%) and (B) area under the disease progress curve (AUDPC) for yellow rust in six wheat cultivars and the Yr15 line across the 2024 and 2025 seasons

3.2. Qualitative characterization

Six crosses were made between the selected wheat cultivars and the *Yr15* line to identify and introgress the *Yr15* resistance gene at the adult plant stage (Table 2; Fig. 2). Disease severity in the resulting F_2 populations showed a wide distribution, ranging from 0% to 60%. The F_2 wheat plants resulting from crosses *Yr15*xGiza-171 and *Yr15*xSids-14 displayed low disease severity (L) and segregated into 173 L: 41H and 179 L: 78H, respectively. In contrast, a high disease severity of yellow rust was noted in F_2 plants from crosses *Yr15*xGemmeiza-11, *Yr15*xSids-12, *Yr15*xMisr-1 and *Yr15*xMisr-2. These crosses segregated into 77L: 139H, 70L: 154H, 106L: 137H, and 88L: 164H, with Pb values of 0.432, 0.537, 0.421 and 0.311 respectively. The observed ratios were consistent with the expected ratios of 7:9, 1:3, 1:1, and 7:9 for the aforementioned six crosses (Table 2 and Fig. 2).

Table (2). Distribution of yellow rust frequency among parents and six F_1 and F_2 crosses, assessed at the adult stage during the 2025 growing season

Cross name	**No. of tested plants**		**Rust severity (%) classes**								**Expected ratio**	**X^2**	**P_b**
			Resistant (R)			**Susceptible (S)**			**observed ratio**				
			0-10	**11-20**	**21-30**	**31-40**	**41-50**	**51-60%**	**L**	**H**			
Yr15×Giza 171	P_1	35	35	0									
	P_2	55	34	21									
	F_1	44	21	23									
	F_2	214	76	87	10	21	11	9	173	41	3:1	3.89	0.535
Yr15×Gemm. 11	P_1	39	32	7									
	P_2	51					23	28					
	F_1	46				11	35						
	F_2	216	24	21	32	46	54	39	77	139	7:9	5.76	0.432
Yr15×Sids 12	P_1	34	21	13									
	P_2	55					23	32					
	F_1	49				29	20						
	F_2	224	26	21	23	43	54	57	70	154	1:3	4.66	0.537
Yr15×Misr1	P_1	35	18	17									
	P_2	44				25	19						
	F_1	40				23	17						
	F_2	243	20	19	67	34	54	49	106	137	1:1	3.95	0.421
Yr15×Misr2	P_1	31	19	12									
	P_2	43				22	21						
	F_1	64				33	31						
	F_2	252	32	24	32	46	53	65	88	164	7:9	7.98	0.311
Yr15×Sids 14	P_1	45	31	14									
	P_2	47			30	17							
	F_1	53		25	28								
	F_2	257	47	56	76	23	43	12	179	78	3:1	3.92	0.467

