Estimates of Genetic Effects of Yield, Yield Components, Yellow and Stem Rust Resistance through Generation Mean Analysis in Three Bread Wheat Crosses

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Abstract

This study was carried out during the four winter growing seasons from 2019/2020 to 2022/2023 seasons at Sakha Agricultural Research Station farm, ARC, Egypt to investigate the inheritance and nature of genetic control of yellow and stem rust diseases, yield, and its components in bread wheat. The five populations included P_1, P_2, F_1, F_2 and F_3 of three crosses (cross 1: Misr 2 × Giza171, cross 2: Misr 2 × Sakha 95 and cross 3: Gemmiza 9 × shandweel 1). Results indicated that dominance gene effects were larger in magnitude than the additive gene effects for all the studied traits except for 100-kernel weight in the first cross. Additive × Additive gene effects were positive and highly significant for no of spike/plants in all the three crosses, grain yield/plant in the first and third crosses, no of kernels/spike in the third cross. Dominance × Dominance was highly significant positive for 100 - kernel weight and grain yield/plant in the first and second crosses and no. of kernels /spike in the second cross. Narrow sense heritability estimates were low to relatively high for all the studied crosses, and moderate to low for stripe rust in the three crosses, and was high in the first and third crosses for stem rust. The first cross (Misr 2× Giza171) was the most desirable which had the lowest mean values for the infection disease severity for stripe rust disease, while the third cross (Gemmiza 9 × Shandawel 1) for stem rust disease.

Keywords: Bread wheat, Gene action, Heritability, Stripe rust, Stem Rust

Introduction

Wheat is one of the most important and strategic cereal crops around the world, it provides more calories in the diet than any other crop (Shewry, 2009). The available genetic resources are being utilized by wheat breeders to modify the cultivated varieties for the fulfillment of the demands of ever increasing population and ever changing requirements (Mba *et al*., 2012; Sial *et al*., 2013).

Wheat rusts have major historical and economic importance worldwide and yield losses due to rusts have been reported in many wheat producing countries in most years and periodic epidemics during the last century resulted in famine situations in many parts of the world (Brennan and Murray 1988).

In the present decade, there has been an increasing interest in adult plant resistance because of its widespread occurrence in the germplasm and durability. Genetic diversity for stripe and stem rust resistance is important for incorporating resistance

genes from other species of Triticum to bread wheat to develop new resistant varieties. In this way, genetic analysis for adult plant resistance to stripe and stem rusts is key to understanding the nature and inheritance of resistance gene(s) for further use in breeding programs.

Generation mean analysis is one such useful tool for the estimation of gene effects for polygenic traits which can estimate gene effects (Kearsey and Pooni, 1996), and provides information on the relative importance of average effects of the genes additive effects, dominance deviations, and effects due to non-allelic genetic interactions effects to determine genotypic values of the individuals and consequently, mean genotypic values of families and generations (Mather and Jinks, 1982).

Many wheat breeders studied broad sense heritability to evaluate hybrid populations (Pawar *et al*., 1988; Larik *et al*., 1999; Ansari *et al*., 2002; Sial *et al*., 2013). Heritability in broad sense (h^2 b), genetic advance (G.A), phenotypic and genotypic variances

were used to evaluate the variance magnitude in breeding material of wheat (Khan *et al* 1985,).

Breeding efforts have resulted in various varieties of hexaploid wheat having improved yield and grain traits. Plant breeders need to develop genotypes that can express high grain yield potential and diseases resistance Noorka and Afzal 2009). This requires a search for the selection of yield related -traits, which were considered as highly associated with grain yield (Richards *et al*., 2002).

The present investigation was planned to determine the type of gene action and to estimate some genetic parameters in three bread wheat crosses using analysis of the five populations of each cross for grain yield, its components and resistance to stripe and stem rust.

Materials and Methods

The field experiment was carried out on the Experimental Farm of Sakha Agricultural Research Station, Agricultural Research Center, Egypt, through four seasons; 2019/2020, 2020/2021, 2021/2022, and 2022/2023. Name, pedigree, selection history, and characteristics for stripe and stem rusts of these parental genotypes are presented in Table 1. In the 2019/20 growing season, the parental genotypes were crossed to produce the three F_1 crosses. The studied crosses were cross 1: Misr 2 × Giza171, cross 2: Misr 2 × Sakha 95 and cross 3: Gemmiza 9 × shandawel 1. A part of grains obtained from the F_1s' and F_2's grains of the three crosses were sown to generate F_2's and F_3's in 2020/2021 and 2021/2022, respectively.

