Inheritance of Stripe Rust Resistance in Adult Plants and Some Economic Traits of Some Bread Wheat Crosses

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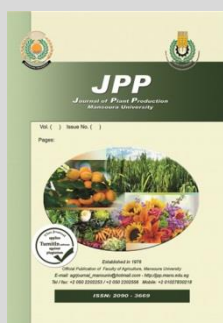
ABSTRACT

The experimental field work was conducted at Gemmeiza and Sakha Agricultural Research Stations, (ARC), Egypt, in 2017/18, 2018/19 and 2019/20 seasons to study the genetic behavior of grain yield and yellow rust resistance in three bread wheat crosses. The Genetic materials included (P_1, P_2, F_1, F_2, BC_1 and BC_2) of Gemmeiza 11× Giza168 (cross 1), Sids12 × Shandaweel1 (cross 2) and Gemmeiza 12 × Shandaweel 1 (cross 3). Significant differences were observed among most genotypes for measured traits. Additive gene effects were negative and highly significant in the first and the third crosses for No. days to maturity and grain yield plant^{-1} and in the second cross for No. spikes plant^{-1}. However, it was positive and highly significant in the second cross for 100-kernel weight, yellow rust resistance and grain yield plant^{-1}. Narrow sense heritability was ranged from moderate to high values for plant height, yellow rust resistance and No. kernels spike^{-1} in all studied crosses. These results could be employed to improve both yield and rust resistance in Egyptian wheat breeding program.

Keywords: Wheat, disease resistance, stripe rust, gene action, grain yield

INTRODUCTION

Wheat (*Triticum aestivum* L.) is the most important crop in Egypt and in the world. In Egypt, there is a serious gap between wheat production and consumption. Therefore, the Egyptian breeding program is interesting to develop high-yielding cultivars to improve wheat production.

The losses of wheat yield due to stripe rust is a severe problem in wheat cultivated regions in the world and Egypt (Fu *et al*., 2008). In Egypt, there were decreasing in wheat yield in the years 1967, 1986, 1995, 1997, 1999 and 2015 caused by yellow rust disease (Abd El-Hak *et al*., 1972 and Omara *et al*., 2018).

Comprehensive understanding the genetic performance of bread wheat resistance to rusts is essential point in breeding for improvement of resistance (El-Seidy *et al*., 2017a). Generally, there were one, two or a few number of genes controlling the resistant to different diseases like rusts (Shahin and Ragab, 2015). Moreover, the resistance was dominant in most cases over susceptibility (Patil *et al*. 2000), while the susceptibility was dominant in few cases over dominant (Ganeva *et al*. 2001). As reported in many studies, additive gene action plays important role in inheritance of this trait. On the other hand, other studies reported that dominance and /or epistasis gene actions were more important in controlling this trait (Sharshar, 2015, Kalim *et al*., 2016, El-Seidy *et al*., 2017a and Shehab-Eldeen and Abou-Zied 2020).

Consequently, the present study was conducted to study the genetic behavior of resistance to yellow rust and grain yield and its components in some bread wheat crosses.

MATERIALS AND METHODS

This study was conducted at Gemmeiza and Sakha Agricultural Research Stations, Agricultural Research Center (ARC), Egypt, during seasons 2017/18, 2018/19 and 2019/20. Three crosses derived from five wide diverse parental bread wheat cultivars and differed in their reaction to stripe rust were used i.e., (I) Gemmeiza 11 × Giza 168, (II) Sids 12 × Shandaweel 1 and (III) Gemmeiza 12 × Shandaweel 1.The name of five Egyptian bread wheat cultivars, pedigree and cross name of the five wheat cultivars are listed in Table (1).

Table 1. Name and pedigree and cross name of the used five bread wheat parents.

Genotype	Pedigree and cross name	Reaction to stripe rust
Gemmeiza 11	BOW"S"/KVZ"S"//7C/SERI82/3/GIZA168/SAKHA61 CGM7892-2GM-1GM-2GM-0GM	Susceptible (S)
Giza 168	MRL/ BUC// SERI CM 93046-8 M-OY-OM-2Y-OB-OGZ	Resistant (R)
Sids 12	BUS//7C//ALD/5/MAYA74/ON//1160.147/3/BB/ GLL/4/CHAT"S"/6/MAYA/VUL//CMH74A.630/4*SX. SD7096-4SD-1SD-1SD-0SD	Susceptible (S)
Shandweel 1	SITE/MO/4/NAC/TH.AC//3*PVN/3/MIRLO/BUC. CMSS93 B005 67S-72Y-010M-010Y-010M-3y-OM-0HTY-0SH	Susceptible (S)
Gemmeiza 12	OTUS/3/SARA/THB//VEE CMSS97YOO227S-5Y-010M-010Y-010M-2Y–1M-0Y-OGM	Moderate Susceptible (MS)

The first and second seasons were conducted on the Experimental Farm of Gemmeiza Agricultural Research Station. In 2017/18 growing season, the used parents were crossed to produce F_1 seeds. In 2018/19 season, for each cross the hybrid seeds of the two back crosses (BC_1 and BC_2) and F_2 were obtained. In season 2019/20, the six populations (P_1, P_2, F_1, BC_1, BC_2 and F_2) of each cross were evaluated using a randomized complete block design with three replications in the Experimental Farm of Sakha Agriculture Research Station, Egypt as a hot spot of stripe rust infection. Each replicate consisted of 20 rows (each row was 4 m length, 30 cm apart and grains were 20 cm apart), one row for each of P_1, P_2 and F_1, three rows for each of BC_1 and BC_2 and nine rows for F_2. Moreover, two border rows were sown high susceptible cultivar (Morocco) used as spreader rows and to avoid the border effects.

Data were recorded for P_1, P_2 and F_1 on 30 individual guarded plants, for BC_1 and $BC_2$120 plants and for F_2 300 plants for each collected cross from the three replications. The studied data were: (1) number of days to maturity (DM), (2) plant height, cm (PH), (3) number of spikes plant^{-1} (S/P), (4) number of No. kernels spike^{-1} (K/S), (5) 100-kernel weight in grams (100-KW) and (6) grain yield plant^{-1} in grams (GY). The recommended field practices for bread wheat production were applied in all growing seasons in the two sites.

