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# Quantitative Studies on Resistance to Stripe and Stem Rust Diseases and on Grain Yield of Bread Wheat

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This work was carried out at the Experimental Farm of Sakha Agricultural Research Station, Kafr El-Sheikh, Egypt, during the three growing seasons 2013/14, 2014/15 and 2015/16, to estimate types of gene action controlling the inheritance of wheat resistance to stripe and stem rust diseases as well as to study the inheritance of grain yield character. Genetic materials used in this study included six populations (P1, P2, F1, F2, BC1 and BC2) of two bread wheat crosses namely, (Sakha 95 X Shandaweel 1) and (Sakha 95 X Sids 13). Results revealed that additive (a) was higher in magnitude than dominance (d) variance for all characters. The most predominant type of epistasis was additive X additive (aa) for both diseases; stripe and stem rust resistance. The values calculated for heritability in broad sense were high, while for narrow sense heritability values were moderate to relatively high for the two crosses in all studied characters. Both crosses are promising and higher in magnitude, which had high genetic advance associated with high heritability estimates were detected. Therefore, these two crosses would be useful in breeding programs for improving the studied characters.

Keywords: wheat, Yellow Rust, Stem Rust, Six Populations, Gene Action, Heritability

## **INTRODUCTION**

Wheat (*Triticum aestivum* L.) is the most important cereal crop in Egypt as well as in many countries. Egypt has a big gap between wheat production and consumption. Therefor, the main goal of the Egyptian breeding program is to increase yield production by developing high-yielding new cultivars through important processes and technics. One of these processes is reducing crop losses by breeding cultivars resistant to diseases, especially the most critical wheat diseases; stripe and stem rusts, caused by *Puccinia striiformis* and *Puccinia graminis tritici*, respectively.

Grain yield losses due to stripe rust disease are very high in many countries all over the world, including Egypt (Omara et al. 2018). Wheat stripe rust in Egypt is considered to be a destructive disease, and it caused significant yield losses under severe epidemics. Understanding the genetic behavior of wheat resistance to the two diseases is critical for deciding the breeding method that maximizes the genetic improvement of resistance. (Shehab El-Din et al. 1991 and El-Seidy et al. 2017 a). In many studies, wheat resistance to rusts was described as a simple inherited character affected by one, two or a few number of genes, (Shahin and Ragab 2015) and (El-Seidy et al. 2017 a). On the other side, many investigators reported that resistance is a quantitative character governed by many genes affected by the prevailing environmental conditions. (Shehab El-Din et al. 1991, Yadav and Narsinghani, 2000, Sharshar, 2015 and El-Seidy et al. 2017 a). In addition, resistance was dominant over susceptibility in most cases, (Shehab El-Din and Abd El-Latif, 1996 and Patil et al. 2000), while the vice versa was true in other studies, (El-Fadly et al. 1991 and Ganeva et al. 2001). Moreover, some cases best fit the simple additive genetic model, while, dominance and / or epistasis were more effective and had important role on the genetic behavior of this

trait, (Sharshar, 2015, Kalim Ullah1 et al. 2016 and El-Seidy et al. 2017 a).

The main objectives of this research were to: 1). Study the genetic behavior of wheat resistance to stripe and stem rust diseases, 2). Study inheritance of grain yield character, and 3). Detecting plant resistance to stripe and stem rusts to be grown through advanced generations to develop improved and advanced wheat cultivars.

# MATERIALS AND METHODS

The field work was conducted at Sakha Experimental farm, Agricultural Research Center (ARC), Egypt, during the three seasons from 2013/14 to 2015/16 to study the genetic behavior of wheat resistance to stripe and stem rust diseases as well as genetics of the grain yield character.

In the first season, 2013/14 the new wheat cultivar Sakha 95 was crossed to both Shandweel 1 and Sids 13. The names, pedigrees and cross name of the three wheat genotypes are presented in Table 1.

In the second season (2014/15), the  $F_1$  hybrid seeds of each cross were separately sown to produce  $F_1$  plants and part of these plants were backcrossed to each of their respective parents. Seeds of the two backcrosses (BC<sub>1</sub> and BC<sub>2</sub>) were obtained. The rest of  $F_1$  plants were self-pollinated to get  $F_2$  plants.

