

Evaluation of New Sources of Resistance to Wheat Stripe Rust (*Puccinia striiformis* f. sp. *tritici*), under Egyptian Field Conditions

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ABSTRACT

Wheat stripe rust caused by *Puccinia striiformis* f. sp. *tritici* is the most destructive rust disease in Egypt and worldwide. The current study was performed during 2014/2015 and 2015/2016 growing seasons to evaluate 57 wheat genotypes, selected from a total of 554 wheat genotypes from CIMMYT for their field reaction to stripe rust infection, as the new sources of resistance. Four epidemiological parameters, i.e. FRS %, ACI, AUDPC and rAUDPC, as well as 1000 kernel weight were used as criteria to evaluate stripe rust resistance and yield potentiality. The analysis of variance data depicted extensive and high significant differences among different wheat genotypes under study for their response to stripe rust infection each year. Out of 57 wheat genotypes, only 12 wheat promising lines; no's 1, 2, 3, 12, 13, 14, 16, 21, 22, 25, 50 and 51 had high resistance potentiality to be used as new sources to enhance the level of stripe rust resistance in the local breeding cultivars, making it possible to minimize the reliance on fungicides without impairing disease control. Correlation analysis gave an evidence to the importance of all parameters under study, especially FRS (%) and ACI as good indicators for the evaluation of adult plant resistance (APR) in the tested wheat lines against stripe rust under field conditions. High heritability estimates (up to 99%) and moderate to high values of genetic advance, expected from selection, were obtained for all the studied traits, revealing that most of the phenotypic variations were due to genetic factors or genetic structure of the studied genotypes. Also, it is an indicative for the possibility to achieve high success in recovering the desired genes for stripe rust resistance in future generations. Moreover, it means that the genetic variations were less affected by the changes in environmental conditions from season to another season. It could be concluded that FRS (%) and ACI are considered to be more appropriate indicators, rather than AUDPC and rAUDPC for screening large numbers of breeding materials, because they were more easily to be applied or handled for the breeders that facilitates the success of selection process, during a national breeding program without more time consumption.

Keywords: Wheat, stripe rust, resistant genotypes, heritability, genetic advance

INTRODUCTION

Wheat stripe rust caused by *Puccinia striiformis* f. sp. *tritici* is the most destructive rust disease in Egypt and worldwide (Line 2002). It is a macrocyclic rust, causing a serious economic loss in the susceptible wheat cultivars (Jin *et al.*, 2010 and Omara *et al.*, 2016). Stripe rust was a dominant disease in Central Asian countries in the late 1990's and early 2000's, accounting for yield losses of 20 and 40% in 1999 and 2000 (Morgounov *et al.*, 2004). Historically, wheat stripe rust is considered a sporadic disease in Egypt. During the last five decades, severe stripe rust epidemics occurred in 1967, 1986, 1995 and 1997, attacking the widely grown wheat cultivars; Giza-144, Giza-150, Gemmeiza-1, Giza-163, Sakha-69 and the long spikes; Sids cultivars (Abd El-Hak *et al.*, 1972, El-Daoudi *et al.*, 1996 and Abu El-Naga *et al.*, 1997).

Host-genetic resistance or growing wheat cultivars having a sustainable stripe rust resistance is still the most effective, economically and environmentally safe control method, not only to minimize crop losses but also to avoid the sudden occurrence of severe epidemics in the future (Singh *et al.*, 2000). The evaluation of different wheat genotypes, as the sources of resistance against stripe rust has been previously studied by many investigators. In Egypt, Abu El-Naga *et al.* (2001) showed that wheat cultivars; Giza-168, Sakha-61, Sakha-93, Gemmeiza-7 and Gemmeiza-9 have satisfactory and an adequate levels of stripe rust resistance during the two years of their study. Recently, Omara *et al.* (2016) reported that the two wheat cultivars newly released, i.e. Gemmeiza-11 and Sids-12, showed susceptible reaction to stripe rust under field conditions in Egypt, although widely cultivation of these cultivars in a large area nationwide.

Likewise, different wheat genotypes were evaluated in several countries worldwide to elucidate their response against stripe rust infection (Cetin *et al.*, 2006). Accordingly, most of these countries depend mainly on wheat genotypes introduced from CIMMYT to develop new wheat cultivars with high and acceptable levels of rust resistance. However, these genotypes are distributed internationally through the CIMMYT nurseries system (Singh *et al.*, 2011).

National wheat breeding program for rust resistance in Egypt is based, to a large extend, upon the wheat resistant genotypes from CIMMYT and ICARDA, besides to the old sources of resistance in the country. Over the last three years, most of the commercial and recommended wheat cultivars exhibited different levels of susceptibility to stripe rust infection under the Egyptian field conditions nationwide (Omara *et al.*, 2016). Thus, it is necessary to search for new sources of resistance to be used for enhancement of resistance to stripe rust in the local breeding materials.

Therefore, the objective of this investigation was to evaluate a total of 57 wheat promising lines, selected from 554 CIMMYT genotypes for their adult plant resistance (APR) to stripe rust infection under field conditions in Egypt. A second objective was to estimate heritability (%) and genetic advance expected from selection of four stripe rust resistance components that used as criteria for evaluating this resistance. Subsequently, the main objective of this study was to facilitate the exploitation and use of these resistant lines into a national breeding program for stripe rust resistance.

MATERIALS AND METHODS

The present work was carried out at Sakha Agricultural Research Station during 2014/2015 and

2015/2016 growing seasons. Fifty seven wheat advanced lines were selected kindly from the International Bread Wheat Screening Nursery (304 lines) and 9th STEMRRSN (250 lines) obtained from CIMMYT. In addition, the highly susceptible variety; Morocco as well as the two commercial wheat cultivars;

Sids-12 and Sids-13 were used as the check cultivars (control). All wheat genotypes were evaluated against stripe rust infection during the two growing seasons of the study. The pedigree of the genotypes evaluated in this study is found in Table (1).

Table 1. Pedigree of wheat genotypes used in this study.