L = Low rust severity ≤ 30 %
H = High rust severity ≥ 30%

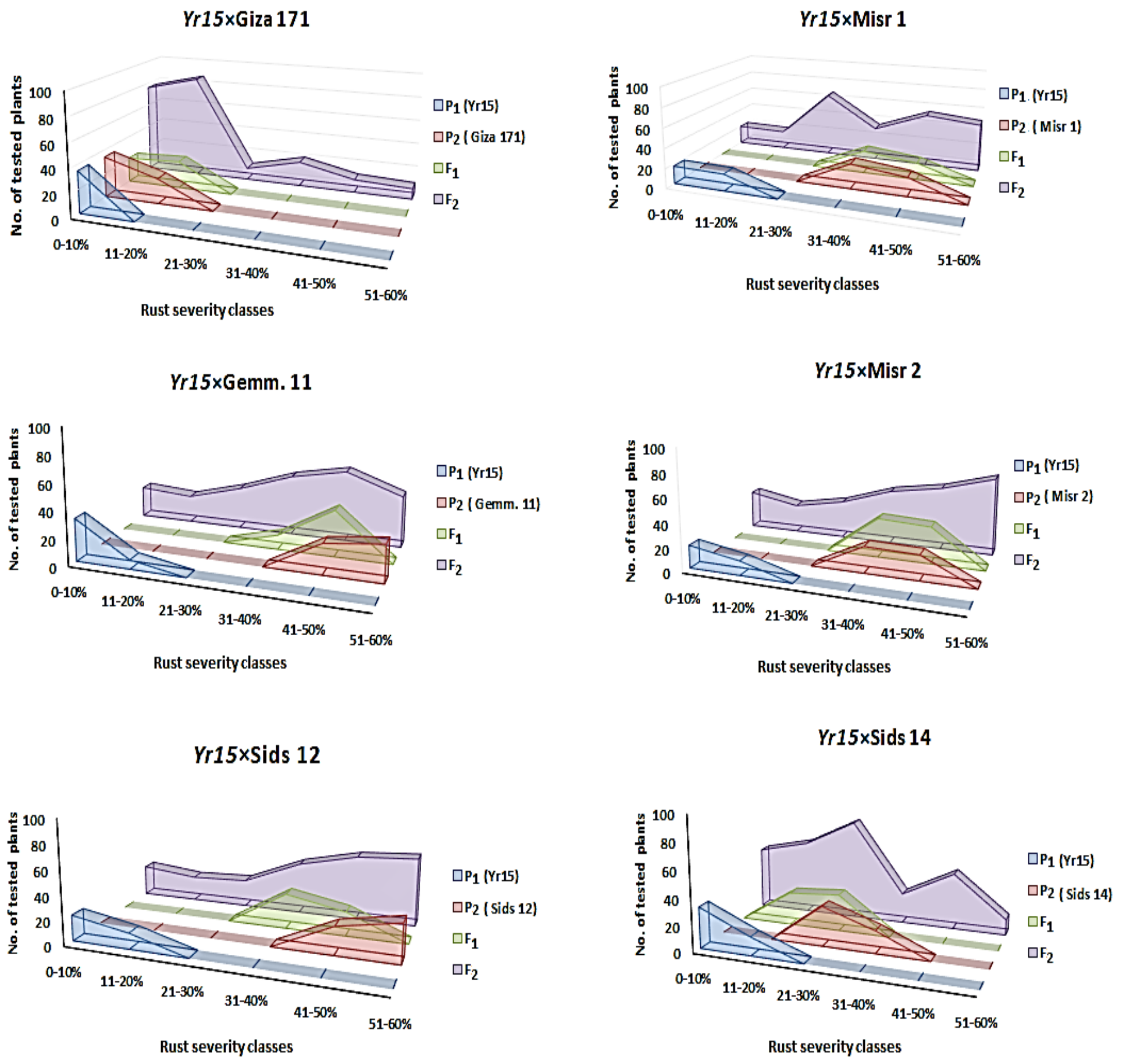

Fig. (2). Distribution of yellow rust severity (%) among the parental lines (P_1 and P_2) and the F_1 and F_2 generations of six wheat crosses between *Yr15* and the cultivars Giza 171, Misr 1, Misr 2, Sids 12, Sids 14, and Gemmeiza 11 at the adult plant stage

3.3. Quantitative analysis

The six parental lines and their corresponding F_1 and F_2 populations from the crosses (*Yr15* × Giza-171, *Yr15* × Gemmeiza-11, *Yr15* × Sids-12, *Yr15* × Misr-1, *Yr15* × Misr-2, and *Yr15* × Sids-14) were assessed under field conditions at the adult plant stage to evaluate quantitative traits associated with yellow rust resistance (Table 3). Mean and variance estimates for the parental, F_1, and F_2 generations were used to determine the dominance coefficients for F_1 (h_1) and F_2 (h_2), in addition to estimating the functional number of resistance genes involved and the broad-sense heritability. Across the six crosses, mean disease severity showed considerable variation, ranging from 6.42 to 35.68%. The F_1 generations displayed moderate levels of severity, with means between 18.19 and 24.97%, indicating partial expression of resistance. The F_2 populations exhibited wider segregation, recording mean severities of 17.10, 34.35, 35.68, 34.46, 35.27, and 24.80, respectively, reflecting the expected genetic variation following recombination. Dominance effects, represented by h_1 and h_2, provided insight into the mode of gene action controlling resistance in each cross, with values indicating differences in the relative influence of dominant versus additive genetic components across the evaluated populations. The h_1 values were -1.16, +0.31, +0.36, -1.05, -0.98, and -3.22, respectively, across six consecutive crosses. The significantly negative h1 values suggested the presence of partially resistant domains. The F_2 degree of dominance values (h_2) were -0.487, -5.829, -65.06, +88.270, -34.670, and -6.170, respectively (Table 3).

