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Estimation of Genetic Parameters for some Agronomic Traits, and Resistance to Stripe and Stem Rusts Using Six Parameters Model in Three Bread Wheat Crosses

Sharshar, A. M.^{1*} and Samar M. Esmail²



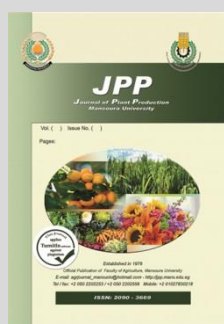
¹Wheat Research Department, Field Crops Research Institute, ARC, Egypt

²Wheat Diseases Research Department, Plant Pathology Research Institute, ARC, Egypt

ABSTRACT

The present investigation was carried out during seasons 2015/2016, 2016/2017 and 2017/2018 at the Experimental Farm of Sakha Agricultural Research Station, to determine type of gene action and some genetic parameters, also study the resistance of stripe and stem rust diseases in three bread wheat crosses (line 1×sids1), (line 1×line 2) and (line 1×misr 3) derived from four parental wheat genotypes. Genetic material included six populations (P₁, P₂, F₁, F₂, BC₁ and BC₂) for each cross. The studied characters were resistance to stripe and stem rust diseases, plant height (cm), number of spikes/plant, number of kernels /spike, 100 - kernel weight (g) and grain yield / plant (g). Results in general indicated that negative heterotic effects relative to the mid- parent and better parent were found for most of the agronomic traits and most crosses of stripe and stem rust traits. Non-allelic interaction was found for all studied traits in all the crosses under study. Dominance gene effects were larger in magnitude than the additive gene affects for most studied traits. The estimates of heritability in broad sense were high in most studied crosses. Narrow sense heritability estimates were low to relatively high for all the studied crosses. Generally, the best crosses were the third cross (Line1 × misr3) and the first cross (Line1 × Sids 1) for resistance to stripe and stem rust diseases, respectively, and could be recommended to be used in the wheat breeding program.

Keywords: *Triticum aestivum*, stripe rust, stem rust, gene action, heritability, heterosis



INTRODUCTION

Wheat (*Triticum aestivum* L.) is the most widely cultivated cereal crop in the world. In Egypt, it is considered as the major winter cereal crop and national wheat production is insufficient to meet the local consumption because of the higher increase in population especially in recent years. The improvement of wheat yield is dependent upon a better understanding of the type of gene action underlying the inheritance of yield and its contributing characters. Wheat grain yield is determined by the environmental factors and the several yield components such as; productive tillers per unit area, number of grains per spike, grain weight per spike, semi-dwarf type plant height and the high 1000-grain weight (Ahmedi and Bajelan, 2008; Mohsin *et al.*, 2009 and Sial *et al.*, 2013).

It has been observed that in breeding programs, the magnitude of genetic inheritance and expected genetic gains are very essential to predict response to selection in diverse environments and provide the basis for effective selection for particular traits in segregating populations.

Stripe rust (yellow rust) (*Puccinia striiformis*) and stem rust (*Puccinia graminis*), are the most destructive foliar diseases of wheat in Egypt and worldwide.

Historically and presently, stripe and stem rusts have caused significant and severe losses on susceptible wheat cultivars worldwide (Wellings, 2011). Many cultivars that possessed resistance to stripe rust lost their

resistance after released due to genetic adaptation of the fungus. Some cultivars, however, have maintained their level of resistance throughout their widespread use and their resistance is considered to be durable.

Information on the genetics and gene effects of breeding materials could ensure the long-term selection and better genetic improvements. The maximum progress in improving any character would be expected in a selection program when the additive gene action was the main component of genetic variance, whereas, the presence of non-additive gene action might suggest the use of a hybridization program for achieving this goal. Many genetic models proposed by Mather (1949), Gamble (1962), Hayman and Mather (1955) and Mather and Jinks (1971) could be used in wheat genetic studies.

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

MATERIALS AND METHODS

The experiment was conducted at the Experimental Farm of Sakha Agricultural Research Station, Kafr El-Sheikh, Egypt, The experimental material comprised three crosses of wheat during three growing seasons (2015/2016, 2016/2017 and 2017/2018). In the first season, three crosses were made by hand. *i.e.* Line 1 x sids1 (cross 1),

* Corresponding author.

E-mail address: anassarshar@yahoo.com

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Line1 x Line2 (Cross 2), Line1x misr3 (Cross 3). In the second season, seeds of F₁'s were sown to produce F₁ plants and some of these plants were selfed to produce F₂ seeds. Each of F₁ plants were crossed back to their respective parents to produce first back cross (BC₁) and second back cross (BC₂).

