ROLE OF RESISTANCE (*YRS*) GENES TO *PUCCINIA STRIIFORMIS* IN FIVE BREAD WHEAT CULTIVARS SUSCEPTIBLE AND VALIDATION BY MOLECULAR MARKERS IN ASSESSMENT OF RESISTANCE

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ABSTRACT

Wheat stripe rust, caused by *Puccinia striiformis f. sp. tritici*, is one of the most destructive diseases of wheat in the world. Emergence of new race of the pathogen in Egypt at last decades, spread of those races pose effect at to wheat production in Egypt, has required assemblage of a broad genetic base of resistance. Five ten crosses between *Yr5, Yr10* and *Yr15* and each of Sids 12, Sids 13, Gemmeiza 10, Gemmeiza 11, and Sakha 93, were performed. Results indicated that the five varieties parents exhibited high susceptible reaction against stripe rust at seedling and adult stage, on the other hand monogenic lines exhibited high resistance. While crosses against stripe rust at seedling and adult stages proved that plant segregation F1 plants of the five ten crosses having *Yr5, Yr10 and Yr15,* were resistant and exhibited low stripe rust reaction (0 - 0, and 1) at seedling stage and low stripe rust severity ranged between(0, 10R and 10MR) at adult stage. The result of F2 plants reaction exhibited wide range of stripe rust reaction (0 to 9) at seedling stage and severity ranged between (0 to 80S) at adult stage but the direction was in the side resistance and this confirmed the results of F1. This result confirmed the presence of resistant gene in the segregations of the resulted crosses and verified that a single dominant pair gene controls stripe rust resistance at adult stages. Resistance gene of the F2 was expression performance to resistance genes to *Yr 5, Yr 10* and *Yr 15*, those tolerant to yellow rust introgressive lines could be widely used as donors of stability in practical selection of bread wheat. Using the molecular marker method, *Yr10* In this study, we used the primer Xpsp3000 to identify markers linked to yellow rust resistance genes. In this respect, specific DNA segment of 52 individual of F2 have linked with primer Xpsp3000 260-bp band. The rest 18 individuals did not linked with the primer Xpsp3000. Segregation in F2 of individual which, reacted with the primer YrSTS/7, 8 and shown in this respect, specific DNA segment of 58 individual of F2 have linked with primer YrSTS/7, 8 439-bp band. The rest 21 individuals did not link with the primer YrSTS/7, 8. These markers provide an important tool to plant breeders for marker-aided wheat breeding and also for pyramiding resistance genes in the absence of distinguishable rust virulence's

Keywords: *Triticum aestivum*, stripe rust, Yr's genes, molecular markers

INTRODUCTION

Stripe rust, caused by *Puccinia striiformis f. sp. tritici*, is one of the most important diseases of wheat in the world. In Egypt, stripe rust attacked most of the commercial wheat cultivars during 1968 to 1995, causing severe infection in North Delta area EI-Daoudi et al. (1996). Stripe rust caused high loss in the production of most Egyptian wheat cultivar in the delta area during 1996/1997 growing seasons EI-Daoudi, (1998). Identifying resistance genes in wheat varieties, even those overcome by new races of the yellow rust pathogen is important for a better understanding of race changes and a better use of various resistance genes with various strategies (Chen 2005). Gene pyramiding, gene deployment and multilane varieties were considered to be useful for prolonging race-specific resistance (McIntosh and Lagudah 2000). There are a few of genes are effective in the seedling stage (Ma *et al*. 2001; Yan *et a*l. 2003). Thus, it is very important to search to identify new resistance genes for wheat breeding programmes. Identification of yellow rust resistance genes and breeding of resistant varieties is an effective approach to minimizing wheat losses due to this disease. To date, more than 70 stripe rust resistance genes, officially or provisionally designated Yr for 'stripe rust', have been reported in wheat (McIntosh *et al.,* 2009; Chen 2005; Cheng and Chen 2010).