Genotype	Pedigree
Line 1	TACUPETO F2001*2/BRAMBLING//KIRITATI/2*TRCH
Line 2	KACHU//KIRITATI/2*TRCH
Line 3	KIRITATI//HUW234+LR34/PRINIA/3/BAJ #1
Line 4	MUTUS//ND643/2*WBLL1
Line 5	ND643/2*WBLL1/4/WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1
Line 6	ND643/2*WBLL1//KACHU
Line 7	SUP152//ND643/2*WBLL1
Line 8	FRNCLN/3/ND643//2*PRL/2*PASTOR/4/FRANCOLIN #1
Line 9	FRNCLN/3/KIRITATI//HUW234+LR34/PRINIA/4/FRANCOLIN #1
Line 10	CHYAK1*2/3/HUW234+LR34/PRINIA//PFAU/WEAVER
Line 11	SHORTENED SR26 TRANSLOCATION/4/3*CHIBIA//PRLII/CM65531/3/KAUZ/BAV92
Line 12	SHORTENED SR26 TRANSLOCATION//FRET2*2/BRAMBLING/3/2*FRET2*2/BRAMBLING
Line 13	SHORTENED SR26 TRANSLOCATION/3/KIRITATI//PBW65/2*SERI.1B/4/2*DANPHE #1
Line 14	TUKURU//BAV92/RAYON/4/WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1
Line 15	QUAIU/3/KIRITATI//PBW65/2*SERI.1B/4/DANPHE #1
Line 16	WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1*2/4/KBIRD
Line 17	CROSBILL #1*2/3/ND643//2*ATTILA*2/PASTOR
Line 18	DANPHE #1*2/SHORTENED SR26 TRANSLOCATION
Line 19	FRNCLN/3/KIRITATI//HUW234+LR34/PRINIA/4/FRANCOLIN #1
Line 20	WBLL1*2/BRAMBLING/5/BABAX/LR42//BABAX*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ
Line 21	MILAN/KAUZ//BABAX/3/BAV92/4/WHEAR//2*PRL/2*PASTOR
Line 22	BABAX/LR42//BABAX*2/3/PAVON.7S3+LR47/4/ND643/2*WBLL1/5/BABAX/LR42//BABAX*2/3/PAVON 7S3, +LR47
Line 23	FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ/5/KIRITATI/2*TRCH/6/BAJ #1
Line 24	FRET2*2/BRAMBLING//KIRITATI/2*TRCH/3/FRET2/TUKURU//FRET2
Line 25	FRET2*2/KIRITATI//KIRITATI/2*TRCH/3/WBLL1*2/BRAMBLING
Line 26	FRET2*2/KIRITATI//KIRITATI/2*TRCH/3/WBLL1*2/BRAMBLING
Line 27	ND643/2*WBLL1/5/PRL/2*PASTOR/4/CHOIX/STAR/3/HE1/3*CNO79//2*SERI
Line 28	ND643/2*WBLL1//MUNAL/3/MUNAL #1
Line 29	KIRITATI//HUW234+LR34/PRINIA/3/CHONTE/5/PRL/2*PASTOR/4/CHOIX/STAR/3/HE1/3*CNO79//2*SERI
Line 30	KIRITATI//HUW234+LR34/PRINIA/3/FRANCOLIN #1/4/BAJ #1
Line 31	ND643/2*WBLL1//2*KACHU
Line 32	ND643/2*WBLL1//KIRITATI/2*TRCH/3/ND643/2*WBLL1
Line 33	MUNAL*2//ND643/2*WBLL1
Line 34	PAURAQ//ND643/2*WBLL1/3/PAURAUQUE #1
Line 35	KISKADEE #1*2/3/ND643//2*PRL/2*PASTOR
Line 36	WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1*2/4/ND643/2*WBLL1
Line 37	WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1/4/PAURAUQUE #1/5/WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1
Line 38	WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1/4/KBIRD/5/WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1
Line 39	HUW234+LR34/PRINIA*2//KIRITATI/3/KINGBIRD #1
Line 40	PASTOR//HXL7573/2*BAU/3/SOKOLL/WBLL1/4/HUW234+LR34/PRINIA//PBW343*2/KUKUNA/3/ROLF07/5/WHEAR/SOKOLL
Line 41	BABAX/LR42//BABAX*2/3/PAVON 7S3, +LR47/4/ROLF07/YANAC//TACUPETO F2001/BRAMBLING
Line 42	ND643/2*WBLL1/4/HUW234+LR34/PRINIA//PBW343*2/KUKUNA/3/ROLF07
Line 43	BABAX/LR42//BABAX/3/ER2000/4/KA/NAC//TRCH/5/SOKOLL/3/PASTOR//HXL7573/2*BAU
Line 44	BABAX/LR42//BABAX/3/ER2000/11/CROC_1/AE.SUARROSA(213)//PGO/10/ATTILA*2/9/KT/BAGE//FN/U/3/BZA/4/TRM/5/ALDAN/6/SERI/7/VEE#10/8/OPATA/12/BAVIS
Line 45	ATTILA*2/PBW65*2//PARUS/3/PRL/4/ATTILA*2/PBW65//KIRITATI/3/WAXWING/KIRITATI
Line 46	WBLL1*2/BRAMBLING//ND643/2*WBLL1
Line 47	ND643/2*WBLL1/3/ND643//2*PRL/2*PASTOR
Line 48	PFAU/MILAN/3/BABAX/LR42//BABAX*2/4/NIINI #1
Line 49	PFAU/MILAN/3/BABAX/LR42//BABAX*2/4/NIINI #1
Line 50	PFAU/MILAN/3/BABAX/LR42//BABAX*2/4/NIINI #1
Line 51	PFAU/MILAN/3/BABAX/LR42//BABAX*2/4/NIINI #1
Line 52	WBLL1*2/BRAMBLING//WHEAR/SOKOLL/3/WBLL1*2/BRAMBLING
Line 53	SNB//CMH79A.955/3*CNO79/3/ATTILA/4/CHEN/AEGILOPS/SUARROSA (TAUS)//BCN/3/2*KAUZ/5/KINGBIRD #1
Line 54	ELVIRA/5/CNDO/R143/ENTE/MEXI75/3/AE.SQ/4/2*OCL/6/VEE/PJN//KAUZ/3/PASTOR/7/TILHI/4/CROC_1/AE.SUARROSA (213)//PGO/3/CMH81.38/2*KAUZ/8/PICAFLO #2
Line 55	WHEAR//2*PRL/2*PASTOR/3/WHEAR/SOKOLL
Line 56	PRL/SARA//TSI/VEE#5/3/TILHI/4/ATTILA/2*PASTOR/5/KINGBIRD #1
Line 57	ATTILA/3/URES/PRL//BAV92/4/WBLL1/5/CROC_1/AE.SUARROSA (205)//BORL95/3/PRL/SARA//TSI/VEE#5/4/FRET2
Sids-12	BUC//7C/ALD/5/MAYA74/ON//1160147/3/BB/GLL/4/CHAT"S"/6/MAYA/VUL//CMH74A.630/4*SX.SD7096-4SD-1SD-1SD-0SD
Sids-13	KAUZ "S"//TSI/SNB"S". ICW94-0375-4AP-2AP-030AP-0APS-3AP-0APS-050AP-0AP-0SD.
Morocco	----