Also, the three crosses were re-crossed again in the same season to produce their F₁ seeds. In the third season, the obtained seeds of the six populations P₁, P₂, F₁, BC₁, BC₂ and F₂ of the three crosses were sown using a randomized complete block design with three replications. Each field plot consisted of 12 rows (one row for each of P₁, P₂ and F₁, two rows for each of BC₁ and BC₂ and five rows for F₂) besides two border rows were planted to avoid the border effects. The rows were 2.8 m long spaced 30 cm apart and seeds were spaced 20 cm between plants. So, each of the P₁, P₂, F₁, BC₁, BC₂ and F₂ generations have the same field plot size to satisfy the equality of the field plot in each replicate for all the treatments, which are required in the randomized complete block design (RCBD). The wheat cultivar 'Morocco' which is highly susceptible to all races of rusts, was grown as spreader around the experimental material.

Names, pedigree and selection history of the studied parents are presented in Table 1.

Table 1. Names, pedigree and selection history of the studied parental bread wheat cultivars.

Parent	Name	Pedigree
1	Line 1	Veroby CMSS96Y02555S-040Y-020M-050SY-020SY-6M-0Y
2	Sids 1	HD2172/Pavon "s"/1158.57/Maya 74 "S" S 46-45D-25D-15D-05D
3	Line 2	ATTILA*2/Giza 168 S.15612-1S-1S-1S-0S
4	Misr 3	Attila*2/PBW65*2/KACHU CMSS06Y00582T-099TOPM-099Y-099ZTM-099Y-009M-10WGY-0B-0EGY

All recommended cultural practices were applied at the proper time to raise a normal healthy plants.

To satisfy the analysis of variance of the characters recorded, 200, 75, and 30, 30 and 30 individual F₂, BC₁, BC₂, P₁, P₂ and F₁, plants respectively, were chosen at random from the six populations and all studied characters were recorded.

Data were recorded on the selected plants of the six populations in each cross for; plant height (cm), the number of spikes/plant, number of kernels/spikes, 100-kernel weight (g), stripe rust, stem rust reactions and grain yield/plant (g).

The infection types for stripe and stem rusts were recorded and estimated as disease severity according to the scale adopted by Stakman *et al.* (1962). In this method, resistance, moderately resistance, medium, moderately susceptible and susceptible field responses were symbolized as R, MR, M, MS and S, respectively.

For the quantitative analysis, field response was converted into an average coefficient of infection (ACI) using 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 could be obtained by multiplying infection severity by 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, respectively.

Heterosis was estimated as a percent of the deviation of F₁ hybrids over its mid-parent (MP) or its better parent (BP) values. Inbreeding depression was estimated as the average percentage decrease of the F₂ from the F₁. Potence ratio (P) was also calculated according to Peter and Frey (1966).

The population means and the variances were used to compute the scaling tests A, B and C. Scaling test was used to check the adequacy of the additive - dominance model for different traits in each cross (Hayman and Mather 1955). The significance of any one of these scales was taken to indicate the presence of epistasis *i.e.* non-allelic interaction. In the presence of non-allelic interaction, various gene effects were estimated using six parameter and to estimate the type of gene effects according to Mather (1949) and Hayman and Mather (1955).

The six parameters model proposed by Gamble (1962) was used to estimate different gene effects. Heritability in broad and narrow sense was calculated according to Mather (1949) and the predicted genetic advance under selection was computed according to Johnson *et al.* (1955).

RESULTS AND DISCUSSION

Mean performance

Mean and variance of the six populations (P₁, P₂, F₁, BC₁, BC₂ and F₂) of the three wheat crosses for the studied characters are shown in Table 2.

The F₁ mean values exceeded the mid-values of the two parental means for all the studied characters in all the three crosses reflecting the presence of dominance towards the better parent except of no. of spikes/plant for all the crosses and No. of kernels/spike, 100-kernel weight and grain yield/plant for the first cross which was lower than the mid-parent indicating partial dominance for these crosses.

Regarding F₂ population, the mean values were intermediate between the two parents and less than the F₁ mean values, for all studied characters except the first cross in each of number of spikes /plant, 100-kernel weight and grain yield/plant indicating that these characters are quantitatively inherited.

However, both BC₁ and BC₂ mean values varied according to the character itself, which tended toward the mean of recurrent parent for the studied traits with some exceptions. Similar results were obtained by Manal H. Eid (2009), Koumber and El-Gammaal (2012) and Hamam (2013).

Generally, from the previous data it was interested to note that the variances of the non-segregating populations (P₁, P₂ and F₁) were the lowest than those of segregating populations (F₂, BC₁ and BC₂). This indicates that they are genetically homogeneous while F₂ and both B.C are heterogeneous populations which showed greater variances.

This is expected because the segregating populations consisted of heterozygous plants.