The analysis of variance was performed using randomized complete block design and LSD were calculated to test the significance of differences among means according to Steel *et al.* (1997).The scaling tests A, B and C and the gene effects were calculated according to Mather (1949) and Hayman and Mather (1955).The six parameters model developed by Gamble (1962) was used to determine the different gene effects. Likewise, heritability in broad and narrow senses were calculated as described by Mather (1949) and the predicted genetic advance under selection was calculated as described by Johnson *et al.* (1955).

Heterosis was determined as the percent of the deviation of F_1 hybrids over its better parent (BP), and inbreeding depression was estimated as the average percentage decrease of the F_2 from the F_1 were calculated according to Mather and Jinks (1971). Potence ratio (P) was calculated as described by Peter and Frey (1966).

Disease filed evaluation

The infection types for stripe rust (YR) were recorded as disease severity according to the scale given by Stakman *et al.* (1962) resistant (R), moderately resistant (MR), moderately susceptible (MS) and susceptible(S). The rust reaction frequency distribution was performed for the six populations of the three crosses under natural field conditions.

The quantitative analysis was calculated from the field response which converted into an average coefficient of infection (ACI) using the method of Stubbs *et al.* (1986). An average coefficient of infection was obtained by multiplying the percentage of disease severity by infection type (0 = immune, R = 0.2, MR = 0.4, X = 0.6, MS = 0.8 and S = 1). The original data of yellow rust were transformed taking square root to decrease the value of variance.

The Chi-square test (χ^2) and corresponding probability (P) values was calculated to test and determine the difference between observed and expected ratios in F_2 populations of stripe rust reactions (Steel *et al.*, 1997).

RESULTS AND DISCUSSION

Mean performance and variance for six populations of the studied wheat crosses are illustrated in Table (2). Means of the six populations significantly differed in most studied characters, indicating to genetic variability for statistical-genetic analyses. Similar results were detected by Elmassry and El-Nahas (2018) and Sharshar and Genedy (2020).

The mean of F_1 population were higher than the best parent in most crosses for most traits, which indicated a high heterotic effect. Also, the F_1 mean was higher than the mid parents mean for K/S and GY at cross 1 and cross 3 respectively, this reflect the presence of partial dominance towards the better parent. However, F_1 plants mean values were less than the better parent in cross 3 for 100kw and K/S, indicating the importance of over dominance component of genetic variance.

In F_2 mean values were higher than the F_1 in most investigated crosses, indicting the importance of the additive genetic component of genetic variance. However, the F_2 mean values were less than the F_1mean for GY at the three crosses, showing the importance of non-additive component of genetic variance. These results are in accordance with Abd El-Rahman (2013). The means of obtained F_2 generation for grain yield were intermediate between the two parents and less than the F_1 mean value in the three crosses, suggesting quantitatively inheritance.

In general, the means of BC_1 and BC_2 were nearly close to those of corresponding parents in most cases (Hammam, 2013, Sharshar and Esmail, 2019 and Shehab-Eldeen and Abou-Zeid, 2020).

The lowest genetic variance components were obtained by the parents and their F_1 because of the homogeneity of such populations, therefore represent the environmental variances (Shehab-Eldeen and Abou-Zeid, 2020).

Gene action

At least, one of the scales A, B and C tests was significant, indicating to non-allelic interaction (epistasis) and validity of six population model. Gene effects of the three studied crosses are shown in Table (3). All the studied crosses showed highly significant mean effects (m) for all traits, indicating quantitative inheritance. These findings are in accordance with Elmassry and El-Nahas (2018) and Sharshar and Genedy (2020).

Additive gene effects were negative and highly significant in cross 1 and cross 3 for No. days to maturity and grain yield plant^{-1} and in cross2 for No. spikes plant^{-1}, respectively. Meanwhile, it was positive and highly significant in cross Sids 12 x Shandaweel 1 for 100-kernel weight and grain yield plant^{-1}.These results suggest the possibility of using pedigree selection for these cases. Similar results were obtained by Patel *et al.* (2018), Sharshar and Esmail (2019) and Shehab-Eldeen and Abou-Zeid (2020).

The dominance effects (d) were positive and significant for grain yield plant[-1], No. spikes plant[-1]and plant height in most crosses and negative and highly significant for No. days to maturity and 100-kernel weight in cross 2 and cross 3. These results showed the important role of additive and dominance effects for No. days to maturity and 100-kernel weight and selection would be effective in late generations. Similar results were observed by Abd El-Hamid and Ghareeb (2018).

Table 2. Means ($\bar{\chi}$) and variances (S^2) of six parameters populations of three Egyptian bread wheat crosses for the studied traits.

