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## Improvement Grain Yield and Yellow Rust Resistance in Four Bread Wheat Crosses

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Cross Mark

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### ABSTRACT

Four bread wheat crosses between Line 1 and each of Misr 1, Misr 3, Sakha 93 and Sakha 95 were studied in F<sub>1</sub>, F<sub>2</sub> and F<sub>3</sub> generations to develop promising wheat lines having high grain yield and yellow rust resistance at Sakha Agricultural Research Station, ARC, Egypt. The experiments were conducted during four successive growing seasons from 2018/19 to 2021/22. For most studied characters in the F<sub>2</sub> and F<sub>3</sub> generations, the genetic variances indicated an important role with moderate to high broad sense heritability. Variations in all studied traits among F<sub>3</sub> families in the four crosses were significant. Regarding yellow rust, the parent Misr 3 was resistant while Sakha 93, Sakha 95 were moderately resistant, Line 1 was moderately susceptible and Misr 1 was susceptible. Yellow rust resistance in the two parents of cross 1 and cross 3 were controlled by one dominant gene for yellow rust. On the other hand, cross 2 and cross 4 were controlled by two dominant genes. The final selection based on grain yield and yellow rust resistant resulted in 11 families from Line 1 × Misr 1 cross, 12 families from Line 1 × Misr 3 cross, 4 families from Line 1 × Sakha 93 cross and 6 families from Line 1 × Sakha 95 cross. These 33 families seemed to be promising genotypes thus, they will be evaluating to select the best lines having highest agronomic traits and yellow rust resistance.

**Keywords:** *Triticum aestivum* L., components of variance, heritability, F<sub>3</sub> families, yellow rust resistance.

### INTRODUCTION

Wheat is Egyptian most important food crop in terms of area and consumption. The production-to-consumption gap is a major economic challenge. To meet this challenge, Egyptian wheat breeding program plans to release new cultivars with high productivity, desirable agronomic characteristics, and rust resistance.

Grain yield is a quantitative trait that is highly controlled by many of genetics factors as well as affected by environmental variability. So that understanding the genetic expression of all its associated components is required for maximizing grain yield.

Rust resistant cultivars are the best choice for controlling the spread of rust diseases, according to Moustafa *et al.* (2009). Showed that, Egyptian wheat breeders are constantly on the lookout for resistance genes and screening for rust resistance in high-risk areas. Breeding wheat for rust resistance is the most effective, cost-effective, and environmentally safe strategy for controlling wheat rust diseases (Aglan *et al.*, 2020).

Many studies in wheat have been conducted to estimate phenotypic and genotypic variances and to derive criteria such as heritability's and predicted selection responses using parents and advanced generations which enables in predicting performance in the next generation (Sultan *et al.*, 2011; Aglan and Farhat, 2014; Abd El-Hamid and El-Hawary, 2015; El-Hawary, 2016; Hussain *et al.*, 2017; Abd El-Hamid and

Ghareeb, 2018; Darwish *et al.*, 2018; Gebrel *et al.*, 2020; and Mohamed *et al.*, 2021).

High heritability with high selection response has additive genetic variation for trait(s) of interest and high heritability with high selection response plays an important role in selecting high yielding genotypes (Iqbal and Khan, 2003).

The present work aimed to: (1) Examine the inheritance of some agronomic traits in the second and third segregating generations of the four crosses Misr 1×Line 1, Misr 3×Line 1, Sakha 93×Line 1, and Sakha 95×Line 1. (2) Select new bread wheat families with high yield potential and resistance to yellow rust diseases. (3) Investigate the inheritance of yellow rust in F<sub>3</sub> families of the four crosses.

### MATERIALS AND METHODS

During the four growing seasons from 2018/19 to 2021/22, five bread wheat genotypes (Table 1) and their F<sub>1</sub>, F<sub>2</sub>, and F<sub>3</sub> generations were studied on the experimental farm of Sakha Agricultural Research Station in Kafr el-Sheikh, Egypt (31° 5' 12" North, 30° 56' 49" East).

In 2018/19, the five parents were crossed to create four crosses in this study as cross 1 = Misr1×Line 1, cross 2 = Misr 3×Line1, cross 3 = Sakha 93×Line1 and cross 4= Sakha 95×Line 1. In order to obtain F<sub>2</sub> seeds, the four hybrid seeds of F<sub>1</sub> crosses were planted in 2019/20. F<sub>2</sub> plants were planted in 2020/21, and 70 plants were selected at random to advance to the F<sub>3</sub> generation.

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**Table 1. Name, pedigree and source of the five parental genotypes.**

Name	Abbrev.	Pedigree	source
Misr 1	M.1	OASIS / SKAUZ // 4*BCN /3/ 2*PASTOR CMSS00Y01881T-050M-030Y-030M-030WGY-33M-0Y-0S	Egypt
Misr 3	M.3	ATTILA*2/PBW65*2/KACHU CGSS 05 B00123T-099T-0PY-099M-099NJ-6WGY-0B-0BGY-0GZ	Egypt
Sakha 93	S.93	Sakha 92/TR 810328 S.8871-1S-2S-1S-0S	Egypt
Sakha 95	S.95	PASTOR // SITE / MO /3/ CHEN / AEGILOPS SQUARROSA (TAUS) // BCN /4/ WBLL1. CMSA01Y00158S-040POY-040M-030ZTM-040SY-26M-0Y-0SY-0S.	Egypt
Line 1	L.1	CROC-1/AE.SQ(224)//OPATA-M-85/3/PASTOR CMSS96Y02555S-040Y-020M-050SY-020SY-6M-0Y	CIMMYT

On November 25, 2020, the four populations (P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub> and F<sub>2</sub>) from each cross were studied in an experiment which designed in a randomized complete block design with three replications. Each replicate consisted of one row for each of the parents and their F<sub>1</sub> and 14 rows for F<sub>2</sub> generation. Planting was done in rows 4 m long with 25 cm between rows and 20 cm between plants within rows. The estimated traits in the parents, F<sub>1</sub> and F<sub>2</sub> for each cross were: plant height (PH, cm), no. of spikes plant<sup>-1</sup> (SP<sup>-1</sup>), 100-kernel weight (100KW, g), no. of kernels spike<sup>-1</sup> (KS<sup>-1</sup>) and grain yield plant<sup>-1</sup> (GYP<sup>-1</sup>, g). Data was collected on individual guarded plants as 30 plants from each parent and F<sub>1</sub> plants, as well as 210 plants from F<sub>2</sub> generation.