Table 1: Pedigrees and infection type of wheat genotypes used in this study

Genotypes	Cross &Pedigree	Reaction to Stripe rust	Reaction to stem rust
Misr 2	Skauz / Bav92 CMSS96M03611S-1M-010SY-010M-010SY-8M-0Y-0S	Susceptible	Susceptible
Giza 171	Sakha 93/ Gemmeiza 9 Gz 2003-101-1Gz- 4Gz-1Gz-2Gz-0Gz	Resistant	Resistant
Sakha 95	PASTOR // SITE / MO /3/ CHEN / AEGILOPS SQUARROSA (TAUS) // BCN /4/ WBLL1. CMA01Y00158S-040POY-040M-030ZTM-040SY-26M-0Y0SY-0S	Moderate	susceptible
Gemmiza 9	Ald "S" / Huac // Cmh 74A. 630 / Sx CGM 4583-5GM-1GM-0GM	Moderate	Moderate
Shandawel 1	SITE//MO/4/NAC/TH.AC//3*PVN/3/MIRLQ/BUC.CMSS93B 00567 S-72Y-010M-010Y-010M-OHTY-OSH	Susceptible	Resistant

In 2022/2023, the parents, F_1, F_2 and F_3 populations of the three crosses were evaluated using the randomized complete block design (RCBD) with three replications. Each experimental plot consisted of 17 rows (one row for each of P_1, P_2 and F_1 and seven rows for each of F_2 and F_3). Two border rows were surrounded the experiment to avoid the border effects. The rows were 3 m long, 20 cm apart and 10 cm among plants within the row. The wheat cultivar 'Morocco' which is highly susceptible to all races of rusts, was grown as a spreader around the experimental materials. All cultural practices were applied during the growing season according to the recommendation. Data on 30 individual randomly selected plants from each parent and F_1 generation and 200 plants from F_2 and F_3 populations were recorded to calculate the studied traits

(number of spikes / plant, number of kernels / spike, 100-kernel weight, stripe rust, stem rust reactions and grain yield per plant) for all populations of the three crosses.

Rust data recorded under field conditions in the adult plant stage were termed infection response (IR, s) according primarily to the size of pustules and associated necrosis or chlorosis. Infection responses (IR, s) were classified into four discrete categories: R = resistant, MR = moderately resistant, MS = moderately susceptible and S = susceptible (Roelfs *et al*., 1992), MR-MS" denoted an infection response class overlapped between the MR and MS categories.

Table 2. Adult plant resistance response (disease severity % and infection type) of tested wheat genotype against stripe (yellow) rust and stem rust under field conditions.

Symptoms	Disease severity %	Host response	Disease response
R	0 – 5 %	Resistant	Resistant no visible infection or some chlorosis or necrosis and no uredia
R-MR	10 – 20 %	Resistant to Moderately Resistant	
MR	20 – 30 %	Moderately Resistant	Moderately Resistant small uredia present ant surrounded by either Chlorotic or necrotic areas
MR – MS	30 – 40 %	Moderately Resistant to Moderately Susceptible	
MS	40 – 50 %	Moderately Susceptible	Moderately Susceptible medium-sized uredia present and possibly surrounded by chlorotic areas
MS - S	50 – 70 %	Moderately Susceptible to Susceptible	
S	70 – 100 %	Susceptible	Susceptible arge uredia present generally with little or no chlorosis and no necrosis

Biometrical and genetically methods:

The population means and the variances were used to compute the scaling tests C and D to estimate the type of gene effects according to Mather and Jinks (1971) and Hayman and Mather (1955). The five parameters model proposed by Hayman (1958) and Jinks and Jones (1958) was used to estimate different gene effects. The scaling test variance, standard error and 't' test were calculated to detect the non-allelic interactions.

Populations mean analysis in this study used biometrical technique as developed by Mather and Jinks (1982) to perform genetic parameters. The population mean of each trait was verified as follows: $Y = m + \beta_1 (d) + \beta_2 (h) + \beta_3 (i) + \beta_4 (1)$, where, Y: the mean of one population, m: the mean of all populations, d: the sum of additive effects, h: the sum of dominance effects, i: the sum of additive x additive interaction, 1: the sum of dominance x dominance interaction and $\beta_1 \dots$ and β_4 are the coefficients of gene effects. The significance of the measured gene effects (m, d, h, i, j and l) was tested by t-test for the studied traits according to the Hayman model (1958) as described by Singh and Chaudhary (1985).

Both broad (h^2_b) and narrow (h^2_n) sense heritability were estimated according to Mather and Jinks (1982). Expected genetic advance (GA %) as a percentage of the F_2 mean was calculated as reported by Allard (1999).

Frequency distribution values were computed for parents, F_1, F_2 and F_3 populations for response to stripe and stem rust infection under field conditions. concerning the mode of inheritance for quantitative analysis, the Roelfs Scale response of the infection in the field was converted to numeric values where symbol R = 1, R-MR = 2, MR = 3, MR-MS = 4, MS = 5, MS-S = 6, S = 7 (Singh *et al*., 2013).