In the final season (2015/16), the obtained seeds from the plants of the six populations i.e.,  $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$ ,  $BC_1$  and  $BC_2$  for the two crosses were planted in randomized complete blocks design (RCBD) experiment with three replications. Each experimental plot consisted of (one row for each of  $P_1$ ,  $P_2$  and  $F_1$ , four rows for each of  $BC_1$  and  $BC_2$  and nine rows for  $F_2$  plants). Moreover, two border rows were sown with a mixture of high susceptible wheat varieties for the two diseases as spreader to get high inoculum for both diseases (Morocco, *Triticum spelta sahariensis* 'TSS', Thatcher and Max) to be used as trap nursery

\* Corresponding author. E-mail address: drmostafa\_tag@yahoo.com DOI: 10.21608/jpp.2020.122667 and source of inoculum to detect infection. Each row was 4 m long spaced 30 cm apart and grains were 20 cm apart.

The experiment was surrounded by a mixture of cultivars highly susceptible to both diseases as a trap nursery to help in the natural and artificial inoculations. The artificial inoculation for stem rust was carried out at the third week of March in the early evening (at sunset) using a mixture of

fresh urediniospores for the most prevalent pathotypes and talcum powder at a rate of 1:25 (w/w) and dusted at booting stages. The inoculation of all wheat plants was carried out at booting stage according to the method of (Tervet and Cassell 1951). Meanwhile, the artificial inoculation for stripe rust was not carried out because it is forbidden in the open fields and it was under natural infection.

Table 1. Names, pedigrees and cross name for three bread wheat genotypes.

Parent	Genotype Name	Pedigree and Selection History
1	Sakha 95	PASTOR // SITE / MO /3/ CHEN / AEGILOPS SQUARROSA (TAUS) // BCN /4/ WBLL1.
1		CMA01Y00158S-040POY-040M-030ZTM-040SY-26M-0Y-0SY-0S.
2	Shandweel 1	SITE/MO/4/NAC/TH.AC//3*PVN/3/MIRLO/BUC
		CMSS93B00567S-72Y-010M-010Y-010M-3Y-0M-0HTY-0SH
3	Sids 13	KAUZ"S"//TSI/SNB"S".
		ICW94-0375-4AP-2AP-030AP-0APS-3AP-0APS-050AP-0AP-0SD.

#### Data recorded

For evaluation experiment of the six populations, data were recorded on 45 individual guarded plants for  $P_1$  and  $P_2$ , 35 plants for  $F_1$ , 75 plants for each of  $BC_1$  and  $BC_2$  and 300 plants for the  $F_2$  for each cross collected from all replications. The following characters were recorded:

## Stripe and Stem rusts diseases assessment

The infection types for stripe and stem rusts were recorded and estimated as disease severity using the method of (Stakman *et al.* 1962) in which resistant (R), moderately resistant (MR), intermediate (M), moderately susceptible (MS) and (S) susceptible.

## Grain yield / plant (GY/P) in g:

It was recorded by weighing the grains of each individual plant.

Data were collected from the selected plants in each cross for stripe rust, stem rust resistance and for grain yield/plant.

The quantitative analysis of field response was applied by converting the average coefficient of infection (ACI) following the method of (Stubbes *et al.* 1986) and modified by (Shehab El-Din and Abd El-latif 1996). In this method, an average coefficient of infection was determined by multiplying infection severity with an assigned constant values namely, 0.05, 0.1, 0.2, 0.4, 0.6, 0.8 and 1 for 0, 0;, R, MR, M, MS and S infection types, sequently, (Abou-Zeid *et al.* 2018 a).

Heterosis was calculated as the deviation percent of  $F_1$  hybrid over its mid-parent (MP) and better parent (BP) estmates.

Inbreeding depression was also calculated as the average percentage decrease of the  $F_2$  from the  $F_1$ . Moreover, potence ratio (P) was also determined according to (Peter and Frey 1966).

The population means and the variances were used to detect the scaling tests A, B and C and to determine the type of gene effects using the method of (Mather 1949 and Hayman and Mather 1955).

In addition, the six parameters model applied by (Gamble 1962) was followed to estimate the different gene effects. Moreover, heritability in broad and narrow senses were using the method of (Mather 1949) and the predicted genetic advance under selection was also estimated according to (Johnson *et al.* 1955).

# RESULTS AND DISCUSSION

Means and variances of  $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$ ,  $BC_1$  and  $BC_2$  populations of the two wheat crosses for the two rusts and for yield characters are presented in Table (2).

For stripe disease rust the data show that  $F_1$  generation mean values lie between  $P_1$  and  $P_2$  mean values in the two crosses, indicating partial dominance for the susceptibility and resistance in the two crosses, respectively. On the other hand, for stem rust, the same reaction was true, in cross II, while in cross I susceptibility was completely dominance resistance. The  $F_1$  mean values for grain yield surpassed the mid values of the two parental means in both crosses indicating that presence of partial dominance towards the better parent.