Randomized complete block design with three replicates was followed, to carry out this experiment. The experimental unit consisted of two rows with 3m. long. The experiment was surrounded by one meter border of the highly susceptible varieties; *Triticum spelta saharenses* (T.S.S.) and Morocco to serve as permanent source, and/or a spreader for rust inoculum. At booting stage, spreader plants were artificially inoculated by the rust pathogen urediniospores, following the procedure adopted by Tervet and Cassel (1951), in addition to the natural infection. The inocula (urediniospores mixture) were obtained from stripe rust greenhouse of Wheat Diseases Research Department, Plant Pathology Research Institute, ARC, and mixed with talcum powder at the rate of 1:20 (w:w). The agricultural practices recommended for the wheat crop were conducted in this experiment.

Disease assessment:

Disease severity (DS %) was recorded four times, one every 10 days interval, during each of the two successive growing seasons, expressed as the percentage coverage leaf area of wheat plants with rust pustules, following the method adopted by Peterson *et al.* (1948). Field reaction of stripe rust as infection type was expressed in five types (Stakman *et al.*, 1962), *i.e.* highly resistant (0), resistant (R), moderately resistant (MR), moderately susceptible (MS) and susceptible (S). Then this reaction was transformed to average coefficient of infection (ACI) values, according to the methods adopted by Saari and Wilcoxson (1974). The obtained data served in the determination of the final rust severity (FRS %), as outlined by Das *et al.* (1993). Area under disease progress curve (AUDPC) was calculated for each genotype under study according to an equation proposed by Pandey *et al.* (1989) as follows:

$$AUDPC = D [1/2 (Y_1 + Y_k) + Y_2 + Y_3 + \dots + Y_{(k-1)}]$$

Where:

D = Time intervals (days between consecutive records)

$Y_1 + Y_k$ = Sum of the first and the last disease scores.

$Y_2 + Y_3 + \dots + Y_{(k-1)}$ = Sum of all in between disease scores.

Relative area under disease progress curve (rAUDPC) was also calculated for each genotype, using the equation of Milus and Line (1986) as follows:

$$rAUDPC = \frac{\text{Line (AUDPC)}}{\text{Susceptible (AUDPC)}} \times 100$$

Yield assessment:

Grain yield expressed as 1000 kernel weight per gram was determined for all the tested genotypes in the two growing seasons, under study.

Genetic components:

To estimate the percentage of heritability in its broad sense (h^2) for final rust severity (FRS %), average coefficient of infection (ACI), area under disease progress curve (AUDPC), and relative area under disease progress curve (rAUDPC), the following formula was applied:

$$\% \text{Heritability}(h^2) = \frac{\text{Genotypic variance } (\sigma^2g)}{\text{Phenotypic variance } (\sigma^2ph)} \times 100$$

(Miller *et al.*, 1958)

Where:

$$\sigma^2g = (\sigma^2e + r\sigma^2g) - \sigma^2e / r$$

$$\sigma^2ph = (\sigma^2e + r\sigma^2g) / r$$

Genetic advance (GA), expected from selection, was also calculated, for each of the epidemiological parameters according to the following formula:

$$\text{Genetic advance } (\%) = (\sigma^2g / \sigma^2ph)k \times \sqrt{\sigma^2ph} \sqrt{\sigma^2ph}$$

(Miller *et al.*, 1958).

Where:

k = 2.06 at 5% selection intensity.

Statistical analysis:

Randomized complete block design with three replicates was followed the analysis of variance (ANOVA) of the data that performed with the software package SPSS13. The least significant difference (LSD) at 5% levels was used to compare treatments means. Also, correlation and regression coefficient “SPSS Regression Modeling” was used to determine the relationship between FRS (%), ACI, AUDPC and rAUDPC and 1000 kernel weight during the two growing seasons.

RESULTS AND DISCUSSION

To evaluate 57 wheat lines, selected from a total of 554 wheat genotypes from CIMMYT for their field reaction to stripe rust infection in order to use as the new sources of resistance, four epidemiological parameters, *i.e.* FRS %, ACI, AUDPC and rAUDPC, as well as 1000 kernel weight were estimated, during 2014/2015 and 2015/2016 growing seasons. The obtained data relevant to these parameters were subjected to an analysis of variance (Tables, 2 and 3). The results of analysis of variance depicted extensive genetic variations and high significant differences among the different genotypes for their response to stripe rust infection each year under study.