The observed expected ratios of the phenotypic classes for stripe and stem rusts infection were determined by Chi-square (X^2) analysis according to Steel and Torrie (1960).

Moreover, the minimum number of effective genes controlling slow-rusting resistance in each cross was estimated by the formula of Wright (1968)**.**

Results and Discussion

1-Yield and yield components traits results
Mean performance

The mean and variance of the five populations $(P_1, P_2, F_1, F_2,$ and $F_3)$ of the three bread wheat crosses for the studied traits are shown in Table 3. F_2 is an ideal generation in which segregation and recombination are maximum for imposing selection. F_3 generation is equally important in the process of selection. The magnitude of recombination potential depends on the genetic diversity of the parents. A population is considered superior when it shows high mean coupled with high variability. Three crosses were studied for yield component traits, stripe and stem rusts in five generations.

Table 3. Means ($\overline{X}$) and variances (S^2) for all the studied traits using five populations for the three bread wheat crosses.

Crosses	Traits	statistical parameters	P₁	P₂	MP	F₁	F₂	F₃
Cross (1) **Misr2 x Giza171**	No of spikes/plant	$\overline{X}$	21.20	22.20	21.70	22.60	20.30	17.14
		S^2	0.51	0.64		0.66	37.60	23.90
	No of kernels/spike	$\overline{X}$	61.10	73.80	67.45	74.57	70.89	66.90
		S^2	0.62	0.83		1.08	66.80	45.30
	100 -kernel weight (g)	$\overline{X}$	2.98	5.05	4.02	4.90	4.85	5.14
		S^2	0.04	0.06		0.09	0.83	0.66
	Grain yield/plant(g)	$\overline{X}$	26.50	59.30	42.90	52.27	50.07	35.93
		S^2	0.25	0.49		1.17	48.42	36.64
Cross (2) **Misr2 x Sakha 95**	No of spikes/plant	$\overline{X}$	21.20	30.10	25.65	26.32	19.90	15.76
		S^2	0.30	0.80		0.81	34.97	23.39
	No of kernels/spike	$\overline{X}$	61.10	71.40	66.25	69.93	55.50	54.40
		S^2	0.69	0.80		1.58	66.02	46.40
	100- kernel weight (g)	$\overline{X}$	2.98	3.57	3.28	5.10	4.98	5.66
		S^2	0.04	0.01		0.09	0.82	0.69
	Grain yield/plant(g)	$\overline{X}$	26.50	78.03	52.27	59.63	39.92	32.21
		S^2	0.25	0.51		1.76	46.63	35.89
Cross (3) **Gemmiza 9x Shandawel 1**	No of spikes/plant	$\overline{X}$	22.13	17.46	19.80	21.87	20.43	17.44
		S^2	0.32	0.46		0.74	40.89	30.13
	No of kernels/spike	$\overline{X}$	72.80	71.16	71.98	72.83	70.71	67.45
		S^2	0.64	0.55		1.25	68.35	48.46
	100- kernel weight (g)	$\overline{X}$	3.84	2.87	3.36	4.68	4.64	4.44
		S^2	0.07	0.06		0.09	0.86	0.63
	Grain yield/plant(g)	$\overline{X}$	44.60	46.70	45.65	48.60	43.66	33.27
		S^2	0.31	0.56		1.83	57.52	43.09

Data showed highly significant differences among the investigated populations and their respective parents for most the studied traits.

Results in Table 3 showed that, among the investigated parents, the second parent (Giza 171) in the first cross (Misr2 × Giza171) was the best parent for no of kernels/spike and 100-kernel weight (g) with mean values of 73.8 and 5.05, respectively while the parent Sakha 95 in the second cross (Misr2 × Sakha 95) gave the highest no of spikes/plant and grain yield /plant with mean values of 30.1 and 78.03, respectively. The F₁ mean values were higher than the mid-values of the two parental means for all studied traits in the three crosses, reflecting the presence of partial dominance towards the better parent. The F₂ mean values were less than the F₁ mean, indicating that these traits are quantitatively inherited.

Generally, from the previous data it was interesting to note that the variances of the non-segregating populations (P₁, P₂ and F₁) were the lowest than those of segregating populations (F₂, F₃). This indicates that they are genetically homogeneous while

F₂ and F₃ are heterogeneous populations that showed greater variances. This is expected because the segregating populations consisted of heterozygous heterogeneous plants. Similar results were reported by El-Hawary, and Morgan (2022), Gebrel *et al* (2020), Shehab-Eldeen, *et al* (2020) and Sharshar *et al* (2020).

