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Effective and Ineffective of some Resistance Genes to Wheat Leaf, Stem and Yellow Rust Diseases in Egypt

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ABSTRACT

One hundred and five wheat genotypes; 38 wheat leaf rust monogenic lines, 46 stem rust monogenic lines and 17 yellow rust monogenic lines, thee commercial wheat cultivars; Sakha 95, Misr 3 and Gemmeiza 11 and the highly susceptible variety Morocco were evaluated for their adult plant resistance and stability of resistance to rust diseases under different field conditions at Sadat City and Elbostan for three successive growing seasons i.e. 2016/2017, 2017/2018 and 2018/2019. Depending on the obtained results, differences between environments, genotypes and the interaction between environments and genotypes were highly significant for all studied characters. These results confirmed that, there are wide variations between genotypes. The wheat genotypes under study were classed into three classes based on the infection type. The first class included the most effective genotypes which included *Lr* 17, *Lr* 18, *Lr* 21, *Lr* 28 and Misr 3 for leaf rust, *Sr* 2, *Sr* 24, *Sr* 32, *Sr* 33, *Sr* 36, *Sr* 38, *Sr* 39 and Misr 3 for stem rust and *Yr* 1, *Yr* 5, *Yr* 10, *Yr* 15, *Yr* SP, Misr 3 and Sakha 95 for yellow rust. The second class was genotypes of differential resistance and the third class included ineffective genotypes. Stability factors during the three growing seasons at the two locations confirmed that, nine wheat monogenic lines; *Lr* 28, *Lr* 22a, *Lr* 14b, *Sr* 20, Sr 25, *Sr* 31, *Sr* 9e, *Sr* 12 and *Yr* 17 were widely adapted and stable in their resistance.

Keywords: Wheat, leaf rust, monogenic lines, major gene resistance, stability of resistance.

INTRODUCTION

Wheat (*Triticum aestivum* L.) is one of the most important field crops in Egypt; it covers less than 60 % of local consumption (FAO, 2016). Rust diseases of wheat i.e. leaf rust (*Puccinia triticina* Eriks.), stem rust (*Puccinia graminis* Pers. f. sp. *tritici* Eriks. & E. Henn.) and stripe rust (*Puccinia striiformis* Westend. f. sp. *tritici*) are still the most dangerous biotic stress that cause significant grain yield losses in Egypt and worldwide. This is mainly because of the presence of new aggressive races (Singh *et al*., 2006).

Grain yield losses due to yellow rust range from 10-70 % (Chen, 2005), moreover, stripe rust can cause 100 % yield loss if infection occurs at early growth stage (Afzal *et al*., 2007). While, grain yield losses to leaf rust can reaches 40% in the susceptible wheat genotypes (Khan *et al*., 2013). Under Egyptian conditions, losses due leaf rust reached to more than 20% (Shahin & El-Orabey, 2016 and El-Orabey *et al*., 2017). On the other hand, wheat stem rust can causes yield losses of up to 100 % due to damaged tillers and shriveled grains (Kokhmetova *et al*., 2011). In Egypt, yield losses due to stem rust ranged from 1.96 % to 8.21 % recorded on the Egyptian wheat cultivars (Ashmawy *et al*., 2013). In most cases susceptible wheat cultivars were changed with new resistant one (Rattu *et al*., 2007).

Developing resistant varieties to rust diseases is the most valuable, economical, effective and environmentally friendly approach to control rust diseases (Line and Chen, 1995). Two main kinds of resistance are identified to rust diseases in wheat i.e. quantitative (race nonspecific) and qualitative (race-specific) resistance. Using of genes for race-specific resistance confirms effective protection to rust diseases (Shah *et al.,* 2010). The race-specific resistance works according to the gene-for-gene concept (Flor, 1956). Meanwhile, race-nonspecific resistance is generally polygenic. This kind of resistance has been described as partial resistance or slow rusting resistance (Parlevliet, 1979) and is known to be more durable and long-lasting (HerreraFossel *et al*., 2007).

At present, more than 77 leaf rust resistance genes (*Lr*,s) have been formally cataloged in wheat genome (McIntosh *et al*., 2017). Most of these resistance genes are effective in seedling stage and stay effective in adult stage. However, some of these genes are ineffective because of the emergence of new virulence leaf rust races (Kolmer *et al*., 2008). Moreover, more than 70 formally named stripe rust resistance genes (*Yr* 1 - *Yr* 78) and many temporarily designated genes have been recorded to stripe rust in wheat and its wild relatives (McIntosh *et al*., 2017). While, 82 stem rust resistance genes (*Sr*,s) have been described (McIntosh *et al*., 2017). Some rust resistance genes in wheat express resistance at adult plant stage only and are known as adult plant resistance genes (APR), which mainly depends on the genetics of the host parasite interaction as well as environmental conditions. The great change in rust resistance gene behavior is mainly because of the new virulent races, so the resistance of a genotype is not a constant trait; the resistance of any genotype depending on a single resistance gene may become susceptible in a short time (Kolmer *et al*., 2008).

Rusts are obligate airborne pathogens and difficult to control when a susceptible cultivar is grown on a huge area. Resistance cultivars may be broken down due to the emergence of new virulences in pathogen population. Therefore, usual monitoring of virulent races and a continuous search and utilization of resistance genes is very important to avoid rust epidemics.

The present study aims to evaluate and monitoring the changes in rust reaction of leaf, stem and stripe rust monogenic lines at adult plant stage under Egyptian filed conditions to detect the effective monogenic lines. Also, to characterize stability of resistance of the tested wheat rust monogenic lines.

MATERIALS AND METHODS

Evaluation of wheat rust monogenic lines at adult plant stage under field conditions

Thirty-eight wheat leaf rust monogenic lines, 46 stem rust monogenic lines and 17 yellow rust monogenic lines, thee commercial wheat cultivars; Sakha 95, Misr 3 and Gemmeiza 11 and the highly susceptible variety Morocco received from Wheat Diseases Res. Dept., Plant Pathology Res. Inst., ARC, Egypt were used in the current study. The experiments were conducted under field conditions at Sadat City, Minufiya governorate and Elbostan, Behira governorate for three successive growing seasons; 2016/2017, 2017/2018

and 2018/2019. The wheat monogenic lines were planted in three replicates with three rows (3 m long and 30 cm apart), each row was sown with 5 g of a given tested monogenic line. The experiment was bordered by spreader rows sown with mixtures of highly susceptible cultivars (Morocco, Thatcher and *Triticum spelta sahariensis*). The spreader plants were artificially inoculated using a mixture of urediniospores of the prevalent leaf, stem and stripe rust races mixed with talcum powder at a rate of 1: 20 (v:v) (spores : talcum powder) (Tervet & Cassell, 1951) in addition to the natural infection during late tillering and late elongation stages. The urediniospores of leaf, stem and stripe rusts received from Wheat Diseases Res. Dept., Plant Pathology Res. Inst., ARC, Egypt.

Disease assessment

Wheat genotypes response to leaf, stem and stripe rust pathogen were recorded after heading stage using modified Cobb,s scale (Peterson *et al.*, 1948). The type of infection i.e. Immune=(0), resistant=(R), moderately resistant=(MR), moderately susceptible=(MS) and susceptible= (S) was recorded according to Roelfs *et al.* (1992). The rust response was transformed to average coefficient of infection (ACI) by multiplying rust severity by an assigned constant value for infection types; Resistant (R)=0.2, Moderately resistant (MR)=0.4, Moderately susceptible (MS)=0.8 and Susceptible (S)=1 for use in the statistical analysis (Stubbs *et al*., 1986).

All of the tested wheat genotypes were divided into three categories according to the infection types at the two locations i.e. first group: Effective genes which include monogenic lines with high resistance at all locations i.e. Immune (0), resistant (R) and moderately resistant (MR). Second group: Ineffective genes which includes susceptible monogenic lines at all locations i.e. moderately susceptible (MS) and susceptible (S) and third group: Genes Differentiated in effectiveness which includes monogenic lines with high degree of resistance at some locations and susceptible at other locations.

