Gene effect estimation for yield–characters and inheritance of yellow rust resistance among generations in three bread wheat crosses

Shehab-Eldeen, M.T[1], M. A. H Darwish[1] and Zeinab, E. Ghareeb[2]

[1] Wheat Res. Dep., Field Crops Res. Inst., ARC, Giza, Egypt –
E mail: m_abdelkareem34@yahoo.com
[2] Central Lab. for Design and Statistical Analysis Res., ARC, Giza, Egypt –
E mail: zeinabghareeb@yahoo.com

ABSTRACT

This study was carried out during 2016/17 to 2019/2020 seasons on the farm of Sakha Agricultural Research Station, ARC, Egypt to investigate the inheritance and nature of genetic control of yellow rust disease and yield traits in bread wheat. Four parental bread wheat genotypes and their F_1, F_2 and F_3 filial generations were evaluated in a randomized complete block design in three replications for three crosses (Shandaweel-1 × Misr-1, Shandaweel-1 × Sakha-95 and Line-2 × Sakha-95). The existence of genetic variability was due to differences among the investigated filial generations for all studied traits except for 100-kernel weight in the 1st hybrid. Scaling test revealed the presence of non-allelic interactions (epistasis) in the most studied cases. Dominance gene effects were generally greater than additive ones in all cases. Gene effects varied among crosses' traits, whereas the dominance and duplicate dominance beside additive gene effects were found to play important role in the inheritance for most studied cases. Therefore, the significantly herotic effect and over-dominance was detected. Narrow sense heritability estimates displayed moderate values in most cases. Inheritance of resistance to yellow-rust disease among generations was governed by one to three genes, whereas depends on the parental genetic background that affects the genetic interaction of cross. Promising F_3 families derived from Shandaweel-1 x Sakha-95 cross recorded the complete dominant tolerant to yellow-rust infection, however Line-2 x Sakha-95 families were promising for grain yield. Selection based on rust infection for individual plants within sixty families recorded 25, 50 and 21 as best families from the three crosses, respectively. Wheat breeders can employ these results to improve both yield and rust-infection and enhance Egyptian wheat genotypes.

Keywords: *Families, Gene action, Genetic advance, Heterosis, Heritability, Inbreeding depression, Mean analysis, parameter, Triticum aestivum L.*

INTRODUCTION

Wheat (*Triticum aestivum* L.) is one of the most important cereal food commodities not only in Egypt but also all over the world. Currently, Egypt is the largest wheat importer in the world. The local consumption reached 18.6 million tons,

meanwhile, total wheat production is not enough (Gomaa et al., 2014). In addition, wheat yield as a complex trait was influenced by many biotic factors as rusts. Stripe or yellow rust of wheat caused by *Puccinia striiformis f. sp. tritici* is the most destructive rust in Egypt. The best approach towards breeding for resistance would be to identify the durable of the resistance and use it to be incorporated in a new cultivar (Johnson et al., 1978).

Genetic improvement of yield and rust-related traits and selection or hybridization breeding program depends on estimates of genetic components for the interested traits consisting of additive, dominance and non-allelic interaction effects, which may provide practical information to the breeders during the development of rust-tolerant wheat varieties (Hussain et al., 2008 and Dehghani and Moghaddam 2004). Resistant genotypes provide an effective and economical way to control the disease, but the genetics of rust resistance knowledge in wheat is little to help breeders to rely on genes when breeding for resistance (Eyal, 1999 and Mohammadi et al., 2012). Genetic analysis of rust resistance in wheat suggested that pathogenicity is controlled by several loci and is likely inherited as a quantitative trait (Kema et al., 1996; Zhan et al., 2005 and Mohammadi et al., 2012). Many studies were undertaken to analyze generation mean data to gather information about genetic interrelationships among parents, crosses, gene action to identify combination for the important traits, that is, grain yield and yellow rust-tolerant wheat and their inheritance. Zhang et al., (2010) characterized wheat stripe rust resistance genes to explain their inheritance.

Plant breeders need to develop genotypes which are able to express high grain yield potential and diseases resistance (Noorka et al., 2009). This requires a search for and selection of yield related-traits, which were considered as highly associated with grain yield (Richards et al., 2002). Breeding program aims to increase the genetic potential of the desired traits continuously. To accumulate a desired gene in genetic pool of improved genotypes, the mode of inheritance is necessary to understand the magnitude of gene effects and gene action forms (Farshadfar et al., 2000). All genetic studies agreed that both additive and non-additive gene actions were involved in the expression of most traits (Hannachi et al., 2013). Primarily, the selection of promising parents is very essential to obtain superior hybrids, depending on the predominance of additive effect (Beche et al., 2013). Keeping in view the importance of yellow-rust tolerance and some grain yield traits, the goal of this research was to investigate the mode of gene action and inheritance pattern of these traits for using them as indicators

of highest grain yield in three bread wheat crosses utilizing P_1, P_2, F_1, F_2 and F_3 populations.

The objectives of this study were 1) to determine the genetic control of yield-traits and yellow-rust resistance by genetic analysis among generation means in wheat and 2) to explain the possibility of development genotypes among different generations, showing the best promising ones.

MATERIALS AND METHODS

Genetic material

The present experiment was conducted on the experimental farm of the Sakha Agricultural Research Station, Agricultural Research Center, Kafr Elsheikh, Egypt (31.10° North, 30.93° East) during 2016/17 to 2019/20 growing seasons. Four bread wheat parental genotypes were selected on the basis of the presence of wide differences among them based on their characteristics (Table 1).

Table 1. Name, pedigree and infection type of four parental bread wheat genotypes.

Code No.	Parent name	Pedigree	Yellow rust
P_1	Shandaweel-1	SITE//MO/4/NAC/TH.AC//3*PVN/3/MIRLQ/BUC.CMSS93B 00567 S-72Y-010M-010Y-010M-OHTY-OSH	MR †
P_2	Misr-1	OASIS/KAUZ//4*BCN/3/2*PASTOR CMSS00Y01881T-050M-030Y-030M-030WGY-00M-0Y-0S	MR
P_3	Sakha-95	PASTOR // SITE / MO /3/ CHEN / AEGILOPS SQUARROSA (TAUS) // BCN /4/ WBLL1. CMA01Y00158S-040POY-040M-030ZTM-040SY-26M-0Y-0SY-0S.	R
P_4	Line-2	SIDS BXD 12-13 #3	S

† R= Resistant, MR= Moderately Resistant, MS= Moderately Susceptible and S= Susceptible.
Hybrid1: Shandaweel-1*Misr-1, Hybrid 2: Shandaweel-1*Sakha-95 andHybrid3: Line-2*Sakha-95.

Disease infection and assessment under natural conditions

The experiment was planted 15 days after the recommended sowing date (the first half of December) to expose the plants to suitable environment for rust infection. Wheat plants were exposed to the current recommended practices. Plots were surrounded by spreader area planted with a mixture of highly susceptible wheat genotypes to rusts, i.e., Morocco and Max to spread rust inocula. Rust disease spreader plants were inoculated by injection method twice in a week during the growing season to provide and maintain the rust

inocula pressure in the experiment. Yellow rust was scored on the flag leaf of individual plants when the severity on the most susceptible parent was about 100%, i.e. most of the leaf surface was covered with uredinia. The modified Cobb scale of Saari and Wilcoxson, (1974) and Pathan and Park (2006), multiplying of disease severity (DS) and constant values of infection type (IT) was expressed in five types based on; resistant = (R), tolerant = (T), moderately tolerant = (MT), moderately susceptible = (MS) and susceptible = (S). Disease severity and host response scores were multiplied together to give the coefficient of infection (C.I.) for data analysis.

The weather reports in Table (2) showed the highest heat waves and moister recorded for the weather of seasons especially in the infection period.

Table 2. Climatic characteristics of the Sakha experimental site through 2019/2020 season.