Genotype		Parameter	DM, day	PH, cm	S/P	K/S	100-KW, g	GY, g plant-1
Gemmeiza 11×Giza168	P$_1$	$\bar{\chi}$	151.03	110.17	16.53	63.37	4.97	28.29
		S^2	1.17	16.35	8.19	18.72	0.12	13.74
	P$_2$	$\bar{\chi}$	154.5	105	23.3	60.08	5.53	46.09
		S^2	1.47	17.24	5.73	19.44	0.17	15.06
	F$_1$	$\bar{\chi}$	153.6	109.67	18.33	60.37	4.92	36.52
		S^2	1.35	17.13	5.61	12.31	0.13	18.79
	F$_2$	$\bar{\chi}$	157.28	110.9	15.52	57.73	5.03	25.0
		S^2	31.72	267.58	107.65	298.95	2.2	302.52
	BC$_1$	$\bar{\chi}$	156.76	115.21	17.94	55.25	4.59	28.69
		S^2	26.66	162.77	94.64	242.24	1.84	264.7
	BC$_2$	$\bar{\chi}$	154.84	110.17	19.41	55.76	4.28	35.61
		S^2	24.89	217.62	88.18	261.9	1.94	277.02
	LSD 0.05		1.02	1.40	2.93	5.31	0.53	5.95
Sids 12 × Shandaweel 1	P$_1$	$\bar{\chi}$	146.07	89.83	14.23	52.97	4.23	9.44
		S^2	0.55	12.9	6.12	11.07	0.15	14.71
	P$_2$	$\bar{\chi}$	154.6	115.17	19.97	58.03	4.75	53.12
		S^2	1.14	24.97	6.52	13.9	0.17	14.73
	F$_1$	$\bar{\chi}$	152.37	110.33	23.33	58.83	4.4	55.1
		S^2	1.18	13.68	7.33	11.52	0.14	19.11
	F$_2$	$\bar{\chi}$	155.66	116.4	22.11	62.82	5.05	32.21
		S^2	27.84	193.18	101.14	349.18	2.01	221.23
	BC$_1$	$\bar{\chi}$	152.42	110.17	21.48	62.59	5.34	53.87
		S^2	25.3	133.59	88.79	271.55	1.81	204.07
	BC$_2$	$\bar{\chi}$	155.77	112.08	24.66	62.45	4.92	35.84
		S^2	24.31	132.6	85.1	278.48	1.83	179.37
	LSD 0.05		0.74	1.62	2.83	4.95	0.47	5.95
Gemmeiza 12 ×Shandaweel 1	P$_1$	$\bar{\chi}$	152.73	110.67	23.1	61.43	4.69	40.46
		S^2	1.58	18.51	7.3	10.6	0.12	14.08
	P$_2$	$\bar{\chi}$	154.6	115.17	19.97	58.03	4.75	53.12
		S^2	1.14	24.97	6.52	13.9	0.16	14.73
	F$_1$	$\bar{\chi}$	154.13	120.17	24.03	52.53	4.15	43.66
		S^2	1.91	30.14	7.41	15.02	0.16	17.37
	F$_2$	$\bar{\chi}$	155.82	126.03	16.21	60	5.09	26.78
		S^2	29.3	242.41	99.66	326.94	2.34	265.07
	BC$_1$	$\bar{\chi}$	151.54	115.33	20.78	61.83	4.93	27.09
		S^2	24.84	188.12	87.52	278.16	1.93	221.93
	BC$_2$	$\bar{\chi}$	156.23	120.25	20.53	56.3	4.5	32.45
		S^2	25.25	154.56	75.24	259.72	1.98	233.6
	LSD 0.05		1.12	3.35	1.81	6.98	0.41	4.57

Table 3. Scaling test and gene effects for the studied traits in the   studied wheat crosses.

Character	Cross	A	B	C	m	a	d	aa	ad	dd
DM, day	1	8.88**	1.58	16.40**	157.28**	1.92**	-5.10**	-5.93**	3.65**	-4.53
	2	6.40**	4.57**	17.23**	155.66**	-3.35**	-4.23*	-6.26**	0.92	-4.71
	3	-3.78**	3.72**	7.67**	155.82**	-4.68**	-7.27**	-7.73**	-3.75**	7.8**
PH, cm	1	10.58**	5.67	9.10*	110.90**	5.04**	9.23**	7.15	2.46	-23.4**
	2	20.17**	-1.33	39.93**	116.40**	-1.92	-13.27**	-21.1**	10.75**	2.27
	3	-0.17	5.17	37.97**	126.03**	-4.92**	-25.72**	-32.97**	-2.67	27.97**
S/P	1	1.02	-2.82	-14.43**	15.52**	-1.47	11.05**	12.63**	1.92	-10.83
	2	5.40**	6.02**	7.56**	22.11**	-3.18**	10.09**	3.86	-0.31	-15.27**
	3	-5.58**	-2.93	-26.31**	16.21**	0.24	20.29**	17.79**	-1.33	-9.27
K/S	1	-13.23**	-8.93**	-13.24**	57.73**	-0.51	-10.27	-8.92	-2.15	31.08**
	2	13.38**	8.03*	22.63**	62.82**	0.14	2.12	-1.21	2.68	-20.21*
	3	9.70**	2.03	15.47**	60.00**	5.53**	-10.93	-3.73	3.83	-8.00
100KW, g	1	-0.70**	-1.89**	-0.24	5.03**	0.31	-2.68**	-2.35**	0.59**	4.95**
	2	2.05**	0.69*	2.41**	5.05**	0.42*	0.24	0.33	0.68**	-3.07**
	3	1.00**	0.09	2.60**	5.09**	0.43*	-2.08**	-1.51**	0.46*	0.42
GY, g plant[-1]	1	-7.43*	-11.4**	-47.42**	25.00**	-6.92**	27.92**	28.59**	1.98	-9.75
	2	43.21**	-36.54**	-43.91**	32.21**	18.03**	74.40**	50.58**	39.87**	-57.25**
	3	-29.95**	-31.88**	-73.78**	26.78**	-5.36**	8.82	11.95*	0.97	49.88**

Cross 1:Gemmeiza 11 × Giza168, cross 2:Sids 12 x Shandaweel 1 and cross 3:Gemmeiza 12 x Shandaweel 1). *, ** significant at 5% and 1% probability levels, respectively. m = mean, a: additive, d: dominance, aa: additive × additive, ad: additive × dominance, dd: dominance × dominance effects.

Moreover, positive and significant additive × additive (aa) epistatic gene effects were observed for spikes number plant[-1] and grain yield plant[-1] in three crosses. Positive and highly significant additive × dominance (ad)

gene effects were determined in most crosses for most characters. Meantime, highly significant negative (ad) effects were exhibited in the third cross for No. days to maturity.

Furthermore, significant and positive dominance × dominance (dd) interallelic interaction were obtained in cross 1 for No. kernels spike[-1] and 100-kernel weight and cross 3 for No. days to maturity, plant height and grain yield plant[-1], indicating that the inheritance of these traits was affected by the duplication effect of epistatic genes. Similar results were given by Sheikh *et al.* (2009). Generally, the additive and additive × additive effects were more important than dominance gene effect for most studied traits in the three crosses. These results are in general agreement with Elmassry and El-Nahas (2018) and Sharshar and Genedy (2020).

Table (4) showed negative and high significant better parent heterosis to for the No. days to maturity and the plant height in the cross 1 and cross 2. Desired positive and significant better parent heterosis were reported for No. of spikes plant[-1], plant height and No. kernel spike[-1] in cross 3, plant height in cross 1 and No. kernel spike[-1]in cross 2 and 3. These results showed that the dominance regulation was toward the best parents. These results were similar to those of Abd El-Hamid and Ghareeb (2018) and Shehab-Eldeen and Abou-Zeid, 2020).