Statistical analysis

Analysis of variance (ANOVA) was calculated to determine the effects of genotype, environment, and GE interactions on rust ACI and infection types according to Gomez & Gomez (1984). The stability of leaf rust resistance for each genotype was calculated by Eberhart and Russell (1966).

Cluster analysis:

Cluster analysis for the tested genotypes against leaf, stem and yellow rust diseases was applied to the data of average coefficient of infection (ACI) and infection type (IF). The infection types were coded as 1, 2, 3 and 4 for infection types; R, MR, MS and S, respectively. A dendrogram based on the un-weighted pair group method with arithmetic mean (UPGMA) was also constructed with R software.

RESULTS

Effect of genotype and environment and their interaction:-

The analysis of variance for all tested genotypes evaluated for leaf, stem and yellow rust under the two locations are given in Tables (1, 2 and 3). The differences between environments (E), genotypes (G) and the interaction between environments and genotypes were highly significant for all studied characters. These results indicated that, the presence of wide variability among the genotypes. The significant estimates of G×E interaction confirmed that the characters were unstable and may considerably fluctuate with change in environments.

Table 1. Analysis of variance for the effects of locations, seasons, cultivars and their interactions on the average coefficient of infection (ACI) and infection type (IF) for leaf rust across locations for 2016/2017-2018/2019 growing seasons.

Source	DF	Mean square	
		ACI	IF
Environment	5	954.79**	1.43**
Rep	2	1011.46	0.088
Rep(Env)	10	285.06	0.06
Geno	41	7851.39**	14.98**
Env*Geno	205	228.52**	0.83**
Error	492	31.34	0.04

**** Significant at 0.001 probability level.**

Table 2. Analysis of variance for the effects of locations, seasons, cultivars and their interactions on the average coefficient of infection (ACI) and infection type (IF) for stem rust across locations for 2016/2017-2018/2019 growing seasons.

Source	DF	Mean square	
		ACI	IF
Environment	5	656.37**	2.42**
Rep	2	80.74	0.13
Rep(Env)	10	49.66	0.21
Geno	20	5762.58**	28.39**
Env*Geno	100	137.78**	1.97**
Error	240	20.23	0.16

**** Significant at 0.001 probability level.**

Table 3. Analysis of variance for the effects of locations, seasons, cultivars and their interactions on the average coefficient of infection (ACI) and infection type (IF) for yellow rust across locations for 2016/2017-2018/2019 growing seasons.

Source	DF	Mean square	
		ACI	IF
Environment	5	56.08**	6.13**
Rep	2	190.27	0.16
Rep(Env)	10	58.33	0.58
Geno	49	2615.60**	24.97**
Env*Geno	245	36.95**	0.92**
Error	588	10.57	0.18

**** Significant at 0.001 probability level.**

Evaluation of wheat leaf rust monogenic lines at adult stage under field conditions:

Thirty eight monogenic lines (*Lr* genes) were evaluated against leaf rust disease to study the efficacy and stability of these monogenic lines to leaf rust resistance at Sadat City, Minufiya and Elbostan, Behira during three successive growing seasons; 2016/2017, 2017/2018 and 2018/2019.

Data in Table (4) showed that the leaf rust monogenic lines can be divided into three groups according to their performance under field conditions during the three growing seasons of study; Group I: Effective genotypes (resistant): This group includes wheat genotypes with high degree of resistance to leaf rust at all locations during the three seasons of study. These genotypes are *Lr* 17, *Lr* 18, *Lr* 21, *Lr* 28 and Misr 3. The tested genes in this group showed leaf rust response ranged from 0 to 20 MR. Group II: Genotypes differentiated in effectiveness (susceptible and/or resistant): This group includes *Lr* genes with high degree of resistance

during growing season (s) and susceptible during other growing season (s) to leaf rust. These genes are *Lr* 2a, *Lr* 2b, *Lr* 9, *Lr* 10, *Lr* 19, *Lr* 29 and *Lr* 30. The tested monogenic lines present in this group showed rust response ranged from 0 to 90 S. Group III: Ineffective genotypes (susceptible): This group includes susceptible wheat genotypes to leaf rust during the three growing seasons of the study at adult stage. These wheat genotypes are *Lr* 1, *Lr* 2c, *Lr* 3, *Lr* 3ka, *Lr* 3bg, *Lr* 11, *Lr* 12, *Lr* 13, *Lr* 14a, *Lr* 14b, *Lr* 15, *Lr* 16, *Lr* 20, *Lr* 22a, *Lr* 22b, *Lr* 23, *Lr* 24, *Lr* 25, *Lr* 26, *Lr* 10+*Lr* 27+*Lr* 31, *Lr* 32, *Lr* 33, *Lr* 34, *Lr* 35, *Lr* 36, *Lr* 37, *Lr* B, Sakha 95, Gemmeiza 1 and Morocco. The genotypes in this group showed rust response ranged from Tr S to 100 S.

Table 4. Response of 38 wheat monogenic lines against leaf rust at Sadat City and Elbostan locations under field conditions during 2016/2017, 2017/2018 and 2018/2019 growing seasons.

Lr gene	Season / Location / Leaf rust response*					
	2016/2017		2017/2018		2018/2019	
	Sadat City	Elbostan	Sadat City	Elbostan	Sadat City	Elbostan
Effective genotypes						
Lr 17	5R	10MR	5MR	10R	10MR	5MR
Lr 18	TrMR	0	5MR	5MR	5MR	10MR
Lr 21	5MR	TrMR	TrMR	10MR	5MR	10MR
Lr 28	0	5R	TrR	TrR	5R	0
Misr 3	0	0	0	0	TrR	5R
Differentiated genotypes						
Lr 2a	20MR	0	60S	30S	30S	40S
Lr 2b	5R	10S	40S	TrR	60S	30S
Lr 19	5S	0	0	TrMS	0	0
Lr 29	0	5S	5MR	0	TrS	5S
Lr 30	0	5S	0	0	10S	20S
Ineffective genotypes						
Lr 1	60S	80S	70S	60S	70S	70S
Lr 2c	60S	70S	50S	50S	70S	60S
Lr 3	20S	10S	30S	30S	30S	20S
Lr 3ka	10S	30S	30S	10S	20S	20S
Lr 3bg	30S	40S	50S	60S	60S	50S
Lr 9	30S	10S	30S	40S	50S	30S
Lr 10	10S	20S	10S	30S	20S	10S
Lr 11	50S	60S	70S	50S	50S	40S
Lr 12	5S	30S	20S	10S	40S	30S
Lr 13	20S	30S	50S	40S	30S	30S
Lr 14a	40S	50S	30S	20S	50S	40S
Lr 14b	5S	10S	20S	10S	10S	5S
Lr 15	20S	10S	10S	20S	10S	30S
Lr 16	10S	5S	10S	5S	30S	20S
Lr 20	5S	TrS	10S	20S	30S	20S
Lr 22a	10S	10S	10S	5S	20S	10S
Lr 22b	70S	80S	90S	70S	80S	90S
Lr 23	50S	30S	40S	50S	60S	40S
Lr 24	5S	TrS	20S	30S	40S	20S
Lr 25	40S	50S	50S	40S	20S	30S
Lr 26	60S	40S	60S	50S	50S	60S
Lr 10+ 27+ 31	5S	TrS	TrS	5S	TrS	5S
Lr 32	20S	10S	10S	20S	30S	20S
Lr 33	30MS	10MS	20MS	20MS	10S	5S
Lr 34	5S	5S	TrS	5S	5S	TrS
Lr 35	60S	30S	40S	50S	50S	30S
Lr 36	30S	20S	30S	10S	40S	20S
Lr 37	20S	40S	30S	50S	50S	40S
Lr B	30S	40S	30S	20S	20S	30S
Sakha 95	5S	5S	TrS	5S	5S	10S
Gemmeiza 11	30S	40S	20S	30S	30S	30S
Morocco(check)	90S	100S	100S	100S	90S	90S

*** Score contains two components: disease severity according to the modified Cobb's scale (Peterson *et al.*, 1948), where 5=5% up to 100=100%, and host response according to the scale described by Roelfs *et al*. (1992), where MR=moderately resistant, MS=moderately susceptible and S=susceptible.**

Evaluation of wheat stem rust monogenic lines at adult stage under field conditions:

Fourty six monogenic lines (*Sr* genes) were evaluated against stem rust disease to study the efficacy of these monogenic lines to stem rust resistance at Sadat City and Elbostan during three successive growing seasons; 2016/2017, 2017/2018 and 2018/2019.