The parental lines exhibited a wide range of variance values, extending from 6.79 to 50.81 across the cultivars Giza-171, Misr-1, Misr-2, Sids-12, Sids-14, Gemmeiza-11, and the *Yr15* line (Table 2). The F_1 variances for the six tested crosses were recorded as 24.94, 18.19, 24.15, 22.14, 24.97, and 24.91, respectively. The F_2 variance values were generally elevated across all tested crosses. Additionally, the heritability percentage was notably high, exceeding 98% for the six crosses. The anticipated counts of resistance genes for these crosses were 0.013, 0.007, 0.001, 0.001, 0.001, and 0.001, respectively (Table 3).

Table (3). Mean disease severity, variance estimates, dominance coefficients, broad-sense heritability (%), and estimated gene number for six wheat crosses evaluated at the adult plant stage during the 2025 growing season

Cross name	No. of tested Plants	$\overline{X}$	S^2	Degrees of dominance		Heritability %	No. of genes
				h_1	h_2		
Yr15×Giza-171	P_1	6.42	12.24				
	P_2	23.60	8.81				
	F_1	24.94	10.22	-1.16			
	F_2	17.10	2748.02		-0.487	99.61	0.013
Yr15×Gemm-11	P_1	14.72	6.79				
	P_2	24.75	50.49				
	F_1	18.19	42.6	+0.31			
	F_2	34.35	1863.63		-5.829	98.46	0.007
Yr15×Sids-12	P_1	23.61	8.82				
	P_2	24.33	50.81				
	F_1	24.15	39.08	+0.36			
	F_2	35.68	1944.03		-65.06	98.46	0.001
Yr15×Misr-1	P_1	24.97	9.85				
	P_2	24.53	39.31				
	F_1	22.44	38.4	-10.50			
	F_2	34.46	1869.61		+88.27	98.68	0.001
Yr15×Misr-2	P_1	23.72	8.87				
	P_2	24.98	39.88				
	F_1	24.97	39.84	-0.98			
	F_2	35.27	1917.12		-34.67	98.72	0.001
Yr15×Sids-14	P_1	21.43	8.11				
	P_2	23.08	28.61				
	F_1	24.91	20.28	-3.22			
	F_2	24.80	1911.90		-6.17	99.04	0.001

3.4. Yield components of the six crosses

Given the importance of yield-related traits, the performance of the six crosses; *Yr15* × Giza-171, *Yr15* × Gemmeiza-11, *Yr15* × Sids-12, *Yr15* × Misr-1, *Yr15* × Misr-2, and *Yr15* × Sids-14 was evaluated for key agronomic characteristics. Descriptive statistics for the parental lines and their F_1 and F_2 populations are summarized in Table (4). Significant differences ($P < 0.05$) were detected among the parents for all measured traits, confirming the presence of substantial genetic diversity. For plant height, number of spikes per plant, number of kernels per plant, 100-kernel weight, and grain yield per plant, the mean values of the F_1 generation were generally comparable to or exceeded those of the respective high parents across the three crosses. Moreover, the F_2 populations exhibited higher average values for all five yield traits compared with the parental means, indicating favorable segregation and the potential for selecting superior recombinants.

The results summarized in Table (5) show clear differences among the three crosses for the evaluated genetic traits. In all cases, phenotypic variance in the F_2 populations was substantially higher than the corresponding environmental variance. Traits such as plant height, number of spikes per plant, number of kernels per plant, and grain yield exhibited the largest phenotypic, genotypic, and environmental components of variation. For every trait assessed, genetic variance exceeded environmental variance, indicating a strong genetic contribution to trait expression. Broad-sense heritability estimates for the measured traits fell within the moderate to high range, supporting the potential for effective selection. Based on the predominance of genetic variance over phenotypic variance and the favorable heritability levels, the use of modified pedigree/bulk and selected bulk methods is recommended for these crosses, as these approaches are well suited for achieving genetic improvement in early segregating generations.