Month	Period	Temperature c°				Mean Relative humidity	Precipitation (mm)
		Mean		Extreme			
		Max.	Min.	Max.	Min.		
Nov.	1-15	29.09	26.29	32.40	29.40	70.93	0.00
	16-31	25.67	23.89	28.10	26.60	64.20	0.00
Des.	1-15	21.35	13.33	25.00	19.60	73.13	24.80
	16-31	20.80	12.40	23.50	16.60	72.57	35.88
Jan.	1-15	18.36	11.75	20.90	16.10	75.67	44.90
	16-31	18.33	12.05	21.10	15.60	72.53	22.60
Febr.	1-15	20.39	12.61	24.00	15.60	69.90	7.40
	16-31	20.54	12.48	28.90	16.00	71.39	6.90
Mar.	1-15	22.66	15.62	29.70	18.20	72.27	59.90
	16-31	22.59	15.49	29.60	22.00	63.23	0.90
Apr.	1-15	26.02	18.89	31.90	20.50	62.77	0.00
	16-31	26.82	20.17	33.80	22.20	62.33	0.00
May	1-15	30.95	23.95	33.40	18.30	55.63	0.00
	16-31	31.92	25.36	41.40	21.30	51.78	0.00

Experimental procedure:

The selected parents were crossed to obtain three F_1's/hybrids, Hybrid 1: Shandaweel-1 × Misr-1, Hybrid 2: Shandaweel-1 × Sakha-95 and Hybrid 3: Line-2 × Sakha-95 in 2016/17 season. Obtained grains from the three hybrids of F_1s' and F_2's were raised to produce F_2's and F_3's in 2017/18 and 2018/19 seasons, respectively. Parents, F_1, F_2 and F_3 (sixty random families from each hybrid) generations of the three hybrids were evaluated in a randomized complete block design with three replications in 2019/20 season under field conditions. Experimental genotypes including parents, F_1's, F_2's and F_3's were sown in rows; 3-m long with 30 cm apart and plants within rows were 20 cm spaced. Three rows were assigned to each parent and F_1's, while 20 rows for each F_2

generation of each hybrid. Data were recorded on randomly 30 individual guarded plants of each parent and F_1's and 250 F_2's plants for plant height, number of spikes per plant, number of kernels per spike, 100-kernel weight and grain yield per plant.

The getting $F_{1:2}$ seeds in 2017/18 were sown in 2018/19. Then, 60 random plants from $F_{2:3}$ were selected and harvested separately to be sown in the next season. The experiment was conducted in RCBD with three replications in 2019-2020. Each plot was one-meter-long row, and distance between plots was 25 cm. In each plot 10 plants were randomly selected and measurements were taken for studied traits. Meanwhile, susceptibility to wheat yellow rust was recorded at the time of disease onset. Four rows were devoted to each family (sixty F_3 families) for the three hybrids. At least, 45 plants from each F_3family were used to obtain the last recorded data under field conditions. Recommended wheat crop production practices were followed.

Biometrical analyses

The collected data were subjected to analysis of variance for the five generation means to perform differences among generations. Means of grain yield traits were used to perform C and D scaling test as given by Hayman and Mather (1955) to study the fit adequacy of additive-dominance model. Standard error of the C and D estimates were obtained by taking the square root of their respective variances, consequently, t-test was calculated by dividing C and D effects on their respective standard error. Under joint scaling test, the five parameters were estimated to obtain information on the nature of gene effects involved in the genetic control of yield traits as established by Singh and Chaudhary (1985). The considered-five parameters concluded mean effects (m), additive (d) and dominance (h) gene effects and types of epistasis (i and l). The variance and standard errors for each of these parameters (m, d, h, i and l) were calculated and the significance of each one was tested using t-test. The type of epistasis was determined only when dominance [h] and dominance x dominance [l] effects were significant, recording complementary epistasis in the same effects sign and duplicate epistasis in different signs (Mather and Jinks 1982).

Both broad and narrow-sense heritability, potence ratio, heterosis above mid and best parent and inbreeding depression (%) were calculated according to Mather and Jinks (1982). Genetic advance as percentage of the F_2 mean were estimated as reported by Allard (1999). The t-test was used to determine the significance of these parameters where the standard error (SE) was calculated.

Obtained F_3 60 family's data were analyzed separately for yield traits and resistance to yellow rust to determine the relationship of the resistant gene/s and their inheritance and determine the best families.

Inheritance studies

Infection to yellow rust at the adult plants under field condition was restricted. Evaluation fit goodness of the observed and expected segregation ratios of F_1, F_2 and F_3 populations used Chi-square (χ^2) and corresponding probability (*P*) values proposed by Steel and Torrie (1960). Then, mode of inheritance of infection types expected ratio according to the divided phenotype groups (observed) of the yellow rust based upon (χ^2). This χ^2-goodness of fit was used to compare the observed distribution in the population with those predicted by various genetic models for each measure of resistance. Models used were single-, two-, and three-gene models, as well as gene interaction models were used to compare sets of data from the segregates and their two parents (as Mendelian-ratios). Infection types (R = 0, T =0.2 and MT =0.4) were classified as resistant and types (MS= 0.8 and S =1.0 was classified as susceptible. Chi-square tests were used to determine the goodness of fit of the segregation ratios in F_2 and F_3 data from the three crosses were analyzed separately for resistance to determine the relationship of the gene or genes for resistance to each generation/cross.

RESULTS AND DISCUSSION

Generation Mean

Data in (Table 3) present mean performance and standard error for the studied traits using the five generations (P_1, P_2, F_1, F_2 and F_3) of the three bread wheat hybrids for the investigated traits. Results of five population means established that significant differences among the investigated generations and their respective parents for all studied traits except for 100-kernel weight in the 1st hybrid, pointing to the presence of genetic variability for these traits in the studied hybrid materials.

In filial generations, F_1's mean presented best performance for yellow rust infection, grain yield plant^{-1} and 100-kernel weight in 2nd hybrid, number of spikes plant^{-1} in 3rd hybrid and number of kernels spike^{-1} in 1st hybrid. In F_2's, results revealed best values for number of spikes plant^{-1}, yellow rust infection and grain yield plant^{-1} in1st hybrid and number of kernels spike^{-1} and 100-kernel weight in 2nd hybrid. Meanwhile, number of spikes plant^{-1}, grain yield plant^{-1} and number of kernels spike^{-1} in 3rd hybrid and yellow rust infection and 100-kernel weight in the 2nd hybrid recorded the best values for F_3's mean.

Among the investigated parents, genotype Sakha-95 revealed the best values for all traits except number of kernels spike^{-1}, recorded the highest mean values for plant height (116.17 cm), number of spikes plant^{-1} (33.87 spike), 100-kernel weight (3.56 g) and grain yield plant^{-1} (52.23 g) with the lowest yellow rust infection (0.27). However, parent Shandaweel-1 had the maximum number of kernels spike^{-1} (74.10 kernels).

In hybrids, the second hybrid (Shandaweel-1 x Sakha-95) exceeded its parents for plant height and 100-kernel weight, meanwhile, third hybrid Line 2 x Sakha-95 surpassed its parents for number of kernels spike^{-1} and 100-kernel weight, indicating to over-dominance.

Table 3. Means ($\bar{x}$ ± se) for the studied traits using the five populations for the three bread wheat crosses.