Heterosis, Inbreeding Depression and Potence Ratio:

Heterosis percentage relative to mid and better parents, inbreeding depression and potence ratio for all the studied characters in the three crosses are presented in Table 3

Highly significant positive values relative to mid parent were found at second and third crosses in all the studied traits except all crosses in N.of spikes/plant and the first cross in each of No. of kernels/spike, 100-kernel weight and grain yield/plant which revealed significant and highly significant negative values.

Table 2. Means (\bar{X}) and variances (S^2) of the six populations (P₁, P₂, F₁, BC₁, BC₂ and F₂) for all the studied characters in three bread wheat crosses.

Traits	Crosses	Statistical parameter	P ₁	P ₂	F ₁	BC ₁	BC ₂	F ₂
Plant height (cm)	1	\bar{X}	115.00	111.60	113.97	107.22	109.62	113.48
	(Line 1 x Sids1)	S^2	0.11	0.10	0.417	1.48	1.53	0.46
	2	\bar{X}	118.00	101.67	112.50	108.96	100.57	103.94
	(Line 1 x Line2)	S^2	0.14	0.13	0.185	1.60	1.57	0.45
	3	\bar{X}	116.67	110.00	120.00	115.89	113.82	114.40
	(Line 1 x Misr3)	S^2	0.13	0.15	0.296	1.62	1.64	0.46
No. of spikes/Plant	1	\bar{X}	21.47	25.41	18.43	18.67	22.48	21.36
	(Line 1 x Sids1)	S^2	0.08	0.08	0.12	0.33	0.39	0.13
	2	\bar{X}	22.28	17.10	19.30	18.28	17.32	17.81
	(Line 1 x Line2)	S^2	0.08	0.07	0.16	0.35	0.35	0.12
	3	\bar{X}	22.70	21.53	21.27	20.94	20.32	20.64
	(Line 1 x Misr3)	S^2	0.06	0.08	0.17	0.41	0.48	0.17
No. of kernels/ Spike	1	\bar{X}	78.60	57.52	67.07	68.00	62.86	60.46
	(Line 1 x Sids1)	S^2	0.05	0.11	0.24	1.16	1.26	0.38
	2	\bar{X}	74.97	55.43	74.90	73.34	65.56	57.89
	(Line 1 x Line2)	S^2	0.14	0.13	0.28	1.15	0.96	0.37
	3	\bar{X}	79.80	69.47	78.00	73.44	72.33	73.30
	(Line 1 x Misr3)	S^2	0.15	0.16	0.28	1.07	1.12	0.36
100- kernel weight (g)	1	\bar{X}	3.56	4.35	2.41	3.82	4.04	4.05
	(Line 1 x Sids1)	S^2	0.002	0.002	0.002	0.007	0.009	0.003
	2	\bar{X}	3.73	2.20	3.74	3.59	3.38	2.93
	(Line 1 x Line2)	S^2	0.002	0.002	0.004	0.005	0.010	0.003
	3	\bar{X}	2.90	3.02	3.35	3.20	3.06	3.46
	(Line 1 x Misr3)	S^2	0.002	0.001	0.004	0.005	0.009	0.003
Grain yield/ plant (g)	1	\bar{X}	53.67	30.01	37.96	40.38	34.39	38.40
	(Line 1 x Sids1)	S^2	0.11	0.13	0.20	0.95	0.80	0.30
	2	\bar{X}	46.86	21.06	46.14	36.23	33.27	38.85
	(Line 1 x Line2)	S^2	0.13	0.13	0.35	0.92	0.68	0.24
	3	\bar{X}	49.34	30.48	47.98	36.61	35.71	41.77
	(Line 1 x Misr3)	S^2	0.10	0.17	0.22	0.92	1.11	0.32

For heterotic effects relative to the better parent, highly significant positive values were found in the third cross in both of plant height and 100-kernel weight while the negative values were found in the second cross for plant height and all crosses in both of No.of spikes/plant

and grain yield/plant, first and second crosses in No. of kernels/spike and the first cross in 100-kernel weight. These results are similar to the earlier results reported by Khattab (2009), Darwish (2011), Zaazaa, *et al.* (2012), Hammam (2013) and Abd El-Aty *et al.* (2014).

Table 3. Estimates of heterosis, inbreeding depression percentages and potence ratio (%) for all the studied characters in the three wheat crosses.