Evaluation of the tested wheat genotypes for stripe rust resistance, under field conditions:

Rust response of 57 wheat promising lines under study was recorded as rust severity (%), starting from the first appearance of disease symptoms in each genotype, until the disease severity reached its maximum and final level on the check variety (Morocco). Four epidemiological parameters, *i.e.* final rust severity (FRS %), average coefficient of infection (ACI), area under disease progress curve (AUDPC) and relative area under disease progress curve (rAUDPC) were estimated to characterize stripe rust resistance in the tested wheat genotypes, compared to the check variety; Morocco, as well as the two local wheat cultivars; Sids-12 and Sids-13, during 2014/15 and 2015/16 growing seasons.

Data presented in Tables (4 and 5) show that thirty wheat lines; no's 1, 2, 3, 4, 12, 13, 14, 15, 16, 17, 18, 20, 21, 22, 23, 25, 27, 29, 30, 36, 38, 40, 43, 44, 45, 48, 49, 50, 51 and 57, in 2014/15 and only twelve lines; no's 1, 2, 3, 12, 13, 14, 16, 21, 22, 25, 50 and 51 in 2015/16 have displayed high levels of adult plant resistance to stripe rust infection under field conditions. Where, no disease symptoms (pustules) could be

observed or recorded in wheat plants of these advanced lines. Therefore, they should be characterized as the completely resistant lines. However, the exploitation

and deployment of this disease resistance are amongst the major contribution in genetic improvement of many crops including wheat.

Table 2. ANOVA of the disease response for wheat genotypes, expressed as four epidemiological parameters of stripe rust and 1000 kernel weight during 2014/15 growing season.

S.O.V.	DF	MS				1000 kernel weight	F prob				1000 kernel weight
		Epidemiological parameters					Epidemiological parameters				
		FRS ^a (%)	ACI ^b	AUDPC ^c	rAUDPC ^d		FRS (%)	ACI	AUDPC	rAUDPC	
Replications	2	6.505	0.265	66.822	27.572	3.207	0.062	0.850	0.099	0.004	0.002
Genotypes	59	1554.287	1540.684	474040.248	1343.907	52.891	4.512	1.699	4.103	1.141	1.632
Error	118	2.301	1.709	28.443	3.368	0.535	-	-	-	-	-
Total	179	-	-	-	-	-	-	-	-	-	-

FRS^a (%) = Final rust severity, ACI^b = Average coefficient of infection, AUDPC^c = Area under disease progress curve and rAUDPC^d = Relative area under disease progress curve.

Table 3. ANOVA of the disease response for wheat genotypes, expressed as four epidemiological parameters of stripe rust and 1000 kernel weight during 2015/16 growing season.

S.O.V.	DF	MS				1000 kernel weight	F prob				1000 kernel weight
		Epidemiological parameters					Epidemiological parameters				
		FRS ^a (%)	ACI ^b	AUDPC ^c	rAUDPC ^d		FRS (%)	ACI	AUDPC	rAUDPC	
Replications	2	26.316	0.838	711.016	4.312	0.023	0.047	0.701	2.864	0.003	0.950
Genotypes	59	1496.347	1519.534	534297.932	610.653	50.968	1.793	2.152	1.950	1.378	1.308
Error	118	8.002	2.408	30.456	0.780	0.606	-	-	-	-	-
Total	179	-	-	-	-	-	-	-	-	-	-

FRS^a (%) = Final rust severity, ACI^b = Average coefficient of infection, AUDPC^c = Area under disease progress curve and rAUDPC^d = Relative area under disease progress curve.

Meanwhile, wheat lines; no's 5, 6, 7, 9, 28, 31, 32, 33, 34, 35, 37, 39, 41, 42, 46, 47, 52, 53, 54, 55 and 56 in 2014/15, as well as the promising lines; no's 4, 5, 6, 8, 9, 15, 17, 18, 20, 23, 27, 29, 30, 31, 32, 33, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 53, 55, 56 and 57 in 2015/16, exhibited susceptible disease reaction to stripe rust, but they have the ability to retard or delay the disease onset or development and showed low to moderate final rust severity (less than 29.66), during the two growing seasons of the study. Also, their AUDPC estimates did not exceed up to 265.33 as they were ranged from (28.66 to 265.33) and from (12.66 to 265.00) during the two seasons, respectively. These wheat promising lines could be characterized or identified as the partially resistant (PR) genotypes, and proved to have an adequate levels of slow-rusting resistance to stripe rust under field conditions (Singh *et al.*, 2011 and Qamar *et al.*, 2012). However, no or limited deployment of partial resistance genes in breeding program in Egypt, and it's application has remained little and it perhaps less appreciated than it should be.

On the other hand, other lines under evaluation; no's 8, 10, 11, 19, 24 and 26 in 2014/15 and lines; no's 7, 10, 11, 19, 24, 26, 28, 34, 52 and 54 in 2015/16 show, in general, the highly susceptible field reaction to stripe rust. Thus, they classified as the fast-rusting group of genotypes. The values of AUDPC were ranged from (380.33 to 1175.00) and from (315.33 to 1300.66) compared to the check variety, Morocco (1595.00 and 1652.33), as well as the fast-rusting cultivars, Sids-12 (1051.00 and 1048.66) and Sids-13 (1850.33 and 1953.33) in the two seasons of the study, respectively. Moreover, the decrement in the level of stripe rust severity, expressed as the lower estimates of FRS %, ACI, AUDPC and rAUDPC in the first season less than those in the later season, could be due to the slight differences in environmental conditions between the two

years under study (Shah *et al.*, 2010). In addition to, the high diversity or variation of the prevalent stripe rust virulent pathotypes from one year to another within the pathogen populations (Wan and Chen 2012). A successful breeding program aim to combine high and adequate level of resistance to stripe rust with high grain yield potential in advanced wheat lines. The obtained results relevant to 1000 kernel weight show significant differences between the tested wheat lines as affected by the level of disease severity. (Tables, 4 and 5). The highest values of 1000 kernel weight (more than 46 gm) were recorded with the highly resistant wheat lines followed by partially resistant (PR) lines. In contrast, the lowest values of 1000 kernel weight were obtained from the highly susceptible or fast-rusting wheat lines. Similar results were previously obtained by Omara *et al.* (2016).

