THE GENETIC SYSTEM CONTROLLING LEAF RUST RESISTANCE IN BREAD WHEAT
(*Triticum aestivum* L)

Awaad, H. A. *, A. H. Salem*, M.M. M. Atia ** and Minaas, E. A. Sallam***

*Agronomy Dept., Fac. Agric., Zagazig Univ., Egypt
**Agric. Bot. and Pl. Path. Dept., Fac. Agric., Zagazig Univ., Egypt
***Wheat Dis. Res. Dept., Pl. Path. Res. Institute, ARC, Giza, Egypt

ABSTRACT: P_1, P_2, F_1, F_2, F_1 x parent 1(Bc_1) and F_1 x parent 2 (Bc_2) generations resulting from four crosses i. e., 1) ACSAD 945 x Sakha 69, 2) Giza 168 x Gemmeiza 5, 3) Gemmeiza 9 x PAT10/ALD'S' and 4) Sakha 69 x Sahel 1) among seven genetically diverse bread wheat cultivars for leaf rust resistance, were artificially infected by a mixture of eleven physiological races of *Puccinia recondita* Rob. Ex Desm. f. sp. *tritici* Eriks & Henn urediospores and evaluated for their reaction to leaf rust resistance, infection type, disease severity (%), grain yield/plant and predicted loss at the Experimental Farm, Faculty of Agriculture, Zagazig University, Egypt. Correlation coefficient, genetic analysis and heritability were estimated for the studied characters. The obtained results could be summarized as follows:

Significant differences between parental wheat genotypes and their populations were detected for the studied characters. The most resistant wheat cultivars were Giza 168 (3 R) followed by PAT10/ALD'S' (5 R), ACSAD 945 (10 R) and Gemmeiza 9 (20 R-MR). Whereas, Gemmeiza 5 (60 S-MS), Sakha 69 (50.6 MS) and Sahel 1 (40.8 MS) expressed as susceptible ones. The F_1 plants showed highly resistant in 1st cross, complete dominance in 2nd cross and partial dominance in 3rd one towards their respective resistant parent.

Negative and highly significant correlation was detected between grain yield and each of infection type and disease severity in most studied crosses.

Scaling test revealed that, the digenic model was involved in the inheritance of the studied characters in most crosses. Whereas, the simple additive-dominance genetic model was valid for explaining the inheritance of leaf rust resistance in 4th cross, with prevailed type of additive (d) gene effect. The additive (d), dominance (h) and their digenic interaction types, additive x additive (i), additive x dominance (j) and dominance x

dominance (l) were highly significant and involved in the genetics of infection type and disease severity in most cases. This result is hold true for grain yield / plant in 1st cross, while dominance (h), additive x dominance (j) and dominance x dominance (l) were significant and more pronounced in 3rd cross. Duplicate type of epistasis was detected for infection type in 1st cross; disease severity in 1st and 4th crosses as well as grain yield / plant in 1st and 3rd crosses. However, complementary type has been reported for infection type in 2nd cross (confirmed with 9: 7 ratio of χ^2 result) as well as disease severity in 2nd and 3rd crosses.

The additive genetic variance (A) was highly significant and considered the prevailed type controlling disease resistance assessment in most cases, whereas the dominance genetic variance (D), was more important in the inheritance of grain yield in all crosses.

Narrow sense heritability was high for infection type and disease severity in three out of the studied four crosses and moderate for grain yield in all crosses.

Genetic analysis using simple χ^2 test suggest that, adult leaf rust resistance was controlled by two interacting gene pairs in 1st cross; two complementary gene pairs in 2nd cross; two double dominant gene pairs in 3rd cross as well as two recessive complementary genes in the 4th one.

INTRODUCTION

The prospects of sustaining increased production in wheat depends on various factors from which leaf rust resistance, is important. Leaf rust caused by *Puccinia recondita* f. sp. *tritici.* is an important disease of wheat in Egypt and many parts of the world. 20 to 25 % yield loss has been recorded following leaf rust infection, more than 350 physiological races for *Puccinia recondita* f. sp. *tritici* and more than 43 gene for leaf rust resistance have been genetically characterized in wheat germplasm (McIntosh *et al.*, 1995 and 1995a and Anonymous, 1997).

Understanding the inheritance of host wheat genotype x pathogen interaction should permit planning of breeding program for pyramiding the resistance genes in the promising varieties against the disease.

Resistance against leaf rust has been documented to be a simple inherited character controlled by a single major dominant gene (Sibikeev *et al.*, 1995 and Brown *et al.*, 1997) or a single recessive one (Sudhakar and Joshi, 1996 and Barcellos *et al.*, 2000) and a few number of major gene pairs (Abd

El-Latif *et al.*, 1995; Shehab El-Din *et al.*, 1996 and Singh *et al.*, 2001), whereas five to six groups of genes (Ageez and Boulot,1999) as well as 10 *Lr*-gene combinations (Sibikeev *et al.*, 1996) have been identified .

The resistance to leaf rust is dominated over susceptibility and controlled by both additive and non- additive gene effects with great importance to additive one, functioning partial dominant genes (Ageez and Boulot, 1999). Whereas, additive, dominance and epistasis especially dominance x dominance were involved in the genetic system controlling leaf rust resistance with duplicate and complementary types of epistasis have been detected by Singh *et al.*(1999) and Yadav *et al.* (1999), respectively. Heritability estimates in narrow sense for resistance was high (>70%) (Shehab El-Din *et al.*, 1996 and Ageez and Boulot, 1999).