Scaling test and gene effects:

Quantitative traits which are of great interest are governed by a large number of genes having their effects. These are too modified by several environmental factors (Johansen, 1926). Thus, analysis at the level of individual genes becomes impractical and whole genome analysis over the totality of the gene should be undertaken (Wright, 1956). The genetic variability, thus, should be partitioned into its broad components.

Scaling test estimates of the investigated traits for all the studied traits in the three crosses are presented in Table 4.

The results revealed the presence of non-allelic interactions for all studied traits in all crosses. It should

be mentioned that at least one of the C and D tests were significant for the previous traits, indicating the adequacy of the five-parameter model to explain the type of gene action controlling the traits in these crosses. The getting results are similar to those obtained by Shehab-Eldeen *et al* (2020), Sharshar *et al* (2020), Gebrel *et al*. (2020), Aglan *et al*. (2020), Sharshar, A. M. and Samar M. Esmail(2019), Yassin and Ghareeb (2019).

Table 4. Estimates of scaling tests and gene effects for all the studied traits in the three bread wheat crosses.

Crosses	Traits	Scaling test		Genetic components					Type of epistasis
		C	D	(m)	(a)	(d)	(aa)	(dd)	
Cross (1) **Misr2 × Giza171**	No of spikes/plant	-7.3800**	-15.45**	20.305**	-0.50**	9.97**	8.0700**	-10.76**	duplicate
	No of kernels/spike	-0.55	-8.85**	70.895**	-6.33**	12.87**	-6.85**	-11.06**	duplicate
	100- kernel weight (g)	1.57**	2.8**	4.854**	-1.04**	-0.72**	-3.67**	1.62**	duplicate
	Grain yield/plant(g)	9.966**	-42.25*	50.075**	-16.40**	39.19**	2.14**	20.98**	complementary
Cross (2) **Misr2 × Sakha 95**	No of spikes/plant	-24.00**	-28.19**	19.95**	-4.47**	15.36**	5.86**	-5.59	duplicate
	No of kernels/spike	-50.14**	-25.80**	55.58**	-5.13**	12.47**	-1.42	32.46**	Complementry
	100- kernel weight (g)	3.18**	6.12**	4.99**	-0.29**	-1.73**	-4.13**	3.92**	duplicate
	Grain yield/plant(g)	-64.12**	-55.53**	39.92**	-25.77**	33.70**	-25.19**	11.44**	complementary
Cross (3) **Gemmiza 9 × Shandawel 1**	No of spikes/plant	-1.59	-10.71**	20.44**	2.33**	8.94**	11.54**	-12.15**	duplicate
	No of kernels/spike	-6.79**	-15.57**	70.71**	0.82**	10.09**	10.87**	-11.69*	duplicate
	100- kernel weight (g)	2.52**	1.77**	4.65**	0.48**	0.56**	0.21	-1.01	duplicate
	Grain yield/plant(g)	-13.84**	-45.53*	43.67**	-1.05**	30.99**	25.94**	-42.25**	duplicate

M:mean, a: additive, d: dominance, aa: additive × additive, dd: dominance × dominance, C and D: scalling test parameters
*, ** Significant at 0.05 and 0.01 levels, respectively

The estimated mean effect parameter (m) which reflects the contribution due to the overall mean plus the locus effects and interactions of the fixed loci was found to be highly significant for all the studied traits in the three crosses indicating that these traits are quantitatively inherited.

The additive (a) gene effects (Table 4) were positive and highly significant for no of spikes/plant, no of kernels/spike, 100- kernel weight in the third cross, indicating the contribution of additive gene effect in the inheritance of these traits and the potential for obtaining an additional improvement of these traits by selection using the pedigree method. Moreover,

highly significant negative additive effects were detected for all the studied traits in the first and second crosses, and grain yield/plant in the third cross, indicating that the additive effects were less important in the inheritance of these traits**.**

Dominance gene effects (d) were positive and highly significant for no of spikes/plant, no of kernels/spike and grain yield/plant in the first and second crosses, and all the studied traits in the third cross indicating the importance of dominance gene effects in the inheritance of these traits. On the other hand, highly significant negative effects were obtained for 100-kernel weight in the first and second crosses,

indicating that the alleles responsible for less value of these traits were over dominant over the alleles controlling high value. These results are in harmony with those obtained by Shehab-Eldeen *et al* (2020), Gebrel *et al* (2020), El-Hawary and Morgan (2022), they found that both additive and dominance gene action were significant in the inheritance of yield components and the dominance effects were negative and higher than additive effects.

Additive × additive gene effects (aa) were positive and highly significant for no of spike/plants in the three crosses, grain yield/plant in the first and third crosses and no of kernels/spike in the third cross suggesting that these traits have increasing gene effects and the selection for its improvement could be effective in early generation for the wheat breeding program. Meanwhile, negative and highly significant values of additive × additive gene action were obtained for no of kernels/spike in the first cross, 100- kernel weight in the first and second crosses and grain yield/ plant in the second cross, so selection for these traits will not be effective in the early generations because there is no additive genetic effect to be fixed in these traits.