Table 4. Heterosis (%), inbreeding depression %, heritability and genetic advance for the studied traits in Gemmeiza 11× Giza168, Sids 12 × Shandaweel 1 and Gemmeiza 12 × Shandaweel 1 crosses.

Characters	Crosses	Heterosis BP%	Inbreeding depression %	h² b	h²n	Ga %
	Cross 1	1.7**	-2.4**	95.79	37.48	2.76
DM, day	Cross 2	4.31**	-2.16**	96.36	21.76	1.52
	Cross 3	0.92**	-1.09**	94.41	29.05	2.08
	Cross 1	4.44**	-1.12	93.66	57.84	17.58
PH, cm	Cross 2	22.82**	-5.5**	91.56	62.21	15.30
	Cross 3	8.58**	-4.88**	89.30	58.63	14.92
	Cross 1	-21.32**	15.36**	94.16	30.17	41.56
S/P	Cross 2	16.86**	5.26**	93.25	28.07	26.30
	Cross 3	4.04**	32.57**	92.82	36.69	46.55
	Cross 1	-4.73**	4.36**	94.75	31.36	19.35
K/S	Cross 2	1.38**	-6.78**	96.56	42.48	26.03
	Cross 3	-14.49**	-14.21**	95.83	35.48	22.03
	Cross 1	-11.08**	-2.14**	93.82	28.48	17.31
100KW, g	Cross 2	-7.43**	-14.73**	92.65	19.16	11.10
	Cross 3	-12.62**	-22.52**	93.62	33.08	20.49
	Cross 1	-20.75**	31.55**	94.51	20.92	29.99
GY, g plant[-1]	Cross 2	3.72**	41.54**	92.35	26.68	25.38
	Cross 3	-17.81**	38.66**	94.01	28.15	35.25

*, ** significant at 5% and 1% probability levels, respectively.

Inbreeding depression, measures the reduction of F_2 population due to inbreeding. In general, values of inbreeding depression were positive and highly significant in all crosses for the No. spikes plant[-1], No. kernels spike[-1] and grain yield plant[-1]. Meanwhile, it was negative and highly significant for No. days to maturity, plant height and 100-kernel weight in all crosses. These results are in line with those reported by Koumber and El-Gammaal (2012), Zaazaa *et al.* (2012) and Shehab-Eldeen and Abou-Zeid, 2020).

Broad sense heritability values were higher than the corresponding narrow sense heritability, suggesting the existence of non-additive gene action. Broad sense heritability values were high in all crosses for all studied traits and ranged from 89.3% for plant height in cross 3 to 96.56% for No. kernels spike[-1] in the cross 2.

The heritability estimates in narrow sense ranged from moderate for plant height and No. kernelsspike[-1] to low in all crosses for No. days to maturity, 100-kernel weight and grain yield plant[-1], explaining the presence of non-additive gene action. These results are in line with El-Seidy *et al.* (2017b).

The expected genetic advance from selection for all traits in all crosses is presented in Table (4).The highest genetic advance values were observed for No. spikes plant[-1] (46.55%) in cross 3 and plant height (41.65%) in cross 1. Meanwhile, the low genetic advance values were obtained for No. days to maturity (1.52%) in cross 3. These results are in line with Abd El-Fattah and Mohammad (2009) and Abd El-Hamid and Ghareeb (2018).

Inheritance mode of yellow rust (YR) resistance

For the cross (1) Gemmeiza 11 (S) × Giza 168 (R), data of yellow rust reaction as average coefficient of infection (ACI) is illustrated in Table (5) and Figure (1).The two parental means were significantly differed in their reaction to ACI. The reaction to yellow rust ranged from 5.5 to 1 in Gemmeiza 11 with an average of 3.72 and from 1 to 0.3 in Giza 168 with an average of 0.34. It was noticed that Gemmeiza 11 and Giza 168 had distinctly non-over lapping ranges. The parental line Giza 168 was more resistant than Gemmeiza 11.

The F_1 mean value was very close or shifted toward the susceptible parent Gemmeiza 11, where their values were 3.15 for F_1 and 3.74 for Giemmaza11, suggesting partial dominance toward the high parent mean or toward susceptibility parent .

Support to the inheritance of yellow rust reaction as average coefficient of infection could be shown by the segregation of BC_1 plants. They segregated into two classes with a ratio of 87.5 -12.5%. The first class was distributed within the range of P_1 (toward susceptibility parent), while the second class was distributed within the range of P_2 (low infection type or more resistant to yellow rust. This means that the ratio 3:13 was confirmed by the chi- square test (χ^2), as shown in Table (5). This is expected when the character is controlled by single or two pair of genes and receives of

high infection types or toward the susceptibility to rust.

All plants of BC_2 were resistant except 26 were distributed within the range of F_1 and P_1 without any segregation. This is expected when the character is controlled by single or two pair of genes dominance and receives of low value to resistance or toward the resistant to rust.

The means of F_1 and F_2 populations were significantly differed; the F_2 mean (3.35) was higher than F_1 mean (3.15).It might be due the small sizable magnitude of segregation effects in the F_2 generation. The expected ratio when the character is controlled by additive gene effects was 9: 7 in F_2 with ($\chi^2 = 0.31$; $P> 0.58$).

This segregation ratio indicated the presence of two genes for resistance, suggesting duplicative recessive epistatic effect of genes responsible inheritance of resistant to yellow rust. Meanwhile, expected ratios recorded 3: 13with ($\chi^2 = 03.08$; $P> 0.08$) and 13: 3 with ($\chi^2 = 0.67$; $P> 0.41$) for$_{BC1}$ and BC_2, respectively. These results indicated the presence of dominant and recessive epistatic in the direction of susceptible parent and direction of resistant parent for$_{BC1}$ and BC_2, respectively.

Regarding to cross (2) Sids 12(S) × Shandaweel 1(S), the data of yellow rust reaction as average coefficient of infection are presented in Table (5) and illustrated in Figure (2).