Data in Table (5) showed that the stem rust monogenic lines can be divided into three groups according to their performance under field conditions at all locations and during the three seasons of study; Group I: Effective genotypes (resistant): This group includes wheat genotypes with high degree of resistance to stem rust during the three seasons of study. These genotypes are *Sr* 2 complex, *Sr* 24, *Sr* 32, *Sr* 33, *Sr* 36, *Sr* 38, *Sr* 39 and Misr 3. The tested genotypes in this group showed stem rust response ranged from 0 to Tr MR. Group II: Genotypes differentiated in effectiveness (susceptible and/or resistant): This group includes wheat genotypes with high degree of resistance during growing season (s) and susceptible during other growing season (s) to stem rust. These genotypes are *Sr* 11, *Sr* 12, *Sr* 13, *Sr* 15, *Sr* 23, *Sr* 25, *Sr* 26, *Sr* 27, *Sr* 28, *Sr* 29, *Sr* 31, *Sr* 34, *Sr* 37, *Sr* 40 and *Sr* Wld-1. The tested monogenic lines present in this group showed rust response ranged from 0 to 10 S. Group III: Ineffective genotypes (susceptible): This group includes susceptible wheat genotypes to stem rust during the three growing seasons of the study. These genotypes are *Sr* 5, *Sr* 6, *Sr* 7a, *S* 7b, *Sr* 8a, *Sr* 8b, *Sr* 9a, *Sr* 9b, *Sr* 9d, *Sr* 9e, *Sr* 9g, *Sr* 10, *Sr* 14, *Sr* 16, *Sr* 17, *Sr* 18, *Sr* 19, *Sr* 20, *Sr* 21, *Sr* 22, *Sr* 30, *Sr* 35, *Sr* Tmp, *Sr* McN Sakha 95, Gemmeiza 1 and Morocco. The genotypes in this group showed rust response ranged from Tr S to 90 S.

Evaluation of wheat stripe rust monogenic lines at adult stage under field conditions:

Seventeen monogenic lines (*Yr* genes) were evaluated against stem rust disease to study the efficacy and stability of these monogenic lines to stem rust resistance at Sadat City and Elbostan during three successive growing seasons; 2016/2017, 2017/2018 and 2018/2019.

Data in Table (6) showed that the stripe rust monogenic lines can be divided into three groups according to their performance under field conditions during the three seasons of the study; Group I: Effective genotypes (resistant): This group includes wheat genotypes with high degree of resistance to yellow rust during the three seasons. These genes are *Yr* 1, *Yr* 5, *Yr* 10, *Yr* 15, *Yr* SP, Misr 3 and Sakha 95. The tested genes in this group showed yellow rust response ranged from 0 to Tr R. Group II: Genotypes differentiated in effectiveness (susceptible and/or resistant): This group includes wheat genotypes with high degree of resistance during growing season (s) and susceptible during other growing season (s) to yellow rust. These genotypes are *Yr* 2, *Yr* 17, *Yr* 18, *Yr* 27, *Yr* 31 and *Yr* 32. The tested monogenic lines present in this group showed rust response ranged from 0 to 30 S. Group III: Ineffective genotypes (susceptible): This group includes susceptible wheat genotypes to yellow rust during the three growing seasons. These genotypes are *Yr* 6, *Yr* 7, *Yr* 8, *Yr* 9, *Yr* 28, *Yr* A, Gemmeiza 11 and Morocco. The genotypes in this group showed rust response ranged from Tr S to 90 S.

Table 5. Response of 46 wheat monogenic lines against stem rust at Sadat City and Elbostan locations under field conditions during 2016/2017, 2017/2018 and 2018/2019 growing seasons.

Sr gene	Season / Location / Stem rust response*					
	2016/2017		2017/2018		2018/2019	
	Sadat City	Elbostan	Sadat City	Elbostan	Sadat City	Elbostan
Effective genotypes						
Sr 2 complex	0	0	TrMR	0	TrMR	5MR
Sr 24	0	0	0	0	0	0
Sr 32	0	0	TrMR	0	0	0
Sr 33	0	0	0	0	0	0
Sr 36	0	0	0	0	0	0
Sr 38	0	0	0	0	0	0
Sr 39	0	0	0	0	0	0
Misr 3	0	0	0	0	0	0
Differentiated genotypes						
Sr 11	5MS	TrMS	TrMR	5MR	TrMR	5MR
Sr 12	TrS	0	TrS	5S	5S	TrS
Sr 13	10MR	TrMR	5MR	5MS	TrMS	TrS
Sr 15	TrMR	5MR	10S	TrS	10S	TrS
Sr 23	0	5R	0	0	5S	5MS
Sr 25	0	TrMS	TrMS	0	TrMS	5MS
Sr 26	0	0	5MR	0	0	TrS
Sr 27	0	0	0	0	TrMS	5MS
Sr 28	0	0	TrS	5S	5S	5S
Sr 29	10MR	5MR	5MS	5MS	TrS	5S
Sr 31	0	0	0	0	TrMS	5MS
Sr 34	0	TrS	TrS	0	TrS	5S
Sr 37	5 S	TrMR	TrS	5S	TrS	5S
Sr 40	10MS	5MS	TrMR	5MR	TrMS	TrS
Sr Wld-1	0	0	0	0	0	TrMS
Ineffective genotypes						
Sr 5	5S	10S	10S	10S	10S	5S
Sr 6	5S	10S	TrS	TrS	5S	TrS
Sr 7a	5S	5S	10S	TrS	10S	5S
S 7b	10S	5S	10S	20S	20S	10S
Sr 8a	30S	20S	40S	30S	30S	20S
Sr 8b	30S	20S	20S	20S	20S	30S
Sr 9a	5S	10S	10S	5S	TrS	5S
Sr 9b	10S	5S	TrS	10S	20S	5S
Sr 9d	20S	30S	20S	10S	30S	20S
Sr 9e	TrS	5S	5S	TrS	5S	10S
Sr 9g	5MS	5S	TrMS	5S	10S	10S
Sr 10	20S	10S	5S	20S	10S	20S
Sr 14	TrS	5S	5S	5S	5S	10S
Sr 16	TrS	5S	10S	10S	10S	10S
Sr 17	20S	10S	5S	TrS	20MS	20S
Sr 18	5MS	5S	TrS	5S	TrS	10S
Sr 19	20S	20S	30S	10S	30MS	20S
Sr 20	5S	10S	5S	TrS	10S	5S
Sr 21	5S	20S	20S	10S	20S	10S
Sr 22	TrMS	5S	TrS	5S	TrS	TrS
Sr 30	5S	TrS	5S	TrS	TrS	5S
Sr 35	5S	10S	5S	10S	10S	5S
Sr Tmp	20MS	20MS	10S	20S	10S	20S
Sr McN	30S	40S	40S	50S	60S	40S
Sakha 95	5S	5S	TrS	5S	5S	10S
Gemmeiza 11	10S	20S	30S	20S	20S	30S
Morocco (check)	70S	80S	80S	90S	80S	80S

*** Score contains two components: disease severity according to the modified Cobb's scale (Peterson *et al.*, 1948), where 5=5% up to 100=100%, and host response according to the scale described by Roelfs *et al.* (1992), where MR=moderately resistant, MS=moderately susceptible and S=susceptible.**

Table 6. Response of 17 wheat monogenic lines against stripe rust at Sadat City and Elbostan locations under field conditions during 2016/2017, 2017/2018 and 2018/2019 growing seasons.