Yr5 was described first in 1966 by Macer in *Triticum spelta album* (Macer. 1966). *Yr5* is located on chromosome arm 2BL, 21 cM away from the centromere (Law. 1976). (Kema 1992) transferred this gene into some commercial cultivars. Gerechter-Amitai., *et al* 1970). reported that accession G-25 of Triticum dicoccoides Korn was resistant to many races of Puccinia striiformis from different geographical origins. (Gerechter-Amitai *et al.,* 1974 and 1989) Later, it was shown that this stripe rust resistance was conferred by the dominant gene *Yr15*. (McIntosh *et al.,*1996) showed that it is located on the short arm of chromosome 1B . Yr15 was introgressed into tetraploid and hexaploid wheats . With the use of molecular markers and a genetic linkage map, various wheat genes that control yellow rust resistance have been successfully tagged (Prasad *et al*. 2003). Identify potential molecular markers associated with yellow rust resistance in wheat. These markers shall be used for selecting yellow rust resistance in segregating populations. A number of genes affect yellow rust resistance in wheat. (McIntosh *et al*. 2005). Molecular markers have been linked to many yellow rust resistance genes in wheat, such as *Yr5, Yr10, Yr15, Yr17, Yr24, Yr26*, *Yr29, Yr32, Yr34* and *YrH52* (Chague *et al*. 1999; Robert et al. 2000; Peng *et al.* 2000; Sun *et al.* 2002; and Wang *et al.* 2008). These markers provide an

important tool to plant breeders for marker-aided wheat breeding and also for pyramiding resistance genes in the absence of distinguishable rust virulence's (Kaur *et al*. 2008). In this study, we used these primer sets to identify markers linked to yellow rust resistance genes in wheat by bulk sergeant analysis. Here, we report the identification of Xgwm382 marker that is associated with yellow rust resistance and can potentially be used to select yellow rust resistant wheat germplasm. Molecular markers are relatively short sequences which can be specifically amplified by PCR and detected in the presence of all other genomic sequences whose location in the genome is mapped. These markers produce simple and reproducible patterns on agarose or poly-acrylamide gel. Some STS markers reported for Yr genes include YrSTS(7,8), YrSTS (Lagudah , 2011) and S19M93-140 for Yr5 (Chen. *et. al* 2003), Yr10 Smith et. al., 2003)

MATERIALS AND METHODS

The cultivars used in this study included *i.e.* Sids 12, Sids 13, Gemmeiza 10, Gemmeiza 11,and Sakha 93 exhibited a wide range of variability in their susceptibility to stripe rust, and known *Yr* gene carrier monogenic lines, *Yr5,Yr10* and *Yr15* exhibited high level of resistance to stripe rust at adult stage under Egyptian condition. These parents were sown at Sakha station and Nubaria Agric. Res. Sta. Development of crosses and generations: From 2012-2013 to 2014-2015, five cultivars, as female parent, was crossed with known genes carrier lines (male parent), the seed was sown to get the F1 seeds and the F1 plants were self-pollinated to obtain F2 seeds.

Infection assessment and statistical analysis

Through the methods of classical genetics, allelic analysis, wheat yellow rust resistant genes were analyzed at seedling stage. Each cultivar, F1 and F2 were grown in standard peat soil in 10 cm square pots containing 10 plants. Seedlings at the two leaf stage when the first leaf was fully expelled were inoculated with *Pst* isolates (Stubbs, 1988). After inoculation, the seedlings were placed in a dew chamber at 10ºC and 100% of relative humidity for 24 h and then transferred to greenhouse maintained with 16 h light/8 h dark photoperiod at 14-18 C. Infection type (IT) was recorded 15-17 days after inoculation when rust was fully developed on the susceptible check Morocco according to scale described by McNeal *et al.*. (1971). Based on the traditional 9 scale of infection types (IT), 4 classes were used in this study, the infection types i.e. 0, 1 and 2 were resistant; 3, 4 and 5 types, moderate resistant; 6 and 7 moderate susceptible and 8 and 9 high susceptible. . The division standard to resistant and

susceptible was adapted according to infection type levels and infection type number in the parents, F1 and F2 generation to determine resistant or susceptible Infection type (Liu, 1988).