The mean of the two parents were not significantly different in their reaction to yellow rust, the reaction in Sids 12 was6.16 and in Shandaweel 1 with an average of 4.39, as shown in Table (5). It was noticed that both the parental genotypes Sids 12 and Shandaweel1were susceptible to yellow rust disease.

The F_1 mean was relatively decreased outside (low

severity) the tow-parent mean value, they were 4 and 2, respectively, suggesting over dominance toward resistance, indicating that the effects of additive genes are involved in the inheritance of this character.

Variances of the non-segregating populations, i.e., P_1, P_2 and F_1 differed, indicating that the environmental variance varies considerably among different genotypes. However, they showed the least variations comparing with the segregating populations as shown by the lowest C.V. % values; this indicates that they are more homogeneous than the F_2, BC_1 and BC_2 populations which had greater variances, these results support that the inheritance of yellow rust reaction as average coefficient of infection could be shown by the segregation of BC_1 plants.

The F_2 population segregated into two classes with a ratio of 61.0: 39.0 %. The first class was distributed within the range of P_1 and P_2 while the second class distributed out of the range of both parents and F_1 populations. This ratio was fit a 7: 9 ratio using χ^2 test with 0.07 and probability 0.79, suggesting the duplicative recessive epistatic effect of genes responsible inheritance of resistant to yellow rust. Expected ratio 1: 3 with ($\chi^2 = 1.60$; $P > 0.21$) was obtained in BC_1, indicating to one gene ratio, however ratio 1: 1 with ($\chi^2 = 0.13$; $P> 0.72$) in BC_2, indicating to test cross progenies.

All plants of BC_2, divided into two equal groups were distributed within the range ousted two parents (low value to resistance or toward the resistant to rust). This is expected when the character is controlled by two independent genes and recessive of resistant to yellow rust.

For cross Gemmeiza12 (MS) × Shandaweel 1 (S), data of yellow rust reaction as average coefficient of infection is illustrated in Table (5) and Figure (3).
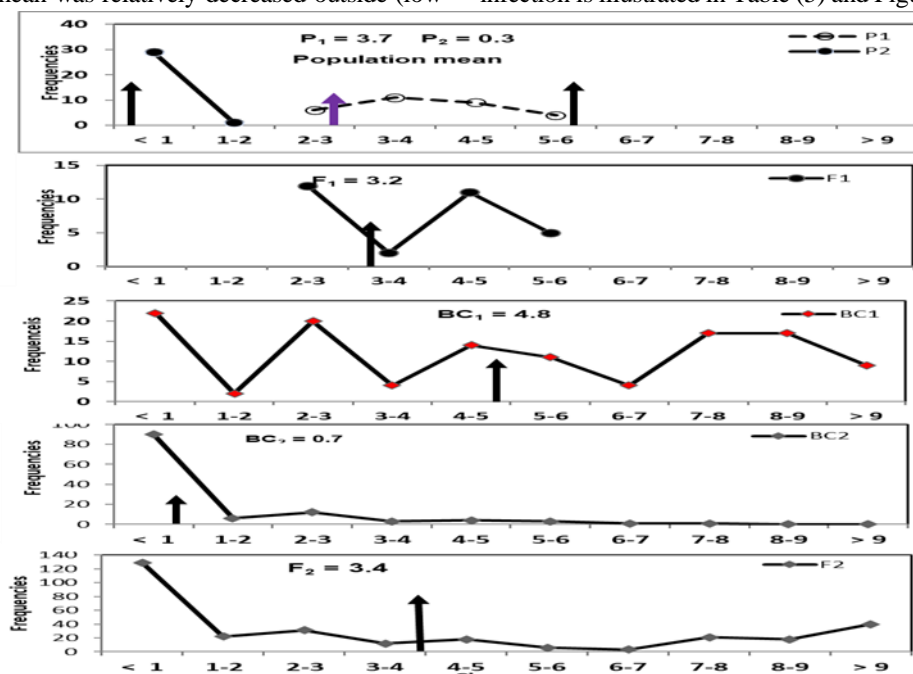