In general, early attempts have been carried out at CIMMYT, aimed to enhance stripe rust resistance based on additive interaction of slow-rusting genes. They researchers in this International center have successfully combined high levels of resistance to stripe rust with high grain yield potential in wheat lines such as; Tukuru, Kukuna and Vivits. They added that genetic analysis of such resistance indicated that at least 4 or 5 minor genes with additive effect, conferred resistance to both leaf and yellow rusts (Singh *et al.*, 2000). Fully utilization of advanced lines received from International centers, such as CIMMYT and ICARDA as sources of resistance to rust disease, in particular stripe rust with high yield potentiality and other desirable agronomic characteristic for possible use in crossing blocks, is the main objective of national breeding program in Egypt. As discussed before, further studies are needed to confirm and emphasized the effectiveness and stability of the evaluated genotypes for stripe rust resistance as useful advanced lines under different climatic conditions.

Table 4. Adult plant reaction of 57 wheat genotypes against stripe rust, expressed as the four epidemiological parameters; FRS (%), ACI, AUDPC and rAUDPC as well as 1000 kernel weight, during 2014/15 growing season.

Genotype	Epidemiological parameters				1000 kernel weight (gm)
	FRS ^a (%)	ACI ^b	AUDPC ^c	rAUDPC ^d	
Line 1	0.00	0.00	0.00	0.00	46.33
Line 2	0.00	0.00	0.00	0.00	46.15
Line 3	0.00	0.00	0.00	0.00	46.83
Line 4	0.00	0.00	0.00	0.00	47.50
Line 5	9.33	8.00	107.00	5.78	43.00
Line 6	20.33	16.00	212.00	11.50	42.24
Line 7	10.33	10.00	173.00	9.35	44.16
Line 8	30.33	24.33	380.33	20.50	40.00
Line 9	3.00	3.00	32.66	1.78	45.33
Line 10	30.33	30.33	474.66	25.70	40.66
Line 11	50.33	50.33	875.33	47.30	37.66
Line 12	0.00	0.00	0.00	0.00	47.66
Line 13	0.00	0.00	0.00	0.00	48.33
Line 14	0.00	0.00	0.00	0.00	47.33
Line 15	0.00	0.00	0.00	0.00	46.33
Line 16	0.00	0.00	0.00	0.00	46.66
Line 17	0.00	0.00	0.00	0.00	46.00
Line 18	0.00	0.00	0.00	0.00	47.00
Line 19	60.33	60.33	1024.33	55.40	36.66
Line 20	0.00	0.00	0.00	0.00	48.33
Line 21	0.00	0.00	0.00	0.00	47.66
Line 22	0.00	0.00	0.00	0.00	46.33
Line 23	0.00	0.00	0.00	0.00	48.66
Line 24	69.66	70.33	1175.00	63.50	32.66
Line 25	0.00	0.00	0.00	0.00	46.66
Line 26	50.33	50.33	776.00	41.90	35.00
Line 27	0.00	0.00	0.00	0.00	45.66
Line 28	9.00	8.00	104.33	5.62	41.00
Line 29	0.00	0.00	0.00	0.00	46.33
Line 30	0.00	0.00	0.00	0.00	47.66
Line 31	10.00	10.00	169.66	9.19	42.66
Line 32	19.66	16.33	220.00	11.90	40.33
Line 33	8.66	4.00	59.00	3.19	41.66
Line 34	20.33	19.66	265.33	14.30	38.66
Line 35	9.00	9.00	109.66	5.95	42.00
Line 36	0.00	0.00	0.00	0.00	47.66
Line 37	5.00	5.00	91.33	4.97	44.33
Line 38	0.00	0.00	0.00	0.00	48.33
Line 39	3.00	2.46	30.00	1.62	44.33
Line 40	0.00	0.00	0.00	0.00	46.33
Line 41	5.00	2.00	28.66	1.51	44.66
Line 42	5.00	5.00	79.33	4.27	43.66
Line 43	0.00	0.00	0.00	0.00	47.33
Line 44	0.00	0.00	0.00	0.00	46.00
Line 45	0.00	0.00	0.00	0.00	48.00
Line 46	10.00	10.00	129.66	7.03	42.66
Line 47	9.33	8.66	110.33	5.95	43.33
Line 48	0.00	0.00	0.00	0.00	47.00
Line 49	0.00	0.00	0.00	0.00	46.00
Line 50	0.00	0.00	0.00	0.00	47.66
Line 51	0.00	0.00	0.00	0.00	47.00
Line 52	20.33	16.00	208.33	11.50	41.33
Line 53	9.66	8.00	104.00	5.62	43.66
Line 54	10.10	11.00	186.33	10.10	43.33
Line 55	29.66	7.66	109.66	5.95	43.00
Line 56	20.00	8.33	111.33	6.05	44.33
Line 57	0.00	0.00	0.00	0.00	46.33
Sids-12	90.33	90.33	1595.00	86.50	25.33
Sids-13	59.66	60.33	1051.00	56.80	30.66
Morocco	99.33	99.66	1850.33	100.00	23.33
LSD _{0.05}	2.42	2.74	8.53	2.93	1.17

FRS^a (%) = Final rust severity, ACI^b = Average coefficient of infection, AUDPC^c = Area under disease progress curve and rAUDPC^d = Relative area under disease progress curve.

Table 5. Adult plant reaction of 57 wheat genotypes against stripe rust, expressed as the four epidemiological parameters; FRS (%), ACI, AUDPC and rAUDPC as well as 1000 kernel weight, during 2015/16 growing season.