Dominance × dominance epistasis type was highly significant positive for 100- kernel weight and grain yield/plant in the first and second crosses and no of kernels /spike in the second cross. These results confirm the important role of dominance × dominance gene action in the genetic system controlling this character and selection should be effective in late generations. Highly significant negative dominance × dominance gene effects was attained for no of spikes/plant and no of kernels /spike in the first and third crosses and grain yield /plant in the third cross, indicating their reducing effect in the expression of this character and there is no breeding importance in proceeding generations. These results are in line with those obtained by Sharshar and Genedy (2020), Shehab-Eldeen *et al* (2020), Sharshar *et al* (2020) and Gebrel *et al* (2020) El-Hawary and Morgan (2022), Sharshar and Samar M. Esmail (2019) which confirms the important role of dominance × dominance gene interaction in the genetic system.

The type of epistasis According to Kearsey and Pooni (1996) was determined as duplicate when dominance (d) and dominance × dominance (dd) have different signs in crosses that exhibited significant epistasis, while similar signs of (d) and (dd) reflect complementary epistasis. These results illustrated that duplicate epistasis was prevailing for most studied traits in the three crosses except for grain yield/plant in the first and second cross, no of kernels/spike in the second cross which were complementary epistasis. This indicates that duplicate epistasis was greater and more important when compared with complementary epistasis for most studied traits, as non-additive effects were higher than additive effects in most of the studied traits, intensive selection through later generations was needed to improve these traits. These results agree mostly with those obtained by Abd El-Aty and Katta 2007, Sharshar *et al* (2020).

Heritability and percentage of genetic advance:

Both broad and narrow-sense heritability and genetic advance estimates are given in Table 5.

The knowledge of heritability guides the plant breeder to predict the behavior of the succeeding generation, making a describable selection and accessing the magnitude of genetic advance improvement that is possible through selection. Broad-sense heritability h2(b) includes different types of genetic variances, whereas plant breeders are concerned with narrow-sense heritability h2(n) which estimates the additive portion of genetic variance.

Heritability estimates in the broad sense were high for all the studied traits in the three crosses, ranging from 91.14 % for 100- kernel weight in the first cross to 98.87 for no of spike/plant in the third cross, indicating that most of the phenotypic variability was due to genetic effects. Heritability estimates in a narrow sense were moderate for most studied traits in all crosses and ranged from 31.24% for 100- kernel weight in the second cross to 72.24% for no of spikes/plant in the first cross, indicating that these traits were greatly affected by additive and non-additive effects and there is an appreciable amount of heritable variation.

The results indicated that these traits were greatly controlled by additive and non-additive effects and there is an effective amount of heritable variation. Therefore, the selection for these traits will be easier and have low environmental influence.

The expected genetic advance (Δg) ranged from 0.58 for 100-kernel weight in the second cross to 10.83 for no of kernels /spike in the first cross. The expected genetic advance as a percent of F_2 mean was low to moderate in most of the traits in the three crosses and ranged from 11.71 % for 100-kernel weight in the third cross to 45.28 % for no of spikes/plant in the first cross, indicating the possibility of practicing selection in early generations to enhance selecting high yielding genotypes. Meanwhile, the remaining traits, showed the low values of expected genetic advance, suggesting the role of environmental factors and dominance gene action in the inheritance system of these traits. Similar results were reported by Gebrel *et al* (2020) and Mohamed *et al* (2021). Sharshar and Samar M. Esmail (2019), Shehab-Eldeen (2020), El-Hawary and Morgan (2022).

Table 5. Estimates of Heritability and percentage of genetic advance for all the studied traits in three bread wheat crosses.

Crosses	Traits	Heritability percentage		Expected genetic advance	
		$h^2(b)$	$h^2(n)$	Δg	Δg %
Cross (1) **Misr2 × Giza171**	No of spikes/plant	98.49	72.74	9.19	45.28
	No of kernels/spike	97.97	64.34	10.83	15.28
	100 kernel weight (g)	93.84	40.66	0.76	15.71
	Grain yield/plant (g)	98.53	48.65	6.97	13.93
Cross (2) **Misr2 × Sakha 95**	No of spikes/plant	98.19	66.20	8.07	40.43
	No of kernels/spike	97.38	59.17	9.90	17.82
	100- kernel weight (g)	94.61	31.24	0.58	11.71
	Grain yield/plant (g)	98.12	46.07	6.48	16.23
Cross (3) **Gemmiza 9 × Shandawel 1**	No of spikes/plant	98.87	52.59	6.93	33.90
	No of kernels/spike	97.62	58.20	9.91	14.02
	100- kernel weight (g)	91.14	53.59	1.02	21.99
	Grain yield/plant (g)	98.10	50.19	7.84	17.96

2- Results of stripe and stem rust resistance.
1- Qualitative analysis:
1- Inheritance mode of stripe rust resistance at adult plant stage in three bread wheat crosses.