On Nov.27, 2021, 70 F<sub>3</sub> families were evaluated from each cross along with their parents as checks and the RCBD design was performed three replicates. Two rows of 1.75 m long and 35 cm apart represented the F<sub>3</sub> families and their parents. The studied traits in parent (checks) and F<sub>3</sub> for each cross were: days to heading (DH, day), days to maturity (DM, day), plant height (PH, cm), no. of spikes m<sup>-2</sup> (SM<sup>-2</sup>), no. of kernels spike<sup>-1</sup> (KS<sup>-1</sup>) 1000-kernel weight (1000KW, g), grain yield m<sup>-2</sup> (Gym<sup>-2</sup>, kg) and yellow rust reaction (YR). Data was collected on row means for F<sub>3</sub> families and their checks. The plants were bordered by a combination of wheat genotypes that were especially very sensitive to yellow rust to disseminate the spores of yellow rust.

The yellow rust reaction was recorded under field conditions at heading and anthesis stages and clustered into R, R-MR, MR, MR-MS, MS, MS-S, S, where R is resistant, S is susceptible and M is moderate, and disease severity percent was assessed according to Stakman *et al.* (1962) and Singh *et al.* (2013).

Wheat plants with infection types 0, R, R-MR, MR, MR-MS were considered resistant, whereas MS, MS-S and S were considered susceptible. After that, the significance of the deviation of observed from expected ratios was detected by chi-square test ( $\chi^2$ ) according to Steel *et al.*, (1997).

To determine the significance of parent differences, the t-test was used. Data from parents and their F<sub>1</sub> and F<sub>2</sub> plants were used to calculate phenotypic, genotypic, and environmental variances (Acquaah, 2012). The F ratio was calculated to determine the significance of differences between F<sub>2</sub> variance and parallel environmental variance, broad sense heritability (H<sup>2</sup> %) was calculated as reported by Acquaah (2012). Moreover, potence ratio was also determined according to (Peter and Frey, 1966). The 70 F<sub>3</sub> families and their checks (the two parents) of each cross were analyzed according to Steel *et al.* (1997) and differences between means of genotypes were tested with LSD at 5% level of probability. The variance components were estimated

using the expected mean squares as stated by Acquaah (2012).

## RESULTS AND DISCUSSION

Generations mean: The means of the two parents, F<sub>1</sub> and F<sub>2</sub> generations of each cross, as well as the t-test of differences between parents and the F ratio test of the four crosses in respect to the studied traits are presented in Table 2.

The findings of (t) test results for detected differences between the two parents in each cross were significant in most cases in the four crosses, revealing that there were genetic diversity in all parents. Similar trends were reported by Abd El-Hamid and El-Hawary (2015), El-Hawary (2016), Abd El-Hamid and Ghareeb (2018), Gebrel *et al.* (2020) and Mohamed *et al.* (2021).

The (F) test also showed that F<sub>2</sub> plants genetically differed in the four crosses for all studied traits. The existence of significant genetic variability and significance differences between parents obtained herein in most traits may suggest that the genes of favorite effects were not completely associated in the parents, i.e., these genes are dispersed. Similar trend was reported by Abdelkhalik (2019).

Average of the studied traits for parents, F<sub>1</sub> and F<sub>2</sub> populations of the four bread wheat crosses are given in Table 2.

The parent Line 1 was the tallest genotype comparing with the other studied genotyped, while Misr 1 and Misr 3 had the highest number in SP<sup>-1</sup>, also Misr 3 had the highest number in KS<sup>-1</sup>. Meanwhile, Sakha 95 had the heaviest genotype in 100KW and GYP<sup>-1</sup>.

The F<sub>1</sub> generation's mean values were greater than their respective parents for SP<sup>-1</sup>, KS<sup>-1</sup>, 100KW and GYP<sup>-1</sup> in cross 1 (Misr 1×Line1), PH, SP<sup>-1</sup>, 100KW in cross 2 (Misr 3×Line1), SP<sup>-1</sup>, KS<sup>-1</sup>, GYP<sup>-1</sup> in cross 3 (Sakha 93×Line1) and all traits in cross 4 (Sakha 95×Line1).

Regarding the F<sub>2</sub> means, the values were intermediate between the two parents for the SP<sup>-1</sup>, GYP<sup>-1</sup> in cross 1 (Misr 1×Line1), SP<sup>-1</sup>, 100KW, GYP<sup>-1</sup> in cross 2 (Misr 3×Line1), KS<sup>-1</sup> in cross 3 (Sakha 93×Line1). Furthermore, the F<sub>2</sub> means were less than or close to their corresponding lowest parent mean values for PH, 100KW in cross 1 (Misr 1×Line1), PH, KS<sup>-1</sup> in cross 2 (Misr 3×Line1), 100KW, GYP<sup>-1</sup> in cross 3 (Sakha 93×Line1), PH, SP<sup>-1</sup>, 100KW and GYP<sup>-1</sup> in cross 4 (Sakha 95×Line1). Meanwhile, F<sub>2</sub> means were higher than the means of both parents for KS<sup>-1</sup>, GYP<sup>-1</sup> in cross 1 (Misr 1×Line1), SP<sup>-1</sup>, 100KW in cross 2 (Misr 3×Line1), PH, SP<sup>-1</sup> in cross 3 (Sakha 93×Line1), KS<sup>-1</sup> in cross 4 (Sakha 95×Line1), demonstrates the level of variation produced by segregation in F<sub>2</sub> plants.