Table 2. Means (X<sup>-</sup>) and variances (S<sup>2</sup>) of the six studied populations of the two wheat crosses for diseases reactions and grain yield.

	<del>                                  </del>							
Charac-ter	Cross	Statistical parameter	P <sub>1</sub>	$P_2$	$\mathbf{F}_{1}$	$\mathbf{F}_2$	BC <sub>1</sub>	BC <sub>2</sub>
Stripe Rust	Sakha 95 X Shandaweel 1	X-	0.03	0.22	0.17	0.55	0.15	0.93
		$S^2x^-$	0.02	0.04	0.04	3.45	0.10	3.71
	Sakha 95 X Sids 13	X-	0.03	20.29	5.37	2.97	2.25	3.95
		$S^2x^-$	0.02	0.48	1.12	40.89	20.61	27.67
Stem Rust	Sakha 95 X Shandaweel 1	X-	4.02	1.02	4.66	4.98	2.49	3.90
		$S^2x^-$	3.02	0.02	1.29	33.19	18.16	20.02
	Sakha 95 X Sids 13	X-	4.02	0.02	1.43	2.90	3.74	1.17
		$S^2x^-$	3.02	0.01	1.70	22.18	21.49	6.76
Grain Yield	Sakha 95 X Shandaweel 1	X-	40.10	32.04	37.00	35.54	40.66	33.42
		$S^2x^-$	23.50	18.91	31.21	322.50	284.52	220.08
	Sakha 95 X Sids 13	X-	40.10	25.98	35.60	30.16	33.62	27.48
		$\mathrm{S}^2\mathrm{x}$	23.50	19.63	24.60	221.26	204.58	162.65

Means of  $F_2$  generation were higher than the two parents in cross I (Sakha 95 X Shandaweel 1) for stripe and stem rusts, indicating overdominace towards the susceptible parent. On the other hand, the  $F_2$  mean value for stripe rust in cross II was less than the mid parents indicating partial

dominance towards the resistant parent. Meanwhile, it was higher than the mid parent for stem rust in cross II improving the presence of partial dominance towards the susceptible parent. These results are in accordance with those obtained by (Al-Naggar *et al.*, 2010) and (Sharshar and Esmail 2019).

In addition, means of F<sub>2</sub> generation for grain yield were intermediate and less than the F<sub>1</sub> mean values in both crosses indicating that this character is quantitatively inherited. These results are in harmony with the results obtained by (Sharshar and Esmail 2019).

Generally, BC1 means were close to those of their respective female parents while and BC2 means were close to their respective male parents (P2's) for all rusts reactions and grain yield of both crosses, except for stem rust in the first cross. Similar results were reported by (Gad 2010, Al-Naggar et al. 2012, Hamam 2013 and Sharshar and Esmail 2019).

The highest magnitude of variance was stated by the F<sub>2</sub> generation for the three studied characters followed by those of backcross generations, except for one case in (Sakha 95 X Shandaweel 1) for stripe rust. Mianwhile, the lowest variance magnitude was detected by parents and F<sub>1</sub> populations. These results are in harmony with those obtained by (Al-Naggar and Shehab-Eldeen 2012 and Sharshar and Esmail 2019).

#### Gene effects

Regarding to the scaling test as presented in table (3) showed that at least one of the scales A, B and C tests was significant, proving the presence of (epistasis) and indicating that using the six parameter model to detect different genetic

components was valid for the two wheat crosses and studied characters.

The two crosses exhibited highly significant mean effects (m) for the studied characters indicating that these characters were quantitatively inherited. These results are in harmony with those of (Hendawy 1998, Afiah 1999, El-Hosary et al. 2000, Sharshar 2015, El-Seidy et al. 2017 b and Sharshar and Esmail 2019).

Additive gene effects were highly significant negative and significant negative in cross I for stripe rust and stem rust diseases, respectively. Meanwhile, it was positively and highly significant in the second cross for stem rust. Therefore, practicing selection for the resistance could be started from early generations. The obtained results are in harmony with those of Gad (2010), Al- Naggar and Shehab-Eldeen (2012) and Sharshar and Esmail (2019).

For grain yield, positively significant values were found in both crosses Sakha 95 X Shandaweel 1 and Sakha 95 X Sids 13. This reflects the enhancing effect of type of the additive gene action in the inheritance of such character. These results are in agreement with those reported by (Al-Naggar and Shehab-Eldeen 2012, Hamam 2013, Patel et al. 2018 and Sharshar and Esmail 2019).

Table 3. Estimates of scaling tests and gene effects for three studied characters in the two wheat crosses.

