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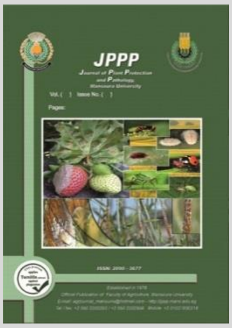
Screening of CIMMYT Wheat Genotypes to Stem Rust Disease under Field Conditions in Egypt

Omara, R. I.*; A. A. Shahin and M. I. M. Ahmed

Plant Pathology Research Institute, ARC, Giza, Egypt.



ABSTRACT

Among 190 wheat genotypes (CIMMYT), 51 lines were evaluated for adult plant resistance (APR) to stem rust infection at Sakha, Kafr El-Hamam and Nubaria locations, as the new sources of this resistance. Extensive and high significant differences of stem rust reaction among the tested wheat lines were obtained, at the three locations under study. Out of 51 wheat genotypes, only eight promising lines; no's 1, 9, 12, 14, 20, 25, 47 and 49 had the highest resistant potentiality at adult stage (completely resistant) and utilized as the new sources to increase stem rust resistance. Twenty nine wheat lines were characterized as partially resistant (PR), at the three locations of the study. The phenotypic variations were attributable to genetic structures of the lines due to high heritability estimates (up to 99%) and high values of genetic advance. The importance of all the selected disease parameters was confirmed through the correlation analysis especially final rust severity (FRS %). It is considered to be the more appropriate indicator, rather than area under disease progress curve (AUDPC) and relative area under disease progress curve (rAUDPC) for screening large numbers of breeding materials to stem rust resistance and facilitate the success of selection process, during a national breeding program.

Keywords: wheat, stem rust, disease parameters, yield components, heritability, genetic advance

INTRODUCTION

Puccinia graminis f. sp. *tritici*, the causal pathogen of wheat stem rust, causes serious yield losses on susceptible cultivars in Egypt, especially in the late sowing dates (Ashmmawy *et al*., 2013 and Abdelaal *et al*., 2018).

It causes severe epidemics in Africa, Middle East, Asia mostly, Australia, New Zealand, Europe and both North and South America (Singh *et al*., 2011).

In Egypt, stem rust found to be early appeared in epidemic level in 1947 and 1968 (Goma 1968). Moreover, in the last five decades, stem rust could be successfully controlled nationwide, under Egyptian field conditions and all over the world. But, recently the sudden emergency of an aggressive race; UG99, which have the ability to overcome stem rust resistance of many wheat varieties, worldwide (Patpour *et al*., 2016 and Soko *et al*., 2018). Then, thirteen races of Ug99 lineage are now known and speeded in different countries, *i.e.* eastern African highlands, South Africa, Sudan, Yemen, Zimbabwe and Iran. This encourages us to find new sources of resistance to combat this aggressive race and its derivatives.

Host-genetic resistance considers the most environmentally safe and effective control methods to stem rust disease, as it avoids the severe epidemics through the reduction of yield losses due to the infection (Singh *et al*., 2011).

Accordingly, several genotypes were previously assessed in different countries to reveal their reaction to wheat stem rust disease, under field conditions (Kokhmetova *et al*., 2011 and Abdelaal *et al*., 2018). Wheat genotypes produced by International Maize and Wheat Improvement Center (CIMMYT) were utilized by most countries to improve and obtain highly resistant cultivars to stem rust pathogen. Then, CIMMYT spreads wheat genotypes all over the world through the nurseries system (Singh *et al*., 2011).

Wheat genotypes obtained from CIMMYT and ICARDA as well as the available resistant cultivars are the main sources of resistance to the breeding programs in Egypt. Recently, the available commercial wheat cultivars showed different levels of susceptibility to stem rust infection in different locations in Egypt (Abdelaal *et al*., 2018). Hence, the needs to examine new sources of resistance to improve stem rust resistance in the local breeding programs.

The first objective of this research is to evaluate 51 wheat lines for their adult plant resistance (APR) to stem rust infection, under field conditions at three different locations in Egypt. The second objective is to assess heritability (%) and genetic advance of three stem rust resistance parameters; FRS (%), AUDPC and rAUDPC that usually used as the criteria for evaluating this resistance. An ultimate goal of this study was to facilitate the good exploitation and full utilization of these promising wheat lines into breeding program for stem rust resistance.

MATERIALS AND METHODS

The experiments were handled under Egyptian field conditions at three locations, *i.e.* Sakha, Kafr El-Hamam and Nubaria Agricultural Research Stations, during 2019/2020 growing season. Fifty one wheat advanced lines were selected from 8th STEMRRSN (190 lines) obtained from CIMMYT. Additionally, Misr-1 (the highly

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* **Corresponding author.**
E-mail address: redaomara43@gmail.com
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susceptible variety) was served as check control. The lines were assessed for stem rust infection. The pedigree of each tested line is presented in Table (1).

The experiment was carried out using randomized complete block design (RCBD) with 3 replicates. Each unit of the experiment included five rows with 3m long. One border of the highly susceptible variety (Morocco) was grown around the experiment as a permanent source and spreader of infection (spores). Artificial inoculation was carried out on the spreader plants at booting stage with urediniospores of the most prevalent races (TTTRC, TTPPC and TTSPB) as described by Tervet and Cassel (1951), in addition to the natural infection. Inoculum of the pathogen was prepared in stem rust greenhouse of Wheat Diseases Research Department, Plant Pathology Research Institute, ARC, Giza, Egypt.