The qualitative analysis of the obtained data was carried out according to the infection response of the tested parents, F_1, F_2 and F_3 populations against wheat stripe and stem rust pathogen at the adult plant Stage, under field conditions. The frequency distributions and Chi- square analysis of segregated generations (F_2 and F_3) plants of the three studied crosses of stripe and stem rust are presented in Table 6.

The Data indicate that the parents Misr 2 and shandawel 1 expressed high susceptibility to stripe rust ranging from MS-S to S, while the parents Sakha 95 and Gemmiza9 showed moderate susceptibility ranging from MS to MS-S, however the parent Giza 171 showed high resistant to stripe rust and ranging from R to R-MR. Meanwhile, the F_1 plants ranged from MS to MS-S indicating that the susceptible was partially dominant over resistance.

For stem rust, the data in Table 6 indicated that the parents Misr2 and Sakha 95 expressed high susceptibility to stem rust and ranged from MS-S to S on the other hand, the parents Giza171, Gemmiza 9 and Shandawel 1 showed resistant to stem rust and ranged from R to R-MR. Meanwhile, the F_1 plants ranged from MS to MR-MS in the first and second cross,

while ranged from MR to R-MR in the third cross indicating partial dominance for resistance over susceptibility.

Segregations and Chi- square analysis revealed that F_2 and F_3 plants showed a wide range of infections from R to S. For the first cross, the F_2 classified into 127 resistant (R) and 73 susceptible(S), confirming the expected ratio (9:7) that indicated to existence two complementary dominant genes. For F_3, the number of plants with Resistant: susceptible in the first cross were 138: 62 confirming the ratio (3: 1) indicated to one recessive gene (decreasing resistance ratios).

For the second cross the F_2 generation revealed 79 resistant: 121 susceptible as a segregation ratio (7:9) indicating the existence of two complimentary recessive genes, meanwhile the F_3 classified into 105 resistant: 95 susceptible which fitted the expected ratio of 9:7 indicating the existence for two complementary dominant genes.

On the other side, the third cross displayed segregation of 93 resistant: 107 susceptible for F_2 confirming the ratio 7:9 suggested the existence of two complementary recessive genes. Meanwhile, F_3 data from the third cross revealed frequencies of 156 resistant and 44 susceptible which fitted the expected ratio of 3:1 these data suggested the existence of one dominant gene.

Table 6. Frequency distribution of Stripe and stem rust for P_1, P_2, F_1, F_2 and F_3 for three bread wheat crosses at the adult stage under field conditions.

Traits.	Cross name	No. of tested plants	R	R-MR	MR	MR-MS	MS	MS-S	S	R	S	Expected ratio	X^2	p[b]
Stripe rust	**Cross (1)** Misr 2 × Giza 171	$P_{1\,30}$						2	28					
		$P_{2\,30}$	27	3										
		$F_{1\,30}$					26	4						
		$F_{2\,200}$	103	11	13		10	18	45	127	73	9: 7	4.272	0.038
		$F_{3\,200}$	114	4	20		27	12	23	138	62	3: 1	3.84	0.05
	Cross (2) Misr 2 × Sakha 95	$P_{1\,30}$						2	28					
		$P_{2\,30}$					24	6						
		$F_{1\,30}$					23	7						
		$F_{2\,200}$	22	18	39		16	5	100	79	121	7: 9	1.476	0.225
		$F_{3\,200}$	90	15			70		25	105	95	9: 7	1.142	0.285
	Cross (3) Gemmeiza 9 × Shandawel 1	$P_{1\,30}$					22	8						
		$P_{2\,30}$					2	28						
		$F_{1\,30}$					20	10						
		$F_{2\,200}$	41	14	52		13	14	66	93	107	7: 9	1.147	0.283
		$F_{3\,200}$	103	15	38		14		30	156	44	3: 1	0.426	0.513
Stem rust	**Cross (1)** Misr 2 × Giza 171	$P_{1\,30}$						1	29					
		$P_{2\,30}$		2	28									
		$F_{1\,30}$				3	27							
		$F_{2\,200}$	25	6	20			9	140	51	149	1:3	0.026	0.87
		$F_{3\,200}$	58				142			58	142	1:3	1.706	0.191
	Cross (2) Misr 2 × Sakha 95	$P_{1\,30}$					4	26						
		$P_{2\,30}$					5	25						
		$F_{1\,30}$				6	24							
		$F_{2\,200}$	20	10	25		35	10	100	55	145	1:3	0.666	0.414
		$F_{3\,200}$	90	38			60		12	128	72	9:7	4.881	0.027
	Cross (3) Gemmeiza 9 × Shandawel 1	$P_{1\,30}$	22	8										
		$P_{2\,30}$		7	23									
		$F_{1\,30}$		9	21									
		$F_{2\,200}$	110	13	17		12	18	30	140	60	3:1	2.667	0.102
		$F_{3\,200}$	110	13	47		13	5	12	170	30	13:3	1.846	0.174