Thus, this work was designed to study the reaction of the six populations derived from four wheat crosses against leaf rust infection. Determination the adequacy of the genetic model, types of gene action and heritability for infection type, disease severity and grain yield/plant were also investigated. Test the goodness of fit of observed ratios to theoretical expectations using Chi-square analysis were also undertaken.

MATERIALS AND METHODS
Crossing technique and experimental layout

The present investigation was conducted during the three winter growing seasons: 1999/2000, 2000 /2001 and 2001/ 2002 at the Experimental Farm, Faculty of Agriculture, Zagazig Univ., Zagazig, Egypt. Four wheat crosses have been used in the present study derived from seven diverse parental bread wheat genotypes (Table 1). These genotypes were used to obtain the following four crosses; 1) ACSAD 945 x Sakha 69, 2) Giza 168 x Gemmeiza 5, 3) Gemmeiza 9 x PAT10/ALD "S" and 4) Sakha 69 x Sahel 1, differed in their resistance to leaf rust.

In the first season of 1999/2000, the seven parental wheat genotypes were evaluated in a randomized complete block design with three replicates, at the meantime, pair crosses were performed to obtain F_1's grains. In the second season, 2000/2001, four F_1 cross grains were sown to produce F_1 plants. Each of the F_1 plants were crossed back to their respective parents to produce first (F_1 x P_1) and second (F_1 x P_2) backcrosses. In the meantime, pair crosses were made to produce

more F_1 grains, also the F_1 plants were selfed to produce F_2 grains. In the third season, 2001 /2002, the obtained grains of six populations (P_1, P_2, F_1, F_2, Bc_1 and Bc_2) for each of the four crosses were evaluated using a randomized complete block design with three replicates. Wheat grains were sown in 21st November. Row was 2m long, row to row and plant to plant spaces was 20 and 5cm, respectively.

Testing procedure:

At adult plant stage (booting stage), the six populations for each cross were artificially infected with a mixture of eleven *Puccinia recondita* Rob. Ex Desm. f. sp. *tritici* Eriks & Henn races urediospores, i.e., 2, 5, 17, 28, 35, 40, 52, 121, 124, 126 and 141 kindly obtained from wheat Dis. Res. Dept., Pl. Dis. Res. Institute, ARC. Urediospores mounted in talic powder were dusted on moistened wheat leaves by baby cyclones as mentioned by Sibikeev *et al.* (1996). Then, additional dose of nitrogen and irrigation were performed to enhance the infection. After 14 days from the artificially infection, the data of infection type, disease severity % and predicted loss were recorded. Grain yield/plant was also estimated at harvest. Infection type was measured using a scale of 0-4

described by Stakman *et al.* (1962) and Knott (1989) where:

O= Immune: no signs uredia or macroscopic signs of infection

O; =Very resistant: no uredia, but hypersensitive necrotic or chlorotic flecks of varying size are present.

1= Resistant: small uredia surrounded by necrosis

2= Moderately resistant: small to medium uredia surrounded by green islands

3= Moderately susceptible: medium–sized uredia without chlorosis or necrosis

4= Susceptible: large uredia with a limited amount of chlorosis, may be diamond – shaped.

For qualitative study O, O; 1 and 2 infection types will be jointly considered as the resistant class, while 3 and 4 infection types will be expressed as susceptible one. However, for quantitative study, infection types O and O; will be given arbitrary numbers 0.25 and 0.50, respectively.

Leaf rust severity (%) was assessed using modified Cobb's scale (0 – 100 %) according to Peterson *et al.* (1948). Predicted loss as a result of disease attack was calculated according to Doling and Doodson (1968) using the following formula:

Loss = 0.268 x disease severity (R) + 3.9.

Statistical analysis and breeding assessment:

The obtained data were statistically analyzed and correlation between grain yield/plant and each of infection type and disease severity (%) were calculated according to Rangaswamy (2000).

The A, B and C scaling tests as outlined by Mather and Jinks (1982) were applied to test the presence of non–allelic interactions as follows, $A= 2\bar{B}_1 - \bar{P}_1 - \bar{F}_1$, $B= 2\bar{B}_2 - \bar{P}_2 - \bar{F}_1$ and $C= 4\bar{F}_2 - 2\bar{F}_1 - \bar{P}_1 - \bar{P}_2$. In the presence of non–allelic interaction, the analysis was proceeded to compute the interaction types involved using the six–parameters genetic model according to Singh and Chaudhary (2001). The signi-

ficance of the genetic components was tested using the "t" test.

The components of genetic variance i.e., additive (VA) dominance (VD) and (VAD) genetic variances as well as the environmental variance were computed using Kearsey and Pooni (1996) formulae as follows:

$VA^* = (2S^2F_2 - S^2Bc_{1.1} - S^2Bc_{1.2})$

$VD^* = (S^2Bc_{1.1} + S^2Bc_{1.2} - S^2F_2 - VE)$

$VAD = (^1/_2)(S^2Bc_{1.2} - S^2Bc_{1.1})$

$VE = (^1/_3)(VP_1 + VP_2 + VF_1)$

The genetic components of variance were used further to compute the dominance ratio and heritability in narrow sense by the following equations.