Several previous studies have investigated the means of the parents, and their F<sub>1</sub> and F<sub>2</sub> and other advanced

generations. El-Hawary (2016); Abd El-Hamid and Ghareeb (2018); Gebrel *et al.* (2020); Farhat *et al.* (2020) and Mohamed *et al.* (2021) who found that, in many cases, that

the mean value of the F<sub>2</sub> population was higher than the highest parent for grain yield and its components.

**Table 2. Descriptive statistics of the studied traits for the two parents and their F<sub>1</sub> and F<sub>2</sub> populations for the four wheat crosses.**

Cross	Trait	Statis.	P <sub>1</sub>	P <sub>2</sub>	Parents mean	F <sub>1</sub>	F <sub>2</sub>	T test	F ratio
Cross 1 Misr 1 × Line 1	PH	$\bar{x}$	107	114	111.5	110	108	**	**
		$S^2$	14.41	13.88		15.9	282.18		
	SP <sup>-1</sup>	$\bar{x}$	26	16	21	23	19	**	*
		$S^2$	20.89	8.06		69.29	52.04		
	KS <sup>-1</sup>	$\bar{x}$	54	58	56	61	75	*	**
$S^2$		31.37	88.42		100.43	396.47			
100KW	$\bar{x}$	4.31	4.76	4.54	4.92	4.32	**	*	
	$S^2$	0.12	0.29		0.38	0.51			
GYP <sup>-1</sup>	$\bar{x}$	57.35	41.51	49.43	69.54	55.26	**	**	
	$S^2$	115.33	106.69		97.18	621.78			
Cross 2 Misr 3 × Line1	PH	$\bar{x}$	108	114	111	113	106	**	**
		$S^2$	10.53	13.88		26.05	91.07		
	SP <sup>-1</sup>	$\bar{x}$	26	16	21	25	22	**	**
		$S^2$	16.05	8.06		51.59	107.55		
	KS <sup>-1</sup>	$\bar{x}$	68	58	63	65	59	**	**
$S^2$		37.82	88.42		97.41	331.01			
100KW	$\bar{x}$	4.46	4.76	4.61	5.09	4.73	*	**	
	$S^2$	0.31	0.29		0.41	0.86			
GYP <sup>-1</sup>	$\bar{x}$	75.39	42.62	59.01	67.39	47.69	**	**	
	$S^2$	73.90	106.69		86.95	666.51			
Cross 3 Sakha 93 × Line 1	PH	$\bar{x}$	110	114	112	106.67	114.62	**	**
		$S^2$	5.95	13.88		10.61	344.88		
	SP <sup>-1</sup>	$\bar{x}$	15.92	16	16	26.50	16.41	n.s	*
		$S^2$	18.27	8.06		19.83	34.37		
	KS <sup>-1</sup>	$\bar{x}$	52.40	58	55	64.67	54.10	*	**
$S^2$		82.04	88.42		112.79	346.11			
100KW	$\bar{x}$	5.24	4.76	5.00	4.99	4.61	**	**	
	$S^2$	0.23	0.29		0.29	1.36			
GYP <sup>-1</sup>	$\bar{x}$	45.5	43.62	44.56	53.27	36.96	n.s	**	
	$S^2$	92.93	106.69		52.80	320.67			
Cross 4 Sakha 95 × Line 1	PH	$\bar{x}$	110	114	112.25	117	108	**	**
		$S^2$	10.53	13.88		12.19	68.52		
	SP <sup>-1</sup>	$\bar{x}$	25	16	20	27	15	**	*
		$S^2$	17.34	8.06		14.78	23.67		
	KS <sup>-1</sup>	$\bar{x}$	62	58	60	73	62	n.s	**
$S^2$		51.08	88.42		107.14	219.37			
100KW	$\bar{x}$	5.03	4.76	4.89	5.22	4.29	*	*	
	$S^2$	0.16	0.29		0.34	0.59			
GYP <sup>-1</sup>	$\bar{x}$	79.06	43.6	63.59	86.29	45.42	**	**	
	$S^2$	108.92	106.69		172.79	432.54			

\*and \*\* indicate significant at 0.05 and 0.01 levels of probability, respectively

PH=Plant height, SP<sup>-1</sup>=No. of Spikes Plant<sup>-1</sup>, KS<sup>-1</sup>= No. of Kernels spike<sup>-1</sup>, 100KW=100 Kernel weight, GYP<sup>-1</sup>=Grain yield plant<sup>-1</sup>.

Genetic parameters based on F<sub>2</sub>: Heterosis percentages, inbreeding depression, potence ratios, component of variance and broad sense heritability for the two parents, F<sub>1</sub> and F<sub>2</sub> of each cross are presented in Table 3.

Heterosis percentages over the better parents were positively significant for 100KW, GYP<sup>-1</sup> in cross 1 (Misr 1×Line1), 100KW in cross 2 (Misr 3×Line1), SP<sup>-1</sup>, KS<sup>-1</sup> and GYP<sup>-1</sup> in cross 3 (Sakha 93×Line1) and all studied traits in cross 4 (Sakha 95×Line1).

Moreover, data presented in Table 3 indicate that inbreeding depression estimates were significant or highly significant with positive signs for most traits in the four crosses except for KS<sup>-1</sup> in cross 1 (Misr 1×Line1) and PH in cross 3 (Sakha 93×Line1) which were highly significant with negative signs. For these studied traits the desirable values are the positive ones. These results agreed with those of El-Hawary (2016); Abd El-Hamid and Ghareeb (2018); Gebrel *et al.* (2020) and Mohamed *et al.* (2021).

Values of potence ratios were more than unity for KS<sup>-1</sup>, 100KW, GYP<sup>-1</sup> in cross 1 (Misr 1×Line1), 100KW in cross

2 (Misr 3×Line1), PH, SP<sup>-1</sup>, KS<sup>-1</sup>, GYP<sup>-1</sup> in cross 3 (Sakha 93×Line1) and for all studied traits in cross 4 (Sakha 95×Line1). These results suggests that these traits were controlled by over dominance, and that they predominated and played the most important role in the inheritance of most traits. On the other hand, potence ratio values were less than unity for PH, SP<sup>-1</sup> in cross 1 (Misr 1×Line1), PH, SP<sup>-1</sup>, KS<sup>-1</sup> in cross 2 (Misr 3×Line1), 100KW in cross 3 (Sakha 93×Line1). According to these findings, partial dominance predominated and played the most important role in the hereditary of these traits. Similar outcomes were obtained by Aglan *et al.* (2020); Farhat *et al.* (2020) and Mohamed *et al.* (2021).