4. Discussion

This investigation examined six Egyptian wheat cultivars; Giza-171, Gemmeiza-11, Sids-12, Misr-1, Misr-2, and Sids-14 alongside the monogenic line *Yr15* to characterize their responses to yellow rust under field conditions. The wide range of disease severity (%) recorded among these genotypes reflects varying levels of partial resistance, which, although incapable of conferring full immunity to specific *Puccinia striiformis* races, can substantially delay infection or attenuate symptom development in adult plants **(Omara *et al*., 2021 and Omara *et al*., 2022a)**. Such quantitative or partial resistance remains a cornerstone of durable rust management strategies in wheat. Consequently, elucidating the inheritance of resistance was essential for facilitating efficient introgression of *Yr15* into locally adapted wheat germplasm.

The *Yr15* gene, originally identified in the 1980s **(Gerechter-Amitai *et al*., 1988)**, has long been regarded as a highly effective resistance factor. However, recent reports of virulent pathotypes in the UK **(Jason, 2025)** and certain Egyptian regions **(Shahin *et al*., 2024)** highlight the evolving nature of the pathogen and the consequent need for continuous evaluation of resistance gene efficacy. Across two field seasons, the studied cultivars were differentiated into slow-rusting and fast-rusting groups. Slow-rusting behavior, characterized by reduced disease development, was observed in Misr-1, Misr-2, Sakha-94, and Giza-171. Conversely, Gemmeiza-11, Sids-12, Misr-1, and Misr-2 exhibited rapid disease progression. The absence of segregation within the F_2 populations of these cultivars indicated that *Yr15* was not expressed in their genetic backgrounds, despite earlier studies reporting its presence in some of these cultivars **(Elkot *et al*., 2016).**

Segregation patterns in the F_2 populations from *Yr15* × Gemmeiza-11, *Yr15* × Sids-12, *Yr15* × Misr-1, and *Yr15* × Misr-2 revealed ratios of 77L:139H, 70L:154H, 106L:137H, and 88L:164H, respectively corresponding to expected Mendelian ratios of 7:9, 1:3, 1:1, and 7:9. These results confirm the involvement of a single recessive gene pair governing resistance in these crosses. The overall pattern supported partial dominance toward reduced disease severity, aligning with previous findings **(Abd El-Latif & Boulot, 2000; Hermas & El-Sawi, 2015; Mabrouk *et al*., 2022 and Omara *et al*., 2017)**.

Table (4). Characteristics of *Yr15*, Giza 171, Gemmeiza 11, Sids 12, Misr 1, Misr 2, Sids 14, and their F_1 and F_2 populations for the 2025 growing season.