R = Resistant   MR = Moderately Resistant   MS = Moderately Susceptible   S = Susceptible

For stem rust, data in Table 8 revealed that in the first cross the F_2 and F_3 was segregated to 51 resistance: 149 susceptible and 58 resistance: 142 susceptible, respectively confirming the ratio (1:3) which indicated the existence of one recessive gene. In the second cross, the F_2 was classified into 55 resistant to 145 Susceptible confirming the ratio (1:3) suggesting the existence of one recessive gene, while the F_3 segregated to 128 Resistant to 72 susceptible confirming the expected ratio of 9:7 indicating the existence of two complementary dominant genes. F_2 segregated in the third cross to 140 Resistant to 60 susceptible which fitted the expected ratio 3:1 suggesting the existence of one dominant gene. The F_3 was classified into 170 resistant: 30 susceptible therefore the expected ratio was 13:3 suggesting the existence of two duplicate dominant genes.

2- Quantitative analysis
Mean of response Stripe and Stem rust diseases in the three bread wheat crosses at the adult stage under field conditions.

The mean of response stripe and stem rust diseases for the five populations of the three studied crosses are presented in Table 7. The data indicated that the F_1 mean values were less than the mid parents in the second and third cross for stripe rust, the first and second cross for stem rust, indicating partial dominance towards the parent of low disease severity, while the F_1 was higher than the mid parent in the first cross for stripe rust and third cross for stem rust indicating the presences of complete dominance for resistance in this crosses.

Table 7. Means(x) and variances (S^2) of response Stripe and Stem rust diseases in the three bread wheat crosses at the adult stage under field conditions.

Crosses	Traits	Statistical parameters	P_1	P_2	MP	F_1	F_2	F_3
Cross (1)	stripe rust	$\overline{X}$	6.93	1.10	4.01	5.13	3.19	2.75
Misr2 x Giza171		S^2	0.06	0.09		0.12	6.69	5.16
	stem rust	$\overline{X}$	6.97	2.93	4.95	4.90	5.66	3.84
		S^2	0.03	0.06		0.09	5.09	3.29
Cross (2)	stripe rust	$\overline{X}$	6.93	5.20	6.07	5.23	3.30	3.23
Misr2 x Sakha 95		S^2	0.06	0.16		0.18	7.34	5.22
	stem rust	$\overline{X}$	6.87	6.83	6.85	4.80	5.25	2.75
		S^2	0.12	0.14		0.16	4.53	4.08
Cross (3)	stripe rust	$\overline{X}$	5.27	6.68	5.97	5.33	4.18	2.63
Gemmiza 9x Shandawel 1		S^2	0.20	0.24		0.22	5.66	4.68
	stem rust	$\overline{X}$	1.27	2.76	2.01	2.70	2.82	2.28
		S^2	0.20	0.17		0.21	5.68	3.19

The F_2 mean values were less than the mid-parent in all the studied crosses for stripe rust, the second cross for stem rust suggesting the importance of partial dominance of resistance in the inheritance of these traits, while the F_2 means were higher than the mid-parent in the first and third cross for stem rust indicating partial dominance towards the susceptible parent. These results are in agreement with those obtained by Sharshar, and Samar Esmail (2019), Shehab-Eldeen *et al* (2020) and Elmassry, *et al* (2020).

Finally, the first cross (Misr2× Giza171) was the most desirable which had the lowest mean values for the infection and low disease severity for stripe rust disease and the third cross (Gemmiza 9 × Shandawel 1) for stem rust disease.

Heritability, degree of dominance and number of genes

Heritability estimates in broad sense were high for stripe and stem rust diseases for all the studied crosses indicating that the phenotypic variability was mostly attributed to genetic effects for these diseases in these crosses as shown in Table 8.