Figure 1. Distribution of stripe rust reaction as average coefficient of infection in parental and hybrid population of the wheat cross Gemmiza11×Giza168
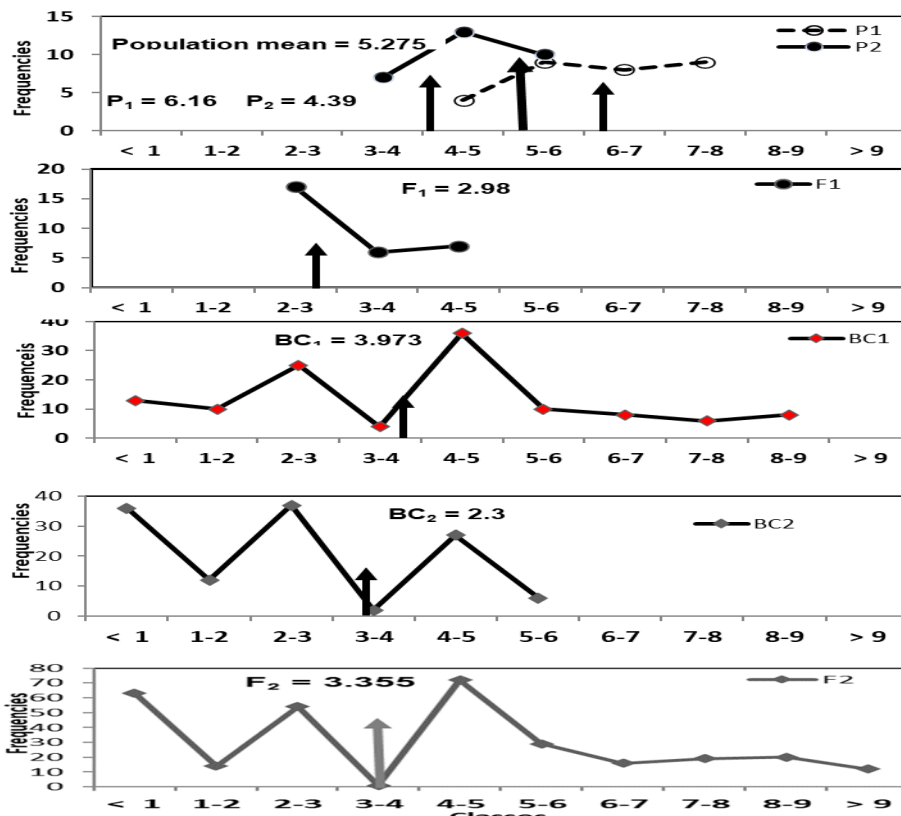
Figure 2. Distribution of stripe rust reaction as average coefficient of infection in parental and hybrid populations of the wheat cross Sids12 × Shandaweel 1.
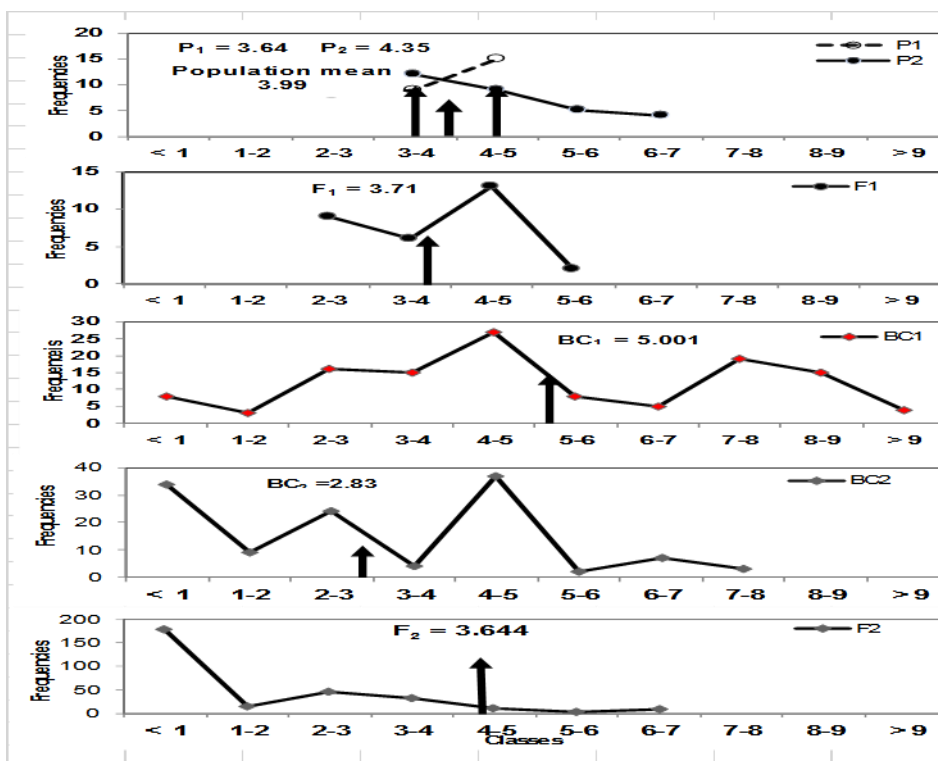

Figure 3. Distribution of stripe rust reaction as average coefficient of infection in parental and hybrid populations of the wheat cross Gemmeiza12 × Shandaweel 1.

The two parental means differed insignificantly in their reaction to yellow rust. The reaction to yellow rust ranged from 4.9 to 2 in Gemmeiza 12 with an average of 3.65 and in Shandaweel 1 was 4.35 as shown in Table (5).

The parental line Gemmeiza 12 was more resistant than Shandaweel 1.

The F_1 mean value was very close or shifted toward the resistant parent Gemmeiza 12, where their values were

3.71 for F_1 and 3.65 for Gemmeiza 12, suggesting partial dominance toward the low parent mean or toward resistant parent. The segregation of BC_1 plants segregated into two classes with a ratio of 16.6:83.3%. The first class was distributed within the range of P_1, while the second class was distributed within the range of P_2 and F_1populations. In general, in the four generations most resistant crosses were generated from two or at least one resistant parent.

Table 5. Segregation ratio and chi square (χ2) analysis of yellow rust for BC_1, BC_2 and F_2 plants from the attempted three crosses between five parents .

Crosses	Parents/ generations	No. of resistant plants	No. of susceptible plants	Total plants tests	% of resistant plants	% of susceptible plants	Expected Ratio R:S	χ2	P. Value
Cross 1 (Gemmeiza 11× Giza168)	Gemmeiza 11	0	30	30	0	100.0	Mean.3.72		
	Giza 168	30	0	30	100	0	Mean.0.34		
	F1	0	30	30	0	100.0	Mean.3.15		
	BC1	15	105	120	12.50	87.50	3 : 13	3.08	0.08
	BC2	94	26	120	78.33	21.67	13:3	0.67	0.41
	F2	164	136	300	54.67	45.33	9 : 7	0.31	0.58
Cross 2 (Sids 12 x Shandaweel 1)	Sids 12	0	30	30	0	100.0	Mean.6.16		
	Shandaweel 1	0	30	30	0	100.0	Mean.4.39		
	F1	0	30	30	0	100	Mean.0.14		
	BC1	36	84	120	30.00	70.00	1:3	1.60	0.21
	BC2	58	62	120	48.33	51.67	1 : 1	0.13	0.72
	F2	129	171	300	43.00	57.00	7 : 9	0.07	0.79
Cross 3 (Gemmeiza 12 x Shandaweel 1)	Gemmeiza 12	0	30	30	0	100.0	Mean.3.65		
	Shandaweel 1	0	30	30	0	100.0	Mean.4.39		
	F1	0	30	30	0	100.0	Mean.3.71		
	BC1	20	100	120	16.67	83.33	3 : 13	0.34	0.56
	BC2	53	66	119	44.54	55.46	7 : 9	0.03	0.86
	F2	185	115	300	61.67	38.33	9 : 7	3.58	0.06

(P_1) Gemmeiza 11 (S), (P_2) Giza 168 (R), (P_3) Sids 12 (S),(P_4) Shandaweel 1 (S) and (P5) Gemmeiza 12 (MS).7: 9complimentary recessive genes and 9: 7complementary dominant genes.