Table 1: Name and pedigree bread wheat cultivar used in the study

No	Genotypes	Pedigree	Reaction to yellow rust
1	Sids 12	BUS//7C//ALD/5/MAYA74/ON//1160.147/3/BB/GLL/4/CHAT"S"/6/MAYA/VUL//CMH74A.630/4*SX. SD720096-4SD-1SD-1SD-0SD.	Susceptible
2	Sids 13	ALMAZ-19=KAUZ"S"//TSI/SNB"S". ICW94-0375-4AP-2AP-030AP-0APS-3AP-0APS-050AP-0AP-0SD.	Susceptible
3	Gemmeiza 10	MAYA 74 "S" / ON//1160 – 147/3/BB/GLL/4/ CHAT "S" /5/ CROW "S" CGM 5820 - 3GM - 1GM - 2GM – OGM	Susceptible
4	Gemmeiza 11	BOW"S"/KVZ"S"//7C/SER182/3/GIZA 168/SAKHA61. GM7892-2GM-1GM-2GM-1GM-0GM.	Susceptible
5	Sakha 93	Sakha 92 / TR 810328 S 8871-1S-2S-1S-0S	Susceptible
6	*Yr5*		Resistant
7	*Yr10*		Resistant
8	*Yr15*		Resistant

Chi-square ($\chi 2$) and corresponding probability (P) values were used to evaluate the goodness of fit of the observed and expected segregation ratios of F2 populations. At the adult tests under field condition was restricted in the spreader plants which were using artificial infection to stripe rust races. Inoculums is virulent for *Yr2, Yr6, Yr7, Yr8, Yr9, Yr11, Yr12, Yr17, Yr18, Yr27and* a virulent for *Yr5, Yr10, Yr15, YrSP* gen. All materials were inoculated at seedling and adult, were considered as the susceptible ones. To clarify, mode of inheritance of expected ratio of the phenotypes classes of the stripe rust, infection types were determined using ($\chi 2$) analysis according to the method of Steel and Torrie (1960).

DNA extraction procedure

Total DNA of each wheat cultivar and isogenic line was extracted from 60 mg leaf tissue which digested in liquid nitrogen with a mortar and pestle using i-genomic plant DNA extraction Mini Kit (iNtRON Biotechnology, Inc, Cat. No. 17371) according to manufacturer's instructions. The eluted DNA was stored at -20.

Polymerase chain reaction was performed in a thermocycler according to the conditions in Table (2). Following the amplification, 2 µl loading buffer was mixed with 5 µl PCR product that ran on 1% agarose gel in 1x TBE buffer at 85V for two hours and the bands were observed

under UV light. The gels were stained using ethidium bromide and either Gene Ruler 100 bp DNA Ladder Plus (Fermentas, Germany) was used as a molecular weight marker. The products of primer YrSTS7/8 did not separate on 1% agarose and therefore were analyzed by Poly-Acrylamide Gel Electrophoresis (PAGE) on a denaturing 6% gel at 200 Vfor 5 hours. Band patterns were visualized using silver staining (Chen *et al.* 2003) and images were captured by a scanner.

Table 2: Sequences of markers used to identify yellow rust resistance genes

Gene	Marker	Primer Sequence	Reference
Yr10	Xpsp3000	F:GCAGACCTGTGTCATTGGTC R:GATATAGTGGCAGCAGGATACG	Bariana *et al*. (2002)
Yr5	*YrSTS(7,8)*	F:GTACAATTCACCTAGAGT R:GCAAGTTTTCTCCCTATT	Chen *et al*. (2003)

Table 3: PCR conditions used for each primer*

Primer	Initial Denaturation**	Number of cycles	Enaturation	Annealing***	Extension***	Final Extension**
YrSTS7/8	94 (3)	30	94 (60)	60 (30)	72 (120)	72 (10)
Xpsp3000	94 (3)	30	94 (60)	60 (30)		72 (10)