Traits	Parents		Filial generations		
Hybrid 1	**Shandaweel-1**	**Misr-1**	**F$_1$**	**F$_2$**	**F$_3$**
Plant height	115.00^{ab} ±0.64	110.00^b ±0.63	115.00^{ab} ±0.80	109.10^b ±0.99	120.92^a ±0.31
No. of spikes plant^{-1}	22.20^{ab} ±0.89	23.77^b ±0.98	23.03^{ab} ±1.12	20.70^{ab} ±0.68	18.42^b ±0.20
Yellow rust infection	6.94 ^{c} ±1.16	13.43^{bc} ±1.61	18.67^b ±1.45	11.91^c ±1.15	27.04^a ±0.41
Grain yield plant^{-1}	40.30 ^{a} ±1.07	35.63 ^{b} ±1.30	34.17 ^{b} ±2.53	36.44 ^{b} ±1.04	20.12 ^{c} ±0.23
No. of kernels spike^{-1}	74.10 ^{a} ±1.19	67.93 ^{b} ±1.18	66.47^{bc} ±1.49	63.89 ^{c} ±1.05	43.65 ^{d} ±0.28
100-kernel weight	3.24 ^{a} ±0.13	3.42 ^{a} ±0.12	3.26 ^{a} ±0.15	3.37 ^{a} ±0.10	3.41 ^{a} ±0.03
Hybrid 2	**Shandaweel-1**	**Sakha-95**			
Plant height	115.00 ^{c} ±0.64	116.17 ^{c} ±0.46	121.83 ^{b} ±0.74	115.70 ^{c} ±1.41	128.83 ^{a} ±0.40
No. of spikes plant^{-1}	22.20^{bc} ±0.89	33.87 ^{a} ±0.80	24.40 ^{b} ±0.91	19.74^{cd} ±0.61	17.99 ^{d} ±0.18
Yellow rust infection	6.94 ^{b} ±1.16	0.27 ^{c} ±0.13	0.40 ^{c} ±0.26	15.98 ^{a} ±1.36	9.81 ^{b} ±0.31
Grain yield plant^{-1}	40.30^{bc} ±1.07	52.23 ^{a} ±0.32	43.54 ^{b} ±2.14	34.39 ^{c} ±1.20	24.53 ^{d} ±0.31
No. of kernels spike^{-1}	74.10 ^{a} ±1.19	63.13^{bc} ±0.13	57.80 ^{c} ±0.17	64.79 ^{b} ±1.51	46.83 ^{c} ±0.36
100-kernel weight	3.24 ^{c} ±0.13	3.56^{bc} ±0.11	3.92^{ab} ±0.12	3.77^{ab} ±0.10	4.00 ^{a} ±0.03
Hybrid 3	**Line-2**	**Sakha-95**			
Plant height	115.00 ^{a} ±0.42	116.17 ^{a} ±0.46	115.33 ^{a} ±0.58	103.68 ^{b} ±0.82	107.80 ^{b} ±0.23
No. of spikes plant^{-1}	23.80 ^{c} ±0.89	33.87 ^{b} ±0.80	27.87 ^{b} ±0.91	18.27 ^{d} ±0.57	21.02^{cd} ±0.20
Yellow rust infection	67.67 ^{a} ±1.06	0.27 ^{c} ±0.13	74.33 ^{a} ±0.92	43.63 ^{b} ±2.66	44.96 ^{b} ±0.82
Grain yield plant^{-1}	21.43 ^{c} ±0.09	52.23 ^{a} ±0.32	34.23 ^{b} ±1.59	32.01 ^{b} ±1.22	33.3 ^{b} ±0.38
No. of kernels spike^{-1}	48.07 ^{b} ±0.21	63.13 ^{a} ±0.13	66.77 ^{a} ±0.13	62.90 ^{a} ±1.24	49.80 ^{b} ±0.35
100-kernel weight	2.62 ^{b} ±0.06	3.56 ^{a} ±0.11	3.64 ^{a} ±0.09	3.58 ^{a} ±0.14	3.68 ^{a} ±0.03

Hybrid1: Shandaweel-1* Misr-1, Hybrid2: Shandaweel-1* Sakha-95 and Hybrid3: Line-2 * Sakha-95.

Means within each row followed by the same letter are not statistically different at 5% level of probability (Duncan 1955).

A comparison of F$_2$'s and F$_3$'s mean with the respective F$_1$'s mean established that only 100-kernel weight in both 2nd and 3rd hybrids for F$_2$'s were not significant. However, F$_3$'s mean with the respective F$_1$'s revealed that plant height recorded observed increase in both 1st and 2nd hybrids and 100-kernel weight in both 2nd and 3rd hybrids.

Generally, results illustrated that parents were selected with large differences to create the desired recombination in the segregated generations. The parental differently responded according to their genetic makeup in most investigated traits. In addition to, the environment had obvious effects on the expression of the studied traits among different generations. These results are in agreement with those obtained by Gebrel *et al.*

(2020), Aglan *et al.* (2020), Yassin and Ghareeb (2019), Abd El-Hamid and Ghareeb (2018) and Koumber and El-Gammaal (2012) for number of spikes plant^{-1}, 100- kernels weight and grain yield plant^{-1}.

Scaling test and gene effects

Results in Table (4) presented the scaling test estimates and gene action parameters of the investigated traits of the three bread wheat hybrids. Estimates of both C and D scaling test were significantly differed than zero within the limits of their standard error for all studied traits in the three crosses, except 100-kernel weight in 1st hybrid, indicating presence of non-allelic interactions. These results pointed to the inadequacy of additive-dominance model to explain the gene effects (Mather and Jinks 1982), and simple additive-dominance model was adequate only for 100-kernel weight in 1st hybrid to estimate the genetic components of variance with free from linkage bias. The getting results are similar to those obtained by Gebrel*et al.* (2020), Aglan *et al.* (2020), Yassin and Ghareeb (2019), Abd El-Hamid and Ghareeb (2018), Al-Bakry*et al.* (2017) and Koumber and El-Gammaal (2012). The simple additive-dominance model was fit to interpret the genetic control for 100-kernel weight in cross (Shandaweel-1* Misr-1). However, other remaining traits/crosses revealed the complexity effects and hence the analysis was further elongated to a digenic interaction.

Gene effects

Gene action and their test of significance of the five parameters described the nature of gene action. The estimated effects for investigated traits varied among the three crosses are in (Table 4). Results indicated that the obtained mean effects of F$_2$ (m) were highly significant for all studied traits in the three wheat crosses, indicating that these traits have quantitative inheritance, which reflect effects due to overall mean plus their fixed loci interactions.

Concerning to the additive component (a), the results were positive and highly significantly for plant height, grain yield plant^{-1} and number of kernels spike^{-1}, in the 1st cross (Shandaweel-1* Misr-1), for yellow rust infection and number of kernels spike-1 in the 2nd cross (Shandaweel-1* Sakha-95) and yellow rust infection in the 3rd cross (Line-2* Sakha-95), indicating the presence of additive gene action. Positive and significant results referred to the importance of additive effect of these traits in the above crosses for selection of superior segregant in breeding program. The additive gene action for yield and yield-traits was reported earlier by many authors (Gebrel et al., 2020, Aglan et al., 2020, Yassin and Ghareeb 2019 and Abd El-Hamid and Ghareeb 2018). Meanwhile, negative and significant values were detected for yellow rust infection in the in 1st cross, number of spikes plant^{-1} and grain yield plant^{-1} in the 2nd cross and number

of spikes plant^{-1}, grain yield plant^{-1}, number of kernels spike^{-1} and 100-kernel weight in the 3rd cross. Negative and significant results indicated that the investigated materials have decreasing alleles for these traits and selection to improve it could be effective especially for yellow rust infection and plant height if shorter genotypes are desired. The results are in accordance with the previous findings of Gebrel et al., (2020), Aglan et al., (2020), Yassin and Ghareeb (2019) and Abd El-Hamid and Ghareeb (2018).

Table 4. Scaling test and gene action parameters of the investigated traits in three bread wheat hybrids.

Traits	Scaling test		Gene actions				
	C	D	m	a	d	aa	dd
Hybrid 1	**Shandaweel-1* Misr-1**						
Plant height	-18.60**	40.50**	109.10**	2.50**	-27.60**	-25.10**	78.80**
No. of spikes plant^{-1}	-9.22**	-11.33**	20.70**	-0.78	6.07**	4.45**	-2.81
Yellow rust infection	-10.08**	60.59**	11.91**	-3.25**	-33.59**	-48.57**	94.23**
Grain yield plant^{-1}	1.47	-67.89**	36.44**	2.33**	41.71**	50.17**	-92.49**
No. of kernels spike^{-1}	-19.41**	-95.22**	63.89**	3.08**	55.70**	66.41**	-101.08**
100-kernel weight	0.29	0.16	3.37**	-0.09	-0.13	-0.25	-0.17
Hybrid 2	**Shandaweel-1* Sakha-95**						
Plant height	-12.03**	50.98**	115.70**	-0.58	-29.74**	-37.16**	84.02**
No. of spikes plant^{-1}	-25.92**	-23.47**	19.74**	-5.83**	7.70**	-0.34	3.26
Yellow rust infection	55.93**	0.56	15.98**	3.34**	5.75**	15.62**	-73.82**
Grain yield plant^{-1}	-42.05**	-63.21**	34.39**	-5.97**	32.40**	23.20**	-28.21**
No. of kernels spike^{-1}	6.32**	-79.51**	64.79**	5.48**	43.24**	65.03**	-114.44**
100-kernel weight	0.43	1.53**	3.77**	-0.16	-0.43**	-1.27**	1.46**
Hybrid 3	**Line-2 * Sakha-95**						
Plant height	-47.10**	-27.90**	103.68**	-0.58	10.50**	9.58**	25.60**
No. of spikes plant^{-1}	-40.33**	-10.13**	18.27**	-5.03**	-0.94	-10.04**	40.27**
Yellow rust infection	-42.07**	24.64**	43.63**	33.70**	16.93**	43.96**	88.95**
Grain yield plant^{-1}	-14.09**	-4.38	32.01**	-15.40**	-2.04	-30.23**	12.96**
No. of kernels spike^{-1}	6.87**	-37.79**	62.90**	-7.53**	37.51**	11.27**	-59.55**
100-kernel weight	0.86**	1.31**	3.58**	-0.47**	-0.18	-1.67**	0.59*

* and ** indicate significant at 0.05 and 0.01 level of probability, respectively.