Trait	Crosses	Heterosis%		Inbreeding Depression %	Potence Ratio%
		MP	BP		
Plant height (cm)	1 (Line 1 x Sids1)	0.59	-0.9	0.43	0.39
	2 (Line 1 x Line2)	2.43**	-4.66**	7.6**	0.33
	3 (Line 1 x Misr3)	5.88**	2.86**	4.67**	2.00
No. of spikes/plant	1 (Line 1 x Sids1)	-21.35**	-27.45**	-15.88**	2.54
	2 (Line 1 x Line2)	-1.99**	-13.39**	7.74**	-0.15
	3 (Line 1 x Misr3)	-3.84**	-6.31**	2.96**	-1.46
No. of Kernels/ Spike	1 (Line 1 x Sids1)	-1.45*	-14.66**	9.86**	-0.09
	2 (Line 1 x Line2)	14.88**	-0.09	22.71**	0.99
	3 (Line 1 x Misr3)	4.51**	-2.26**	6.03**	0.65
100-kernel weight (g)	1 (Line 1 x Sids1)	-38.93**	-44.48**	-67.63**	3.90
	2 (Line 1 x Line2)	25.92**	0.12	21.53**	1.01
	3 (Line 1 x Misr3)	13.22**	11.02**	-3.25**	-6.67
Grain yield/ Plant (g)	1 (Line 1 x Sids1)	-9.28**	-29.27**	-1.16	-0.33
	2 (Line 1 x Line2)	35.88**	-1.52*	15.8**	0.94
	3 (Line 1 x Misr3)	20.21**	-2.77**	12.94**	0.86

*, ** Significant at 0.05 and 0.01 levels, respectively.

MP: mid parent
BP: better parent

With regard to the inbreeding depression percent, positive values of inbreeding depression were detected for all traits in most studied crosses except the first cross for No.of spikes/plant, the first and the third crosses for 100-kernel weight which had negative values. Insignificant inbreeding depressions were also detected in the first cross in each of plant height and grain yield/plant.

This logical since the expression of heterosis in F₁ will be followed by considerable reduction in F₂ performance.

Potence ratio values were more than unity in all crosses in 100-kernel weight, first and third cross in No.of spikes/plant and the third cross in plant height indicating the presence of over dominance towards lower or higher parent.

A partial dominance towards lower or higher parent was at the remaining characters for all the studied crosses. The above results are confirmed by the finding of Darwish (2011), Hammam (2013) and Abd El-Aty *et al* (2014).

Estimation of type of gene Action:

Testing for non-allelic interaction (A, B, and C) together with the six parameters model and type of epistasis are given in Table 4.

The results revealed the presence of non-allelic interactions for all the studied characters in all the studied crosses except for the number of spike/plant in the third cross. It is worthy to mention that at least one of the A, B

and C tests was significant for the previous characters, indicating the adequacy of the six-parameter model to explain the type of gene action controlling the character in these crosses. However, for the excepted cases, the simple additive-dominance model would be adequate.

The estimated mean effect parameter (m) was found to be highly significant for all the studied traits in all crosses indicating that these characters are quantitatively inherited.

The additive gene effects were positively significant and highly significant for plant height in the second cross, number of kernels/ spike and grain yield/plant in the first and second crosses, suggesting the potential for obtaining further improvements of these traits using pedigree selection program. Similar findings have been reported by Abd El-Aty *et al* (2014) and Patel *et al* (2018)

On the other hand, significant and highly significant negative additive effects were detected only in the first cross for number of spike/plant, indicating that the additive effects were less important in the inheritance of this character.

Meanwhile, none of the crosses exhibited positive or negative significant additive effects for 100 kernel weight in all crosses, plant height in the first and third cross, No.of spike/plant in the second and third crosses, No. of kernel/spike and grain yield/plant in the third cross.

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

Traits	Crosses	Scaling test			Genetic Components						
		A	B	C	(m)	(a)	(d)	(aa)	(ad)	(dd)	
Plant height (cm)	1 (Line 1 x sids1)	-14.52**	-6.34*	-0.63	113.48**	-2.39	-19.56**	-20.23**	-4.09*	41.09**	Duplicate
	2 (Line 1 x Line2)	-12.59**	-13.02**	-28.89**	103.94**	8.38**	5.95	3.28	0.22	22.33**	Complementary
	3 (Line 1 x Misr3)	-4.88	-2.36	-9.07*	114.4**	2.07	8.5	1.83	-1.26	5.41	Complementary
No. of spikes/plant	1 (Line 1 x sids1)	-2.57*	1.13	1.7	21.36**	-3.82**	-8.14**	-3.14	-1.85*	4.58	Duplicate
	2 (Line 1 x Line2)	-5.02**	-1.75	-6.76**	17.81**	0.96	-0.4	-	-	-	-
	3 (Line 1 x Misr3)	-2.1	-2.15	-4.22	20.64**	0.61	-0.88	-0.03	0.03	4.28	Duplicate
No. of kernels/spike	1 (Line 1 x sids1)	-9.67**	1.13	-28.42**	60.46**	5.14**	18.89**	19.88**	-5.4**	-11.35	Duplicate
	2 (Line 1 x Line2)	-3.18	0.8	-48.62**	57.89**	7.78**	55.94**	46.24**	-1.99	-43.85**	Duplicate
	3 (Line 1 x Misr3)	-10.93**	-2.81	-12.07**	73.3**	1.11	1.7	-1.67	-4.06**	15.41*	Complementary
100-kernel weight (g)	1 (Line 1 x sids1)	1.68**	1.32**	3.45**	4.05**	-0.22	-2**	-0.46	0.18	-2.54**	Complementary
	2 (Line 1 x Line2)	-0.28	0.82**	-1.68**	2.93**	0.21	2.99**	2.22**	-0.55**	-2.77**	Duplicate
	3 (Line 1 x Misr3)	0.15	-0.26	1.22**	3.46**	0.14	-0.94**	-1.33**	0.2	1.44*	Duplicate
Grain yield/plant	1 (Line 1 x sids1)	-10.87**	0.82	-6*	38.4**	5.99**	-7.93*	-4.05	-5.84**	14.1*	Duplicate
	2 (Line 1 x Line2)	-20.54**	-0.68	-4.8	38.85**	2.96*	-4.24	-16.42**	-9.93**	37.64**	Duplicate
	3 (Line 1 x Misr3)	-24.09**	-7.04**	-8.7**	41.77**	0.91	-14.36**	-22.43**	-8.53**	53.56**	Duplicate