$hn = (VA^*) / (VA^* + VD^* + VE)$

Dominance ratio = $\sqrt{4VD^*/2VA^*}$

The Chi-square (χ^2) test was performed according to Rangaswamy (2000).

Table (1): Name, origin and pedigree of the parental wheat cultivars

No.	Genotype	Origin	Pedigree
1	Sakha 69	Egypt	Inia/RL4220//7cYr'S'CM15430-25-65-0S-0S
2	Sahel 1	Egypt	N.S.732/Pim//Veery'S'd735-4Sd-1sd-Osd
3	Gemmeiza 5	Egypt	Vee'S'/SWM6525GM4017-IGM-6JM-3GM-OGM
4	Gemmeiza 9	Egypt	Ald'S'Huac'S'/CMH74A.630/5xCGM4583-5GM.1GlM-OGM
5	Giza 168	Egypt	MIL/BUC/Seri:CM93046-8M-OY-OM-2Y-OB
6	ACSAD 945	Syria	Mon'S'Ald'S'//Deir Alla4ACS-W-8211-11Z-71Z-11Z-OIZ
7	PAT10/ALD'S'	Mex.	CM87688-O2910PM-5Y-OH-OSY-1M-OY

RESULTS AND DISCUSSION

1. Reaction of genetic materials to leaf rust:

Data presented in Table (2) show the mean performance of infection type, disease severity, grain yield/ plant and predicted loss. The results indicated significant differences between parental wheat genotypes for all the studied characters. This result suggesting the presence of high level of genetic variability valid for further biometrical assessment.

Based on the reaction of leaf rust infection, the four cross populations classified into three different categories as follows:

I. Resistant x Susceptible:
1. ACSAD 945 x Sakha 69
2. Giza 168 x Gemmeiza 5

II. Resistant x Resistant:
3. Gemmeiza 9 x PAT10/ALD'S'

III. Moderate susceptible x Moderate susceptible:
4. Sakha 69 x Sahel 1

The infection type disease measurement of the studied four cross populations revealed that, four parental wheat genotypes were considered as resistant *i.e.*, Giza 168, PAT10/ALD'S', Gemmeiza 9 and ACSAD 945 with values of 0.45, 0.56, 1.80 and 1.84 respectively. Otherwise, the wheat parents, Sakha 69, Gemmeiza 5 and Sahel 1 expressed as susc-eptible or moderate susceptible with infection type of 3.50, 3.15 and 3.00, respectively.

From the first category between (Resistant "R" x Susceptible "S"), 1st cross of the F_1 and F_2 plants were more resistant than their respective resistant parent ACSAD 945, but the F_1 plants showed complete dominance to the resistant parent Giza 168 in the 2nd one, indicating the accumulation of resistance genes. Moreover, the F_2 plants in this category were resistant (R) or moderate resistant (MR), with the presence of type (MS) in a few plants of 2nd cross.

In continuous, the F_1 plants of the 4th cross between (MS x MS) were moderate susceptible (MS) and valued 3.07, also the F_2 plants possessed the infection type (S) and valued 3.37. Meanwhile, the F_1 plants of the 3rd cross between (R x R) behaved the same type (R) with estimate 1.6 and the F_2 plants exhibited type (MR) with value of 2.56.

The backcrosses "Bc_1 and Bc_2" showed different levels of resis-tance and in almost crosses approached to their respective parent. The lowest infection type has been observed in Bc_1 and Bc_2 of both 2nd and 3rd crosses between (R x S) and (R x R). However, the

Table (2): Mean performance for six populations (P₁, F₁, F₂, Bc₁, Bc₂ and P₂) for infection type, disease severity %, grain yield / plant and predicted loss in four wheat crosses.

Cross	Population	Infection type	Type	Disease severity (%)	Grain yield / plant (g)	Predicted loss =0.268 x R+3.9
I. Resistant x Susceptible						
1. ACSAD 945 x Sakha 69	P_1	1.842± 0.032	R	10.0±1.328	8.91±0.254	6.58±0.396
	F_1	0.625±0.125	R	20.0±1.132	9.06±0,281	9.26±0.353
	F_2	1.690±0.245	R	15.0±2.800	7.81±1.430	7.92±1.058
	Bc_1	2.800±0.150	R- MR	12.0±2.161	7.60±1.171	7.12±0.833
	Bc_2	3.400±0.140	MS-MR	40.2±2.125	4.10±1.156	14.67±0.820
	P_2	3.500±0.049	MS	50.6±0.860	5.86±0.110	17.46±0.243
2. Giza 168 x Gemmeiza 5						
	P_1	0.450±0.082	R	3.0±1.212	9.10±0.213	4.70±0.356
	F_1	0.450±0.127	R	5.0±1.284	9.31±0.138	5.24±0.355
	F_2	2.100±0.296	R.-MR-MS	45.0±4.926	6.85±1.540	15.96±1.617
	Bc_1	2.000±0.285	R-MR	35.0±3.126	7.76±0.969	13.28±1.024
	Bc_2	2.250±0.200	MR	42.5±3.269	7.60±1.11	15.29±1.095
	P_2	3.150±0.085	S-MS	60.0±1.236	7.41±0.151	19.98±0.347
II. Resistant x Resistant						
3. Gemmeiza 9 x PAT10/ALD"S"	P_1	1.800±0.056	R- MR	20.0±1.180	8.35±0.252	9.26±0.358
	F_1	1.600±0.067	R	13.0±0.707	7.10±0.144	7.38±0.213
	F_2	2.560±0.123	MR	30.0±3.739	6.93±1.361	11.94±1.262
	Bc_1	2.200±0.112	R- MR	24.7±2.925	6.83±0.856	10.52±0.945
	Bc_2	1.800±0.101	R-MR	25.0±2.516	5.39±0.992	10.60±0.877
	P_2	0.560±0.081	R	5.0±9.164	10.21±0.172	5.24±0.334
III. Moderate susceptible x Moderate susceptible						
4-Sakha 69 x Sahel 1	P_1	3.500±0.049	MS	50.6±0.860	5.86±0.110	17.46±0.243
	F_1	3.070±0.039	MS	40.0±0.509	4.90±0.120	14.62±0.157
	F_2	3.375±0.378	S	75.0±3.671	3.13±1.139	24.00±1.202
	Bc_1	3.700±0.288	MS	50.0±2.415	3.20±0.500	17.30±0.729
	Bc_2	3.285±0.104	MS-MR	32.7±2.135	4.16±0.849	12.66±0.746
	P_2	3.000±0.056	MS	40.8±1.180	5.30±0.167	14.83±0.337