* The numbers before the parentheses indicate temperature 'ºC'.; ** The numbers in the parentheses indicate initial denaturation and final extension in minutes; *** The numbers in the parentheses show duration of each step in seconds

RESULTS

Evaluation of the tested wheat monogenic lines, F1 hybrids and F2 against stripe rust at seedling and adult stages:

Data in Table (3) reveal the distribution of infection type, of parents, and F1 hybrids for the five ten crosses having *Yr5, Yr10* and *Yr15*. In this respect, Sids-12, Sids-13, Gemmeiza-10, Gemmeiza-11, and Sakha-93 exhibited high susceptibility infection type ranged between 7-9. Meanwhile, the monogenic lines *Yr5, Yr10* and *Yr15* exhibited infection type 0, - 1. As for F1 plants of the five ten tested crosses, all plants exhibited low infection type ranged between 0, - 2 (resistance), this result revealed that resistance was dominant over susceptibility in these crosses in F1 stage

Table 4: Response of three wheat monogenic lines, five cultivars and F1 hybrids against stripe rust infection type using race 134E158 at seedling stage

Yr genes , cultivars and F1 hybrids	Phenotypes	
	*R	S
Yr5	R	
Yr10	R	
Yr15	R	
Sids-12		S
Sids-13		S
Gemmiza-10		S
Gemmiza-11		S
Sakha-93		S
Yr5 x Sids-12**,** Sids-13, Gemmiza-10, Gemmiza-11 and Sakha-93	R	
Yr10 x Sids-12**,** Sids-13, Gemmiza-10, Gemmiza-11 and Sakha-93	R	
Yr15 x Sids-12**,** Sids-13, Gemmiza-10, Gemmiza-11 and Sakha-93	R	

R = resistant, S = Susceptible - Disease rating recorded using 0-9 scale McNeal *et al*. (1971)

Table 5: Evaluation of crosses of the five cvs. having resistant *Yr's* genes against stripe rust infection using race 134E158 at seedling stage

Crosses	**Number of F2 plant**	**Phenotypes (observed Ratio)**		**Expected Ratio**	**X^2**	**P.value**
		R	**S**			
Yr5 x Sids-12	135	94	41	**3 : 1**	2.08	**0.25-0.1**
Yr5 x Sids-13	192	143	49	**3 : 1**	0.03	**0.9-0.75**
Yr5 x Gemmeiza-10	175	130	45	**3 : 1**	0.05	**0.9-0.75**
Yr5 x Gemmeiza-11	121	90	31	**3 : 1**	0.03	**0.9-0.75**
Yr5 x Sakha-93	143	105	38	**3 : 1**	0.19	**0.75-0.5**
Yr10 x Sids-12	147	108	39	**3 : 1**	0.18	**0.75-0.5**
Yr10 x Sids-13	180	141	39	**3 : 1**	0.11	**0.75-0.5**
Yr10 x Gemmeiza-10	198	153	45	**3 : 1**	0.55	**0.75-0.5**
Yr10 x Gemmeiza-11	143	101	42	**3 : 1**	1.46	**0.25-0.1**
Yr10 x Sakha-93	180	140	40	**3 : 1**	0.74	**0.75-0.5**
Yr15 x Sids-12	150	105	45	**3 : 1**	2.00	**0.25-0.1**
Yr15 x Sids-13	190	145	45	**3 : 1**	0.18	**0.75-0.5**
Yr15 x Gemmeiza-10	163	118	45	**3 : 1**	0.59	**0.75-0.5**
Yr15 x Gemmeiza-11	140	118	22	**13 : 3**	0.847	**0.75-0.5**
Yr15 x Sakha-93	120	83	37	**3 : 1**	2.18	**0.25-0.1**