*, ** Significant at 0.05 and 0.01 levels, respectively.

Dominance gene effects (d) were found to be positive and highly significant for no. of kernels/spike in the first and second crosses, 100-kernel weight in the second cross.

On the other hand, highly significant negative effects were obtained for plant height and no. of

spikes/plant in the first cross, 100-kernel weight and grain yield/plant in the first and third crosses. Indicating the importance of dominance gene effects in the inheritance of these traits.

Highly significant positive additive × additive types of epistasis were detected in the first and second crosses for

the number of kernels/spike and the second cross for 100-kernel weight. While highly significant negative additive × additive was found for plant height in the first cross, 100-kernel weight in the third cross and grain yield/plant in the second and third cross.

With regard to additive × dominance type of gene action, data in Table 4 showed that none of the crosses exhibited positive significant additive × dominance effects), Meanwhile, highly significant negative additive × dominance type of gene action was found in the first cross for plant height and No.of spikes/plant, first and third cross for No.of kernels/spike, second cross for 100-kernel weight and all the crosses for grain yield/plant.

Dominance × dominance epistasis type was significant or highly significant positive for plant height in the first and second crosses, No. of kernels/spike and 100-kernel weight in the third cross, grain yield/plant in all studied crosses. Otherwise highly significant negative Dominance × dominance was found for No. of kernels/spike in the second cross and 100-kernel weight in both of first and second crosses while none of the crosses exhibited positive or negative significant for No.of spikes/plant. These results agree with those obtained by Hassan *et al* (2013), Koumber and El-Gammaal (2012), Abd El-Aty *et al* (2014). and Patel *et al* (2018).

Duplicate epistasis was observed, as revealed by differences in signs of (d) and (dd) in crosses which exhibited significant epistasis, while similar signs of (d) and (dd) reflects complementary epistasis. These results illustrated that duplicate epistasis was prevailing for most traits, while complementary epistasis was prevailing for plant height in the second and third crosses, N.of kernels/spike in the third cross and 100-kernel weight in the first cross. This indicates that duplicate epistasis was greater and important when compared with complementary epistasis for most studied characters.

Heritability and percentage of genetic advance:

Heritability estimates in broad sense were high for all studied characters in all crosses, ranged from 87.13 % for 100-kernel weight in the third cross to 97.72% for plant height in the third cross, according to the cross and/or character itself as shown in Table 5.

Heritability estimates in narrow sense were low to moderate for all studied characters in all crosses, and ranged from 22.58% for plant height in the second cross to 68.97% for 100-kernel weight in the third one, indicating that these characters greatly affected by non-additive and environmental effects.

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

Trait	Crosses	Heritability percentage		Expected genetic advance	
		h ² (b)	h ² (n)	Δg	Δg %
Plant height (cm)	1 (Line 1 x sids1)	92.74	35.06	8.45	7.45
	2 (Line 1 x Line2)	95.35	22.58	5.38	5.18
	3 (Line 1 x Misr3)	97.72	23.31	5.65	4.94
N.of spikes/plant	1 (Line 1 x Sids1)	90.00	64.42	8.37	39.20
	2 (Line 1 x Line2)	88.04	56.64	7.08	39.74
	3 (Line 1 x Misr3)	90.87	66.20	9.62	46.63
N.of kernels/spike	1 (Line 1 x Sids1)	94.92	43.12	9.54	15.79
	2 (Line 1 x Line2)	92.74	56.35	12.18	21.04
	3 (Line 1 x Misr3)	92.29	49.53	10.65	14.53
100-kernel weight (g)	1 (Line 1 x Sids1)	90.29	63.34	1.22	30.23
	2 (Line 1 x Line2)	87.49	58.83	1.10	37.62
	3 (Line 1 x Misr3)	87.13	68.97	1.29	37.21
Grain yield (g)	1 (Line 1 x Sids1)	93.25	55.60	10.93	28.46
	2 (Line 1 x Line2)	87.44	32.87	5.74	14.76
	3 (Line 1 x Misr3)	92.72	40.67	8.19	19.61