Results presented in Table (5) showed the Chi-square analysis of segregated generations (F_2, BC_1 and BC_2) plants in the three crosses between four bread wheat cultivars for yellow rust infection at adult stage (APR) under natural field conditions. In wheat cross-1 (Gemmeiza 11× Giza168), all the F_1 plants were susceptible with infection type (3.2). The F_2 population of this cross classified into 45.33% susceptible (S) and 54.67% resistant (R) groups. This result indicated that F_2 plants of this wheat cross segregated to 164 resistant: 136 susceptible plants, conforming the ratio of (9 R: 7 S). The F_2 segregating ratio indicated that the presence of two genes controlling the resistance to stripe rust influenced by Giza 168 as a resistant genotype in this cross. The two resistant genes were interacted with the recessive gene Gemmeiza 11 genotype as (Duplicative recessive epistatic (1d, 1r). to help in appearance the susceptibility against resistance effect (Chen and Line 1993). These results suggested that the resistance genes were different for their response and interaction among genotypes in the studied cross which indicated the existence of one or two recessive gene (decreasing resistance ratios). The BC_1 generation revealed infection type (IT)15R: 105S as a segregation ratio (3R: 13S) for cross (Gemmeiza 11× Giza168), indicating that there were two recessive gene pairs found to be conferring resistance, as mentioned previously in Table (5). In contrast, the BC_2 received a double dose from Giza 168 (R) parent, which led to an increase in the resistance (low infection types) rate, which revealed IT (94R: 26S) as a segregation ratio (13R: 3S), indicating that there were one dominant RR and one recessive rr gene with complementary interaction (epistatic effect) for resistance.

Meanwhile, F_2 data from the susceptible × susceptible in the 2nd cross (Sids 12 x Shandaweel 1)

revealed frequencies of 171 susceptible and 129 resistant IT, which fitted the expected ratio of 9S: 7R. This F_2 segregation ratio indicated that presence of two genes for resistance influenced by Shandaweel 1as a resistant genotype in this cross. The two resistant genes were interacted with the recessive gene Sids 12 genotype as (Duplicate recessive epistasis) to help in appearance of 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 cross.In the BC_1 for cross (Sids 12 x Shandaweel 1), all the F_1 plants were moderately resistant (R group) with infection type (2.98 IT). The BC_1 population of this cross classified into 84 susceptible IT (S) and 36 resistant IT (R) groups. This result indicated that BC_1 plants of this wheat cross segregated to 36resistant: 84 susceptible (84 S: 36 R), conforming the ratio (3S: 1R) that indicated to existence one recessive gene (decreasing resistance ratios).

The F_2 data from the 3rd cross (Gemmeiza 12 (Ms) × Shandaweel 1(S) revealed frequencies of 115 susceptible and 185 resistant IT, which fitted the expected ratio of 9: 7. This F_2 segregation ratio indicated that presence of two genes for resistance might be contributed from Gemmeiza 12 as a resistant cultivar in this cross. The two resistant genes were interacted with the recessive gene Shandaweel1 as (Duplicate recessive epistasis) to help in appearance of 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 tested crosses. The BC_1 generation revealed IT (20R: 100S) as a segregation ratio (3R: 13S) indicating that there were two recessive gene pairs found to be conferring resistance as mentioned previously in Table (5).

Average coefficient infection (ACI) mean and variances for wheat stripe rust.

The mean of the studied parents, F_1's and segregating population of the obtained three crosses with respect to yellow rust is given in Table (6).The wheat stripe rust data revealed that F_1plants mean values stand between P_1 and P_2 mean values in two crosses, showed partial dominance for the susceptibility and resistance in the first and second crosses, respectively. While, in cross 3 susceptibility was over dominated resistance.

However, the F_2 mean values for filed stripe rusts data in the second and third crosses was less than the mid parent exhibit partial dominance towards the resistant parent. Meantime, the third cross was higher than the mid parent showing partial dominance in direction to the susceptible parent Sharshar and Esmail (2019).

Generally, means of the $BC_1$and BC_2were in direction to those of their corresponding parents for yellow rust reactions in the cross 1 and cross 3.On the other hand, BC_1's and BC_2's means value was less than the tow parents toward resistances of yellow rust. Similar results were obtained by Al-Naggar *et al.* (2012), Hammam (2013) and Sharshar and Esmail (2019).

Table 6. Means and variances (S^2) of P_1, P_2, F_1, F_2, BC_1 and BC_2 of the three bread wheat crosses for the yellow rust.

Character	Crosses	parameter	P1	P2	F1	F2	BC1	BC2
Yellow rust (YR)	C-1	$\overline{x}$	3.72	0.34	3.15	3.35	4.85	0.83
		S^2	0.15	0.16	0.14	13.61	9.23	10.9
	C-2	$\overline{x}$	6.16	4.39	2.98	3.91	3.97	2.36
		S^2	0.19	0.19	0.15	7.85	5.32	5.96
	C-3	$\overline{x}$	3.65	4.39	3.71	1.82	5.08	2.87
		S^2	0.14	0.19	0.2	11.6	7.94	8.65

The highest values of variance were showed in F_2 population, followed by the backcrosses for all crosses. In contrast, the lowest variance magnitude was displayed by parents and F_1 plants due to the homogeneity of these populations and represent the environmental variances (Sharshar and Esmail, 2019 and Shehab-Eldeen and Abou-Zeid, 2020).

Estimation of the type of gene action:

At least, one of the scales A, B and C tests was significant, showing the presence of non-allelic interaction (epistasis) and the validity of six-parameter model. Gene effects calculated from the generation mean analysis of the three wheat crosses for the yellow rust are presented in Table (7).

The studied crosses showed highly significant mean effects for yellow rust resistance, indicating that these characters were quantitatively inherited. These results are similar to Sharshar (2015), El-Seidy *et al.* (2017a) and Sharshar and Esmail (2019).

Table 7. Scaling tests and gene effects for yellow rust resistance in the studied wheat crosses.