Results presented in Table (4) showed that segregated phenotypes F2 plants of the crosses between *Yr5, Yr10* and *Yr15* and the wheat varieties Sids 12, Sids 13 ,Gemmeiza 10, and Sakha 93 the resistance was dominant over susceptibility in these crosses ,with expected ratio 3:1. This 3:1 ratio verified that single dominant gene pair controls resistance and supported the fact that *Yr5, Yr10* and *Yr15* carried the seedling stage, while the cross *Yr15* x Gemmeiza-11 number of resistant and susceptible plants were 118 and 22, respectively. These frequencies fitted the theoretical expected ratio of 13: 3 with P value 0.5-0.25 indicated that presence of one dominant gene RR causing resistance against yellow rust, in the absence of an other dominant gene, which interacted with it to cause susceptibility by inhibiting the effect of the resistance gene

Data in Table (5) showed that, the wheat monogenic lines *Yr5, Y10* and *Yr15* were completely resistant reaction. Showed zero percent final rust severity compared with the other tested monogenic lines which showed final rust severity ranged from 0 to TrR. While, the tested wheat cultivars *i.e*. Sids 12, Sids 13 ,Gemmeiza 10, Gemmeiza 11 and Sakha 93 showed all of five parents exhibited high susceptibility, where stripe rust severity (%) ranged between (10MS-80S) during the three seasons. As for as F_1 plant of the five ten tested crosses exhibited high resistance where their stripe rust severity. (%) ranged between 0 and 5R these results revealed that resistance was dominant over susceptibility in these crosses in F_1 at adult stage in Table (6).

Table 6: Final stripe rust severity of three wheat monogenic lines and five cultivars at adult plant stage at Sakha station during three successive growing seasons (2012/13 - 2014/15)

Yr genes and cultivars	**Season / rust severity**		
	2012/13	**2013/14**	**2014/15**
Yr5	0	0	0
Yr10	0	0	TrR
Yr15	0	0	0
Sids 12	30S	40S	80S
Sids 13	20S	30S	70S
Gemmiza 10	10MS	10MS	30S
Gemmiza 11	10MS	10MS	40S
Sakha 93	30S	30S	80S

Table 7: Inheritance of yellow rust resistance in F1 hybrids obtained by the crossing of resistance genes *Yr 5, Yr 10* and Yr15 with five Egyptian cultivars under filed condition

F1 hybrids	No .of plants under study	Ratio of resistant and susceptible plants	
		R	**S**
Yr5 x (Sids-12**,** Sids-13, Gemmiza-10, Gemmiza-11 and Sakha-93)	**150**	**150**	**-**
Yr10 x (Sids-12**,** Sids-13, Gemmiza-10, Gemmiza-11 and Sakha-93)	**165**	**165**	**-**
Yr15 x (Sids-12**,** Sids-13, Gemmiza-10, Gemmiza-11 and Sakha-93)	**150**	**150**	**-**

The infection type frequency distribution and the disease severity class of the F2 populations of each of the five ten crosses were performed. Inoculation was accomplished by using a mixture of the most prevalent races in the area at adult stage.

Data presented in Table(7) the obtained results derived from F2 of the five ten tested crosses having resistance genes exhibited a wide range of reaction to stripe rust severity ranged between 0-80S. The segregated phenotypes showed that F2 plants of the crosses between Yr5, Yr10 and Yr15 and the wheat varieties Sids- 12, Sids-13, Gemmeiza-10, Gemmeiza-11 and Sakha-93 were as follow, (96R:32S, 102R:45S, 124R:30S, 153R:54S and 146R:51S), (131R:40S, 120R:46S, 1161R:53S, 101R:42S and 102R:30S) and (166R:49S, 168R:61S, 120R:46S, 98R:47S and 125R:46S), respectively, with expected ratio 3:1. This 3:1 ratio verified that single dominant gene pair controls resistance and supported the fact that Yr5, Yr10 and Yr15 carried the seedling and adult plant resistance gene and showed gene expression of resistance to stripe rust in all tested crosses at adult

Table 8: Evaluation of crosses of the five wheat cvs. having resistant genes *(Yr's)* against stripe rust infection using a mixture races at adult stage