Sr gene	Season / Location / Yellow rust response*					
	2016/2017		2017/2018		2018/2019	
	Sadat City	Elbostan	Sadat City	Elbostan	Sadat City	Elbostan
Effective genotypes						
Yr 1	0	0	0	0	0	0
Yr 5	0	0	TrR	0	0	0
Yr 10	0	0	0	0	0	0
Yr 15	0	0	0	0	0	0
Yr SP	0	0	0	0	0	0
Misr 3	0	0	0	0	0	0
Sakha 95	0	0	0	0	0	0
Differentiated genotypes						
Yr 2	20S	40S	20S	30S	30S	40S
Yr 17	5S	10S	TrS	0	0	5S
Yr 18	TrS	5S	0	0	0	0
Yr 27	5S	20S	20S	0	0	0
Yr 31	0	5MS	0	10MS	TrMS	0
Yr 32	TrS	TrMR	TrS	5S	0	0
Ineffective genotypes						
Yr 6	20S	20S	20S	30S	30S	10S
Yr 7	30S	30S	30S	20S	20S	30S
Yr 8	30S	30S	20S	40S	10S	40S
Yr 9	30S	10S	10S	20S	20S	30S
Yr 28	10S	20S	TrS	20S	5S	30S
Yr A	30S	50S	20S	40S	30S	40S
Gemmeiza 11	20S	30S	10S	20S	20S	30S
Morocco (check)	80S	90S	90S	80S	80S	90S

*** Score contains two components: disease severity according to the modified Cobb's scale (Peterson *et al.*, 1948), where 5=5% up to 100=100%, and host response according to the scale described by Roelfs *et al.* (1992), where MR=moderately resistant, MS=moderately susceptible and S=susceptible.**

Diversity between the tested genotypes against leaf, stem and yellow rust diseases:

1- Leaf rust genotypes:

Clustering analyses based on ACI and host reaction (IF) is shown in Fig. (1). Tested wheat genotypes were grouped into two main clusters against leaf rust. The first cluster consisted of two sub-clusters; the first one consists of the six wheat genotypes; *Lr* 17, *Lr* 18, *Lr* 21, *Lr* 28, *Lr* 19 and Misr 3 which were in group; effective genotypes except *Lr* 19. The second sub-cluster consists of four wheat monogenic lines *Lr* 2a, *Lr* 2b, *Lr* 29 and *Lr* 30 which were in in group; differentiated genotypes. The second main cluster divided into two sub-clusters; the first one consists of the six highly susceptible wheat genotypes; *Lr* 1, *Lr* 2c, *Lr* 11, *Lr* 22b, *Lr* 26 and Morocco. The second sub-cluster consisted of 26 tested genotypes; *Lr* 3, *Lr* 3ka, *Lr* 3Bg, *Lr* 9, *Lr* 10, *Lr* 10+27+31, *Lr* 12, *Lr* 13, *Lr* 14a, *Lr* 14b, *Lr* 15, *Lr* 16, *Lr* 20, *Lr* 22a, *Lr* 23, *Lr* 24, *Lr* 25, *Lr* 32, *Lr* 33, *Lr* 34, *Lr* 35, *Lr* 36, *Lr* 37, *Lr* B, Sakha 95 and Gemmeiza 11 which were present in in group; susceptible genotypes (Fig. 1).

2- Stem rust genotypes:

The tested wheat genotypes against stem rust were grouped into two main clusters. The first cluster consisted of two sub-clusters; the first one consists of all of the eight wheat genotypes; *Sr* 2 complex, *Sr* 24, *Sr* 32, *Sr* 33, *Sr* 36, *Sr* 38, *Sr* 39, Misr 3 which were in group; effective genotypes. The second sub-cluster consists of ten wheat monogenic lines; *Sr* 11, *Sr* 13, *Sr* 23, *Sr* 25, *Sr* 26, *Sr* 27, *Sr*

31, *Sr* 34, *Sr* 40 and *Sr* Wld-1 which were in in group; differentiated genotypes. The second main cluster divided into two sub-clusters; the first one consists of the two highly susceptible wheat genotypes; *Sr* McN and Morocco. The second sub-cluster consisted of 30 wheat genotypes; *Sr* 5, *Sr* 6, *Sr* 7a, *S* 7b, *Sr* 8a, *Sr* 8b, *Sr* 9a, *Sr* 9b, *Sr* 9d, *Sr* 9e, *Sr* 9g, *Sr* 10, *Sr* 12, *Sr* 14, *Sr* 15, *Sr* 16, *Sr* 17, *Sr* 18, *Sr* 19, *Sr* 20, *Sr* 21, *Sr* 22, *Sr* 28, *Sr* 29, *Sr* 30, *Sr* 35, *Sr* 37 *Sr* Tmp, Sakha 95 and Gemmeiza 11 which most of them were present in in group; susceptible genotypes (Fig. 2).

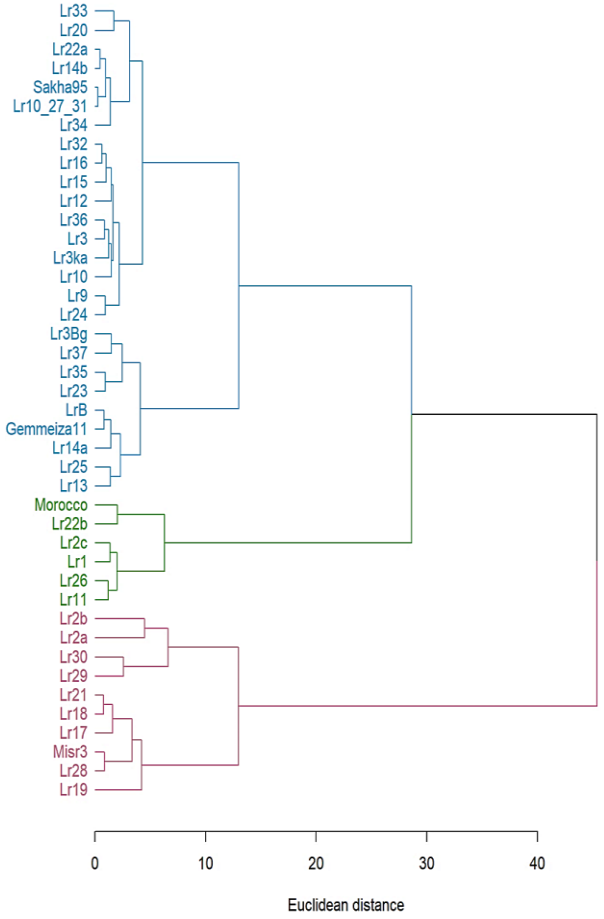

Fig. 1. Dendrogram of cluster analysis of 38 wheat leaf rust monogenic lines, four commercial wheat cultivars and the susceptible wheat variety Morocco (check) based on leaf rust parameters assessed under field conditions during 2016/2017-2018/2019.

2- Yellow rust genotypes:

The tested wheat genotypes against yellow rust were grouped into two main clusters. The first cluster consisted of all of the seven wheat genotypes; *Yr* 1, *Yr* 5, *Yr* 10, *Yr* 15, *Yr* SP, Misr 3 and Sakha 95 which were in group; effective genotypes. The second sub-cluster consists of the first one consisted of the highly susceptible wheat variety; Morocco. The second sub-cluster consists of two sub-clusters; the first sub-cluster consisted of the five wheat monogenic lines; *Yr* 17, *Yr* 18, *Yr* 27, *Yr* 31 and *Yr* 32 which were in in group; differentiated genotypes. The second sub-cluster consisted of the eight wheat genotypes; *Yr* 2, *Yr* 6, *Yr* 7, *Yr* 8, *Yr* 9, *Yr* 28, *Yr* A and Gemmeiza 11 which were present in in group; susceptible genotypes (Fig. 3).