Regarding to the dominance component (d), it was positive and highly significant for number of spikes plant^{-1}, grain yield plant^{-1} and number of kernels spike^{-1} in the 1st cross, for number of spikes plant^{-1}, yellow rust infection, grain yield plant^{-1} and number of kernels spike^{-1} in the 2nd cross and plant height, yellow rust infection and number of kernels spike^{-1} in the 3rd cross, referring the presence of dominance gene effect for the above mentioned traits in the respective crosses. Dominance gene effects were reported by Gebrel et al., (2020), Aglan et al., (2020), Yassin and Ghareeb (2019) and Abd El-Hamid and Ghareeb (2018). Then, these traits indicated above are controlled mainly by

dominance gene effect, suggesting that improvement by simple selection techniques may not be easy and selection should be delayed for several generations and would be possible exploiting heterosis directly in these hybrids.

It is mentioned that both desired additive and dominance gene effects were presented for number of kernels spike^{-1} in the 1st and 2nd crosses and yellow rust infection and grain yield plant-1 in the 1st cross. The appearance of the additive and dominance gene actions simultaneously confirmed the importance of predominance of both additive and dominance gene effects. These results are in harmony with those obtained by Gebrel et al. (2020), Aglan et al. (2020), Yassin and Ghareeb (2019), Abd El-Hamid and Ghareeb (2018) and Al-Bakry et al. (2017).

Considering the type of additive $\times$ additive (aa) gene effect, results demonstrated that positive and highly significant effects were obtained for number of kernels spike^{-1} in all three crosses, for grain yield plant^{-1} in both 1st and 2nd crosses, for wheat yellow rust infection in both 2nd and 3rd crosses and for plant height and number of spikes plant^{-1} in the 1st cross. Then, selection for these desired traits might be effective for wheat breeding program in early generations. These results are in harmony with those obtained by Gebrel et al. (2020), Aglan et al. (2020), Yassin and Ghareeb (2019), Abd El-Hamid and Ghareeb (2018), Koumber and El-Gammaal (2012) and Zaazaa et al. (2012) for most these traits. On the other hand, the desired negative and highly significant effect was detected for wheat yellow rust infection in the 1st cross.

The dominance $\times$ dominance (dd) as epistatic gene effect was positively significant and highly significant effects for plant height in the all three crosses, for yellow rust infection in both 1st and 3rd crosses, for 100-kernel weight in the 2nd and 3rd crosses and number of spikes plant^{-1} and grain yield plant^{-1} in the 3rd cross. These significant positive results proved the importance of dominance x dominance interactions in the genetic control of these traits. However, the desired negative and significant effects were detected for yellow rust infection only in the 2nd cross. The desired positive or negative results pointed to the importance of the heterosis breeding for the development genetic materials and creation superior populations. These results are in conformity with the findings of Yassin and Ghareeb (2019), Abd El-Hamid and Ghareeb (2018), Koumber and El-Gammaal (2012) and Zaazaa et al. (2012) for most traits.

Generally, the dominance and dominance x dominance epistatic effects were more than additive and additive x additive effects, respectively, indicating the importance of dominance and dominance x dominance with the presence of duplicate epistatic effects in the expression of the most investigated traits in these crosses. These results are in conformity with the findings of Yassin and Ghareeb (2019), Abd El-Hamid and Ghareeb (2018), Al-Bakry et al. (2017) and Al-Naggar *et al.* (2015) who

reported that the effectiveness of selection in later segregating generations in improvement of traits controlled by dominance effects with duplicate epistasis.

Heterosis

Cross combinations mean of different bread wheat traits were tested for the relatively expression to mid-parent heterosis (MP) or best–parent or heterobeltiosis (BP) were shown in Table (4). Results revealed that the desired significant and highly significant positive heterotic effects to mid-parents for Plant height in the both 1st and 2nd crosses if tallest plants were the preference, for 100-kernel weight in the both 2nd and 3rd crosses and for number of kernels spike^{-1} in the 3rd cross. On the other side, the desired negatively significant (MP) heterosis was detected for yellow rust infection in the 2nd cross. Therefore, the 2nd cross can be used in breeding for desired lowest yellow rust infection (resistance) with best 100-kernel weight and number of kernels spike^{-1} in the 3rd. These results are in conformity with the findings of Beche et al., (2013) for number of kernels per spike and Gebrel et al. (2020), Aglan et al. (2020), Yassin and Ghareeb (2019), Abd El-Hamid and Ghareeb (2018) and Zaazaa (2012) for most traits

Regarding heterosis over the best-parent (BP), all the desired significantly positive heterotic effects had the same traits/crosses indications of (MP) heterosis with the same interpretations. These results suggested that dominance direction was toward the best respective parent (partial dominance for the highest parent). Meanwhile, none-desired negative (BP) heterosis values were detected. Therefore, the dominance and/or dominance × dominance effects may be caused the significantly heterotic effect. The results of heterosis indicated that hybrid-vigor is helpful for the wheat production and selection of desirable hybrids among the crosses having (MP) and/or (BP) heterotic effects in the studied traits is the best way to improve the bread wheat grain yield (Gebrel et al., (2020), Aglan et al., (2020), Yassin and Ghareeb (2019), Abd El-Hamid and Ghareeb (2018), Zaazaa et al., (2012) and Memon et al., 2005). Differences in heterosis values might be due to genetic variability of the parents and for the allelic and non-allelic interactions, which can either increase or decrease the expression of heterosis. Even in the absence of epistasis, interaction of multiple alleles at a locus could lead to either positive or negative heterosis (Cress 1966).

With respect to the potence ratio, Table (5) presented that over-dominance effect (which their ratios were larger than unity) for all traits except for number of spikes plant^{-1} in all crosses, grain yield plant^{-1} in both the 2nd and 3rd crosses, plant height in the 3rd cross, yellow rust infection in the 2nd cross and 100-kernel weight in the 1st cross that were recording ratios lower than unity, referring partial dominance effect. Similar results were reported by Hendawy (2003) and Koumber and El-Gammaal (2012). Meanwhile, plant height in the 1st cross recorded ratio equal unity, referring to complete-dominance effect.

Table 5. Heterosis (H_{Mp} and H_{BP}), average degree of dominance $(H/D)^{0.5}$, inbreeding depression percentage (ID %), broad and narrow-sense heritability (h^2_b and h^2_n %) and genetic advance percent (GA %) of the studied traits in three bread wheat crosses.