Crosses	**Number of F2 plant**	**Phenotypes (observed Ratio)**		**Expected Ratio**	**X^2**	**P.value**
		R	**S**			
Yr5 x Sids-12	128	96	32	**3 : 1**	0.00	**100**
Yr5 x Sids-13	147	102	45	**3 : 1**	2.469	**0.25-0.1**
Yr5 x Gemmeiza-10	154	124	30	**3 : 1**	2.502	**0.25-0.1**
Yr5 x Gemmieza-11	207	153	54	**3 : 1**	0.130	**0.5-0.25**
Yr5 x Sakha-	197	146	51	**3 : 1**	0.083	**0.9-0.75**

93						
Yr10 x Sids-12	171	131	40	**3 : 1**	0.236	**0.5-0.25**
Yr10 x Sids-13	166	120	46	**3 : 1**	0.651	**0.5-0.25**
Yr10 x Gemmeiza-10	214	161	53	**3 : 1**	0.006	**0.99-0.95**
Yr10 x Gemmeiza-11	143	101	42	**3 : 1**	1.457	**0.25-0.1**
Yr10 x Sakha-93	132	102	30	**3 : 1**	0.364	**0.5-0.25**
Yr15 x Sids-12	215	166	49	**3 : 1**	0.560	**0.5-0.25**
Yr15 x Sids-13	229	168	61	**3 : 1**	0.328	**0.5-0.25**
Yr15 x Gemmeiza-10	166	120	46	**3 : 1**	0.651	**0.5-0.25**
Yr15 x Gemmeiza-11	145	98	47	**3 : 1**	4.251	**0.05-0.01**
Yr15 x Sakha-93	171	125	46	**3 : 1**	0.329	**0.5-0.25**

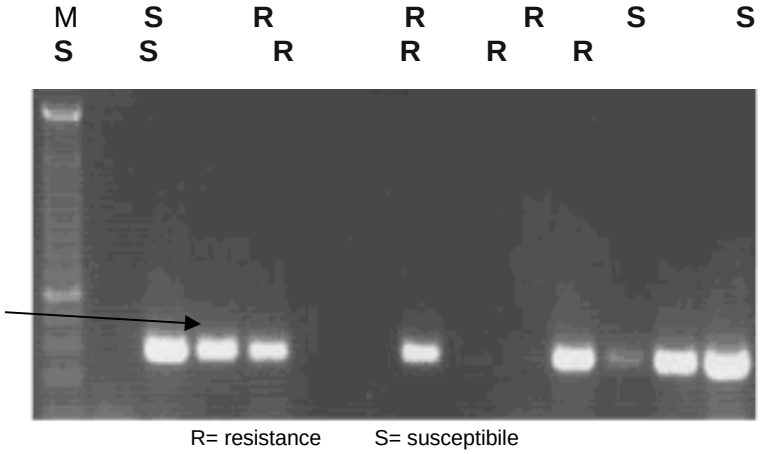

Figure 1: Amplification with marker Xpsp3000 produced 260-bp fragment in F2 resistance segregation carrier gene Yr10

Marker for Yrs gene

Stripe rust resistance gene *Yr10* is race-specific, and was mapped on chromosome 2BS of wheat. The available marker Xpsp3000, for *Yr10.* The results PCR amplification with marker Xpsp3000 produced 260-bp fragment in F2 resistance segregation carry gene *Yr10* and did not show any amplification in F2 susceptible segregation not carry gene *Yr10* (figure 1). Segregation in F2 of *Yr10*x Sids 12 individual which, reacted with the primer Xpsp3000 and shown in fig(1) in this respect, specific DNA segment of 52 individual of F2

have linked with primer Xpsp3000 260-bp band. The rest 18 individuals did not linked with the primer Xpsp3000. this result reveled that the resistance: susceptible individuals are 52:18 with expected ratio 3:1 which verified by X^2. The results of current study suggest that transfer by crosses *Yr10* could be one of the genes responsible for the resistance.