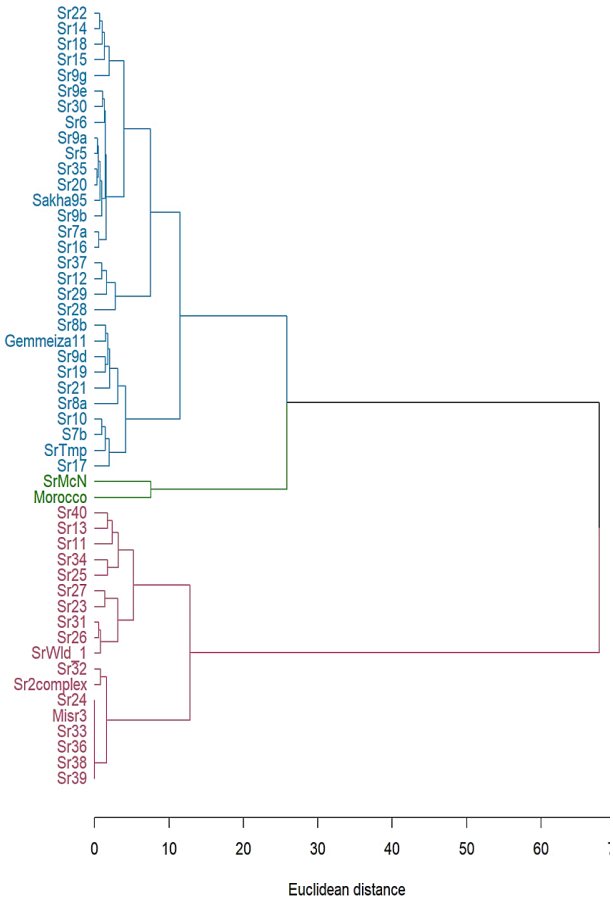

Fig. 2. Dendrogram of cluster analysis of 46 wheat stem rust monogenic lines, four commercial wheat cultivars and the susceptible wheat variety Morocco (check) based on stem rust parameters assessed under field conditions during 2016/2017-2018/2019.

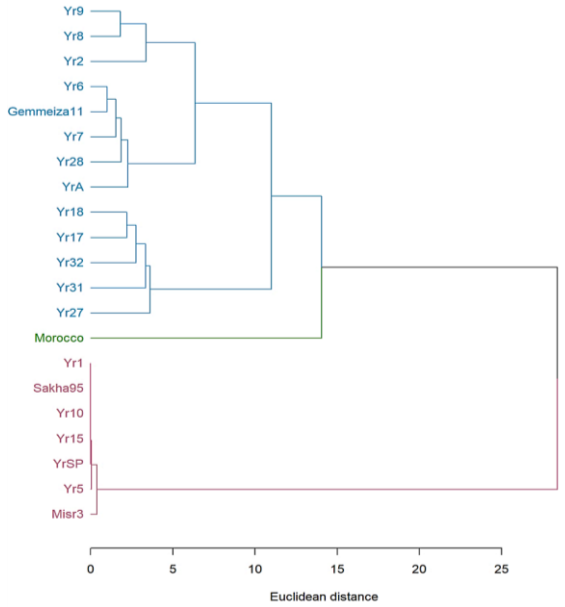

Fig. 3. Dendrogram of cluster analysis of 17 wheat yellow rust monogenic lines, four commercial wheat cultivars and the susceptible wheat variety Morocco (check) based on yellow rust parameters assessed under field conditions during 2016/2017-2018/2019.

Stability parameters:

For each genotype, the values of regression coefficient (bi) and mean performance of ACI and IF for rust resistance for all tested wheat genotypes are presented in Tables (7, 8 and 9). As far as stability analysis is concerned, the wheat variety was stable in its resistance to rust diseases if it had lower mean rust scores, genotypic variance (Si) value was low and regression coefficients (bi) value close to one. Regression coefficients ranged from -0.060 to 7.81 for genotypes tested against leaf rust, -0.12 to 11.53 or genotypes tested against stem rust and 0.00 to 5.40 for genotypes tested against yellow rust. These variations indicate differences in responses to rust resistance for environmental changes.

Table 7. Stability parameters for leaf rust resistance of 42 wheat genotypes grown at two locations during three growing seasons 2016/2017, 2017/2018 and 2018/2019.

Genotype	BLUP ACI	BLUP IF	bi	ri2	Si(1)
Lr 1	61.60	3.97	1.16	68.88	0.30
Lr 2a	24.38	3.97	4.02	295.20	5.00
Lr 2b	20.21	3.97	7.81	420.59	5.50
Lr 2c	51.35	3.97	1.54	78.03	1.33
Lr 3	16.56	3.97	0.77	17.54	1.53
Lr 3ka	17.10	3.97	1.03	67.09	2.77
Lr 3Bg	40.03	3.97	2.79	70.92	1.23
Lr 9	22.77	4.12	2.32	78.34	1.80
Lr 10	13.22	3.97	-0.25	75.35	2.50
Lr 11	46.50	3.97	0.52	88.32	0.90
Lr 12	17.80	3.97	3.91	126.79	3.80
Lr 13	26.00	3.97	0.91	161.45	2.83
Lr 14a	31.40	3.97	0.39	124.70	2.77
Lr 14b	9.23	3.97	1.07	12.50	2.17
Lr 15	13.87	3.97	-0.66	69.48	1.97
Lr 16	11.11	3.97	1.85	39.54	2.33
Lr 17	2.39	2.10	0.17	4.53	0.73
Lr 18	1.97	2.10	0.12	4.91	1.00
Lr 19	1.83	1.17	-0.46	17.28	2.43
Lr 20	11.33	3.97	2.80	42.77	2.67
Lr 21	2.44	1.95	-0.06	8.05	0.63
Lr 22a	8.53	3.97	1.34	4.87	1.20
Lr 22b	73.47	3.97	1.94	81.33	0.10
Lr 23	37.33	3.97	1.97	108.50	1.53
Lr 24	18.40	3.97	4.29	137.80	3.50
Lr 25	33.55	3.97	-2.13	181.83	1.87
Lr 26	49.73	3.97	0.22	55.89	0.57
Lr 10+27+31	4.64	3.97	-0.16	9.29	1.07
Lr 28	1.29	1.17	0.07	5.46	0.40
Lr 29	2.29	1.79	-0.01	9.91	1.80
Lr 30	4.21	2.57	0.54	20.55	3.20
Lr 32	14.94	3.97	1.37	32.55	1.83
Lr 33	10.25	3.50	-0.72	44.55	3.00
Lr 34	4.16	3.50	-0.05	7.77	1.30
Lr 35	38.41	3.97	-0.13	207.17	2.60
Lr 36	18.99	3.97	1.72	62.26	1.77
Lr 37	31.13	3.97	1.93	141.53	1.70
Lr B	24.38	3.97	-1.57	94.86	1.90
Misr 3	2.30	1.17	0.21	14.31	1.83
Sakha 95	6.53	3.97	-0.32	15.20	1.30
Gemmeiza 11	23.57	3.97	-0.02	65.13	1.60
Morocco (check)	87.49	3.97	-0.27	26.32	0.07

The stability of the tested wheat genotypes against leaf rust, only *Lr* 28, *Lr* 22a and *Lr* 14b were stable. They showed low mean of ACI and IF with regression coefficient (0.07, 1.34 and1.07, respectively) and showed lowest genotypic variance (s*i*) (0.40, 1.20, 2.17, respectively) (Table 7).

The stability of the tested wheat genotypes against stem rust, most of the tested wheat genotypes against stem rust showed regression coefficient (bi) values that were different from unity, but some genotypes; *Sr* 20, S*r* 25, *Sr* 31, *Sr* 9e and *Sr* 12 were stable and showed low mean of ACI and IF with regression coefficient (0.83, 1.39, 0.95, 1.08 and 0.94, respectively) and showed lowest genotypic variance (s*i*) (2.67, 2.33, 1.60, 2.83and 4.23, respectively) (Table 8).

The stability of the tested wheat genotypes against yellow rust, most of the tested wheat genotypes against yellow rust showed regression coefficient (bi) values that were different from unity, but only one genotype; *Yr* 17 was stable and showed low mean of ACI and IF with regression coefficient (0.5) and showed lowest genotypic variance (s*i*) (0.90) (Table 9).

Table 8. Stability parameters for stem rust resistance of 42 wheat genotypes grown at two locations during three growing seasons 2016/2017, 2017/2018 and 2018/2019.