Genotype	Epidemiological parameters				1000 kernel weight (gm)
	FRS ^a (%)	ACI ^b	AUDPC ^c	rAUDPC ^d	
Line 1	0.00	0.00	0.00	0.00	47.00
Line 2	0.00	0.00	0.00	0.00	46.66
Line 3	0.00	0.00	0.00	0.00	47.33
Line 4	13.66	2.40	30.33	1.55	44.50
Line 5	5.00	5.00	82.33	4.21	44.00
Line 6	9.33	7.66	107.33	5.49	43.83
Line 7	30.33	30.33	474.66	24.30	38.53
Line 8	19.66	15.66	211.66	10.80	40.66
Line 9	5.00	5.00	79.33	4.06	43.33
Line 10	40.33	40.33	624.66	32.00	37.66
Line 11	70.33	70.33	1300.66	66.60	27.33
Line 12	0.00	0.00	0.00	0.00	47.33
Line 13	0.00	0.00	0.00	0.00	48.33
Line 14	0.00	0.00	0.00	0.00	47.66
Line 15	5.00	5.00	64.00	3.28	43.66
Line 16	0.00	0.00	0.00	0.00	48.33
Line 17	5.00	4.00	56.00	2.87	43.33
Line 18	5.00	5.00	61.00	3.12	43.00
Line 19	60.33	60.33	1050.33	53.8	29.66
Line 20	5.00	5.00	64.33	3.29	44.33
Line 21	0.00	0.00	0.00	0.00	48.33
Line 22	0.00	0.00	0.00	0.00	47.00
Line 23	5.00	4.00	59.33	3.04	43.00
Line 24	49.66	49.66	900.66	46.10	34.00
Line 25	0.00	0.00	0.00	0.00	46.00
Line 26	70.33	70.00	1200.33	61.50	25.33
Line 27	5.00	4.00	59.33	3.04	43.00
Line 28	30.00	30.33	475.00	24.30	38.33
Line 29	2.00	0.60	12.66	0.65	44.00
Line 30	3.00	3.00	30.66	1.57	44.33
Line 31	9.66	7.66	103.66	5.31	42.00
Line 32	19.66	15.66	211.66	10.80	40.33
Line 33	19.66	7.66	110.33	5.65	41.00
Line 34	30.00	24.33	380.00	19.50	40.33
Line 35	9.00	9.00	141.66	7.25	42.33
Line 36	5.00	5.00	70.00	3.58	44.66
Line 37	9.33	4.00	59.00	3.02	44.33
Line 38	5.00	5.00	82.00	4.20	43.33
Line 39	3.00	4.00	59.66	3.05	44.00
Line 40	5.00	2.00	27.66	1.42	45.33
Line 41	10.33	10.33	151.00	7.73	42.66
Line 42	20.33	16.00	212.33	10.90	40.66
Line 43	5.00	5.00	90.66	4.64	43.00
Line 44	10.00	9.00	110.00	5.63	42.00
Line 45	9.00	4.00	59.00	3.02	45.33
Line 46	10.00	10.00	132.33	6.77	42.33
Line 47	20.00	20.00	265.00	13.60	39.33
Line 48	9.00	4.00	59.33	3.04	45.33
Line 49	9.00	8.33	109.66	5.61	44.33
Line 50	0.00	0.00	0.00	0.00	47.33
Line 51	0.00	0.00	0.00	0.00	48.33
Line 52	30.00	24.33	380.00	19.50	39.66
Line 53	20.33	20.33	265.00	13.60	39.33
Line 54	30.00	30.00	315.33	16.10	37.00
Line 55	9.00	8.33	110.00	5.63	43.33
Line 56	9.66	9.66	135.66	6.95	42.33
Line 57	5.00	5.00	95.00	4.86	44.33
Sids-12	80.33	80.33	1652.33	84.60	24.66
Sids-13	60.00	60.00	1048.66	53.70	27.00
Morocco	99.66	99.66	1953.33	100.00	20.00
LSD _{0.05}	4.52	2.48	8.83	1.42	1.24

FRS^a (%) = Final rust severity, ACI^b = Average coefficient of infection, AUDPC^c = Area under disease progress curve and rAUDPC^d = Relative area under disease progress curve.

Relationship between the four epidemiological parameters and 1000 kernel weight:

The association between the four epidemiological parameters, i.e. FRS (%), ACI, AUDPC and rAUDPC, and

1000 kernel weight was determined through correlation analysis over the two growing seasons of the study. Data illustrated in Figs. (1 and 2) show, in general, that there was a significant negative correlation between each of the four epidemiological parameters under study and 1000 kernel weight. In 2014/15, the estimated values of correlation coefficient (R2) were 0.919, 0.916, 0.900 and 0.901, for the aforementioned disease parameters, respectively. Likewise, in 2015/16, these values were 0.950, 0.954, 0.926 and 0.926, for the above mentioned four epidemiological parameters, respectively. Similar results were previously obtained when correlation statistics were performed between different disease parameters of wheat rusts and grain yield of the studied certain wheat genotypes (Boulot *et al.*, 2015). Accordingly, it could be concluded that the relationship between each of FRS (%), ACI and 1000 kernel weight were more pronounced, and higher than the other relations, where the estimated values of R2 were (0.919 and 0.950) and (0.916 and 0.954) during the two growing seasons, respectively.