Generally, the most biometrical parameters resulted from the second and third crosses which were higher in magnitude in comparison with those from other crosses.

Consequently, it could be concluded that these cross would be of interest in a breeding program for improving characters of yield and its components.

The expected genetic advance (Δg) ranged from 1.10 for 100-kernel weight in the second cross to 12.18 for number of kernels/spike in the second one. The expected genetic advance was moderate in all studied characters except for number of spikes/plant in the third cross which was high. These values depend on narrow sense heritability values, standard deviation of F_2 and the character under study. Similar results were obtained by Abd El-Aty (2007), Mahboob *et al* (2013) and Abd El-Aty *et al* (2014).

Results of stripe and stem rust resistance:

Mean of the average coefficient infection (ACI) and variances for stripe and stem rust diseases.

The mean of the average coefficient infection (ACI) of stripe and stem rust diseases for the six populations of the three studied crosses are presented in Table 6.

Table 6. Mean of the average coefficient infection (ACI) for the six populations of the three bread wheat crosses for stripe and stem rust diseases.

Traits	Crosses	Statistical Parameter	P ₁	P ₂	F ₁	F ₂	BC ₁	BC ₂	
Stripe Rust	1 (Line1 x Sids 1)	X ⁻ S ²	0.05 0.01	40.00 0.02	0.13 0.00	3.39 0.03	0.16 0.00	3.10 0.13	
	2 (Line1 x Line 2)	X ⁻ S ²	0.10 0.01	3.60 0.00	0.24 0.00	5.92 0.00	0.07 0.00	0.42 0.01	
	3 (Line1 x Misr3)	X ⁻ S ²	0.07 0.01	0.19 0.00	0.08 0.00	0.57 0.00	0.09 0.00	0.30 0.01	
	Stem Rust	1 (Line1 x Sids 1)	X ⁻ S ²	42.33 0.01	0.26 0.00	0.69 0.00	2.20 0.02	8.55 0.06	0.42 0.01
		2 (line1 x Line 2)	X ⁻ S ²	49.67 0.11	3.50 0.05	38.33 0.21	37.52 0.66	56.32 1.60	35.26 2.40
		3 (Line1 x Misr3)	X ⁻ S ²	50.00 0.15	2.17 0.00	15.63 0.31	21.77 0.59	35.40 1.64	10.61 1.51

The F_2 mean value was less than the mid parent indicating partial dominance towards the resistant parent except the second cross which indicating partial dominance towards the susceptible parent, BC₁ and BC₂ men values, indicated that segregation were in the direction of their respective recurrent parents.

Finally, the third cross (Line1 × Misr3) was the most desirable which had the lowest mean values for the infection low disease severity for stripe rust disease and the first cross (Line1 × Sids 1) for stem rust diseases.

Heterosis, Inbreeding Depression and Potence Ratio:

The resistant crosses to stripe and stem rust diseases (desirable) should have significant negative heterotic effects relative to mid-parent and better parent.

For stripe and stem rusts the data indicated that the F_1 mean values were less than the mid parent in all crosses indicating partial dominance towards the parent of low disease severity. The F_2 mean values were higher than the F_1 , indicating the partial dominance towards the resistant parent. BC₁ and BC₂ mean values indicated that segregation was in the direction of the respective recurrent parents.

With respect to stem rust the data in Table 6 indicated that the F_1 mean values were less than the mid parent in the first and third crosses indicating partial dominance towards the parent of low disease severity while the F_1 mean values was higher than the mid parent in the second cross indicating partial dominance towards the parent of high disease severity.

All crosses in both of stripe and stem rust in Table 7 exhibited high significant negative heterotic effects relative to mid-parent and better parent, except for the second cross in stem rust which had highly significant positive (undesirable) relative to the mid and better parent. These superior and promising genotypes and their progenies might be used in the future in wheat breeding programs for improving the resistance to stripe and stem rust disease.

With respect to inbreeding depression data in Table 7 showed that all the studied crosses in stripe and stem rust exhibited highly significant negative for leaf rust disease except for the second cross (Line1 × Line 2) which had significant positive inbreeding depression for stem rust disease.