highest values were recorded in 4th cross between (MS x MS).

With regard to disease severity (DS), the parental genotypes displayed high level of genetic variability as well as their populations. In general, the results of disease severity coupled with those of infection type.

From the crosses between the resistant cultivar ACSAD 945 (DS 10) and the susceptible one Sakha 69 (DS 50.6), the F_1 (20 R), F_2 (15 R) and Bc_1 (12 R-MR) were resistant (R) or moderate resistant (MR). Moreover, when the resistant parent Giza 168 (3 R) was hybridized with the susceptible one Gemmeiza 5 (60 S-MS), the resultant populations possessed different levels of resistance, i.e.; (5 R) in F_1; (45 R-MR- MS) in F_2; (35 R-MR) in Bc_1 and (42.5 MR) in Bc_2.

The higher disease severity was developed in the populations of the category between (MS x MS) of 4th cross, which varied from (32.7 MS-MR) in Bc_2 to (75.0 S) in F_2 generation.

Moreover, the resistant plants in the category (R X R) of 3rd cross, exhibited relatively reactions ranged from (5 R) in PAT10 /ALD′S′ to (30 MR) in F_2 generation of this cross.

Generally, based on the response patterns of the studied populations, the genetic materials were classified into three groups the first group, including the resistant plants exhibited relatively reactions varied from (O R to 25 R-MR) which were 3R (Giza 168), 5 R (PAT10/ALD′S′ and F_1 of 2nd cross), 10 R (ACSAD 945), 12 R-MR (Bc_1 of 1st cross), 13 R (F_1 of 3rd cross), 15 R (F_2 of 1st cross), 20 R or R-MR (F_1 of 1st cross and Gemmeiza 9) and 24.7 R-MR (Bc_1 of 3rd cross) and 25 R. MR (Bc_2 of 3rd cross). These materials produced the highest grain yield averages 8.15g. with the lowest (7.62) predicted loss, and in general classified as resistant or moderate resistant.

The second group, showed a relatively response range (> 25 R-MR to 50 MS), including 30 MR (F_2 of 3rd cross); 32.7 MS-MR (Bc_2 of 4th cross); 35 R-MR (Bc_1 of 2nd cross); 40 MS (F_1 of 4th cross); 40.2 MS-MR (Bc_2 of 1st cross); 40.8 MS (Sahel 1); 42.5 MR (Bc_2 of 2nd cross); 45 R-MR-MS (F_2 of 2nd cross) and 50 MS (Bc_1 of 4th cross) which classified as moderate either resistant or susceptible. This category exhibited slightly moderate grain yield averages 5.64 g with predicted loss of 13.055. The third group, showed disease assessment varied from (>50 MS to 75 S). This category included the values 50.6 MS (Sakha 69); 60

S-MS (Gemmeiza 5) and 75S (F_2 of 4th cross). The genotypes of this group were moderate susceptible or susceptible and attained wheat grain yield varied from 3.13 (F_2 of 4th cross) to 7.41 g. (Gemmeiza 5), with the maximum values of the predicted loss averages 19.75. In this respect, significant genetic variations were existed among wheat cultivars for both leaf rust resistance and grain yield (Atteia *et al.*, 2000 and Atteia, 2001).

2.Correlation study:

Leaf rust infection of wheat causes a significant loss in wheat grain yield and quality, due to the lack of translocation of nutrients towards the ear and the less effective of photosynthetic activities of leaf area.

Data presented in Table (3) indicate that, positive and significant associations were recorded between infection type and disease severity in three out of the studied four wheat crosses.

Consequently each one of them could be used as satisfactory criterion for measuring resistance. In this connection, values of area under disease progress curve (AUDPC) and rate of disease progress were closely related to the severity of leaf rust infection and might be of importance in selection of wheat varieties with higher resistance to leaf rust as mentioned by Atteia (2001).

It is important to notice that, negative and significant correlation coefficient has been recorded between each of infection type and disease severity on one hand, and grain yield / plant in 1st, 2nd and 3rd crosses, on the other hand. Thus increasing infection type and disease severity led to substantial reduction in wheat grain yield. In this respect, significant

Table (3): Simple correlation coefficient among infection type, disease severity of leaf rust and grain yield / plant in four wheat populations.