Genotypic variances were higher than the environmental variances for all studied traits in the four crosses except for SP<sup>-1</sup> in the two crosses (Misr 1×Line1) and (Sakha 95×Line1), pointing to the possibility of improving for these traits. Similar trends were reported by El-Hawary (2016); Abd El-Hamid and Ghareeb (2018); Gebrel *et al.* (2020) and Farhat *et al.* (2020).

**Table 3. Estimates of heterosis based on better parents, potence ratio, inbreeding depression (ID), variance components and broad sense heritability (H<sup>2</sup>) for the studied traits of the four wheat crosses.**

Cross	Trait	Heterosis (BP)	ID	Potence ratio	$\sigma_e^2$	$\sigma_p^2$	$\sigma_g^2$	H <sup>2</sup>
cross 1	PH	-3.72**	1.99	-0.21	14.69	282.18	267.49	94.79
	SP <sup>-1</sup>	-10.16**	17.37**	0.47	32.75	52.04	19.29	37.07
	KS <sup>-1</sup>	4.66	-24.04**	2.35	73.41	396.47	323.06	81.48
	100KW	3.45**	12.18**	1.73	0.25	0.51	0.26	50.61
	GYP <sup>-1</sup>	20.14**	14.28**	2.55	106.4	621.78	515.38	82.89
cross 2	PH	-0.88	6.19**	0.67	16.82	91.07	74.25	81.53
	SP <sup>-1</sup>	-6.94**	8.82**	0.66	25.23	107.55	82.32	76.54
	KS <sup>-1</sup>	-5.21*	9.09**	0.3	74.55	331.01	256.46	77.48
	100KW	6.94**	7.09**	3.19	0.33	0.86	0.53	61.33
	GYP <sup>-1</sup>	-10.61**	29.23**	0.51	89.18	666.51	577.33	86.62
cross 3	PH	-6.64**	-7.45**	-2.67	10.15	344.88	334.73	97.06
	SP <sup>-1</sup>	66.49**	38.07**	1.82	15.39	34.37	18.98	55.23
	KS <sup>-1</sup>	11.49**	16.34**	3.38	94.42	346.11	251.69	72.72
	100KW	-4.78**	7.63**	-0.05	0.27	1.36	1.09	80.16
	GYP <sup>-1</sup>	17.08**	30.62**	9.27	84.14	320.67	236.53	73.76
cross 4	PH	2.63*	7.69**	2.5	12.2	68.52	56.32	82.19
	SP <sup>-1</sup>	7.51**	44.79**	1.42	13.4	23.67	10.28	43.41
	KS <sup>-1</sup>	17.89**	15.30**	6.75	82.23	219.37	137.14	62.52
	100KW	3.81**	17.83**	2.43	0.26	0.59	0.32	54.88
	GYP <sup>-1</sup>	9.14**	47.36**	1.41	129.47	432.54	303.07	70.06

cross 1= Misr1×Line1, cross 2= Misr3×Line1, cross 3= Sakha 93×Line1, cross 4= Sakha 95×Line1, PH=Plant height, SP<sup>-1</sup>=No. of Spikes Plant<sup>-1</sup>, KS<sup>-1</sup>=No. of Kernels spike<sup>-1</sup>, 100KW=100 Kernel weight, GYP<sup>-1</sup>=Grain yield plant<sup>-1</sup>, ID=Inbreeding depression,  $\sigma_e^2$ =Environmental variance,  $\sigma_p^2$ =phenotypic variance,  $\sigma_g^2$ =genotypic variance, H<sup>2</sup>= broad sense heritability. \*and \*\* indicate significant at 0.05 and 0.01 levels of probability, respectively

Heritability estimates in broad sense for all studied traits are presented in Table 3. Robinson *et al.*, (1949) divided heritability into three classes, low (from 0 to 30), moderate (from 30 to 60), and high (more than 60). Generally, heritability values in broad sense were slightly high in the four studied crosses for all studied traits, except for SP<sup>-1</sup> and 100KW in cross 1 (Misr 1×Line1) and cross 4 (Sakha 95×Line1) in which the heritability values were moderate which indicate that the environmental variances were higher than the genetic ones. These findings are consistent with those reported by Abd El-Hamid and El-Hawary (2015); El-Hawary (2016); Abd El-Hamid and Ghareeb (2018); Gebrel *et al.* (2020) and Mohamed *et al.* (2021).

**Analysis of variance of F<sub>3</sub> Families:** Table 4 shows the variance analysis of the studied traits for F<sub>3</sub> families.

Variations among F<sub>3</sub> families for all the studied traits in the four crosses were found to be significant (P < 0.05 or 0.01). These findings suggest that there is sufficient genetic variation to estimate a variety of genetic parameters. Similar findings have been reported by Hussain *et al.* (2017); Aziz *et al.* (2018); Darwish *et al.* (2018); Aglan *et al.* (2020); Farhat *et al.* (2020).

In the four crosses, the two parents differed significantly for all studied traits, except for PH, 1000KW and Gym<sup>-2</sup> in cross 1 (Misr 1×Line1), PH, KS<sup>-1</sup> in cross 2 (Misr 3×Line1), SM<sup>-2</sup>, KS<sup>-1</sup>, 1000KW and Gym<sup>-2</sup> in cross 3 (Sakha 93×Line1), 1000KW in cross 4 (Sakha 95×Line1). Similar trend was reported by Khan *et al.* (2014); Ul Haq *et al.* (2016); Hussain *et al.* (2017); Aziz *et al.* (2018); Darwish *et al.* (2018); Aglan *et al.* (2020); Farhat *et al.* (2020).