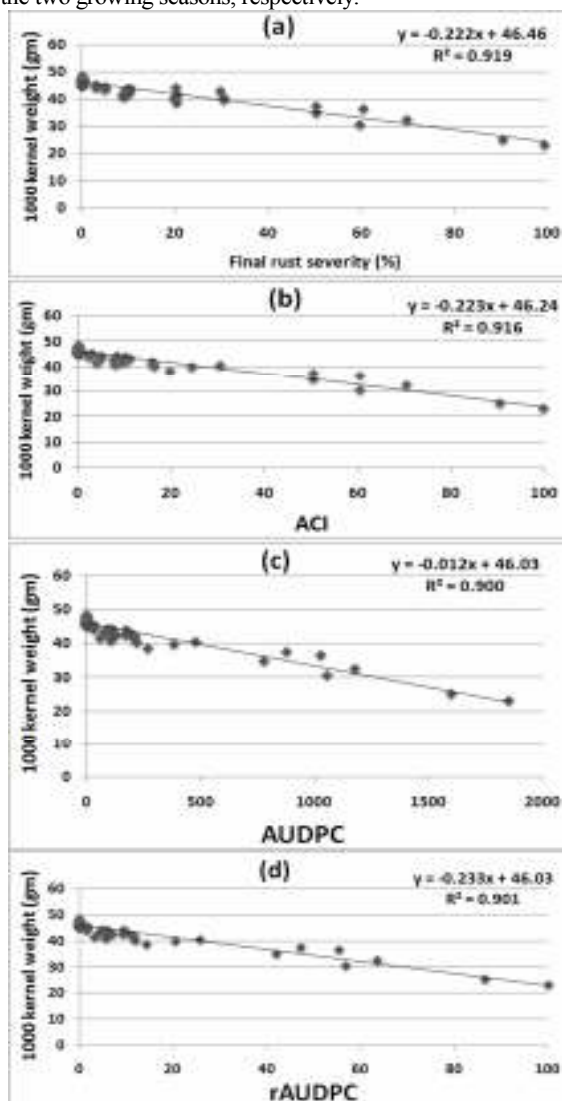


Fig. 1. Correlation coefficient between each of FRS % (a), ACI (b), AUDPC (c) and rAUDPC (d) and 1000 kernel weight (gm) of 57 wheat genotypes during 2014/15 growing season.

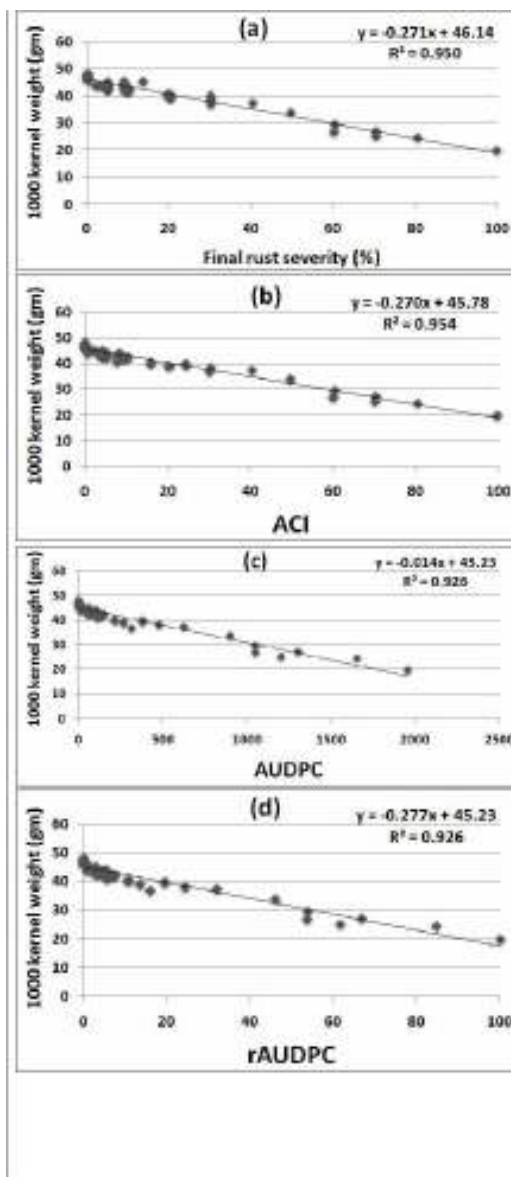


Fig. 2. Correlation coefficient between each of FRS % (a), ACI (b), AUDPC (c) and rAUDPC (d) and 1000 kernel weight (gm) of 57 wheat genotypes during 2015/16 growing season.

Correlation analysis gave evidence to the importance of these parameters, especially FRS (%) and ACI as good indicators for the evaluation of field resistance of the tested wheat genotypes against stripe rust. Thus, the selection of an acceptable and adequate level of resistance will be achieved easier if a large number of breeding materials will be under evaluation. The previous results obtained by Xiaowen *et al.* (2008) showed, in general, that it is more practical to use disease severity (%) for genotype screening rather than AUDPC, where there was high significant correlation between them ($R^2 = 0.91-0.93$)

Genetic components:

High values of broad sense heritability (up to 99%) for FRS (%), ACI, AUDPC and rAUDPC were obtained, being 99.85, 99.88, 99.99 and 99.74% during 2014/15,

respectively. While, in 2015/16, these estimates were 99.46, 99.84, 99.99 and 99.87%, for the aforementioned epidemiological parameters, respectively (Table, 6). The high heritability (%) estimates clearly demonstrated that most of the phenotypic variations were due to genetic factors or genetic structures (genetic make-up) of the studied genotypes. This result also is considered an

indicative for the possibility to achieve high rates of success in recovering the desired and more effective genes for stripe rust resistance in future generations. Moreover, these variations were less affected by the changes in environmental conditions from season to another season (Xiaowen *et al.*, 2008 and Hermas and El-Sawi 2015).

Table 6. Heritability in it's broad sense (h^2), and genetic advance (GA) expected from selection for final rust severity (FRS %), ACI, AUDPC and rAUDPC, during 2014/15 and 2015/16 growing seasons.

Growing season	FRS ^a (%)		ACI ^b		AUDPC ^c		rAUDPC ^d	
	h^2	GA	h^2	GA	h^2	GA	h^2	GA
2014/15	99.85	46.82	99.88	46.63	99.99	81.88	99.74	43.49
2015/16	99.46	45.76	99.84	46.28	99.99	86.93	99.87	29.35

FRS^a (%) = Final rust severity, ACI^b = Average coefficient of infection, AUDPC^c = Area under disease progress curve and rAUDPC^d = Relative area under disease progress curve.