Traits	Heterosis		PR	ID%	Heritability		GA%
	H_{Mp}	H_{BP}			h^2_b %	h^2_n %	
Hybrid 1	Shandaweel-1* Misr-1						
Plant height	2.22*	4.55*	1.00	5.13	94.36	51.03	27.94
No. of spikes plant^{-1}	0.22	-3.09	-0.06	10.11	73.87	38.28	78.51
Yellow rust infection	83.30**	169.04**	-2.61	36.22	80.43	65.39	252.96
Grain yield plant^{-1}	-10.00**	-15.21**	-1.63	-6.63	69.88	12.54	65.23
No. of kernels spike^{-1}	-6.41**	-10.30**	-1.48	3.88	82.49	27.52	44.16
100-kernel weight	-2.00**	-4.69**	0.71	-3.25	81.16	50.61	80.72
Hybrid 2	Shandaweel-1 * Sakha-95						
Plant height	5.41**	5.94**	-10.71	5.03	97.93	40.09	38.96
No. of spikes plant^{-1}	-12.96**	-27.95**	0.62	19.11	76.61	38.08	77.08
Yellow rust infection	-88.81**	51.63**	-0.96	-3863**	97.62	20.91	269.85
Grain yield plant^{-1}	-5.89*	-16.64**	0.46	21.01	87.58	30.42	99.39
No. of kernels spike^{-1}	-15.76**	-22.00**	-1.97	-12.09	98.05	25.40	74.19
100-kernel weight	15.35**	10.11**	-3.23	3.90*	85.50	54.69	77.40
Hybrid 3	Line-2 * Sakha-95						
Plant height	-0.22	0.29	0.43	10.10	95.81	37.71	24.66
No. of spikes plant^{-1}	-3.35**	-17.72**	0.19	34.44**	73.15	54.42	74.55
Yellow rust infection	118.84**	27430**	1.20	41.30	99.15	53.08	196.90
Grain yield plant^{-1}	-7.07**	-34.47**	0.17	6.49	94.42	51.73	116.82
No. of kernels spike^{-1}	20.08**	5.96**	-1.48	5.79	99.81	39.63	64.18
100-kernel weight	17.74**	2.25**	-1.17	1.60	95.15	20.24	124.64

* and ** indicate significant at 0.05 and 0.01 level of probability, respectively.

Inbreeding depression:

Concerning inbreeding depression percentage (ID %), measured as relatively reduction in F_2's mean compared to F_1's one (Table 5). positively significant and highly significant values were attained for 100-kernel weight trait in the 2nd cross and number of spikes plant^{-1} in the 3rd cross. On the other side, negative inbreeding depression estimate was obtained for yellow rust infection in the 2nd cross, meanwhile the rest of traits over all crosses were non-significant. Detected significant effects for the both heterosis and inbreeding depression appear logic because the expression of heterosis in F_1's was followed by considerable decrease in the F_2's performance. In addition, reduction in values of non-additive genetic components is expected due to homozygosity means by inbreeding. As well as, the conflicting estimates heterosis and

inbreeding depression were associated in some other traits. Similar conclusion was reviewed by Zaazaa et al., (2012) for number of spikes per plant.

Heritability estimates:

The predictive role of quantitative traits is the most important functions of heritability estimates in the genetic studies. Heritability assisted plant breeder to predict the genetic behavior and the response to selection among generations. Both broad (h^2_b %) and narrow-sense (h^2_n %) heritability estimates were illustrated in Table (5). Broad-sense heritability depending on magnitudes of its genetic variance component to phenotypic variance recorded the highest values for number of kernels spike^{-1}, yellow rust infection and plant height among the three studied crosses. However, the highest narrow-sense heritability values were obtained for yellow rust infection in the 1st cross (65.39%), for 100-kernel weight (54.69%) in the 2nd cross and No. of spikes plant^{-1} (54.42%) in the 3rd cross. Moreover, lowest narrow-sense heritability was estimated for grain yield plant^{-1} in the 1st cross, indicating that environmental effect was larger than genetic effect for this trait. Similar approaches of broad-sense heritability estimates were agreed with those obtained by Hammad et al. (2012) for plant height and number of kernels spike^{-1}. On the other side, heritability in narrow-sense results were similar to these obtained by Farshadfar et al. (2013) for plant height and Khattab et al. (2010) for number of spikes plant^{-1} and grain yield plant^{-1}.

Generally, heritability estimates presented a moderate to low narrow-sense heritability for most cases. Results showed the considerable differences between broad and narrow-sense heritability in all crosses, suggesting the responsibility of the dominance gene action for the inheritance of most traits in the studied crosses and delayed selection may be more effective for improving traits of these genotypes.

Genetic advance

Assessment of expected genetic advance provides knowledge of possible advance through selection based on phenotypic values from the ratio of genotypic and phenotypic variance. It is clear that high genetic gain would be associated with heritability that mainly due to additive effects, however low genetic gain due to non-additive (Singh and Narayanan 1993). The expected genetic advance percent estimates for the evaluated traits of the three crosses are shown in Table (5). Results of genetic advance percent of F_2 mean ranged from (24.66) for plant height in 3rd cross to (269.85) for yellow rust infection in the 2nd cross.

It is noticed that plant height recorded the lowest estimates overall the three crosses. Meanwhile, yellow rust infection values were the highest (very huge values over hundred percent) overall crosses that suggested decrease environmental variance

causing increase the degree of correspondence between the genetic components and F_2 variance. Then, the huge genetic components enhanced the high values of genetic advance.

The estimated genetic advances for the remaining traits were high, concluding that selection for these traits would be effective. The highest estimates of genetic advance were coupled with highest narrow-sense heritability for most cases, indicating sufficient variability to improve these traits. These results pointed the possibility of applying selection in early generations for these traits. These results are in general conformity with the findings of Sultan et al. (2011).

F_3 families' differences restriction

Infection to yellow-rust was restricted for sixty F_3 families' populations at the adult plants under field condition. Means comparison of divided groups based on segregating infection types for grain yield and yellow-rust infection in three bread wheat crosses were presented in (Table 6). Results revealed highly significant differences between the sixty F_3 families for grain yield and yellow-rust infection traits in the three studied crosses (Abbasi et al., 2014).

These families' phenotype was characterized into the five infection type's classes. The infection types (IT) were resistant of 0.0 to 20% being R, tolerant, 21 to 40% being T, moderately tolerant 41 to 60% being MT, moderately susceptible 61 to 80% being MS and susceptible 81 to 100% being S. Wheat stripe rust resistance genes were characterized previously by Zhang et al. (2010). The comparison between the different F_3 infection types (IT) showed highly significant differences for resistance to yellow-rust and grain yield/plant in the three studied crosses. These results revealed the genetic variability for resistance to yellow rust caused by *P. striiformis* f. sp. *tritici.* Then, the restricted groups were classified as observed resistant and susceptible with comparing to those predicted by various genetic models for each measure of resistance using Chi-square (χ^2).

In the first cross, the 60 families were classified into 25 families in the 1st group, 22 families in the 2nd group, 10 families in the 3rd group and 3 families in the 4th group. The segregation of (25R+22T+10MT): 3S, counting observed 57R: 3S against suggestion fits an expected (56.25: 3.75) as 15: 1 di-genic ratio with ($\chi^2 = 0.16^{ns}$; $P > 0.689$). The validity of test this model χ^2 test confirmed that families were divided into two groups with good fitness to 15: 1 suggestion ratio, referring to involvement of two genes with duplicative dominant epistatic interaction. These results are in general conformity with the findings of Moozhan Serpoush et al. (2018), Navabi et al. (2003) and Chen and Line (1993).

Table 6. Means comparison of divided groups based on sixty families segregating types for grain yield and yellow-rust infection in three bread wheat crosses.