**Table 4. Mean squares of the studied traits for the 70 F<sub>3</sub> families and their two parents of each cross as checks.**

cross	SOV	df	DH	DM	PH	SM <sup>-2</sup>	KS <sup>-1</sup>	1000KW	Gym <sup>-2</sup>
Cross 1 Misr 1 × Line 1	Replications	2	462.91**	3.39	214.40	1744.83	81.67*	13.86*	2.58**
	Genotypes	71	108.59**	31.00**	878.23**	9114.36**	380.01**	51.85**	0.20**
	Families (F)	69	106.75**	31.58**	897.11**	9074.49**	390.58**	51.91**	0.20**
	Checks (C)	1	130.67**	13.50*	160.17	19780.49**	24.48	3.33	0.03*
	F vs C	1	213.68**	8.40	293.19	1199.35	6.25	95.76**	0.01
	Error	142	7.72	3.07	101.39	748.37	22.89	4.02	0.01
	Total	215							
Cross 2 Misr 3 × Line1	Replications	2	34.01**	31.35**	2405.64**	30926.58**	894.60**	447.38**	0.34**
	Genotypes	71	31.81**	13.85**	117.47**	16258.33**	160.48**	27.32**	0.08**
	Families (F)	69	31.07**	13.59**	120.25**	16159.90**	164.35**	28.04**	0.08**
	Checks (C)	1	88.17**	20.17**	37.50	5720.91*	48.17	3.05	0.08**
	F vs C	1	26.79**	25.72**	5.70	33587.76**	6.03	1.94	0.00
	Error	142	3.69	2.81	56.15	1002.36	17.34	9.54	0.01
	Total	215							
Cross 3 Sakha 93 × Line 1	Replications	2	78.34**	57.56**	516.23**	32848.52**	226.25**	1421.04**	0.21**
	Genotypes	71	54.79**	20.69**	651.75**	9075.89**	159.36**	136.63**	0.21**
	Families (F)	69	53.32**	20.74**	652.29**	8804.40**	154.64**	139.85**	0.21**
	Checks (C)	1	192.67**	13.50*	937.50**	1600.67	1.36	23.90	0.00
	F vs C	1	18.50	25.03**	328.13	35283.71**	643.24**	27.17	0.12**
	Error	142	7.54	3.45	107.37	976.58	43.75	20.67	0.01
	Total	215							
Cross 4 Sakha 95 × Line 1	Replications	2	28.23**	26.03**	2202.96**	64562.91**	3031.52**	522.25**	0.26**
	Genotypes	71	139.59**	31.17**	60.79**	8898.62**	453.73**	37.51**	0.04**
	Families (F)	69	139.59**	31.23**	57.81**	8849.53**	449.87**	37.73**	0.04**
	Checks (C)	1	37.50*	28.17**	150.00**	18150.00**	323.55*	8.87	0.27**
	F vs C	1	243.58**	29.97**	177.22**	3034.41	850.77**	51.42*	0.01
	Error	142	5.72	3.42	16.64	1200.36	51.55	8.70	0.00
	Total	215							

DH= days to heading, DM= days to maturity, PH=Plant height, SM<sup>-2</sup>=No. of Spikes M<sup>-2</sup>, KS<sup>-1</sup>=No. of Kernels spike<sup>-1</sup>, 1000KW=1000 Kernel weight, Gym<sup>-2</sup>=Grain yield m<sup>-2</sup>

\*and \*\* indicate significant at 0.05 and 0.01 levels of probability, respectively

**F<sub>3</sub> Families mean performance:** Some descriptive statistics for the studied traits in the F<sub>3</sub> families of each cross are presented in Table 5.

Regarding to F<sub>3</sub> families mean compared to the two parents of each cross, F<sub>3</sub> families had higher values for SM<sup>2</sup> and KS<sup>-1</sup> in cross 2 (Misr 3×Line1), SM<sup>2</sup> in cross 3 (Sakha 93×Line1). On the other hand, F<sub>3</sub> families' mean had lower values for KS<sup>-1</sup>, 100KW, Gym<sup>2</sup> in cross 1 (Misr 1× Line1), DM, 1000KW in cross 2 (Misr 3×Line1), KS<sup>-1</sup> in cross 3 (Sakha 93×Line1), KS<sup>-1</sup>, 100KW in cross 4 (Sakha 95 ×

Line1). While, in the remaining cases, F<sub>3</sub> families mean had intermediate values between the two parents of each cross.

For all four crosses, the maximum values of the F<sub>3</sub> families outperform their two parents. except for KS<sup>-1</sup> in cross 4 (Sakha 95×Line1). These findings reveal the existence of transgressive segregation and allow for the selection of the best families with a desired performance. Similar trends were reported by Aglan *et al.* (2020); Farhat *et al.* (2020).

**Table 5. Descriptive statistics and variance parameters estimate for the studied traits of the 70 F<sub>3</sub> families and their two parents of each cross for the four wheat crosses.**

Cross	Family/parent	DH	DM	PH	SM <sup>2</sup>	KS <sup>-1</sup>	1000KW	Gym <sup>2</sup>
cross 1	Families' maximum	108	157	150	609.24	87.8	50.62	1.18
	Families' minimum	78.33	138.67	73.33	385.12	20	28.32	0.14
	Families' mean	93.17	147.84	111.67	497.18	53.90	39.47	0.66
	Misr 1	87.33	144.67	110.67	551.21	64.93	44.84	0.84
	Line 1	96.67	147.67	121	436.38	60.89	46.33	0.69
	Parents mean	92.00	146.17	115.84	493.80	62.91	45.59	0.77
cross 2	Families' maximum	97.67	151	132.5	619.45	78	52.69	1.17
	Families' minimum	81	137	97.5	337.36	38.53	36.59	0.38
	Families' mean	89.34	144.00	115.00	523.41	58.27	44.64	0.78
	Misr 3	88	146	115	384.28	52	45.35	0.91
	Line 1	95.67	149.67	120	446.04	57.67	46.77	0.68
	Parents mean	91.84	147.84	117.50	415.16	54.84	46.06	0.80
cross 3	Families' maximum	97.67	149.67	148.33	620.52	71	55.35	0.96
	Families' minimum	79	140	77.5	378.81	30.9	33.37	0.39
	Families' mean	88.34	144.84	112.92	499.67	50.95	44.36	0.68
	Sakha 93	83.67	145	100	392.67	58.07	41.98	0.63
	Line 1	95	148	122	425.33	59.02	45.98	0.68
	Parents mean	89.34	146.50	111.00	409.00	58.55	43.98	0.66
cross 4	Families' maximum	107.33	156.33	128.33	628.72	74.6	53.07	1.2
	Families' minimum	77	138.67	109.17	364	41.6	36.88	0.55
	Families' mean	92.17	147.50	118.75	496.36	58.10	44.98	0.88
	Sakha 95	91.33	144.33	110	558.33	75.95	50	1.1
	Line 1	96.33	148.67	120	448.33	61.27	47.57	0.68
	Parents mean	93.83	146.50	115.00	503.33	68.61	48.79	0.89