Charac-ter	Cross -	Scaling test			Type of gene action					
Cnarac-ter		A	В	С	(m)	(a)	(d)	(aa)	(ad)	(dd)
Stripe Rust	Sakha 95 X Shandaweel 1	0.1	1.48**	1.62**	0.55**	-0.78**	0	-0.04	-0.69**	-1.53
	Sakha 95 X Sids 13	-0.91	-17.75**	-19.2**	2.97**	-1.71*	-4.24	0.55	8.42**	18.11**
Stem Rust	Sakha 95 X Shandaweel 1	-3.69**	2.11*	5.58**	4.98**	-1.4*	-5.02*	-7.16**	-2.9**	8.74**
	Sakha 95 X Sids 13	2.03	0.89	4.71**	2.9**	2.57**	-2.39	-1.79	0.57	-1.12
Grain Yield	Sakha 95 X Shandaweel 1	3.38	-3.05	-9.82*	34.5**	7.24**	11.92	10.15	3.21	-10.49
	Sakha 95 X Sids 13	-8.78*	-6.62*	-16.66**	30.16**	5.98**	3.81	1.26	-1.08	14.15

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

The estimates of dominance (d) effects were significant and negative only in the cross I for stem rust trait, suggesting that dominance gene effects were important in the inheritance of resistance traits in this cross. Negative and highly significant additive X additive (aa) gene effects were detected only in cross I for stem rust. On the other side, positively highly significant additive X dominance (ad) gene effects were estimated in the second cross for stripe rust. Meanwhile, highly significant negative (ad) effects appeared in first cross for stripe rust and stem rust. In addition, positively and significant gene effects due to dominance X dominance (dd) appeared in second cross for stripe rust and in first one for stem rust, reflecting enhancing effects due to (dd) type of epistasis in the inheritance of resistance in these crosses. Results also showed that epistasis played an important role in the inheritance of resistance of stripe and stem rusts, while it was not important in grain yield. These results are coincide with these reported by (Al-Naggar and Shehab-Eldeen 2012, Kalim Ullah1 et al. 2016, El-Seidy et al. 2017 b, Khilwat et al. 2019 and Sharshar and Esmail 2019).

#### Heterosis, inbreeding depression and potence ratio:

Favorable (desirable) heterosis percentages for resistance traits those with negative signs to mid-parent and / or better parent.

For stripe rust, Table 4 illustrates that negatively highly significant heterotic effects relative to better parent were detected in the two crosses, while it was negative comparing to mid-parent in the second cross only.

For stem rust, the negative and highly significant heterotic values over both mid and better parents were detected in the second cross, while positive values (undesirable) were found in the first cross. This means that resistant plants could be detected in early generation. Therefore, practicing selection for resistant genotypes could be effective in early generations.

On the other side, highly significant positive heterotic values relative to mid parents were found in both crosses to mid-parent for grain yield character. Thus, to find promising genotypes having high grain yield ability, selection would be better to be postponed to later generations.

Table 4. Heterosis (%) relative to mid-parent (MP) and better parent (BP), inbreeding depression (ID %) and potence ratio (PR) for studied traits of the two wheat crosses.

Character	Cross	Heterosis MP	Heterosis BP	Inbreeding depression ID%	Potence Ratio PR
Strip	Sakha 95 X Shandaweel 1				0.49
Rust	Sakha 95 X Sids 13				-0.47
Stem	Sakha 95 X Shandaweel 1	84.64**	15.79**	-7.03**	1.42
Rust	Sakha 95 X Sids 13	-29.33**	-64.48**	-103.15**	-0.30
Grain	Sakha 95 X Shandaweel 1	4.9**	-5.64**	6.08**	0.44
Yield	Sakha 95 X Sids 13	7.74**	-11.22**	15.29**	0.36
*and *	= significant at 0.05 and 0.	.01 proba	bility level	s, respective	elv.

In general, inbreeding depression values were highly significant negative in cross I (Sakha 95 X Shandaweel 1) for stripe rust and in the two crosses for stem rust. Meanwhile, it was highly significant positive for stripe rust in cross II. On the other side, positive estimates for inbreeding depression were observed for grain yield in both crosses. Similar results were reported by (Shehab Eldeen 2012 and Sharshar and Esmail 2019).

For stripe rust, potence ratio values were less than unity with positive signs of first cross. Meanwhile, these values were less than unity with negative signs in the second cross for stripe and stem rusts, reflecting the important role of partial dominance in the inheritance of these traits.

On the other hand, for stem rust the potence ratio values of cross 1 were more than unity revealing that over dominance controls the inheritance of resistance to that disease. Whereas, potence ratio values were less than unity with positive signs in both crosses for grain yield character. The obtained results are matching with those of (Darwish 2011, Hammam 2013, Abd El-Aty *et al.* 2014, El-Seidy *et al.* 2017 and Sharshar and Esmail 2019).