Cross / Group range	No. of families	R / S ratios	χ^2	Grain yield/plant Range	Mean	Yellow-rust infection Range	Mean
Cross 1 0 – 20 (R)	25			14.46– 46.00	21.72**	0.60 -18.00	10.88**
21 - 40 (T)	22	57 R / 3 S	0.16^{ns}, $P > 0.689$	11.70– 27.40	20.18**	20.91- 38.16	31.36**
41 - 60 (MT)	10			12.19– 22.80	17.80**	41.93- 53.00	44.81**
61 - 80 (MS)	3	15: 1		11.65– 16.70	14.11**	71.69 -72.00	71.90**
81 - 100 (S)	-			-	-	-	-
Mean square differences between families				1637.74**		13447.50**	
F_3 CV%				5.80%		9.70%	
$LSD_{0.05}$				3.64		6.54	
Best 25 families			Family no. 2, 1, 31, 60, 25, 6, 35, 5, 34, 17, 50, 4, 33, 9, 38, 7, 36, 57, 14, 43, 47, 3, 32, 30 and 22.				
Cross 2 0 – 20 (R)	50			14.42– 39.63	26.05**	0.03 – 18.44	5.85**
21 - 40 (T)	9	60 R /0 S		21.13– 38.33	16.58**	21.13 - 38.33	28.22**
41 - 60 (MT)	1		-	20.07	20.07**	42.13	42.13**
61 - 80 (MS)	-	Complete dominant		-	-	-	-
81 - 100 (S)	-			-	-	-	-
Mean square differences between families				1711.00**		4814.20**	
F_3 CV%				6.70%		15.20%	
$LSD_{0.05}$				6.15		4.98	
Best 50 families			Family no. of 6, 14, 47, 13, 2, 60, 49, 58, 15, 34, 12, 53, 51, 7, 33, 16, 40, 52, 32, 50, 57, 4, 46, 21, 39, 10, 38, 11, 45, 56, 5, 54, 8, 44, 1, 59, 37, 17, 55, 31, 43, 27, 42, 41, 18, 22, 36, 25, 26 and 48.				
Cross 3 0 – 20 (R)	21			11.48– 61.44	37.31**	0.01 – 18.64	8.33**
21 - 40 (T)	10	38 R /22 S	1.22^{ns}, $P>0.269$	19.86– 56.41	32.57**	20.85 – 37.79	27.78**
41 - 60 (MT)	7			28.31– 51.29	39.13**	41.42 – 53.40	49.07**
61 - 80 (MS)	7	9: 7		22.05– 31.77	27.18**	60.45 – 76.89	65.49**
81 - 100 (S)	15			14.34– 51.76	28.42**	84.00 – 100.00	96.19**
Mean square differences between families				5483.00**		57470.80**	
F_3 CV%				7.50%		6.40%	
$LSD_{0.05}$				6.75		9.90	
Best 21 families			Family no.46, 40, 1, 45, 7, 48, 56, 57, 47, 53, 15, 41, 12, 54, 5, 24, 19, 6, 30, 32 and 50.				

ns and ** meaning non-significant and highly-significant, respectively.

$P_1 x P_2$: Shandaweel-1* Misr-1, $P_1 x P_3$: Shandaweel-1 * Sakha-95, $P_4 x P_3$: Line-2 * Sakha-95, R: resistant, T: tolerant, MT: moderately tolerant, MS: moderately susceptible and S: susceptible.

However, in the 2nd cross, the observed segregated families were divided into 50 families in the 1st group, 9 families in the 2nd group and 1 family in the 3rd group without any susceptible families. This result demonstrated that the resistance infection type of the all 60 families, indicating to the presence of complete dominant for yellow rust trait.

On the other hand, the 3rd cross recorded 21 families in the 1st group, 10 families in the 2nd group, 7 families in the 3rd group, 7 families in the 4th group and 15 families in the 5th group. The observed ratio of 38R/22S was close to the expected ratio of 33.75: 26.25 for 9: 7 ratios of two segregating loci ($\chi^2 = 1.22^{ns}$; $P > 0.269$).

The best families showed that the 1st group restricted the best desired response for both yellow-rust resistance and grain yield per plant in the three studied crosses as shown in Table (6).

Yellow-rust resistant genes identification among generation

Results presented in Table (7) showed the minimum numbers of genes and Chi-square analysis of segregated generations (F_2 and F_3) plants in the three hybrids between four bread wheat genotypes for yellow rust infection at adult stage under field conditions. Estimates of the minimum numbers of additive genes based on the F_2 and F_3 data in the investigated crosses were between 0.07 and 2.64. Therefore, results revealed that some numbers were in agreement with Mendelian (single locus) and other some 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 Serpoush et al., (2018), Navabi et al., (2003), Chen and Line (1993) and Vanderplank 1984). All the F_1, F_2 and F_3 plants from the various crosses showed differences in their infection types (IT) depending upon their genotype reaction under field conditions. Results showed that all of advanced 250 F_2 and 2700 F_3 segregate plants/cross classified into susceptible (S) and resistant (R) groups with different ratios as shown in Figure (1).

In the wheat cross-1 (Shandaweel-1* Misr-1), all the F_1 plants were moderately resistant (R group) with infection type (18.67 IT). The F_2 population of this cross classified into 168 susceptible IT (S) and 82 resistant IT (R) groups. This result indicated that F_2 plant of this wheat cross segregated to 82 resistant: 168 susceptible (168 S: 82 R), conforming the ratio (3 S: 1 R) that indicated to existence one recessive gene (decreasing resistance ratios), confirming the gene action effect in Table (4) and relationship between generations in Figure (1). The F_2 generation revealed IT (57 S: 193 R) as a segregation ratio (3 S: 13 R) for 2nd cross (Shandaweel-1 * Sakha-95), indicating that there were one dominant RR and one recessive rr gene with complementary interaction (epistatic effect) for resistance as mentioned previously in Table (4). This was in agreement with Chen and Line (1993). Another explanation was existence of one dominant gene for resistance against yellow rust, in the absence of another dominant gene, which interacted with it to cause susceptibility by broken the resistance or inhibiting the effect of the gene (Abu Aly and Abd El-Kreem 2016, Navabi et al., (2003) and Chen and Line (1993).

Table 7. Segregation and Chi-square analysis of F_2's and F_3's of the three crosses, infection types of the four bread wheat genotypes and inheritance mode and numbers of genes for yellow-rust infection.

Generation	Cross	Observed		Expected ratio	Genes no.	χ^2	Inheritance mode genes
		S	R				
F₂ (250 plant)	P_1 (MT) x P_2 (MT)	168	82	3 :1	0.16	0.90[ns] $P> 0.689$	Simple recessive gene (1r*).
	P_1 (MT) x P_3 (R)	57	193	3 : 13	0.10	2.69[ns] $P> 0.752$	Dominant and recessive epistatic (1r, 1d**).
	P_4 (S) x P_3 (R)	154	96	9 : 7	2.09	2.90[ns] $P> 0.148$	Duplicative recessive epistatic (1r, 1d**).
F₃ (2700 plant)	P_1 (MT) x P_2 (MT)	2544	156	15 : 1	0.20	1.03[ns] $P> 0.655$	Duplicative dominant epistatic (2r**).
	P_1 (MT) x P_3 (R)	669	2031	1 : 3	0.07	0.07[ns] $P> 0.791$	Simple dominant gene (1d*).
	P_4 (S) x P_3 (R)	2568	132	61:3	2.64	0.25[ns] $P> 0.104$	Three dominant genes (2r, Id**).

* Mendelian inheritance, ** Epistatic genes effect.
P_1xP_2: Shandaweel-1* Misr-1, P_1xP_3: Shandaweel-1 * Sakha-95, P_4xP_3: Line-2 * Sakha-95, S: susceptible, R: resistant and MT: moderately tolerant.

Meanwhile, F_2 data from the susceptible × resistant in the 3ʳᵈ cross (Line-2 * Sakha-95) revealed frequencies of 154 susceptible and 96 resistant IT, which fitted the expected ratio of 9: 7. This F_2 segregation ratio indicated that presence of two genes for resistance influenced by Sakha-95 as a resistant genotype in this cross. The two resistant genes were interacted with the recessive gene Line-2 genotype as (Duplicate recessive epistasis) to help in appearance the susceptibility against resistance effect (Chen and Line 1993). These results suggested that the resistant genes were different for their response and interaction among genotypes in the studied crosses.

The infection types of the observed F_3 progeny (families) were shown in Table (7) and Figure (1). Cross Shandaweel-1* Misr-1displayed 2544 susceptible plants and 156 resistant plants fitted the theoretical expected ratio of 15: 1 for the presence of two resistance genes, pointing to the presence of duplicative dominant gene action. Meaning, complete dominance at both gene pairs; however, when either gene is dominant, it hides the effects of the other gene. Generation mean analysis in Table (4) also revealed duplicate epistasis for yellow rust resistance in this particular cross.