Table 7. Heterosis relative to mid parent and better parent, inbreeding depression percentage and potence ratio (%) for stripe and Stem rust in three bread wheat crosses.

Traits	Crosses	Heterosis %		Inbreeding depression %	Potence ratio%
		MP	BP		
stripe rust	1 (Line1 x Sids 1)	-99.38**	-99.69**	-2611.64**	1.00
	2 (Line1x Line 2)	-2.47**	-93.43**	-2400.08**	0.10
	3 (Line1 x Misr3)	-39.87**	-59.65**	-646.07**	0.81
Stem rust	1 (Line1 x Sids 1)	-96.75**	-96.75**	-218.36**	-0.98
	2 (Line1x Line 2)	52.61**	52.61**	2.13*	0.57
	3 (Line1 x Misr3)	-40.06**	-40.06**	-39.24**	-0.44

(*) and (**) significant at 0.05 and 0.01 levels of probability, respectively

For potence ratio, the values were less than unity with positive sign for stripe rust in the second cross (line1x Line 2) and third cross (Line1 × Misr3) indicating the

presence of partial dominance in the inheritance of this trait. Meanwhile the values were more than unity for the first cross indicating the presence of over dominance

controlling the inheritance of this trait, on the other hand the values were less than unity with negative sign for stem rust in the first cross (Line1 x Sids 1) and third cross (Line1 x Misr3) and positive sign in second cross indicating the presence of partial dominance in the inheritance of this trait.

Estimation of type of gene action:

Type of gene action and scaling test for stripe and stem rust diseases characters are shown in Table 8.

Table 8. Estimates of scaling tests and gene effects for stripe and stem rusts in three bread wheat crosses.

Traits	Crosses	Scaling test			Genetic Components						
		A	B	C	(m)	(a)	(d)	(aa)	(ad)	(dd)	
Stripe rust	1 (Line1 x Sids1)	0.14*	-33.92**	-26.75**	3.39**	-2.94**	-26.94**	-7.03**	17.03**	40.81**	Duplicate
	2 (Line1 x Line2)	-0.2*	-3**	19.5**	5.92**	-0.35**	-24.31**	-22.69**	1.4**	25.89**	Duplicate
	3 (Line1 x Misr3)	0.05	0.33	1.88**	0.57**	-0.2	-1.56**	-1.51**	-0.14	1.13*	Duplicate
Stem rust	1 (Line1 x Sids1)	-25.92**	-0.12	-35.17**	2.2**	8.14**	-11.47**	9.13**	-12.9**	16.9**	Duplicate
	2 (Line1 x Line2)	24.64**	28.69**	20.23**	37.52**	21.06**	44.85**	33.1**	-2.02	-86.43**	Duplicate
	3 (Line1 x Misr3)	5.17	3.43	3.64	21.77**	24.79**	-5.49	-	-	-	

(*) and (**) significant at 0.05 and 0.01 levels of probability, respectively

The estimated mean effect parameter (m) was highly significant for both rusts, indicating that these traits were quantitatively inherited.

The additive (a) gene effects was highly significant negative for the stripe rust except the third cross which exhibited non-significant negative value, while the additive gene effect was highly significant positive in all crosses for stem rust disease, indicating that the additive gene effect is more important in the inheritance of these traits.

High negative significant dominance effects was detected for stripe and stem rust diseases for all the studied crosses except for the second cross which exhibited highly significant positive effects for stem rust disease, indicating the importance of dominance gene effects in the inheritance of these traits.

Highly significant negative additive x additive gene effects was obtained for stripe rust in all crosses while highly significant positive effects for stem rust were in the first and second cross, indicating the main role of additive x additive gene effect in inheritance of these traits.

Highly significant positive values of Additive x dominance were detected for all studied crosses except the

Most values of A, B and C were significant for all the studied crosses except for stem rust in the third cross, indicating the presence of non-allelic interaction in these crosses. Indicating the adequacy of the six parameters model to explain the type of gene action controlling the traits in these crosses.

third cross for stripe rust disease, while highly significant negative values in the first cross for stem rust.

Dominance x dominance epistatic type was highly significant positive for stripe and stem rust diseases for all the studied crosses except for the second cross in stem rust which had a significant negative value. These results were harmony with Kalim Ullah *et al* (2016) and Khilwat *et al* (2019)

These results illustrated that duplicate epistasis was prevailing for stripe and stem rusts. This indicates that duplicate epistasis was greater and important when compared with complementary epistasis for most studied characters.

Heritability estimates and predicted genetic advance from selection:

Heritability estimates in broad sense were high for stripe and stem rust diseases for all the studied crosses, indicating that the phenotypic variability was mostly attributed to genetic effects for these diseases in these crosses as shown in Table 9. These results were in the same line with Cheruiyot *et al* (2014), Kalim Ullah (2016) and Reena Rani *et al* (2018).