Character	Population	Disease severity	Grain yield/ plant
Infection type	1	0.663*	-0.847**
	2	0.992**	-0.877**
	3	0.944**	-0.717*
	4	0.388	-0.452
Disease severity	1		-0.795**
	2		-0.919**
	3		-0.763**
	4		-0.479

*, ** Significant and highly significant at 0.05 and 0.01 levels of probability, respectively.

reduction in wheat grain yield due to leaf rust attack varied from 20 to 25% in Egypt (Anonymous, 1997).

3. Adequacy of genetic model:

In the present study, scaling test (A, B and C) was employed to test the presence of epistasis (Table 4). The results stated insignificant non–allelic interaction for infection type in 4th cross only with main importance of additive gene effect, suggesting that, the simple additive–dominance genetic model proved to be satisfactory in explaining the inheritance of leaf rust resistance. Hereby, backcross technique with phenotypic selection in early segregating generations might be effective for improving leaf rust resistance in this cross. Similar finding has been reported by Brown *et al.*, 1997).

Significant non- allelic interactions were recorded for infection type in 1st, 2nd and 3rd crosses; disease severity and grain yield / plant in all crosses. This result suggests the presence of epistasis and the digenic model was adequate to explain the genetic system for these characters. This result is expected, since the artificially infection was performed by urediospores mixture of eleven physiological races, and the reaction for these races was done.

Six parameter genetic model presented in Table (4) indicate that, additive (d), dominance (h) and their all digenic interaction types i.e., additive x additive (i), additive x dominance (j) and dominance x dominance (l), were highly significant and involved in the genetic system controlling the inheritance of infection type and disease severity in most cases. The significant estimates of six parameters, indicate that, both additive and dominance as well as epistasis are all important in controlling these characters. In this connection, additive, dominance and epistasis were involved in the inheritance of leaf rust resistance (Shehab El-Din *et al.*, 1996, Singh *et al.*, 1999 and Yadav *et al.*, 1999).

It is important to mention that, the negative values have been recorded in the six parameters were in favour of decreasing infection type and disease severity, then increasing leaf rust resistance. Since increasing alleles for resistance were more frequent than decreasing ones.

The all types of gene effects and their digenic interaction were significant and involved in the inheritance of grain yield / plant in 1st cross. This result coupled with those obtained of infection type and disease severity, suggesting

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Table (4): Scaling test, adequacy of genetic model, genetic components of variance and heritability for the studied characters in four wheat crosses.

Character cross	Infection type				Disease severity (%)				Grain yield / plant			
	1	2	3	4	1	2	3	4	1	2	3	4
Scaling test :												
A	2.68**	0.90**	1.00**	0.83	9.8**	20.0**	16.4**	9.4**	-6.724**	-1.52	-1.79	-4.360**
B	3.13**	3.10**	1.44**	0.50	-6.0**	62.0**	32.0**	-15.4**	-2.774*	-2.89**	-6.53**	-1.886
C	0.17	3.90**	4.68**	0.86	-40.6**	107.0**	96.0**	128.6**	-1.658	-7.73**	-5.04*	-8.440
Appropriate genetic model :												
m	1.69**	2.10**	2.56**	2.78**	15.00**	45.00**	30.00**	75.00**	7.810**	6.850**	6.930**	3.130**
d	0.60**	0.25**	0.40**	0.25*	28.20**	7.50**	-0.30	17.30**	-3.500**	-0.160	1.440	-0.957
h	3.59**	-1.25**	-1.82**	2.09	34.10**	-51.50**	-20.10**	-140.30**	-6.161*	4.375*	-5.460*	1.514
i	5.64**	0.10	-2.24**		44.40**	-25.00**	-20.60**	-134.60**	-7.840*	3.320	-3.280	2.194
j	-0.23**	-1.10**	-0.22**		7.90**	-21.00**	-7.80**	12.40**	-1.975*	0.685	2.370*	-1.237
l	-11.45**	-4.10**	-0.20		-48.20**	-57.00**	-27.80**	140.60**	17.338**	1.090	11.600*	4.052*
Genetic components of variance												
VA*	0.179**	0.735**	0.172**	0.585*	11.434**	3.474*	15.368**	15.669**	4.202*	2.124*	4.338*	2.720*
VD*	0.018*	0.059*	0.031*	0.024*	1.045*	18.173**	0.571*	0.287*	5.985**	3.914**	4.996*	3.084**
VAD	0.0025	0.061	0.046	0.046	0.500	3.894	4.11	2.257	0.950	0.462	1.943	0.950
VE	0.115	0.174	0.160	0.081	2.271	2.495	1.817	1.772	1.114	0.449	0.778	1.606
Dominance ratio $\sqrt{4\,VD^*/VA^*}$	0.448	0.400	0.600	0.286	0.428	3.235	0.273	0.191	1.688	1.919	1.518	1.506
Heritability (hn)	57.37	75.93	47.38	84.78	77.52	14.38	86.55	88.39	37.18	32.74	42.89	36.70

*,** Significant and highly significant at 0.05 and 0.01 levels of probability.

VA*= Additive genetic variance

VD* = Dominance genetic variance

VE = Environmental variance

that grain yield and leaf rust resistance could be improved simultaneously through crossing and selection (pedigree method), to make the utmost of the types of gene effects. Whereas, the dominance (h) and the digenic interactions additive x dominance (j) and dominance x dominance (l) were significant in 3rd cross. Also, the dominance (h) was only significant and accounted the major part of gene effects in controlling grain yield in 2nd cross and dominance x dominance (l) in 4th cross. The considerable amount of non fixable gene action type displayed by these crosses might suggested that, improving grain yield could be achieved through hybrid breeding method. Similar result was detected by Hassan (1993) and Awaad (2002).