Character	Crosses	A	B	C	m	a	d	aa	ad	dd
Yellow rust (YR)	C 1	2.82**	-1.84**	3.05**	3.35**	4.02**	-0.95	-2.07	2.33**	1.1
	C 2	-1.2**	-2.65**	-0.87	3.91**	1.61**	-5.27**	-2.98**	0.73*	6.83**
	C 3	2.81**	-2.37**	-8.17**	1.82**	2.22**	8.3**	8.61**	2.59**	-9.05**

*and **= significant at 0.05 and 0.01 probability levels, respectively

Additive gene effects were positive and high significant in all crosses for stripe rust resistance, indicating that selection could be achieved in early generations.

Additive genetic variance (a) was higher than the corresponding dominance one (d) for yellow rust resistance in cross 1 and cross 2, indicating that pedigree method would be more useful. Moreover, the dominance effects were higher than additive one for in cross 3, indicating that dominance gene effects play akey role and selection through advanced generations using bulk method or modified bulk method would be useful in this cross.These results are in line with those of Al-Naggar and Shehab-Eldeen (2012) and Sharshar and Esmail (2019).

The dominance (d) effects were negative and highly significant only in cross2 for yellow rust resistance.

Negative and highly significant additive × additive gene effects were only showed in cross2 for yellow rust resistance. In contrast, positive and significant additive × dominance (ad) gene effects were resulted in the cross 3. Moreover, positive and significant gene effects caused by the third type of interallelic interaction (dominance × dominance) (dd) exhibited in cross2 for yellow rust resistance. These results are line with those obtained by Kalim *et al.* (2016), El-Seidy *et al.* (2017a), Khilwat *et al.* (2019) and Sharshar and Esmail (2019).

Heterosis, Inbreeding Depression and Potence Ratio

Favorable heterosis percentages for resistance to yellow rust those with negative signs or better parent. Table (8) showed negative and high significant better parent heterosis in the cross 2, even-though it was positive and high significant in cross 1 and cross 3. Potence ratio values were less than unity with positive signs in the first and third crosses for yellow rust resistance indicating the presence of partial dominance.

Table 8.Better parent Heterosis (%) (BP), inbreeding depression (ID %) and potence ratio (PR) for yellow rust resistancein thestudied wheat crosses.

Character	Crosses	Potence ratio	Heterosis BP%	Inbreeding depression %
Yellow rust (YR)	C 1	0.66	829.75**	-6.42**
	C 2	-2.59	-32.05**	-31.09**
	C 3	0.84	1.66**	50.89**

*and **= significant at 0.05 and 0.01 probability levels, respectively

On the other side, potence ratio values were more than unity for yellow rust resistance in cross 2, showing the presence of over dominance governing the inheritance in this trait. The obtained results are matching with those of Hammam (2013), Abd El-Aty *et al.* (2014), El-Seidy *et al.* (2017b) and Sharshar and Esmail (2019).

Generally, inbreeding depression values were negative and highly significant in cross 1 and cross 3 for

yellow rust resistance. Meantime, it was positive and highly significantin cross 3.Similar results were reported by Zaazaa *et al.* (2012), Abd El-Rahman (2013) and Sharshar and Esmail (2019).

The average degree of dominance, heritability and percentage of genetic advance

The average degree of dominance $(H/D)^{1/2}$ is presented in Table (9). Results revealed values more than unity for yellow rust resistance, indicating the presence of over-dominance towards the better parent and early selection might improve this trait. Similar results were obtained by Abd- El Rahman (2013) and Abd El-Hamid and Ghareeb (2018).

Estimates of heritability in broad sense were high for stripe rust resistance in all crosses, suggesting that the phenotypic variability was mostly attributed to genetic impact.These findings were consistent with Cheruiyot *et al.* (2014), Kalim *et al.* (2016), Reena *et al.* (2018) and Sharshar and Esmail (2019).

Table 9. Heritability in broad (h^2b) and narrow (h^2n) sensesand expected genetic advance for yellow rust resistance in the studied wheat crosses.

Character	Crosses	$h^2 b$	h^2n	Δg	Δg %
Yellow rust (YR)	C 1	98.91	52.08	3.96	117.99
	C 2	97.82	56.17	3.24	82.88
	C 3	98.44	56.92	3.99	219.14

*, ** significant at 5% and 1% probability levels, respectively.

On the other side, heritability approximate in narrow sense were moderate to high for yellow rust resistance for all studied crosses, exhibiting the importance of additive gene action. These results were in the same line with Khilwat *et al.* (2019) and Sharshar and Esmail (2019).

It is worthy to note that the expected genetic advance (Δg) estimates for wheat stripe rust, in the three obtained crosses were high, indicating that selection in segregated population would be useful for improving yellow rust resistance. Similar results were obtained by Abd El-Aty *et al.* (2014).

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وراثة المقاومة للصدأالأصفرفي طور النبات البالغ وبعض الصفات الاقتصادية في بعض هجن قمح الخبز

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أجريت هذه الدراسة خلال ثلاث مواسم شتوية من 2017/20 إلى 2019/20 بمزرعة محطة البحوث الزراعية في كل من الجميزة وسخا ـ مركز البحوث الزراعية ـ مصر لدراسة وراثة محصول الحبوب ومقاومة الصدأ الأصفر في ثلاث هجن من قمح الخبز. تم تقييم العشائر الستة عشائر من الهجن جيزة168 × جميزة (هجين رقم 1)، سدس12 × شندويل 1 (هجين رقم 2) وجميزة12× شندويل 1 (هجين رقم 3). وقد أظهرت النتائج فروق معنوية بين كل التراكيب الوراثية في كل الصفات في الهجن الثلاثة. أظهرت النتائج أن الفعل الجيني المضيف كان معنويا وموجبا إلى عالي المعنوية وسالب لصفة عدد الأيام حتى النضج وعدد الفروع للنبات ومحصول الحبوب في الهجين الأول والثالث؛ في حين كان معنويا وموجبا لصفات وزن 100 حبة ومحصول النبات ومقاومة الصدأالأصفر في الهجين الثاني. كانت درجة التوريث بالمعنى الضيق متوسطة إلى مرتفعة لصفات طول النبات ومقاومة الصدأ الأصفر وعدد حبوب السنبلة في الهجن الثلاثة. وبالتالي يمكن توظيف هذه النتائج لتحسين محصول الحبوب، ومقاومة مرض الصدأ الأصفر في البرنامج المصري لتربية للقمح.