Table 8. Estimates of heritability percentage in broad (h^2b) and narrow (h^2n) senses, degree of dominance and number of genes for stripe and stem rust in three bread wheat crosses

Crosses	Traits	Heritability percentage		Degree of Dominance		No. of genes
		$h^2(b)$	$h^2(n)$	h_1	h_2	
Cross (1)	Stripe Rust	98.66	45.82	0.38	0.74	0.65
Misr2 x Giza171	Stem Rust	98.70	70.44	0.00	0.00	0.41
Cross (2)	Stripe Rust	98.17	57.16	0.97	0.28	0.05
Misr2 x Sakha 95	Stem Rust	96.95	20.14	2.88	0.78	0.001
Cross (3)	Stripe Rust	96.08	34.79	0.68	8.66	0.002
Gemmiza 9x Shandawel 1	Stem Rust	96.57	87.67	0.01	0.01	0.50

Heritability estimate in narrow-sense presented a moderate to low for stripe rust in the three crosses and ranging from 34.79% in the third cross to 57.16% in the second cross and the second cross for stem rust with value 20.14% suggesting the responsibility of the dominance gene action for the inheritance stripe and stem rust in this studied crosses and delayed selection may be more effective for improving trait of these genotypes. Moreover, high heritability in narrow sense was in the first and third cross for stem rust with value

70.44% and 87.67 respectively, reflecting the importance of additive gene action and their effects in resistance to stem rust diseases. These results are in agreement with Khilwat *et al.* (2019), Reena *et al.* (2018) and Sharshar, and Samar M. Esmail (2019).

The degree of dominance h_1 and h_2 were positive values in the three crosses for stripe and stem rust, which revealed the presence of over dominance for resistance in this crosses. Hermas and El- Sawi (2015), Abd El Badeea (2015).

The numbers of genes in the studied crosses were between 0.002 in the third cross to 0.65 in the first cross for stripe rust and 0.001 in the second cross to 0.50 in the third cross for stem rust. Therefore, results revealed that some numbers were in agreement with Mendelian (single locus) and others more than a single locus (two or three) in the inheritance of resistance. The estimated gene numbers differed based on the quantitative methods of genetic analysis that may be biased and influenced by the observed estimates of disease severity (Moozhan *et al*., (2018), Navabi *et al*., (2003), and Chen and Line (1993).

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تقدير الثوابت الوراثية للمحصول و مكونات المحصول وصفتي المقاومة للصدأ المخطط والصدأ الأسود بإستخدام تحليل متوسطات الأجيال فى ثلاثة هجن من قمح الخبز

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أجريت هذه الدراسة بمزرعة محطة البحوث الزراعية بسخا– كفرالشيخ خلال أربع مواسم 2019/2020 الي 2022/2023 لتقدير طبيعة التأثير الجينى وإيجاد تراكيب وراثية جديدة يمكن الإنتخاب من خلالها فى الأجيال الإنعزالية التالية للحصول على سلالات جديدة من قمح الخبز مقاومة لمرض الصدأ المخطط (الاصفر) وصدأ الساق (الاسود) ومتفوقة فى صفاتها المحصولية على الأصناف التجارية المنزرعة ، وقد استخدم لذلك ثلاثة هجن (مصر2 × جيزة 171) ، (مصر2× سخا95) و (شندويل1 × جميزة 9) بإستخدام تحليل متوسطات الخمس عشائر(الأب الأول والثانى والأجيال الأول والثانى والثالث) ، وأشارت النتائج الي أن تأثير الفعل الجينى السيادي أكبرمن تأثير الفعل الجينى المضيف لمعظم الصفات المدروسة ، كما دلت النتائج على أن التأثير السيادى × السيادي أكبر من التأثير المضيف × المضيف لمعظم الصفات المدروسة. أظهرت نتائج التأثير المضيف ×المضيف قيم موجبة وعالية المعنوية لصفة عدد السنابل/ نبات في جميع الهجن وصفة محصول الحبوب/النبات في الهجين الأول والثالث وصفة عدد الحبوب/السنبلة في الهجين الثالث، وأظهر التاثير السيادي × السيادي قيم موجبة وعالية المعنوية لصفة وزن 100حبه ومحصول الحبوب/النبات في كل من الهجين الأول والثاني وصفة عدد الحبوب/السنبلة في الهجين الثاني. أظهرت درجه التوريث بالمعني الواسع قيم عالية في كل الهجن في جميع الصفات المدروسة، وكانت قيم معامل التوريث بمعناه الضيق منخفضة إلى عالية في جميع الصفات لكل الهجن المدروسة، وكانت متوسطه إلي منخفضه لصفة الصدأ المخطط في جميع الهجن، بينما كانت عالية في الهجين الاول والثالث لصفة الصدأ الاسود .عموما أفضل الهجن كان الهجين الأول (مصر2×جيزه171) لصفة المقاومة للصدأ المخطط والهجين الثالث (شندويل1 × جميزة 9) لصفه المقاومة لصدأ الساق وبالتالي يمكن إستخدامهم في برنامج تربية القمح لتحسين صفه المقاومه للصدأ المخطط (الاصفر) وصد أالساق.