cross 1 = Misr1×Line1, cross 2 = Misr3×Line1, cross 3 = Sakha 93×Line1, cross 4 = Sakha 95×Line1 , DH= days to heading, DM= days to maturity, PH=Plant height, SM<sup>2</sup>=No. of Spikes M<sup>2</sup>, KS<sup>-1</sup>=No. of Kernels spike<sup>-1</sup>, 1000KW=1000 Kernel weight, Gym<sup>2</sup>=Grain yield m<sup>2</sup>

\*and \*\* indicate significant at 0.05 and 0.01 levels of probability, respectively

**Genetic parameters based on F<sub>3</sub> families:** Some genetic parameters for the two parents and F<sub>3</sub> families of each cross under study are shown in Table 6.

Genotypic variances were higher than environmental variances for all studied traits in the four crosses except for PH, 100KW in cross 2 (Misr 3×Line1), KS<sup>-1</sup> in cross 3 (Sakha 93×Line1) and PH in cross 4 (Sakha 95×Line1). Similar trends were previously found by Khan *et al.* (2014); Amein and Atta

(2016); Aziz *et al.* (2018); Aglan *et al.* (2020) and Farhat *et al.* (2020).

All four crosses revealed moderate to high broad sense heritabilities for all traits indicating the possibility of improving these traits. Similar trend was reported by Khan *et al.* (2014); Amein and Atta, (2016); Ul Haq *et al.* (2016); Hussain *et al.* (2017); Aziz *et al.* (2018); Darwish *et al.* (2018); Aglan *et al.* (2020); Farhat *et al.* (2020).

**Table 6. Variance parameters and broad-sense heritability estimated for the studied traits of the four wheat crosses.**

Cross	Parameter	DH	DM	PH	SM <sup>2</sup>	KS <sup>-1</sup>	1000KW	Gym <sup>2</sup>
Cross 1	σ <sub>e</sub> <sup>2</sup>	33.01	9.48	264.43	2769.18	122.90	16.11	0.07
	σ <sub>p</sub> <sup>2</sup>	40.73	12.62	368.25	3536.13	144.78	19.69	0.07
	σ <sub>e</sub> <sup>2</sup>	7.71	3.15	103.81	766.95	21.87	3.57	0.01
	H <sup>2</sup>	0.81	0.75	0.72	0.78	0.85	0.82	0.91
	σ <sub>e</sub> <sup>2</sup>	9.12	3.60	21.06	5055.79	48.89	6.18	0.03
Cross 2	σ <sub>p</sub> <sup>2</sup>	12.82	6.39	78.12	6048.31	66.57	15.69	0.03
	σ <sub>e</sub> <sup>2</sup>	3.70	2.79	57.06	992.52	17.68	9.51	0.01
	H <sup>2</sup>	0.71	0.56	0.27	0.84	0.73	0.39	0.79
	σ <sub>e</sub> <sup>2</sup>	15.30	5.74	180.76	2600.75	36.76	39.64	0.07
	σ <sub>p</sub> <sup>2</sup>	22.73	9.26	290.77	3602.90	81.12	60.58	0.08
Cross 3	σ <sub>e</sub> <sup>2</sup>	7.44	3.52	110.01	1002.15	44.36	20.94	0.01
	H <sup>2</sup>	0.67	0.62	0.62	0.72	0.45	0.65	0.83
	σ <sub>e</sub> <sup>2</sup>	44.60	9.24	13.65	2564.40	132.98	9.62	0.01
	σ <sub>p</sub> <sup>2</sup>	50.37	12.74	30.50	3720.74	183.91	18.49	0.02
	σ <sub>e</sub> <sup>2</sup>	5.77	3.50	16.85	1156.34	50.93	8.87	0.00
Cross 4	H <sup>2</sup>	0.89	0.73	0.45	0.69	0.72	0.52	0.79

cross 1 = Misr1×Line1, cross 2 = Misr3×Line1, cross 3 = Sakha 93×Line1, cross 4 = Sakha 95×Line1 , DH= days to heading, DM= days to maturity, PH=Plant height, SM<sup>2</sup>=No. of Spikes M<sup>2</sup>, KS<sup>-1</sup>=No. of Kernels spike<sup>-1</sup>, 1000KW=1000 Kernel weight, Gym<sup>2</sup>=Grain yield m<sup>2</sup>, σ<sub>e</sub><sup>2</sup>=Environmental variance, σ<sub>p</sub><sup>2</sup>=phenotypic variance, σ<sub>e</sub><sup>2</sup>=genotypic variance, H<sup>2</sup>= broad sense heritability. \*and \*\* indicate significant at 0.05 and 0.01 levels of probability, respectively

**Selected F<sub>3</sub> families:** The means of the selected families from the four wheat crosses based on their agronomic traits and yellow rust reaction are shown in Tables 7 and 8.

The selection method was based on yellow rust resistance first, then grain yield potentiality second, and

finally the appropriate plant height. The reaction to yellow rust, plant height, and grain yield for each family were considered to select the best families in the F<sub>3</sub> population to be advance as F<sub>4</sub> families (Tables 7 and 8).