Genotype	BLUP ACI	BLUP IF	bi	ri2	Si(1)
Sr 2complex	0.59	1.42	0.76	-0.15	0.50
Sr 5	6.13	3.94	0.19	4.60	2.83
Sr 6	3.94	3.94	-1.20	3.83	4.13
Sr 7a	6.07	3.94	2.98	14.87	2.27
S 7b	10.02	3.94	2.42	21.00	2.10
Sr 8a	24.20	3.94	-1.34	50.56	0.53
Sr 8b	16.81	3.94	2.17	17.45	0.77
Sr 9a	4.81	3.94	-0.29	1.55	1.90
Sr 9b	6.84	3.94	1.48	15.17	5.60
Sr 9d	15.49	3.94	-4.41	44.33	1.00
Sr 9e	4.16	3.94	1.08	1.04	2.83
Sr 9g	5.02	3.39	3.22	5.16	3.13
Sr 10	10.18	3.94	-3.92	25.35	2.23
Sr 11	1.83	2.21	-0.58	1.10	1.87
Sr 12	3.12	3.23	0.94	2.11	4.23
Sr 13	2.41	1.97	0.32	1.08	1.30
Sr 14	4.54	3.71	1.56	2.98	3.23
Sr 15	6.15	3.39	3.61	7.01	4.00
Sr 16	7.77	3.94	4.62	12.40	3.57
Sr 17	9.63	3.71	0.84	33.83	4.60
Sr 18	4.31	3.47	0.94	3.90	2.67
Sr 19	15.88	3.71	1.34	42.61	1.53
Sr 20	5.36	3.94	0.83	5.37	2.67
Sr 21	11.88	3.94	5.57	48.69	1.93
Sr 22	3.25	3.55	-0.12	0.80	1.43
Sr 23	1.20	1.81	2.38	1.51	2.60
Sr 24	0.10	1.10	0.00	0.13	0.80
Sr 25	1.64	2.05	1.39	0.66	2.33
Sr 26	0.61	1.26	0.66	0.37	1.27
Sr 27	1.02	1.42	1.89	1.02	2.30
Sr 28	2.46	2.29	2.52	2.03	3.77
Sr 29	3.77	3.00	-0.60	3.32	2.33
Sr 30	3.66	3.71	0.54	0.66	1.50
Sr 31	0.67	1.10	0.95	1.48	1.60
Sr 32	0.28	1.26	0.11	0.25	1.40
Sr 33	0.10	1.10	0.00	0.13	0.80
Sr 34	2.07	2.76	2.13	1.57	4.60
Sr 35	5.47	3.94	0.72	3.26	2.33
Sr 36	0.10	1.10	0.00	0.13	0.80
Sr 37	3.24	3.15	-0.12	2.10	2.37
Sr 38	0.10	1.10	0.00	0.13	0.80
Sr 39	0.10	1.10	0.00	0.13	0.80
Sr 40	3.85	2.76	-3.59	15.21	4.00
Sr Wld1	0.37	1.10	0.44	0.24	0.33
Sr McN	37.89	3.94	11.53	124.26	0.13
Sr Tmp	10.73	3.47	-2.89	11.58	0.87
Misr 3	0.10	1.10	0.00	0.13	0.80
Sakha 95	6.07	3.94	-0.44	4.57	1.50
Gemmeiza 11	14.62	3.94	4.65	42.13	2.03
Morocco (check)	74.04	3.94	4.77	32.30	0.00

Table 9. Stability parametersfor stripe rust resistance of 17 wheat genotypes grown at two locations during three growing seasons 2016/2017, 2017/2018 and 2018/2019.

Genotype	BLUP IF	BLUP ACI	bi	ri2	Si(1)
Yr 1	1.29	0.27	0.0	9.1	0.3
Yr 2	3.40	17.64	5.4	225.9	1.9
Yr 5	1.29	0.33	0.0	9.7	0.8
Yr 6	3.67	18.98	0.6	50.1	0.8
Yr 7	3.67	20.33	0.0	51.4	0.9
Yr 8	1.56	14.30	4.4	168.4	1.2
Yr 9	1.56	9.94	2.9	77.2	1.9
Yr 10	1.29	0.27	0.0	9.1	0.3
Yr 15	1.29	0.27	0.0	9.1	0.3
Yr 17	2.48	3.36	0.5	6.8	0.9
Yr 18	2.48	1.57	0.2	10.7	1.4
Yr 27	3.67	6.07	-0.8	77.3	1.8
Yr 28	3.67	13.66	3.0	59.6	0.6
Yr 31	2.08	2.24	0.3	9.7	1.2
Yr 32	2.48	1.96	0.0	13.4	1.4
Yr A	3.67	29.01	3.2	74.2	0.2
Yr SP	1.29	0.27	0.0	9.1	0.3
Misr 3	1.16	0.27	0.0	9.1	0.3
Sakha 95	1.29	0.27	0.0	9.1	0.3
Gemmeiza 11	3.54	17.02	0.1	45.1	1.0
Morocco (check)	3.67	77.27	1.4	30.3	0.0

DISCUSSION

There are two methods to control rust diseases; using chemical and growing resistant cultivars. Genetic control is the most valuable, effective, economically and environmentally friendly approach, as it reduces the need for using fungicides and reduces the production cost (Vida *et al*., 2009). Two kinds of resistance were found to control rust diseases; first kind is qualitative resistance, which also called race non-specific resistance, slow-rusting resistance, partial resistance, horizontal resistance and minor gene resistance (Lowe *et al*., 2011). The second kind is qualitative resistance, which also called race-specific resistance, gene-for-gene resistance, vertical resistance and major gene resistance. The first type of resistance is explained by the ability of wheat cultivar to slow down the development of rust infection, even though the infection type on this cultivar is susceptible to rust or (Caldwell, 1968). Such resistance is effective against a broad spectrum of the prevalent races or sudden race changes of leaf rust pathogen (Midaner and Korzun, 2012). It likely, lasts longer and remains effective over a wide range of environmental conditions for many seasons.

It is consequently, considered to be more durable than other kinds of resistance (Broers and Parlevliet, 1989). The second kind of resistance is associated with a rapid death of infected cells, and this phenomenon is called "hypersensitive response". Most of rust resistance genes discovered and deployed in wheat are grouped as major resistance genes. Effectiveness of the genes in this type of resistance mainly depends on the pathogen population composition. The resistance of a gene is not a constant trait because of the new pathotypes virulent to resistance gene multiply from time to time (Ellis *et al*., 2014). More durable resistance can be established by combining several genes into a genotype by gene pyramiding (Nelson, 1978). For successful breeding program for leaf rust resistance requires annually evaluated the rust monogenic lines at adult plant stage under field conditions to determine the effective monogenic lines and incorporate into breeding program for producing new resistant wheat cultivar to rust diseases.

In the present study, thirty-eight leaf rust monogenic lines were evaluated at adult plant stage at two locations during three growing seasons; 2016/2017, 2017/2018 and 2018/2019. The four leaf rust resistance genes; *Lr* 17, *Lr* 18, *Lr* 21 and *Lr* 28 were resistant during the three seasons of the study. *Lr* 17 resistance gene is located on chromosome 2AS (Dyck and Kerber, 1977). It has two alleles; *Lr* 17a which found in the two wheat cultivars Rafaela and EAP 26127 (Dyck and Kerber 1977) and *Lr* 17b, also found in the Australian cultivar Harrier (Singh *et al*., 2001). The two alleles; *Lr* 17a and *Lr* 17b have the same infection type to the same pathotypes, depending on leaf rust pathotype and the temperature (Singh *et al*., 2001). *Lr* 18, transferred from *Triticum timopheevii* Zhuk, and located on the long arm of the 5B chromosome (McIntosh, 1983). Seedling resistance using *Lr* 18 is most effective at (15°C - 18°C), and when temperatures increase this gene becomes less effective; at 25°C it becomes ineffective (McIntosh, 1983 and Carpenter *et al*., 2018). *Lr* 21 found on chromosome 1DS and also linked with the two stem rust resistance genes; *Sr* 21 and *Sr* 33 (Jones *et al*., 1990). *Lr* 28 transferred from *Aegilops speltoides* (Riley *et al*., 1968). It was effective against all Indian leaf rust pathotypes in many genetic backgrounds (Tomar and Menon, 1998). Skolotneva *et al*. (2018) found that the four leaf rust resistance genes; *Lr* 17, *Lr* 18, *Lr* 21 and *Lr* 28 were effective in Western Siberia during 2008-2017.