## Heritability and expected genetic advance from selection:

The values of heritability were high in broad sense for stripe and stem rust diseases in both crosses, revealed that the phenotypic variability was due to the genetic effects for the two diseases in the two crosses, as illustrated in Table (5). The obtained results are similar to those of (Cheruiyot *et al.* 2014, Kalim Ullah1 2016, Reena *et al.* 2018 and Sharshar and Esmail 2019).

On the other hand, for stripe and stem rust diseases heritability values in narrow sense were moderate to high in both crosses, except the second cross in stem rust, indicating the important role of additive gene effects in controlling the resistance to both diseases. These results are in harmony with those reported by (Khilwat *et al.* 2019 and Sharshar and Esmail 2019).

For grain yield, values of heritability were high in broad sense in both crosses, and for narrow-sense heritability values were lower than the corresponding broad sense heritabilities which ranged from low in the second cross to moderate in the first cross, proving the presence of non-additive gene action suggesting that the inheritance is complex. These results are in agreement with those of Abd El-Aty 2002, Salama 2002 and El-Seidy *et al.* 2017 b).

Table 5. Heritability percentage in broad  $(h^2_b)$  and narrow  $(h^2_n)$  sense and expected genetic advance for the three studied characters in the two wheat crosses.

Character	Cross	Heritability	Genetic advance		
Character	Cross	$h^{2}(b) h^{2}(n)$	Δg	Δg %	
Gt ;	Sakha 95 X Shand. 1	99.04 89.72	3.43	621.89	
Stripe rust	Sakha 95 X Sids 13	98.32 81.92	10.79	363.90	
Stem rust	Sakha 95 X Shand. 1	95.76 84.96	10.08	202.28	
Stem rust	Sakha 95 X Sids 13	92.76 72.61	7.04	242.73	
Grain Yield	Sakha 95 X Shand. 1	91.87 43.53	16.10	45.32	
Giani Field	Sakha 95 X Sids 13	89.57 34.03	10.43	34.58	

It is worthy to note that the expected genetic advance ( $\Delta$  g) estimates for grain yield, in both crosses were high, revealing that selection to improve yield could be effective in the segregating populations. This results were matched with Al-Naggar *et al.* (2012).

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دراسات كمية على مقاومة أمراض الصدأ المخطط وصدأ الساق و محصول الحبوب في قمح الخبز مصطفى تاج الدين شهاب الدين 1\* و محمد عبدالحليم أبو زيد2 1 قسم بحوث القمح- معهد بحوث المحاصيل الحقلية- مركز البحوث الزراعية- مصر 2قسم بحوث امراض القمح- معهد بحوث امراض النياتات - مركز البحوث الزراعية – مصر

تم اجراء هذا البحث بالمزرعة البحثية لمحطة البحوث الزراعية بسخا- كفر الشيخ خلال الثلاث مواسم المتتالية 2015/2014 و2015/2016 و 2015/2015 بهدف تقدير طبيعة الفعل الجينى المتحكمة في توارث صفة المقاومة لكل من الصدأ المخطط وصداً الساق و توارث صفة المحصول في هجن الصنف الجديد سخا 95 مع كل من شندويل 1 وسدس 13 تم الحصول على العشائر الستة (الأب الأول، الأب الأول، الجيل الاول، الجيل الثاني، الجيل الثاني، الجيل الثاني، الجيل الثاني، الجيل الثاني، الجيل الثاني، جيل التهجين الرجعى للأب الأول وجيل التهجين الرجعى للأب الأول وجيل التهجين الرجعى للأب الأول وحيل التهجين الرجعى للأب الأتهابي وزرعت في تجربة باستخدام تصميم قطاعات كاملة العشوائية في ثلاثه مكررات في الموسم النهائي وذلك في هجينين من قمح الخبز (سخا 28٪ شاندويل 1) و (سخا 25٪ سدس 13). وأوضحت النتابج أن التباين الجيني المديدي، أما تأثير التفاعل فكان (المضيف X المضيف) هو الأكثر أهمية في توراث صفة المقلومة للصدأ المخطط وصدأ الساق. كانت قيم المكافيء الوراثي بالمعنى الواسع مرتفعة بينما كانت قيم المكافيء الوراثي بالمعنى الواسع مرتفعة بينما كانت قيم المكافيء الوراثي بالمعنى الوسع وذلك بيدة المحال المحال على سلالات جديدة ذات محصول متفوق ومقلومة للصدأ المخطط وصدأ الساق.