Parent/ generation		Plant height (cm)	No. of spikes/ plant	No. of Kernels/ spike	100-kernel weight (g)	Grain yield/ plant(g)
***Yr15* (P_1)**	Mean	82.2	7.4	63.4	2.6	18.4
	SE	0.32	0.3	1.3	0.13	1.22
	Variance	16.1	2.26	52.6	0.26	54.21
Giza-171 (P_2)	Mean	103.15	14.2	67.45	5.23	47.32
	SE	0.33	0.43	0.34	0.15	1.21
	Variance	10.2	22.23	16.32	1.34	147.66
F_1	Mean	103.34	15.11	72.43	3.14	35.3
	SE	0.31	0.23	3.23	0.04	1.34
	Variance	22.22	16.12	229.9	0.05	165.23
F_2	Mean	97.13	11.2	88.2	5.72	36.2
	SE	1.05	0.34	1.15	0.03	1.13
	Min	49	4	29	3.24	15
	Max	130	25	105.2	5.80	89
Gemm.-11 (P_3)	Mean	112.22	16.8	78.2	5.28	55.2
	SE	0.31	0.21	0.22	0.03	2.24
	Variance	14.2	35.21	19.22	0.18	179.11
F_1	Mean	119.2	15.2	91.2	3.01	43.2
	SE	0.2	0.51	3.42	0.02	1.19
	Variance	26.12	17.83	241.4	0.01	180.43
F_2	Mean	126.32	14.3	97.3	5.25	45.2
	SE	1.02	0.32	1.03	0.03	1.11
	Min	64	9	36	3.81	15
	Max	146	27	115.6	7.10	96
Sids-12 (P_4)	Mean	101.17	17.2	76.1	4.24	47.3
	SE	0.32	0.33	0.32	0.16	1.24
	Variance	13.2	29.25	15.32	0.19	165.22
F_1	Mean	115.2	15.2	89.21	2.55	40.3
	SE	0.4	0.43	2.13	0.05	1.33
	Variance	25.12	20.21	238.2	0.02	172.21
F_2	Mean	104.2	11.3	94.4	4.42	37.2
	SE	1.11	0.32	1.13	0.04	1.12
	Min	50	6	32	2.33	16
	Max	130	25	105.1	4.12	95
Misr-1 (P_4)	Mean	82.2	٨.٢	6٦.4	٦.6	٢٠.4
	SE	0.32	0.٦	٣.3	0.1٧	٥.22
	Variance	16.1	2.٤٨	5٥.6	0.2٩	٦٠.21
F_1	Mean	103.15	٣٨.2	6٤.45	٨23	4٩.32
	SE	0.33	0.٧٥	0.3٨	0.15	1.2٥
	Variance	10.2	2٦.2٦	1٨.3٤	1.34	14٩.66
F_2	Mean	103.34	1٩.٤٤	7٥.43	٧.14	3٨.3
	SE	0.31	0.٤٦	٦.23	0.0٧	1.3٨
	Min	22.22	١٨12	2٣٢.9	0.0٣	16٦.23
	Max	97.13	١٦.2	٩٠.2	٩.72	3٩.2
Misr-2 (P_4)	Mean	1.١٩	0.٧	٣.15	0.0٦	1.1٦
	SE	٥١	٨	٣٢	3.٢٦	1٨
	Variance	13٣	2٨	10٨.2	٩.80	٩١
F_1	Mean	11٥.2١	١٩.8	٨٠.2	5.٣١	5٨.2
	SE	0.٢1	0.٢٤	0.٢٥	0.0٦	2.2٨
	Variance	1٥.٢١	٣٨.21	٢٢.22	0.٢١	1٨١.11
F_2	Mean	11٧.٢١	1٨.2	9٥.2	٦.01	4٦.2
	SE	0.٣٢	0.5٤	٦.42	0.0٦	٤.19
	Min	2٨.1٢	1٩.83	24٦.4	0.0٥	18٦.43
	Max	12٨.3١	1٩.3	9٩.3	٩.25	٥٠.2
Sids-14 (P_4)	Mean	1.٢٣	0.٣٦	1.0٦	0.0٦	٥.11
	SE	6٦	٥	3٩	٥.81	1٨
	Variance	14٩	٢٥	11٨.6	٩.10	١٠٠
F_1	Mean	10٣.1٤	1٩.2	7٩.1	4.٢٩	٥٠.3
	SE	0.٤٣	0.3١	0.٣٥	0.1٩	1.2٧
	Variance	1٥.٢	٢٤.25	1٨.32	0.٢١	16٨.22
F_2	Mean	11٨.٣	1٠.2	٩٤.21	٥.55	4٤.3
	SE	0.٢	0.4٠	٥.13	0.0٨	1.3٨
	Min	2٧.1٤	2٥.21	2٤٠.2	0.0٥	17٦.21
	Max	10٢.٢١	١٤.3	9٩.4	٦.42	3٩.2

Table (5). Phenotypic (σ_p^2), genotypic (σ_g^2) and environmental (σ_E^2) variances and broad sense heritability (H^2) for the tested traits in F_2 population of the six crosses