The seven resistance genes; *Lr* 2a, *Lr* 2b, *Lr* 9, *Lr* 10, *Lr* 19, *Lr* 29 and *Lr* 30 showed differentiated response against leaf rust disease during the three growing seasons of the current study. The variability of the efficacy of these monogenic lines during different seasons may be also due to different distribution of leaf rust pathotype (s). Also, may be due to the emergence of new leaf rust pathotype (s) and/or changes in environmental conditions during the three seasons of the study, especially temperature. Dyck and Johnson (1983) found that the two resistance genes; *Lr* 16 and *Lr* 17 were sensitive to temperature. Moreover, Kolmer *et al*. (2007) found that resistance genes *Lr* 1, *Lr* 2a, *Lr* 3ka, *Lr* 10, *Lr* 1, *Lr* 11 and *Lr* 17 become ineffective after the rapid emergence of virulent races. Browder (1980) characterized *Lr* 10 as moderately sensitive to environmental influences. Pretorius & Roelfs (1996) have shown that the optimum expression of *Lr* 13 and *Lr* 34 are strongly influenced by temperature. Bariana (1991) reported that *Lr* 37 was more resistant to *P. triticina* when tested at cooler (17 ±2º C) temperatures.

Previous Egyptian reports confirmed that, resistance genes; *Lr* 2a, *Lr* 2b, *Lr* 9 and *Lr* 19 were effective in adult plant stage (El-Orabey and Nagaty, 2013 and Sallam *et al*., 2014). The differentiation response of these genes may be due to the emergence of new virulent leaf rust pathotypes. Mabrouk (2016) studied the response of 32 leaf rust monogenic lines at adult plant stage in four locations; Qalyubia, Gharbia Sharqia and Beni Suef during three growing season 2012/13, 2013/14 and 2014/15. She found that, the response of the *Lr* 9 ranged from Tr MS - 10 MS and Tr S - 5 S during 2012/13 and 2014/15, respectively. While, the response of *Lr* 19 ranged from 10 MS - 10 S and Tr S - 5 S during 2012/13 and 2014/15, respectively. El-Orabey (2018) also detected virulence to *Lr* 9 and *Lr* 19 genes in

Egypt during 2015/2016 growing season at El-Minufiya, El-Qalubiya, El-Behira and El-Fayom. The rust responses of the two genes were ranged from 20 S - 40 S for *Lr* 9 and Tr S - 5 S for *Lr* 19 during 2015/16 growing season at the four locations. Also, El-Orabey (2018) isolated and identified eight leaf rust races i.e. KTSPT, GBTMT, NPTNK, NJTPK, NTKTS, PRSTT, PTTNS and TTTMS from *Lr* 9 and two pathotypes CTTTT and PKTST from *Lr* 19. This study was the first study for identification and explains the virulence occurred to the two genes in Egypt. El-Orabey *et al*. (2018) identified 24 leaf rust races in Minufiya during 2016/2017 growing season and 14 pathotypes during 2017/2018. The two races; STTTK and TTTMS were identified in Minufiya during 2016/2017 growing season and were virulent to *Lr* 2a, *Lr* 2b, *Lr* 9, *Lr* 10 and *Lr* 30. Also, the two leaf rust pathotypes MTTTT and NTTTT were identified in Minufiya during 2017/2018 growing season and were virulent to the four leaf rust resistance genes; *Lr* 2b, *Lr* 9, *Lr* 10 and *Lr* 30. Moreover, the leaf rust pathotype TTTTT was identified in Minufiya during 2017/2018 growing season and showed 1.18% frequency, this pathotype virulent to *Lr* 2a, *Lr* 2b, *Lr* 9, *Lr* 10 and *Lr* 30. Same results were found by Kolmer *et al*. (2007) who reported that, *Lr* 1, *Lr* 2a, *Lr* 3ka, *Lr* 10, *Lr* 11 and *Lr* 17 lost their efficacy after the emergence of virulent races.

Moreover, results of the present study showed that, the seven stem rust monogenic lines; *Sr* 2, *Sr* 24, *Sr* 32, *Sr* 33, *Sr* 36, *Sr* 38 and *Sr* 39 were resistant during the three seasons of the study. The stem rust resistance gene; *Sr* 2 is located on chromosome 3BS and transferred from Yaroslav emmer wheat (*Triticum turgidum* var. *dicoccum*) into hexaploid wheat (Hare and McIntosh, 1979). This gene linked with morphological character; pseudo-black chaff (PBC), has been used for years in breeding programs. PBC is a dark pigmentation that occurs on the glumes, peduncle and below stem internodes, but its levels of expression vary with genetic backgrounds and environments (Bhowal and Norkhede, 1981). This gene is effective at adult stage against all known races of stem rust including recently Ug99 race and its variants in wheat (Singh *et al*., 2011). *Sr* 24 found on chromosome 3DL and completely associated with *Lr* 24 gene (McIntosh *et al*., 1976). This gene showed resistance to most stem rust pathotypes including the virulent Ug99 race; TTKSK. Virulence to this major resistance gene has been found in South Africa (Mago *et al*., 2005) and India (Bhardwaj *et al*., 1990). Also, *Sr24* is not effective against more recent variant of UG99, designated TTKST. *Sr* 32 is found on the short arm of chromosome 2D and derived from *Aegilops speltoides* and translocated to hexaploid wheat (Mago *et al*., 2013).*Sr* 33 was first discovered in *Aegilops tauschii* and transferred to chromosome arm 1DS of wheat. This gene provides an intermediate level a resistance to several *Puccinia graminis* sp. *tritici* races including Ug99 related races (Kerber and Dyck, 1979). *Sr* 36 derived from *Triticum timopheevi* and found on chromosome arm 2BS (Bariana *et al*., 2001). *Sr* 38 is located on chromosome 2AS and completely linked with the two genes *Lr* 37 and *Yr* 17 (Bariana and McIntosh, 1993). *Sr* 39 was transferred to the hexaploid wheat cultivar Marquis from *Aegilops speltoides*. The gene is found on a translocated segment of *A. speltoides* chromosome 2S to wheat chromosome 2B (Kerber and Dyke, 1990). Egyptian report showed that, the four genes; *Sr* 2, *Sr* 24, *Sr* 32 and *Sr* 33 were effective at adult plant stage under Egyptian field conditions during 2012/2013 growing seasons. While, the three resistance genes; *Sr* 36, *Sr* 38 and *Sr* 39 were ineffective.

In the current study, *Sr* 31 gene was effective during the two growing seasons; 2016/2017 and 2017/2018, while was ineffective (Tr MS) during 2018/2019 growing season. This resistance gene was effective had been effective for more than 30 years worldwide till Ug99 is the first identified to be virulent to this widely deployed resistance gene (Pretorius *et al*., 2000) and till 2012/13 growing season under Egyptian field conditions. In 2013/14, virulence to *Sr* 31 was detected for the first time in Egypt, this mainly due to the presence of three variants of Ug99 i.e. TTKST, TTKTK and TTKSK in Egypt (Patpour *et al*., 2016). The efficacy of this resistance gene broken during 2018/2019 may be due to the appearance of any variants of Ug99. In Hungary, both *Sr* 31 and *Sr* 36 still effective against stem rust infection. However, due to the advent of a highly virulent race TTKS (Ug99) detected in Uganda in 1999 (Pretorius *et al*., 2000) and its variants like TTTSK (Jin *et al*., 2007) which is virulent to most of the *Sr* genes including *Sr* 31and *Sr36*, respectively, there is a need to introduce new, effective *Sr* genes against stem rust into new wheat cultivars. Resistance against Ug99 race is retained by genes *Sr* 2, *Sr* 13, *Sr* 14, *Sr* 22, *Sr* 24, *Sr* 25, *Sr* 26, *Sr* 27, *Sr* 28, *Sr* 29, *Sr* 32, *Sr* 33, *Sr* 35, *Sr* 36, *Sr* 37, *Sr* 39, *Sr* 40, *Sr* 43, *Sr* 44, *Sr* 45, *Sr* 47, and *Sr* Tmp (Singh *et al*., 2006).