It is worthily to notice that, the dominance (h) and its digenic interaction, dominance x dominance (l) were significant and has different signs for infection type in 1st cross, disease severity in 1st and 4th crosses as well as grain yield / plant in 1st and 3rd crosses, indicating that interaction is predominantly of duplicate type (Singh et al., 1999). Whereas, the sign of (h) and (l) was similar for infection type in 2nd cross (confirmed with 9:7 ratio of χ^2 result) and disease severity in 2nd and 3rd crosses,

suggesting that interaction is predominantly of complementary type. Similar interpretation has been reported by Yadav et al., (1999).

4. Components of genetic variance and heritability:

Data presented in Table (4) clearly indicate that, additive and dominance genetic variances were significant, with the predominant of additive component in controlling infection type in all crosses; disease severity in 1st, 3rd and 4th crosses, resulting in dominance ratio was less than unity, suggesting the effectiveness of phenotypic selection for improving leaf rust resistance. Similar conclusion was reported by Ageez and Boulot (1999).

The dominance genetic variance was the prevailed type controlling the inheritance of disease severity in 2nd cross as well as grain yield / plant in all crosses, resulting in dominance ratio was more than unity, indicating the effectiveness of using hybrid-breeding method when commercial seed production of wheat is feasible. Similar conclusion was reported by Yadav et al., (1999) for leaf rust resistance and Awaad (2002) for grain yield.

Heritability estimates depend on the magnitude of its portions, additive and dominance genetic

components to the phenotypic variance (Table 4). In this regard, narrow sense heritability "hn" reflects the fixable type of gene action transmissible from the parents to the progeny or from generation to generation, was high for infection type and disease severity on three out of four crosses studied. These results allowing for considerable progress from selection. In this connection, high narrow sense heritability values have been reported for leaf rust resistance (Shehab El-Din *et al.*, 1996 and Ageez and Boulot, 1999).

Whereas, low (14.38%) "hn" estimate was reported for disease severity in 2nd cross and moderate (47.38 %) for infection type in 3rd cross, also moderate for grain yield /plant in all crosses. This result supported those obtained from adequacy genetic model which revealed that additive and dominance as well as epistasis were involved in the expression of these characters in aforementioned crosses. These results are confirmed by those of Awaad (2002) for grain yield /plant.

5.Chi square (χ^2) test:

Simple χ^2 tests were applied to compare the observed segregations to expected ratios (Table 5).

The results showed that the F_2 of ACSAD 945 x Sakha 69 cross gave 163 resistant:47 susceptible plants provide a ratio of 13 R:3 S ($\chi^2=1.817$) for two interacting gene pairs conferring resistance. Whereas, the observed resistant: susceptible ratio for F_2 population (Giza 168 x Gemmeiza 5) was 125 resistant: 75 susceptible, fitting the expected ratio 9:7 ($\chi^2 = 3.174$), suggesting the function of two complementary gene pairs controlling the resistance and confirmed with previous results of infection type.

The number of resistant: susceptible plants were 191:19 for F_2 population of Gemmeiza 9 x PAT10/ ALD'S', fitting the theoretical ratio 15:1 ($\chi^2 = 2.805$). This result suggested the presence of high levels of adult plant resistance in both Gemmeiza 9 and the exotic PAT10/ALD'S' one, thus could be used as donor for resistance genes. The previous result indicating the functioning of two double dominant gene pairs. Whereas, the number of resistant: susceptible plants in F_2 population of Sakha 69 x Sahel 1 were 62:148, provide a ratio of 1R: 3S ($\chi^2 = 2.292$), for two recessive complementary genes conferring resistance.

The various ratios have been recorded for resistance reflects the

differences in the genetic makeup of the parental materials for resistance. In this respect, leaf rust resistance has been documented to be a simple inherited as monogenic character (Dyck, 1991, Sibikeev *et al.*, 1995; Sudhakar and Joshi, 1996; Brown *et al.*, 1997 and Barcellos *et al.*, 2000), or controlled by a few number of major gene pairs (Abd El-Latif *et al.*, 1995; Shehab El-Din *et al.*, 1996 and Singh *et al.*, 2001). Whereas some recent researchers showed that resistance is a polygenic trait governed by many gene pairs (Sibikeev *et al.*, 1996 and Ageez and Boult, 1999).

Thus, pyramiding leaf rust resistance genes from the studied resistant germplasm may prove to be useful in breeding for diseases resistant varieties.

Table (5): Segregation of reaction to *Puccinia recondita* f. sp. *tritici* in F_2 progenies of four wheat crosses.

Cross	Number of plants		Expected ratio	χ^2
	Resistant (R)	Susceptible (S)		
I. Resistant x Susceptible				
1. ACSAD 945 x Sakha 69	163	47	13 :3	1.817
2. Giza 168 x Gemmeiza 5	125	75	9:7	3.174
II. Resistant x Resistant				
3. Gemmeiza 9 x PAT10/ALD'S"	191	19	15:1	2.805
III. Moderate susceptible x Moderate susceptible				
4. Sakha 69 x Sahel 1	62	148	1:3	2.292

For 1 df , the value of χ^2 is 3.84 (P=0.05)

REFERENCES

Abd El-Latif, A. H.; T. M. Shehab El-Din; M. M. El-Shami and S. A. Aboul–Naga (1995). Genetics of *Triticum aestivum: Puccinia recondita tritici* interaction in three Egyptian wheat cultivars. J. Agric. Res. Tanta Univ., 21: 182 – 188.