Likewise, the genetic advance (GA) expected from selection, based on FRS (%), ACI, AUDPC, rAUDPC values during 2014/15 were 46.82, 46.63, 81.88 and 43.49, respectively. While, in 2015/16, the genetic advance values were 45.76, 46.28, 86.93 and 29.35 with the aforementioned disease parameters, respectively (Table, 6). The high environmental stability of these epidemiological parameters would greatly facilitate the effective use to improve stripe rust resistance through the selection process. Therefore, it seems reasonable from a genetic point of view to suggest that any of the four epidemiological parameters under study could be used as the more reliable estimators for evaluating and screening wheat genotypes with high and adequate levels of stripe rust resistance under field conditions. Meanwhile, from a practical point of view, FRS (%) and ACI are considered to be more appropriate rather than other parameters for screening large numbers of breeding materials, because it is more easily to be applied. Also, it would greatly facilitate a good and effective selection over a numerous numbers of genetic materials, during a breeding program, without more time consumption (Boulot *et al.*, 2015).

CONCLUSION

Twelve wheat promising lines; no's 1, 2, 3, 12, 13, 14, 16, 21, 22, 25, 50 and 51 have a good performance (stable disease resistance) with high yield potentiality over the two years of the study. Out of the tested genotypes, 35 lines having the potentiality to retard and delay stripe rust development under field conditions during the two years of the study. Thus, they characterized as the partial resistance (PR) lines. Therefore, these advanced lines could be released directly for cultivation or be used as the new sources of resistance in future breeding programs. From the previous reports, there are two main breeding strategies for resistance to wheat rust disease, especially stripe rust. The first strategy depends upon the major gene resistance (MGR) also, called a complete resistance. Whereas, the second one, is based on the use and exploitation of partial resistance (PR). The first strategy is easy to handle for the breeders and preferable for the farmer's use but this type of resistance prone to lose its effectiveness by the rapid changes in pathogen population. While, the later is similarly effective against all races (race-non-specific resistance or polygenic resistance), and assumed to be sustainable or more durable.

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تقييم مصادر جديدة لمقاومة مرض الصدأ المخطط في القمح المتسبب عن *Puccinia striiformis* f. sp. *tritici* تحت ظروف الحقل المصرية

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يعتبر مرض الصدأ المخطط الذي يسببه الفطر *Puccinia striiformis* f. sp. *tritici* من أشد أمراض الأصداء تأثيراً على محصول القمح في مصر والعالم. وقد أجريت هذه الدراسة لتقييم 57 سلالة قمح نباتية منتخبة من إجمالي 554 سلالة مسنودة من منظمة السميث لتحديد مدى استجابتها للإصابة بمرض الصدأ المخطط تحت ظروف الحقل خلال موسم الزراعة 2014/2015 و 2015/2016. تم تقييم واختيار تلك السلالات كمصادر جديدة للمقاومة لمرض الصدأ المخطط باستخدام أربعة مقاييس وراثية كمية للمرض وهي النسبة المئوية لشدة المرض النهائية (FRS %) ومتوسط معامل الإصابة (ACI) والمساحة الواقعة تحت منحنى الإصابة المرضي (AUDPC) والمساحة النسبية الواقعة تحت منحنى الإصابة المرضي (rAUDPC) بالإضافة الي قياس أحد مكونات المحصول وهو وزن الألف حبة بالجرام خلال موسمي الدراسة. أظهرت نتائج تحليل التباين وجود فروق معنوية كبيرة بين المقاييس الوراثية السابق ذكرها نتيجة لإختلاف إستجابة السلالات النباتية لمرض الصدأ المخطط وذلك خلال موسمي الدراسة. كما أوضحت تلك الدراسة أن إثني عشر سلالة نباتية مباشرة وهم (1 ، 2 ، 3 ، 12 ، 13 ، 14 ، 16 ، 21 ، 22 ، 25 ، 50 ، 51) قد أظهرت مقاومة عالية (كاملة) لمرض الصدأ المخطط وبالتالي فمن الممكن إستخدامهم كمصادر جديدة للمقاومة ضد المرض. أظهر تحليل معامل الارتباط أهمية إستخدام النسبة المئوية لشدة المرض النهائية (FRS %) وكذا متوسط معامل الإصابة (ACI) كأحد المقاييس الهامة في تقييم المقاومة الحقلية للسلالات النباتية لمرض الصدأ المخطط. وثبتت من الدراسة أيضاً وجود قيم عالية لكفاءة التوريث (تصل إلى 99%) وقيم متوسطة إلى عالية لنسبة التحسن الوراثي المتوقع من إجراء الإنتخاب مما يدل دلالة واضحة على أن الإختلاف بين السلالات النباتية في رد فعلها للإصابة بالمرض يعد إختلافاً وراثياً إذ يرجح أساساً إلى التركيب الوراثي لتلك السلالات النباتية. وتعتبر هذه النتيجة أيضاً مؤشراً على وجود إهتمام كبير لتحقيق معدلات نجاح عالية في إجراء عملية الإنتخاب للتركيب الوراثية المرغوبة للمقاومة لمرض الصدأ المخطط. علاوة على ذلك ، فقد كانت تلك الإختلافات أقل تأثيراً بالتغيرات الحادثة في الظروف البيئية من موسم إلى آخر. ومن الممكن أن نستخلص من تلك الدراسة أهمية إستخدام كلاً من النسبة المئوية لشدة المرض النهائية (FRS %) وكذا متوسط معامل الإصابة (ACI) ، كدلائل جيدة ومناسبة لتقييم وإنتخاب أعداداً كبيرة من السلالات النباتية (التركيب الوراثية) التي من الممكن إستخدامها كمصادر جيدة للمقاومة في برامج التربية المقاومة لأمراض أصداء القمح عموماً، وذلك لسهولة إستخدامها في إجراء عملية الإنتخاب بنجاح بواسطة المرابي وفي وقت قصير الي حد ما أو دون إهدار مزيداً من الوقت كما في المقاييس الأخرى للمقاومة مثل إستخدام المساحة الواقعة تحت منحنى الإصابة المرضي والمساحة النسبية الواقعة تحت منحنى الإصابة المرضي ، والتي تحتاج الي مزيداً من الوقت لتطبيقها خلال عملية تقييم وإنتخاب التركيب الوراثية المرغوبة.