Also, results of the efficacy of yellow rust monogenic lines showed that, the five yellow rust resistance genes; *Yr* 1, *Yr* 5, *Yr* 10, *Yr* 15 and *Yr* SP were resistant during the three seasons of the study. The yellow rust resistance genes *Yr* 1, *Yr* 5, *Yr* 10, *Yr* 15 and *Yr* SP were resistant during the three seasons of the study. Yellow rust resistance gene; *Yr* l is found in the long arm of chromosome 2A (Bariana and McIntosh, 1993). *Yr* 5 derived from *Triticum spelta* and found on the long arm of chromosome 2B (Macer 1966), still shows high resistance against all of isolates in China (Wang *et al*., 1996). *Yr* 10 located on the short arm of chromosome 1B (Metzger and Silbaugh, 1970). Alternative sources for the stripe rust resistance gene *Yr* 10 were identified in *T. spelta* accession 415 (Kemma and Lange, 1992) and in *T. vavilovii* accession AUS22498 (Bariana *et al*., 2002). The *Yr* 10 gene still provide effective resistance to stripe rust in wheat in most wheat growing areas but virulent Pst races have been reported (Chen *et al*., 2010). *Yr* 15 found on the short arm of chromosome 1B (McIntosh and Silk, 1996). *Yr* SP is located on the short arm of chromosome 2B (McIntosh *et al*., 1995). Shahin (2017) evaluated the above four yellow rust resistance genes under Egyptian field conditions and found that, these genes were resistant at adult plant stage and showed rust response ranged from 0 to 5 MR. Chen *et al*. (2009) reported that the yellow rust resistance genes; *Yr* 5, *Yr* 10, *Yr* 15, and *Yr* 24/26 confer resistance to the race CYR32.

In the current study, combined analysis of variance for the tested wheat genotypes for rust diseases resistance showed that the differences between environments (E), genotypes (G) and the interaction between the environments and genotypes were highly significant. These results indicated that genotypes interacted differently in terms of rust severity with the environments. Singh and Narayanan (2000) found that, if G X E interaction was significant, therefore,

stability analysis can be carried out. According to the Eberhart & Russell (1966) model, a stable resistant genotype is one of high resistance, unit regression coefficient (bi=1) and standard error as small as possible. According to stability parameters, nine wheat monogenic lines; *Lr* 28, *Lr* 22a, *Lr* 14b, *Sr* 20, Sr 25, *Sr* 31, *Sr* 9e, *Sr* 12 and *Yr* 17 were stable and widely adapted in their resistance during the three successive growing seasons. They have regression coefficient nearly of 1 with low value of standard error and gave low mean of rust severity. This data is in agreement with Letta and Tilahun (2007) who found that the two durum wheat varieties Ilani and Kilinto are stable varieties to stem rust resistance under Ethiopian conditions. Also, Sallam *et al.* (2014) reported that the leaf rust monogenic line *Lr* 33 was the most stable monogenic line during 2011/12-2013/14 growing seasons.

The breeder needs to design their breeding program very carefully for releasing varieties with different genetic background to resistance for rust diseases. The results of the present study gave enough information for planning of wheat breeding programs for rust resistance according to the response of the tested genotypes at adult stage. The value of information about the tested wheat genotypes is ultimately to control rust diseases by transferring effective leaf, stem yellow rust resistance genes singly or in combination to commercially grown wheat cultivars through breeding program to develop high-yielding resistant wheat cultivars in wheat-growing areas of Egypt. So using of these wheat genotypes; *Lr* 14b, *Lr* 17, *Lr* 18, *Lr* 21, *Lr* 22a, *Lr* 28 and Misr 3 for leaf rust; *Sr* 2, *Sr* 9e, *Sr* 12, *Sr* 24, *Sr* 20, Sr 25, *Sr* 31, *Sr* 32, *Sr* 33, *Sr* 36, *Sr* 38, *Sr* 39 and Misr 3 for stem rust and *Yr* 1, *Yr* 5, *Yr* 10, *Yr* 15, *Yr* 17, *Yr* SP, Misr 3 and Sakha 95 for yellow rust are useful in breeding programs in developing new wheat varieties with stable resistance to rust diseases under Egyptian conditions.

CONCLUSION

Sixteen wheat rust monogenic lines (four leaf rust resistance genes i.e. *Lr* 17, *Lr* 18, *Lr* 21 and *Lr* 28; seven stem rust resistance genes i.e. *Sr* 2, *Sr* 24, *Sr* 32, *Sr* 33, *Sr* 36, *Sr* 38 and *Sr* 39 and five yellow rust resistance genes i.e. *Yr* 1, *Yr* 5, *Yr* 10, *Yr* 15 and *Yr* SP) were resistant and effective at adult plant stage under field conditions during the three growing seasons of the current study. Thus can efficiently be used in devising future breeding program for rust resistance in building a long lasting defense against these diseases. These effective resistance genes can be recommended as resistance sources for incorporation in Egyptian breeding programmes into new released cultivars to increased durability of resistance.

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فاعلية وعدم فاعلية بعض جينات المقاومة فى القمح لأمراض صدأ الأوراق ، الساق والأصفر فى مصر

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تم تقييم ١٠٥ تركيب وراثى من القمح إشتملت على ٣٨ سلالة نباتية تحمل جين أحادى لمقاومة صدأ الأوراق ، ٤٦ سلالة نباتية تحمل جين أحادى لمقاومة صدأ الساق ، ١٧ سلالة نباتية تحمل جين أحادى لمقاومة الصدأ الأصفر فى القمح ، ثلاثة أصناف قمح تجارية وهى سخا ٩٥ ، مصر ٣ و جميزة ١١ والصنف موروكو الحساس للإصابة بالأصداء لمقاومتهم وثبات صفة المقاومة لأمراض الصدأ فى طور البلوغ تحت ظروف الحقل فى الموقعين وهم مدينة السادات والبستان خلال ثلاثة مواسم زراعية متتالية وهى ٢٠١٦/٢٠١٧ و ٢٠١٧/٢٠١٨ و ٢٠١٨/٢٠١٩ . بناءاً على النتائج المتحصل عليها فأن الاختلافات بين البيئات ، التراكيب الوراثية والتفاعل بينهم كان عالى المعنوية لجميع الصفات المدروسة وهذه النتائج تدل على أنه يوجد تنوع عالى بين التراكيب الوراثية .كما أن التراكيب الوراثية تحت الدراسة تم تقسيمها إلى ثلاثة مجاميع طبقاً لطرز الاصابة. المجموعة الأولى تضمنت التراكيب الوراثية الأكثر كفاءة فى مقاومتها حيث إشتملت على *Lr* 17, *Lr* 18, *Lr* 21, *Lr* 28 ومصر ٣ لصدأ الأوراق ، *Sr* 2, *Sr* 24, *Sr* 32, *Sr* 33, *Sr* 36, *Sr* 38, *Sr* 39 ومصر ٣ لصدأ الساق و *Yr* 1, *Yr* 5, *Yr* 10, *Yr* 15, *Yr* SP ، مصر ٣ وسخا ٩٥ للصدأ الأصفر. المجموعة الثانية وهى التراكيب الوراثية ذات المقاومة المتابينة والمجموعة الثالثة إشتملت على التراكيب الوراثية غير الفعالة. طبقاً لمقاييس الثبات الوراثى كان هناك تسعة سلالة نباتية تحمل جين أحادى وهى صدأ الساق *Lr* 12 *Sr* 9e, *Sr* 31, *Sr* 25, *Sr* 20, *Lr* 14b, *Lr* 22a, *Lr* 28و *Yr* 17 أكثر ثباتاً وتأقلماً فى مقاومتهم.