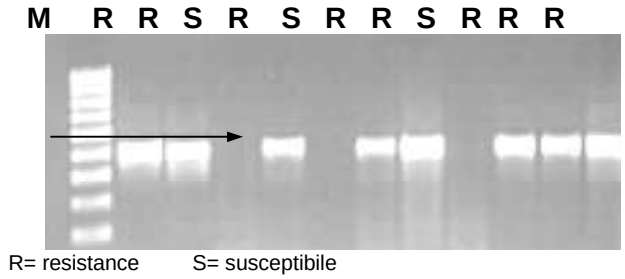

Figure 2: Amplification with marker YrSTS/7,8 produced of 439bp fragment in F2 resistance segregation carrier gene Yr5

The results PCR amplification with marker *YrSTS/7,8* produced 439-bp fragment in F2 resistance segregation carry gene *Yr5* and did not show any amplification in F2 susceptible segregation not carry gene *Yr5* (figure2). Segregation in F2 of individual which, reacted with the primer *YrSTS/7,8* and shown in fig(2) in this respect, specific DNA segment of 58 individual of F2 have linked with primer *YrSTS/7,8* 439-bp band. Twenty-one of individual plants in F2 did not show any amplification to primer *YrSTS/7, 8* , therefore, the status of *Yr10* gene in these individual plants. This result reveled that the resistance: susceptible individuals are 58:21 with expected ratio 3:1 which verified by X^2. The results of current study suggest that transfer by crosses Yr5 could be one of the genes responsible for the resistance.

DISCUSSION

Yellow rust is one of the most aggressive diseases on common wheat *Triticum aestivum* worldwide. In the Egypt, the north country are the most affected, although is becoming more important in the country . Stripe rust is caused by the fungus *Puccinia striiformis*. *f. sp. tritici Eriks*. The preferred way of controlling the disease is through the use of resistant cultivars. There are many genes that can express resistance to this disease. However, changes in pathogen virulence can render them useless for breeding after period of time. Most of the Egyptian cultivars exhibited considerable level of susceptibility, with

few exception EI-Dauodi *et al*. (1998).

Results studied five ten crosses to stripe rust infection at seedling stage under greenhouse condition, the infection types of F_1 plants indicated that the five ten tested crosses having *Yr5, Yr10* and *Yr15* it's resistant. As well as, F_2 segregation of crosses having *Yr5, Yr10* and *Yr15* confirmed the results of F_1 and indicated that resistance was dominant over susceptibility. At adult stage *Yr5, Yr10* and *Yr15* and its crosses with tested , (F_1), exhibited high resistance. The rest of tested parents showed different degrees of susceptibility. Conversely F_2 segregations of crosses having *Yr5, Yr10* and *Yr15* showed that resistance was dominant over susceptibility. Also, results indicated that crosses fitted the expected ratio 3:1. This ratio verified that single dominant gene pair controls stripe rust resistance and supported the F-i result at seedling and adult stages. This data similarly results (Tokubayeva and Shulembaeva 2012), The population analysis of F1 hybrids received from crossings of l-344 and l-345 lines with the lines carrying effective Yr genes all the hybrids F1 showed dominant character of inheritance for the resistance. . In F2 progeny analysis showed that the ratio of resistant and susceptible plants, resistance was dominant over susceptibility in these crosses, with expected ratio 3:1. (Li *et al.* 2011) Report that the adult plants of 103 F2 progeny were tested in the field under the natural infection of *P. striiformis f. sp. tritici*. Seedlings of the parents and F2 were tested with races PST of the pathogen under controlled greenhouse conditions. The genetic study showed that (PI 181434), Yr45 has a single dominant gene conferring all-stage resistance. (Zhang *et al*. 2010). They screened 442 F2 plants derived from two crosses between Shaanmai 139, (YrSM139) and two susceptible cultivars .In F2 progeny analysis showed that the ratio of resistant and susceptible plants, resistance was dominant over susceptibility in these crosses. Using the molecular marker method, *Yr10* In this study, we used the primer Xpsp3000 to identify markers linked to yellow rust resistance genes, in this respect, specific DNA segment of 52 individual of F2 have linked with primer Xpsp3000 260-bp band. The rest 18 individuals did not linked with the primer Xpsp3000. Segregation in F2 of individual which, reacted with the primer YrSTS/7, 8 and shown in this respect, specific DNA segment of 58 individual of F2 have linked with primer YrSTS/7, 8 439-bp band. The rest 21, individuals did not link with the primer YrSTS/7, 8. (Bariana *et al.* 2002), (Chen *et al.* 2003), (Yan *et al.* 2003), (Zahra *et al.* 2014), When the molecular markers with the primers YrSTS/7,8 and Xpsp3000 were used to detect *Yr5* and *Yr10*, the targeted bands were only observed in entries genotype carry *Yr5* and *Yr10* genes and none in the entries not carry these genes.