**Table 7. Means of the selected families and the two parents as checks for the agronomic traits and yellow rust reaction for wheat cross 1 and cross 2.**

Cross	Family No.	DH	DM	PH	SM <sup>2</sup>	KS <sup>-1</sup>	1000KW	Gym <sup>2</sup>	YR
Cross 1 Misr 1 × Line 1	45	85	143	118	548	54	41.72	0.97	0
	55	80	141	118	428	71	43.16	1	0
	58	83	145	103	422	62	50.62	1.01	0
	54	82	146	118	461	78	40.52	1.03	0
	15	87	144	120	579	71	45.43	1.04	TRMR
	1	93	146	120	559	54	45	1.04	TRMR
	28	92	148	123	525	62	42.88	1.05	0
	42	86	145	113	531	50	42.21	1.06	0
	39	79	140	117	461	65	47.66	1.07	0
	26	84	143	115	441	78	38.18	1.1	0
	64	82	142	119	450	66	34.44	1.12	0
	Mean	84.82	143.91	116.73	491.36	64.64	42.89	1.04	
	Min	79	140	103	422	50	34.44	0.97	
	Max	93	148	123	579	78	50.62	1.12	
Misr 1	87.33	144.67	110.67	551.21	64.93	44.84	0.84	20S	
Line 1	96.67	147.67	121	436.38	60.89	46.33	0.69	20MS	
LSD <sub>0.5%</sub>	4.48	2.83	16.25	44.15	7.72	3.24	0.13		
Cross 2 Misr 3 × Line1	66	92	147	121	501	49	46.93	0.93	0
	6	89	144	117	511	46	52.69	0.94	0
	55	84	146	122	427	57	44.89	0.96	0
	47	89	144	115	458	56	47.54	0.96	0
	52	95	146	123	494	59	43.67	0.97	0
	32	85	144	115	509	53	49.48	0.99	10MR
	29	92	148	115	533	54	43.27	1.05	0
	60	87	144	115	460	43	48.72	1.06	0
	21	93	145	117	493	58	47.16	1.06	TRMR
	15	90	147	118	550	61	39.9	1.07	0
	56	88	146	112	547	59	45.43	1.08	0
	50	89	146	123	512	60	45.18	1.17	0
	Mean	89.42	145.58	117.75	499.58	54.58	46.24	1.02	
	Min	84	144	112	427	43	39.9	0.93	
Max	95	148	123	550	61	52.69	1.17		
Misr 3	88	146	115	384.28	52	45.35	0.91	0	
Line 1	95.67	149.67	120	446.04	57.67	46.77	0.68	30MS	
LSD <sub>0.5%</sub>	3.1	2.64	12.09	51.1	6.72	4.98	0.13		

DH= days to heading, DM= days to maturity, PH=Plant height, SM<sup>2</sup>=No. of Spikes M<sup>2</sup>, KS<sup>-1</sup>=No. of Kernels spike<sup>-1</sup>, 1000KW=1000 Kernel weight, GYm<sup>2</sup>=Grain yield m<sup>2</sup>, YR= yellow rust reaction

**Table 8. Means of the selected families and the two parents as checks for the agronomic traits and yellow rust reaction for wheat cross 3 and cross 4.**

Cross	Family No.	DH	DM	PH	SM <sup>2</sup>	KS <sup>-1</sup>	1000KW	Gym <sup>2</sup>	YR
Cross 3 Sakha 93 × Line 1	22	81	141	117	517	37	46.32	0.95	10R
	4	82	141	118	486	45	48.15	0.96	0
	12	88	146	112	456	48	55.35	0.96	0
	36	88	146	126	478	46	55.09	0.96	10 R
	Mean	84.75	143.50	118.25	484.25	44.00	51.23	0.96	
	Min	81	141	112	456	37	46.32	0.95	
	Max	88	146	126	517	48	55.35	0.96	
	Sakha 93	83.67	145	100	392.67	58.07	41.98	0.63	5MR
	Line 1	95	148	122	425.33	59.02	45.98	0.68	20MS
LSD <sub>0.5%</sub>	4.43	2.99	16.73	50.44	10.68	7.34	0.19		
Cross 4 Sakha 95 × Line 1	34	89	147	123	532	42	45.49	1.01	10 R
	62	83	144	117	465	53	46.76	1.02	10R
	57	82	140	122	461	50	51.86	1.05	10 R
	1	85	143	115	430	51	42.92	1.09	10 R
	54	78	141	120	455	64	49.11	1.1	10 R
	63	84	143	118	511	51	50.75	1.2	5MR
	Mean	83.50	143.00	119.17	475.67	51.83	47.82	1.08	
	Min	78	140	115	430	42	42.92	1.01	
	Max	89	147	123	532	64	51.86	1.2	
Sakha 95	91.33	144.33	110	558.33	75.95	50	1.1	20MR	
Line 1	96.33	148.67	120	448.33	61.27	47.57	0.68	20MS	
LSD <sub>0.5%</sub>	3.86	2.98	6.58	55.92	11.59	4.76	0.09		

DH= days to heading, DM= days to maturity, PH=Plant height, SM<sup>2</sup>=No. of Spikes M<sup>2</sup>, KS<sup>-1</sup>=No. of Kernels spike<sup>-1</sup>, 1000KW=1000 Kernel weight, GYm<sup>2</sup>=Grain yield m<sup>2</sup>, YR= yellow rust reaction

Using LSD, the means of F<sub>3</sub> families were compared to the means of the two parents as checks, and as a result, 20 families were selected from cross 1 (Misr 1×Line1), 18 families from cross 2 (Misr 3×Line1), 6 families from cross 3 (Sakha 93×Line1) and 6 families from cross 4 (Sakha 95×Line1) which exceeded the highest parent in grain yield with or without a significant difference with a total of 50 families from the four crosses.

Only 33 out of the 50 families were resistant or moderately resistant to yellow rust as shown in Tables 7 and 8, and the final selection based on grain yield and yellow rust resistance resulted in 11 families from cross 1 (Misr

1×Line1), 12 families from cross 2 (Misr 3×Line1), 4 families from cross 3 (Sakha 93×Line1) and 6 families from cross 4 (Sakha 95×Line1). These 33 families will be evaluated in the next season through the wheat program as F<sub>4</sub> families to select the best lines with highest agronomic traits and yellow rust resistance.