Ageez, A. A. and O. A. Boulot (1999). Quantitative determination of the gene action of leaf rust resistance. Egypt J. Appl. Sci., 14 (6): 216-226.

Anonymous (1997). Wheat rusts in Egypt: Symposium of wheat rusts in Egypt. Egyptian Society of Plant Pathology. Held in

Genetic Engineering Institute. ARC Giza. 10 November.

Atteia, M. F. (2001). Response of some Egyptian wheat cultivars to leaf rust infection. J. Adv. Agric. Res., 6 (1): 221-230.

Atteia, M. F.; A. I. Nawar and I. F. Rehab (2000). Yield of local wheat cultivars as affected by leaf rust and date of potassium application J. Adv. Agric. Res., 5 (1): 1117-1129.

Awaad, H. A. (2002). Genetic analysis, response to selection and prediction of new recombinant lines in bread wheat (*Triticum aestivum* L.) Zagazig J. Agric. Res., 29 (5): 1343-1365.

Barcellos, A. L.; A. P. Roelfs and M. I. B. DE Mouraes–Fernandes (2000). Inheritance of adult plant leaf rust resistance in the Brazilian wheat cultivar Toropi. Plant Disease 84 (1): 90-93.

Brown, G. L. G.; B. S. Bill; T. S. Cox and S. Leath (1997). Transfer of disease resistance genes from *Triticum araraticum* to common wheat. Plant Breeding 116 : 105 – 112.

Doling, D. A. and J. K. Doodson (1968). The effect of yellow rust on yield of spring and winter wheat. Br. Mycol. Soc. Trans., 5: 427-434.

Dyck, P. L. (1991). Genetics of adult- plant leaf rust resistance in Chinese spring and Sturdy wheats. Crop Sci., 31: 309-311.

Hassan, E. E. (1993). Genetic analysis of some main spike characteristics in four wheat crosses (*Triticum aestivum*, L.). Zagazig J. Agric. Res., 20: 611-621.

Kearsey, M. J. and H. S. Pooni (1996). The genetical analysis of Quantitative Traits. 1st ed. Chapman and Hall. London pp. 46

Knott, D. R. (1989). The wheat rusts breeding for resistance. In: Monographs on Theoretical and Applied Genetics, Vol. 12. Springer–Verlag, Berlin.201 pp.

Mather, K. and J. L. Jinks, 1982. Biometrical genetics. 3rd ed. Chapman and Hall, London.

McIntosh, R. A.; G. E. Hart and M. D. Gale (1995). Catalogue of gene symbols for wheat. Pages 1333 – 1500 in Z.S. Li. and Z. Y. Xin (eds). Proc. 8th Int. Wheat Genet. Syml., July 20–25,1993, Beijing , China .

McIntosh, R. A.; C. R. Vetlings and R. F. Park (1995 a). Wheat rusts. An atlas of resistance genes. CSTRO Publications, East Melbourne , Australia.

Peterson, R. F.; A. B. Cammpell and A. E. Hannah (1948). A diagrammatic scale for estimating rust intensity on leaves and stem of cereals. Can. J. Res., 60: 496-500.

Rangaswamy,R.(2000).A textbook of agricultural statistics. New Age International (P) Limited Publishers, New Delhi.

Shehab El-Din, T. M.; M. M. Shami and A. H. Abd El-Latif (1996). Qualitative and quantitative genetic studies on *Triticum aestivum: Puccinia recondita* interaction. J. Agric. Sci. Mansoura Univ., 21 (11): 3769-3778.

Sibikeev, S. N.; S. A. Voronina and V. A. Krupnov (1995). Genetic control for resistance to leaf rust in wheat- Agropyron lines: Agro 139 and Agro 58. Theor.Appl.Genet.,90:618–620.

Sibikeev, S. N.; V. A. Krupnov; S. A. Voronia and V. A. Elesin (1996). First report of leaf rust pathotypes virulent to highly effective *Lr*-genes transferred from *Agropyron* species to bread wheat. Plant. Breeding 115 : 276-278.

Singh R. K. and B. D. Chaudhary (2001). Biometricial methods in quantitative genetic analysis. Kalyani Publishers, New Delhi. Ludhiana.

Singh, D.; R. F. Park and R. A. McIntosh (2001). Inheritance of spring and English winter wheat varieties. Plant Breeding 120 (6): 503-507.

Singh G.; G. S. Nanda and V. S. Sohu (1999). Quantitative analysis of adult plant resistance to stripe and leaf rust in wheat (*Triticum aestivum* L). Agricultural Science Digest (Karnal) 19 (4): 235-238.

Stakman, E. C.; D. M. Stewart and W. Q. Loegering (1962). Identification of physiologic races of *Puccinia graminis* var tritici . ARS, USDA, Agric. Res. Serv. Bull. E.617 . 53pp.

Sudhakar, Y. and A. K. Joshi (1996). Genetics of resistance to *Puccinia recondita* in two wheat crosses. Plant Breeding 115: 85-88.