However, number of susceptible and resistant plants were 669 and 2031, respectively in the Shandaweel-1 * Sakha-95 cross with frequencies fitted the 1: 3 segregation ratio, suggesting that the resistance trait was mono-genically controlled by dominant gene. This dominant resistance may be due to using the resistant parent (Sakha-95) that assisted in the genetic factor's homogeneity.
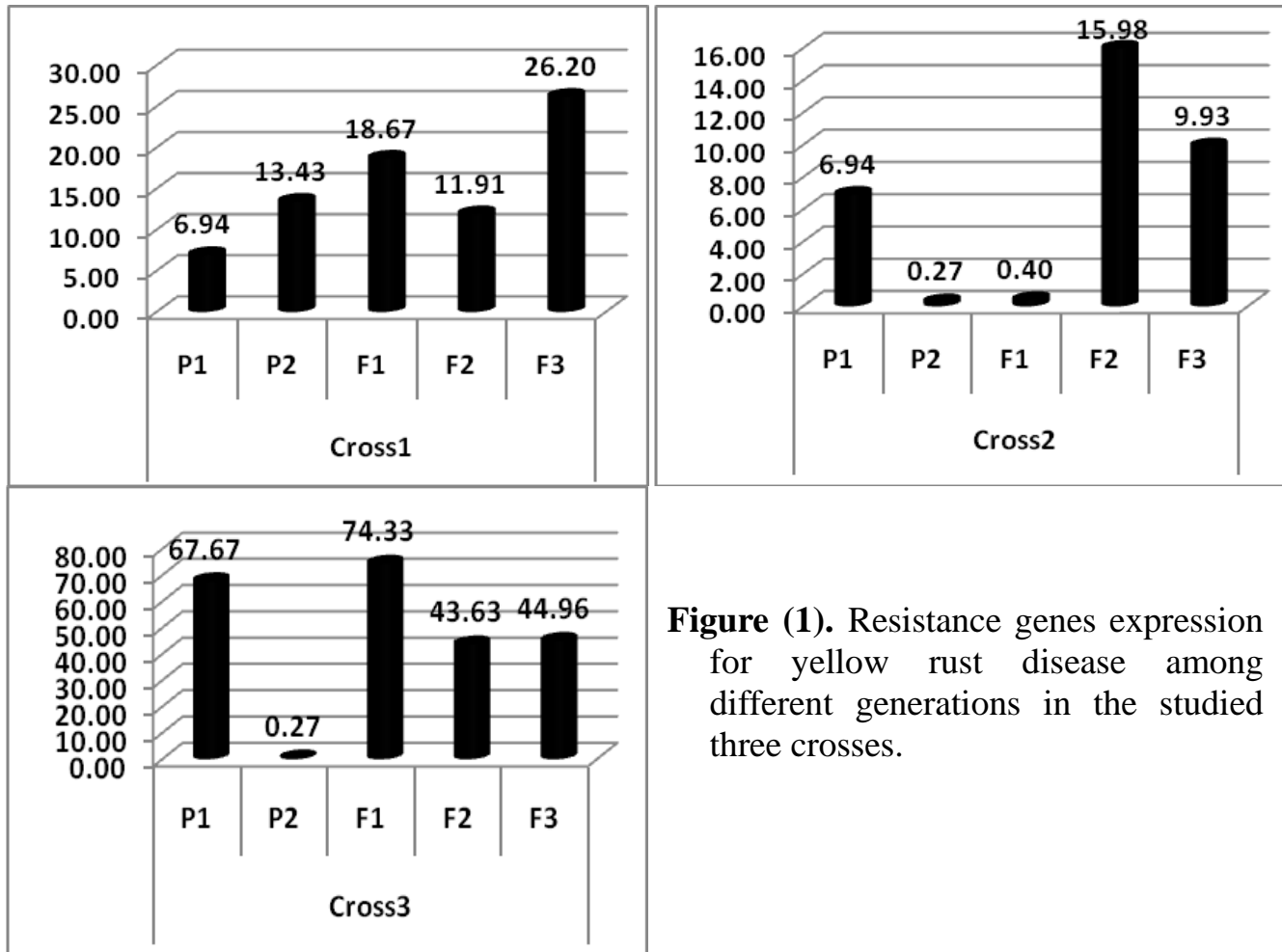
Figure (1). Resistance genes expression for yellow rust disease among different generations in the studied three crosses.

Cross1: Shandaweel-1* Misr-1, Cross2: Shandaweel-1 * Sakha-95, Cross3: Line-2 * Sakha-95 and F_1, F_2 and F_3: the 1st, 2nd and 3rd filial generations, respectively.

On the other side, cross (Line-2 * Sakha-95) displayed segregation ratio of 61: 3 for the observed 2568 susceptible and 132 resistant IT plants, respectively. This segregation ratio indicated that resistance in this cross was controlled by three genes, suggesting that two genes may be recessive and one dominant gene for resistance. The reaction may be that one dominant gene against yellow rust, in the absence of others which interacted with it to cause susceptibility by inhibiting and decrease the effect of the resistance gene. Data from the present study confirmed those results and showed that there are three genes for resistance that were estimated by the Mendelian method of segregation analysis.

The result of fitting the models indicated that epistatic effect was present for yellow-rust infection with differences the significance of gene interactions among the generations of crosses.

The obvious results were agreed with those in Table (4) cross Line-2 x Sakha-95 that referred to dominant resistant x recessive susceptible showed infection types according three genes ratios, confirming the same gene action parameters. Cross Shandaweel-1 (medium tolerant) x Misr-1 (medium tolerant) revealed duplicative the recessives genes interaction to great the appearance of susceptible types. Meanwhile, existence complete dominant in cross Shandaweel-1(medium tolerant) x Sakha-95 (resistant) was cause greatest the resistant alleles among non-allelic interactions.

CONCLUSION

The variability in populations is the basis of progress in the breeding program of a certain crop traits which the desirable traits are heritable in this respect. However, the information of the genetic parameters for parents and their hybrids may be helpful for breeders to identify the best combiners which may be hybridized to build up favorable fixable genes in Egypt. This information offers a great opportunity to improve yield and the resistance inheritance in bread wheat.

The simple additive-dominance model was inadequate to interpret the genetic control for all cases except for 100-kernel weight in cross (Shandaweel-1 x Misr-1). Most cases were controlled mainly by dominance and dominance x dominance gene effect that may be caused the significantly heterotic effect, suggesting that the presence of duplicate epistatic effects in the expression of these traits. Inheritance of resistance to rust-infection depends on the parental genetic background that affects the genetic interaction of cross. The number of genes controlling resistance to yellow-rust disease ranged between one to three genes among different generations. As a general rule, estimated inheritance ratios based on individual plants were best than families ratios for hiding some genetic forms (infection types) behind the dominant infection type of family. This study revealed many inherited ratios types a monogenic inheritance (3: 1) with simple dominance recessive or the opposite. Digenic inheritance with epistatic effects as (3: 13) ratio referred to dominant and recessive, (9: 7) ratio that indicated duplicative recessive and (15: 1) ratio that pointed to duplicative dominant effects. Meanwhile, cross Line-2 x Sakha-95 that referred to dominant resistant x recessive susceptible showed infection types according three genes ratios, confirming the same gene action parameters.

REFERENCES

Abbasi S., A. Baghizade, G. Mohammadi-Nejad and B. Nakhoda(2014). Genetic analysis of grain yield and its components in bread wheat (*Triticum aestivum* L.). Annual Research & Review in Biology 4(24): 3636-3644.

Abd El-Hamid E. A. M, and Zeinab E. Ghareeb (2018). Generation mean analysis for estimating some genetic parameters in four bread wheat crosses. The Seventh Field Crop Conference 8-9 December, ARC, Egypt. 12 - 25.

Abu Aly A. M.A. and Thanaa H. A. Abd El-Kreem (2016). Role of resistance (Yrs) genes to *Puccinia Striiformis* in five bread wheat cultivars susceptible and validation by molecular markers in assessment of resistance. J. Agric. Res. Kafr El-Sheikh Univ. 42(1): 154-168.

Aglan M. A., Eman N. M. Mohamed and A. Shahin (2020). Selection for yield, rust resistance and quality traits in early generations of Giza 171 X Sids 12 cross of bread wheat. J. of Plant Production, Mansoura Univ., 11(3):259 – 266.

Al-Bakry M. R., I. Al-Naggar, Zeinab E. Ghareeb and Samia G. A. Mohamed (2017). Gene effects and interrelationships of spike traits in bread wheat. Egypt. J. Plant Breed. 21(1):85-98.