**F<sub>3</sub> inheritance of yellow rust resistance:** frequency distribution and chi square ( $\chi^2$ ) estimates of F<sub>3</sub> families for yellow rust disease reaction under field conditions are displayed in Table 9. The parent Misr 3 was resistant, Sakha 93, Sakha 95 were moderately resistant, Line 1 was moderately susceptible and Misr 1 was susceptible.

**Table 9. Frequency distribution and chi square ( $\chi^2$ ) analysis of yellow (stripe) rust response for P<sub>1</sub>, P<sub>2</sub> and F<sub>3</sub> of the four wheat crosses under field conditions.**

Cross Name	Parents/ generation	Yellow rust infection response class							Observed ratio		Expected ratio		Chi-square Value	
		R	R-MR	MR	MR-MS	MS	MS-S	S	R	S	X <sup>2</sup>	P.value		
Misr 1×Line 1	P <sub>1 30</sub>						9	21						
	P <sub>2 30</sub>				20	10								
	F <sub>3 70</sub>	25	7	13	11	3	7	4	56	14	3	1	0,993	0,334
Misr 3×Line 1	P <sub>1 30</sub>	22	9											
	P <sub>2 30</sub>				20	10								
	F <sub>3 70</sub>	29	11	16	11	1	2		67	3	13	3	0,862	0,353
Sakha 93×Line 1	P <sub>1 30</sub>	24	6											
	P <sub>2 30</sub>				20	10								
	F <sub>3 70</sub>	10	15	8	17	1	15	4	50	20	3	1	0,476	0,490
Sakha 95×Line 1	P <sub>1 30</sub>	5	25											
	P <sub>2 30</sub>				20	10								
	F <sub>3 70</sub>			25	37	1	7		62	8	13	3	2,463	0,117

R = resistant, S = susceptible and M = moderate

The F<sub>3</sub> families of both crosses (Misr 1×Line1) and (Sakha 93×Line1) were segregated at the ratio of 3 resistant: 1 susceptible. On the other hand, cross 2 (Misr 3×Line1) and cross 4 (Sakha 95×Line1) were segregated at the ratio of 13 resistant : 3 susceptible. These findings suggest that yellow rust resistance in both parents of cross 1 (Misr 1×Line1) and cross 3 (Sakha 93×Line1) were a simple inherited trait that governed by a single dominant gene, while the two crosses (Misr 3×Line1) and (Sakha 95×Line1) were controlled by two dominant genes.

**CONCLUSION**

Regarding yellow rust, the parent Misr 3 was resistant, Sakha 93, Sakha 95 were moderately resistant, Line 1 was moderately susceptible and Misr 1 was susceptible. Yellow rust resistance in the two parents of cross 1 and cross 3 were controlled by one dominant gene for yellow rust. Meanwhile, cross 2 and cross 4 were controlled by two dominant genes.

From total of 280 families of the four crosses only 33 families were selected based on grain yield and yellow rust resistant as 11 families from cross 1 (Misr 1×Line1), 12 families from cross 2 (Misr 3×Line1), 4 families from cross 3 (Sakha 93×Line1) and 6 families from cross 4 (Sakha 95×Line1). These 33 families will be evaluating in the F<sub>4</sub> generation in the coming season to be used through wheat program in releasing high yielding wheat lines coupled with yellow rust resistant.

The four crosses under study, Misr 1×Line 1, Misr 3×Line 1, Sakha 93×Line 1 and Sakha 95×Line 1 are promising crosses for wheat breeders and can help to improve breeding strategies for both grain yield and yellow rust resistance

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## تحسين محصول الحبوب ومقاومة الصدأ الأصفر في أربعة هجن من قمح الخبز

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### الملخص

تم دراسة الجيل الأول والثاني والثالث لأربعة هجن مختلفة من قمح الخبز وهي: السلالة 1 × مصر 1، السلالة 3 × مصر 3، السلالة 1 × سكا 93 والسلالة 1 × سكا 95 لانتخاب تراكيب وراثية تتميز بارتفاع محصول الحبوب بالإضافة لمقاومة الصدأ الأصفر وذلك بمحطة البحوث الزراعية بسخا- مركز البحوث الزراعية خلال أربعة مواسم زراعية من 2018/2019 وحتى 2022/2021. أشارت النتائج إلى أهمية التباين الوراثي لمعظم الصفات المدروسة على مستوى الجيلين الثاني والثالث للأربعة هجن تحت الدراسة، وتراوحت درجة التوريث بالمعنى الواسع من متوسطة إلى مرتفعة في معظم الحالات. كانت الاختلافات معنوية بين عائلات الجيل الثالث لكل هجين في معظم الصفات المدروسة على مستوى الأربعة هجن تحت الدراسة. أظهر الصنف مصر 3 مقاومة للصدأ الأصفر، بينما أظهر الصنفين سكا 95 وسكا 93 مقاومة متوسطة في حين كانت السلالة 1 متوسطة الإصابة والصنف مصر 1 مصاب. كما أظهرت النتائج أن مقاومة الصدأ الأصفر للجيلين الأول والثالث يتحكم بها جين واحد سائد بينما الهجينين الثاني والرابع يتحكم بها جينين سائدين. بناء على محصول الحبوب ومقاومة الصدأ الأصفر تم انتخاب 11 عائلة من الهجين الأول، 12 عائلة من الهجين الثاني، 4 عائلات من الهجين الثالث و 6 عائلات من الهجين الرابع بإجمالي 33 عائلة من الهجن الأربعة على أن يتم تقييمها في الموسم القادم كجيل رابع لانتخاب أفضلها من حيث الصفات المحصولية والمقاومة للصدأ الأصفر حيث يمكن استخدام هذه التراكيب الوراثية في استنباط سلالات تتميز بالمحصول المرتفع والمقاومة للصدأ الأصفر.