Table 9. Estimates of heritability percentage in broad (h²b) and narrow (h²n) senses and expected (Δg) genetic advance from selection for Stripe and stem rust in three bread wheat crosses.

Traits	Crosses	Heritability Percentage		Expected genetic Advance	
		h ² (b)	h ² (n)	Δg	Δg %
Stripe rust	1 (Line1 x Sids 1)	97.30	84.96	5.09	150.26
	2 (line1 x Line 2)	94.34	91.19	1.26	21.43
	3 (Line1 x Misr3)	98.44	92.47	1.76	308.84
Stem rust	1 (Line1 x Sids 1)	98.65	90.54	4.25	193.44
	2 (Line1 x Line 2)	97.17	49.18	14.28	38.07
	3 (Line1 x Misr3)	95.94	67.24	18.49	84.96

(*) and (**) significant at 0.05 and 0.01 levels of probability, respectively.

On the other hand, heritability estimates in narrow sense were moderate to high for stripe and stem rust diseases for all the studied traits, according to the cross and/or traits itself, reflecting the importance of additive gene action and their effects in resistant for stripe and stem rust diseases except the second cross in stem rust. These results are in agreement with Khilwat *et al* (2019).

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تقدير الثوابت الوراثية لبعض الصفات المحصولية وصفتي المقاومة للصدأ المخطط والصدأ الاسود باستخدام العشائر الستة في ثلاثة هجن من قمح الخبز

أنس محمد صفاء الدين شرشر¹ و سمر محمد إسماعيل²

¹قسم بحوث القمح- معهد بحوث المحاصيل الحقلية- مركز البحوث الزراعية

²قسم بحوث امراض القمح- معهد بحوث امراض النباتات - مركز البحوث الزراعية

أجريت هذه الدراسة بمزرعة محطة البحوث الزراعية بسخا- كفر الشيخ خلال ثلاثة مواسم 2016/2015، 2017/2016 و 2018/2017 لتقدير طبيعية التأثير الجيني وإيجاد تراكيب وراثية جديدة يمكن الانتخاب من خلالها في الأجيال اللاحقة للحصول على سلالات جديدة من القمح مقاومة لمرض الصدأ المخطط وصدأ الساق ومتفوقة في صفاتها المحصولية على الأصناف التجارية المنزرعة ، وقد استخدم لذلك أربعة أباء متباينة في صفاتها وهي (سلالة 1 ، سلالة 2 ، سنس 1 ، مصر 3) وتم عمل ثلاثة هجن من هذه الأباء وهي (سلالة 1 × سنس 1) ، (سلالة 1 × سلالة 2) و (سلالة 1 × مصر 3) ، والحصول على العشائر الستة من كل هجين (الأب الأول والثاني والجيلين الأول والثاني والهجينين الرجعيين الأول والثاني) لكل هجين وتمت دراسة كل من الصفات الآتية: طول النبات ، عدد حبوب السنبل ، عدد السنابل للنبات، وزن المائة الحبه(جرام) ، محصول النبات الفردي(جرام)، الصدأ المخطط وصدأ الساق. أوضحت النتائج بالنسبة للصفات المحصولية تفوقت قيم متوسطات الجيل الأول على قيم متوسطى الأباء لمعظم الصفات المدروسة مما يشير الي وجود السيادة تجاه افضل الأباء ، بالنسبة لوراثته مقاومه الصدأ المخطط وصدأ الساق أظهرت النتائج ان أكثر الهجن مقاومه للصدأ المخطط كان الهجين الثالث في حين أن الهجين الاول كان أكثر الهجن مقاومه بالنسبة لصدأ الساق ، أظهرت قوه الهجين بالنسبة لمتوسط الابوين وأفضل الاباء قيم ساليه وعالية المعنويه لمعظم الهجن في الصفات المدروسة، كان تأثير الفعل الجيني السيادةي أكثر أهمية من تأثير الفعل الجيني المضيف لمعظم الهجن في الصفات المدروسة. أظهرت درجة التوريث علي النطاق الواسع قيما عاليه في كل الهجن في كل الصفات المدروسة. كانت قيم معامل التوريث بمعناه الضيق منخفضة إلى عالية في معظم الصفات المدروسة مما يدل علي أهمية الفعل الاضافي وتأثيره في صفه المقومه ، عموما تشير النتائج الي أن افضل الهجن كان الهجين الثالث لصفه الصدأ المخطط والهجين الاول لصفه صدأ الساق وبالتالي يمكن استخدامهم في برنامج تربيته القمح لتحسين صفه المقاومه لصدأ المخطط وصدأ الساق.