Allard R. W. (1999). Principles of Plant Breeding, 2nd edition, John Wiley and Sons, New York, USA**.** pp. 254.

Al-Naggar A. M. M., R. Shabana, M. M. Abd El-Aleem and Zainab El-Rashidy (2015). Response of the gene actions governing grain yield and quality traits in wheat parents and their F_1 progenies to decreasing soil-N rate. Annual Research and Review in Biology. 8 (5): 1-16.

Beche E., C. L. Da Silva, E. S. Pagliosa, M. Z. Capelin, J. Franke, G. Matei and G. Benin (2013). Hybrid performance and heterosis in early segregant populations of Brazilian spring wheat. Australian J. Crop Sci.7 (1): 51–57.

Chen X. M. and R. F. Line (1993). Inheritance of stripe rust (yellow rust) resistance in the wheat cultivar Carstens V. Euphytica 71: 107-113.

Cress C. E. (1966). Heterosis of the hybrid related to gene frequency differences between two populations. Genetics, 53: 269-274.

Dehghani H. and M. Moghaddam. (2004). Genetic analysis of the latent period of stripe rust in wheat seedlings. J. Phytopathology 152: 325–330.

Duncan D. B. (1955). Multiple ranges and Multiple F- test. Biometrics 11:1-42.

Eyal Z. (1999). Breeding for resistance to septoria and stagonospora diseases. In: Lucas J. A., Bowyer P. and Anderson H.M. (eds). Septoria of Cereals, a Study of Pathosystems. CAB International, Wallingford, UK, pp. 332-344.

Farshadfar E., M. Farshadfar and J. Sutka (2000). Combining ability analysis of drought tolerance in wheat over different water regimes. Acta Agronomica Hungarica 48: 353–361.

Farshadfar E, F. Rafiee and H. Hasheminasab (2013). Evaluation of genetic parameters of agronomic and morpho-physiological indicators of drought tolerance in bread wheat (*Triticum aestivum* L.) using diallel mating design. AJCS 7(2):268-275.

Gebrel E. M. A., M. N. A. El-Hawary and M. Y. El-Masry (2020). Genetic behavior of some agronomic traits in three bread wheat crosses using five population model. J. of Plant Production, Mansoura Univ., 11(5):413 – 418.

Gomaa M. A., M. N. M. El-Banna, A. M. Gadalla, E. E. Kandil and A. R. H. Ibrahim (2014). Heterosis, combining ability and drought susceptibility index in some crosses of bread wheat (*Triticum aestivum* L.) under water stress conditions. Middle East J. of Agric. Res., 3(2): 338-345.

Hammad S. M., E. H. El-Seidy and M. A. H. Darwesh (2012). Inheritance of yield and its components in some spring wheat crosses. Proc. 13th International Conf. Agron. Fac. of Agic., Benha Univ., Egypt, 9-10 September 2012. 206 - 221.

Hannachi A., Z. Fellahi, H. Bouzerzour and A. Boutekrabt (2013). Diallel-cross analysis of grain yield and stress tolerance-related traits under semi-arid conditions in durum wheat (*Triticum durum* Desf.). Electronic J. Plant Breeding 4 (1): 1027–1033.

Hayman B. I. and Mather K. (1955). The description of genetic interaction in continuous variation. Biometrics 11: 69-82.

Hendawy H. I. (2003). Genetic architecture of yield and its components and some other agronomic traits in bread wheat. Menufiya J. of Agric. Res. 28 (1): 71-86.

Hussain, F.; R. A. Sial and M. Ashraf (2008). Genetic studies for yield and yield related traits in wheat under leaf rust attack. Int. J. Agri. Biol., 10(5): 531–539.

Johnson R., R. H. Priestley and E. C. Taylor (1978). Occurrence of virulence in *Puccinia striiformis* for compare wheat in England. Cereal Rusts Bull. 6: 11–13.

Kema G. H. J. (1992). Resistance in spelt wheat to yellow rust I. Formal analysis and variation for gliadin patterns. Euphytica, 63:207-217.

Khattab S. A. M., R. M. Esmail and A. M. F. AL-Ansary (2010). Genetical analysis of some quantitative traits in bread wheat (*Triticum aestivum* L.). New York Science Journal, 3(11) 152-157.

Koumber R. M. and A. A. El-Gammaal (2012). Inheritance and gene action for yield and its attributes in three bread wheat crosses (*Triticum aestivum* L.). World Journal of Agricultural Sciences, 8 (2): 156-162.

Mather K. and J. K. Jinks (1982). Biometrical Genetics. Great Br. Univ. Press, 3rd ed.

Memon S. M., B. A. Ansari and M. Z. Balouch (2005). Estimation of genetic variation for agroeconomic traits in spring wheat (*Triticum aestivum* L.). Ind. J.Pl. Sci. 4:171-175.

Mohammadi M., S. Ramezanpour, S. Navabpour, H. Soltanloo, M. Kalateharabi and S. Kia (2012). Genetic analysis and heritabilities of resistance to *Mycosphaerella graminicola* in wheat. Crop Breeding Journal 2(1):35-42.

Moozhan Serpoush, Manoochehr Khodarahmi and Farzad Afshari (2018). Inheritance of resistance to stripe rust (*Puccinia Striiformis* f.sp. *Tritici*) race 198E154A+ in wheat cv. Morvarid. Acta Scientific Agriculture 2(7):27-31.

Navabi A., R. P. Singh, J. P. Tewari, and K. G. Briggs (2003). Genetic analysis of adult-plant resistance to leaf rust in five spring wheat genotypes. Plant Disease, 87(12):1522-1529.

Noorka I. R., S. Rehman, J. R. Haidry, I. Khaliq, S. Tabassam and M. Din (2009). Effect of water stress on physico-chemical properties of wheat (*Triticum aestivum* L.). Pak J Botany, 41(6): 2917–24.

Pathan A. K. and R. F. Park (2006). Evaluation of seedling and adult plant resistance to leaf rust in European wheat cultivars. Euphytica 149: 327–342.

Richards R. A., G. J. Rebetzke, A. G. Condon and A. F. Van Herwaarden (2002). Breeding opportunities for increasing the efficiency of water use and crop yield in temperate cereals. Crop Sci., **42**: 111–121.

Saari E. E., and R. D. Wilcoxson (1974). Plant disease situation of high yielding durum wheat in Asia and Africa. Annu. Rev. Phytopathol. 2, 49–68.

Singh R. K. and B. D. Chaudhary (1985). Biometrical methods in quantitative genetic analysis. Kalyani Publisher, New Delhe, Ludhinana, India.

Singh P. and S. S. Narayanan (1993). Biometrical Techniques in Plant Breading. Kalyani Publishers, New Delhe, Ludhinana, India.

Steel R. D. and T. H. Torrie (1960). Principles and procedures of statistic: Mc-Grow-Hill, N.Y., USA.

Sultan M. S., A. H. Abd Elatife, M. A. Abdel-Moneam and M. N. A. El-Hawary (2011). Genetic parameters for some yield and yield components characters in four crosses of bread wheat under two water regime treatments. J. Plant Prod., Mansoura Univ., 2(2): 351-366.

Vanderplank J. E. (1984). Disease Resistance in Plants. Pages 26-27 in: 2nd ed. Academic Press, Inc., London.

Yassin M. M. M. and Zeinab, E. Ghareeb (2019). Genetic behavior of some economic characters in three wheat crosses. Egypt. J. Plant Breed. 23(7):1511–1523.

Zaazaa E. I., M. A. Hager and E. F. El-Hashash (2012). Genetical analysis of some quantitative traits in wheat using six parameters genetic model. American-Eurasian J. Agric. & Environ. Sci. 12 (4):456-462.

Zhan J., C. C. Linde, T. Juergens, U. Merz, F. Steinebrunner, and B. A. McDonald (2005). Variation for neutral markers is correlated with variation for quantitative

traits in the pathogenic fungus *Mycosphaerella graminicola*. Mol. Ecol. 14: 2683–2693.

Zhang H., R. E. N. Zhi-Long, H. U. Yin-Gang, W. A. Chang-You and J. I. Wan-Quan (2010). Characterization of wheat stripe rust resistance genes in Shaanmai 139. Acta Agronmicacinica, 36:109-114.