	Cross Name	***Yr*15×Giza-171**				***Yr*15×Gemm.-11**				***Yr*15×Sids-12**			
		σ_P^2	σ_E^2	σ_g^2	H^2	σ_P^2	σ_E^2	σ_g^2	H^2	σ_P^2	σ_E^2	σ_g^2	H^2
Yield parameters	Plant height	290.65	15.23	275.42	75.2	277.77	14.54	263.23	336.64	17.32	319.32	82.4	336.64
	No. of spikes/plant	43.39	18.23	25.16	55.7	41.48	19.21	22.27	48.49	21.34	27.15	68.3	48.49
	No. of kernels/spike	460.64	121.32	339.32	73.23	471.75	128.32	343.43	489.08	129.35	359.73	84.32	489.08
	100 kernel weight	0.64	0.23	0.41	54.46	0.58	0.25	0.33	0.47	0.15	0.32	65.21	0.47
	Grain yield/plant	319.46	136.23	183.23	52.13	319.58	139.34	180.24	337.27	149.14	188.13	62.34	337.27
	Cross Name	***Yr*15×Misr-1**				***Yr*15×Misr-2**				***Yr*15×Sids-14**			
		σ_P^2	σ_E^2	σ_g^2	H^2	σ_P^2	σ_E^2	σ_g^2	H^2	σ_P^2	σ_E^2	σ_g^2	H^2
	Plant height	342.46	19.12	323.34	84.3	328.61	15.21	313.4	80.1	337.93	17.43	320.5	89.4
	No. of spikes/plant	55.44	25.23	30.21	62.5	36.28	15.12	21.16	54.3	43.99	16.45	27.54	59.6
	No. of kernels/spike	496.72	134.27	362.45	88.42	462.47	120.21	342.26	75.22	480.8	126.45	354.35	79.35
	100 kernel weight	0.47	0.13	0.34	60.23	0.46	0.14	0.32	55.36	0.6	0.17	0.43	60.56
	Grain yield/plant	344.57	152.23	192.34	60.12	326.36	140.15	186.21	54.17	334.79	145.45	189.34	62.22

Quantitative assessment across the six *Yr15* crosses demonstrated that mean disease severity in F_1 and F_2 generations consistently fell below mid-parent values, further substantiating partial dominance for resistance **(Abd El-Latif & Boulot, 2000; Hermas & El-Sawi, 2015 and Omara *et al*., 2017)**. Negative dominance coefficients (h_1 and h_2) indicated partial dominance of resistance alleles, whereas positive values suggested over-dominance toward susceptibility. The elevated variance estimates in parents, F_1, and F_2 underscore the considerable genetic variability available for selection. Correspondingly, the high broad-sense heritability estimates signify strong genetic control, implying that resistance alleles can be effectively fixed in subsequent generations. Although early-generation selection is plausible due to high heritability, the notable influence of dominance effects suggests that postponing selection until later generations may yield superior outcomes **(Menshawy & Youssef, 2004; Da-Silva *et al*., 2012; Loladze *et al*., 2014 and Omara *et al*., 2017)**.

The number of genes underlying rust resistance remains a subject of debate. Some reports describe rust resistance as oligogenic, governed by one or a few major gene pairs **(Abd El-Latif & Boulot, 2000; Hermas & El-Sawi, 2015; Abdelbacki *et al*., 2018)**. In contrast, others emphasize its quantitative nature, controlled by multiple genes with additive effects alongside environmental interactions **(Navabi *et al*., 2005)**. This complexity is further supported by **Herrera-Foessel *et al*. (2008)**, who demonstrated that slow-rusting resistance in several durum wheat lines was governed by at least two to three independently inherited genes.

The evaluation of agronomic traits including plant height, spike number, kernel number, 100-kernel weight, and grain yield per plant revealed that the mean values of F_2 populations exceeded those of their respective parents across all three examined crosses. This pattern highlights substantial genetic variability and supports the reliability of estimating genetic parameters from these populations **(Aglan *et al*., 2020)**. Given the continual emergence of virulent races capable of overcoming existing resistance, wheat breeders must integrate effective resistance genes such as *Yr15* into breeding programs. Comprehensive understanding of resistance inheritance and genetic behavior thus remains essential for strategic gene deployment and long-term improvement of yellow rust resistance in wheat.

5. Conclusion

The present study highlights the considerable variation in yellow rust response among the evaluated wheat cultivars and confirms the continued effectiveness of *Yr15* under Egyptian field conditions. The segregation patterns observed in the F_2 populations demonstrated that *Yr15* is absent from the tested cultivars, underscoring the importance of its introgression into locally adapted germplasm. The superior performance of F_2 generations in key yield components further indicates substantial genetic variability and favorable recombination, offering valuable opportunities for selection. Given the dynamic evolution of *Puccinia striiformis* and the emergence of new virulent races, breeding strategies should not rely exclusively on single major resistance genes. Instead, integrating durable, quantitative, and diverse resistance sources remains essential for securing long-term protection and enhancing wheat productivity. The genetic insights gained from this study provide a strong foundation for developing improved wheat cultivars with enhanced resistance and yield potential.

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