This work could be usefully applicable in the breeding wheat program against rust disease in general and stripe rust in particular under Egyptian conditions.

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دور جينات المقاومة (*Yrs*) لفطر *Puccinia striiformis* فى خمسة اصناف من قمح الخبز قابلة للاصابة والتحقق بواسطة الدلائل الجزئية فى تقييم المقاومة

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صدأ القمح المخطط (الأصفر) الناتج عن فطر ***Puccinia striiformis*** أحد أكثر الامراض المدمرة لمحصول القمح فى العالم. ظهور سلالات جديدة للمسبب المرضى فى السنوات الاخيرة فى مصر وانتشار تلك السلالات تشكل تأثير على انتاج القمح فى مصر .و قد تطلب ذلك تجميع قاعدة جينية واسعة من المقاومة. تم اجراء خمسة عشر هجين بين *Yr15* , *Yr5, Yr10* وكلأ من سدس 12 و سدس13 و جميزة 10 وجميزة 11 و سخا 93 . وأضحت النتائج أن الاباء الخمسة من الاصناف أظهرت قابلية عالية للاصابة للصدأ الاصفر فى طور البادرة والنبات البالغ بينما على الجانب الاخر اظهرت الثلاث جينات مقاومة عالية. فى حين أظهرت الهجن مقاومة ضد الصدأ الاصفر فى مرحلة البادرة والبلوغ وأظهرت نتائج نباتات الجيل الأول (F1) مقاومة عالية حيث كان الطراز المرضى (0 – 0, and 1) فى مرحلة البادرة والشدة المرضية فى طور البلوغ تراوحت بين (0, 10R and 10MR) .أظهرت نتائج الجيل الثانى رد فعل واسع للشدة المرضية تراوحت بين (0 to 9) فى مرحلة البادرة وتراوحت بين (0 to 80S) ولكن كان الاتجاة فى جانب المقاومة وهذا تاكيد لنتائج F1 . وأكدت هذة النتائج عن وجود جين المقاومة فى انعزالات الهجن وأن المقاومة للصدأ المخطط يتحكم فيها زوج واحد من جين المقاومة السائدة فى طور النبات البالغ . والتعبير عن جينات المقاومة *Yr5, Yr10* and*Yr15* فى جيل ال F2 يمكن استخدامها على نطاق واسع . باستخدام طريقة الدلائل الجزئية (PCR) لجين المقاومة *Yr1*0 أستخدم البرايمر (xpsp3000) لتحديد العلامة المرتبطة لجين المقاومة فىF2. فى هذا الشأن أوضحت النتائج البرايمر المتخصص (xpsp3000) أرتبط مع 52 نبات فردى من الجيل الثانى F2 عند 260bp . باقى 18 نبات فردى لا يظهر ارتباط مع البرايمر . فى حين البرايمر YrSTS/7, 8.لجين المقاومة *Yr5* أرتبط مع 58 نبات فردى من الجيل الثانى F2 عند 439bp باقى 21 نبات فردى من الجيل الثانى F2 لا يظهر ارتباط مع البرايمر . تعتبر هذة العلامات الجزئية أداة هامة لمربى القمح فى التربية الهرمية للمقاومة للصدأ الاصفر (المخطط) .