Yadav, B.; M. Yunus and N. K. Dudi (1999). Genetics of field resistance to leaf rust of wheat under rainfed conditions. Rachis 18 (1): 1-3.

النظام الوراثى المتحكم فى مقاومة مرض صدأ الأوراق فى قمح الخبز

حسن عودة عواد*، عبد الحميد حسن سالم*، محمود محمد محمد عطية**،
ميناس السيد على سلام***

• قسم المحاصيل ـــ كلية الزراعة – جامعة الزقازيق- مصر

**قسم النبات الزراعى و أمراض النبات ـــ كلية الزراعة – جامعة الزقازيق- مصر

*** معهد بحوث أمراض النباتات مركز البحوث الزراعية – الجيزه – مصر

أجريت هذه الدراسة بالمزرعة التجريبية بكلية الزراعة- جامعة الزقازيق مستخدما نظام الستة عشائر لاربعة هجن من قمح الخبز هى ١) أكساد ٩٤٥ × سخا ٦٩ ،

٢) جيزة ٢٦٨ × جمـيزة ٥ ، ٣) جمـيزة ٩ × PAT10/ALD"S" ، ٤) سخا ٦٩×
ساحل١ ناتجة من التهجين بين سبعة أباء متباينة فى مقاومتها لمرض صدأ الأوراق ، حيـث
أجريت العدوى بمخلوط من أحد عشر سلاله فسيولوجية مــن الجراثيـم اليوريديـة للفطـر
Puccinia recondita Rob. Ex Desm. f. sp. *tritici* Eriks & Henn بـهدف
دراسة الاختلافات فى ردود أفعال التراكيب الوراثية للمقاومة من خلال تحديد طراز الاصابـة
وشدة الاصابة (%) ومحصول حبوب النبات والخسارة المتوقعه ، ويمكن تلخيص أهم النتائج
فمايلى:-

أظهرت النتائج وجود أختلافات معنوية بين أباء القمح وعشائرها للصفات المدروسـة،
وكانت أكثر الاصناف مقاومة جيزة ١٦٨ (3R) يليه "PAT10/ALD"S (5 R) واكساد
٩٤٥ (10 R) وجميزة ٩ (20 R-MR) ، فى حين كانت الاصناف جمـيزة ٥-S (60
MS)، سخا ٦٩ (50.6 MS) وساحل ١ (40.8 MS) قابلة للاصابة. وأبـدت نباتـات
الجيل الأول مقاومة عالية ، كاملة وجزئية تجاة الاب المقاوم فى الهجن الأول والثانى والثالث
تجاه الاب المقاوم، على الترتيب.

أظهرت النتائج وجود أرتباط سالب وعالى المعنوية بين محصول الحبوب وكـل مـن
طراز الاصابة وشدة الاصابة فى معظم الهجن .

أشارت نتائج أختبار المقياس (A, B and C) أن الموديل الوراثى غير البسيط هــو
الملائم لتفسير وراثة المقاومة لمرض صدأ الأوراق للصفات المدروسة فى معظم الهجن. فـى
حين كان النظام الوراثى البسيط هو الملائم لتفسير وراثة المقاومة للمرض مع سـيادة الفعـل
الجينى المضيف فى الهجين الرابع. وكان الفعل الجينى المضيف، والسيادى والتفاعل (مضيف
× مضيف)، (مضيف × سيادى) و (سيادى× سيادى) هو المتحكم فى وراثة طراز الاصابـة
وشدة الاصابة فى جميع الهجن مع قليل من الاستثناءات، كما كانت تلك الطرز مـن الفعـل
الجينى هى المتحكمة فى وراثة محصول حبوب النبات فى الهجين الأول. فى حين كان الفعـل
الجينى السيادى والتفاعل (مضيف × سيادى) و(سيادى × سيادى) معنويا لمحصول الحبـوب
فى الهجين الثالث.

كان التفاعل غير الاليلى من النوع المضاعف Duplicate هو السائد لصفة طـراز
الاصابة فى الهجين الأول ، شدة الاصابة فى الهجين الأول والرابع ومحصول الحبوب فـى
الهجين الأول والثالث. بينما كان طراز التفاعل من النوع المكمل Complementary أكثر
وضوحا لطراز الاصابة فى الهجين الثانى (متوافقة مع النسبة ٩:٧ لنتائج أختبار مربع كـاى)
وشدة الاصابة فى الهجين الثانى والثالث.

كان التباين الوراثى المضيف عالى المعنوية وأكثر أهمية فى وراثة مقاييس المقاومـة
لصدأ الاوراق فى معظم الحالات. بينما لعب التباين الوراثى السيادى دوراً مهما فـى وراثـة
محصول حبوب النبات فى جميع الهجن.

كانت كفاءة التوريث فى المعنى المحدود عالية لطراز الاصابة وشدة الاصابة فــى
ثلاث هجن من الاربعه المدروسة' إلا أنها كانت متوسطة لمحصول الحبوب فى جميع الهجن.

أظهر التحليل الوراثى باختبار مربع كاى أن المقاومة لمرض صدأ الأوراق محكومـة
بزوجين من العوامل الوراثية المتداخلة فى الهجين الأول ، وزوجين من الجينات المكملة فـى
الهجين الثانى، وزوجين من العوامل الوراثية المتضاعفة فى الـهجين الثالث وأثنين مـن
الجينات المكملة المتنحية فى الهجين الرابع .