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

Line	Pedigree
Line 1	CMSS08Y00140S-099Y-099M-099NJ-7WGY-0B
Line 2	CMSS08Y00140S-099Y-099M-099NJ-099NJ-4WGY-0B
Line 3	CMSS08Y00140S-099Y-099M-099NJ-099NJ-33WGY-0B
Line 4	CMSS08Y00152S-099Y-099M-099NJ-099NJ-41WGY-0B
Line 5	CMSS08Y00174S-099Y-099M-099NJ-099NJ-12WGY-0B
Line 6	CMSS08Y00274S-099Y-099M-099NJ-099NJ-10WGY-0B
Line 7	CMSS08Y00274S-099Y-099M-099NJ-099NJ-12WGY-0B
Line 8	CMSS08Y00299S-099Y-099M-099NJ-099NJ-19WGY-0B
Line 9	CMSS08Y00316S-099Y-099M-099NJ-17WGY-0B
Line 10	CMSS08Y00400S-099Y-099M-099NJ-099NJ-13WGY-0B
Line 11	CMSS08Y00404S-099Y-099M-099NJ-099NJ-34WGY-0B
Line 12	CMSS08Y00415S-099Y-099M-099NJ-21WGY-0B
Line 13	CMSS08Y00477S-099Y-099M-099NJ-099NJ-3WGY-0B
Line 14	CMSS08Y00489S-099Y-099M-099Y-8M-0WGY
Line 15	CMSS08Y00616T-099TOPM-099Y-099M-099NJ-4WGY-0B
Line 16	CMSS08Y00655T-099TOPM-099Y-099M-099Y-8M-0WGY
Line 17	CMSS08Y00781T-099TOPM-099Y-099M-099NJ-099NJ-4WGY-0B
Line 18	CMSS08Y00927T-099TOPM-099Y-099M-099NJ-099NJ-2WGY-0B
Line 19	CMSS08Y01088T-099M-099Y-099M-099NJ-5WGY-0B
Line 20	CMSS08Y01099T-099M-099Y-099M-099NJ-17WGY-0B
Line 21	CMSS08Y01115T-099M-099Y-099M-099NJ-14WGY-0B
Line 22	CMSS08Y01116T-099M-099Y-099M-099NJ-099NJ-23WGY-0B
Line 23	CMSS08Y01122T-099M-099Y-099M-099Y-1M-0WGY
Line 24	CMSS08B00024S-099M-099Y-12M-0WGY
Line 25	CMSS08B00137S-099M-099NJ-099NJ-50WGY-0B
Line 26	CMSS08B00212S-099M-099NJ-30WGY-0B
Line 27	CMSS08B00391S-099M-099Y-10M-0WGY
Line 28	CMSS08B00485S-099M-099NJ-099NJ-2WGY-0B
Line 29	CMSS08B00527S-099M-099NJ-099NJ-7WGY-0B
Line 30	CMSS08B00600S-099M-099NJ-099NJ-14WGY-0B
Line 31	CMSS08B00684T-099TOPY-099M-099NJ-099NJ-9WGY-0B
Line 32	CMSS08B00866T-099TOPY-099M-099NJ-099NJ-9WGY-0B
Line 33	CMSS08B00914T-099TOPY-099M-099NJ-099NJ-3WGY-0B
Line 34	CMSS08B00923T-099TOPY-099M-099NJ-099NJ-12WGY-0B
Line 35	CMSS08B00928T-099TOPY-099M-099NJ-099NJ-22WGY-0B
Line 36	CMSA08M00406S-040ZTM-050Y-37ZTM-010Y-0B
Line 37	CMSS08B00256S-099M-099NJ-099NJ-26RGY-0B
Line 38	CMSS08B00712T-099TOPY-099M-099NJ-099NJ-10RGY-0B
Line 39	CMSS08B00798T-099TOPY-099M-099NJ-12RGY-0B
Line 40	MN18-3-61-0B
Line 41	MN18-3-69-0B
Line 42	MN18-3-105-0B
Line 43	MN18-4-81-0B
Line 44	MN34-10-28-0B
Line 45	MN34-10-61-0B
Line 46	MN34-10-73-0B
Line 47	MN50-4-25-0B
Line 48	MN50-4-46-0B
Line 49	MN50-5-14-0B
Line 50	MN82-25-20-0B
Line 51	MN82-35-6-0B
Misr-1 (check)	OASIS/SKAUZ//4*BCN1312*PASTOR.CMSSOOY O1881T-050M-030Y-030M-030WGY-33M-0Y-0S.

Disease assessment:

Disease severity (DS %) was recorded five times from the first appearance of symptoms and every 7 days intervals of the tested wheat genotypes, during the growing season at the three locations under study. Rust severity was assessed by calculating the percentage of stem area covered with rust pustules (Peterson *et al*., 1948). The final rust severity (FRS %) was measured as described by Das *et al.* (1993). Area under disease progress curve (AUDPC) and relative area under disease progress curve (rAUDPC) were estimated for each line according to Pandey *et al.* (1989) and Milus and Line (1986), respectively.

Yield assessment:

The weight of 1000 kernel was used as a grain yield. Additionally, the yield per plot (kg) was measured for all lines in different locations.

Genetic components:

The following formula was used to estimate the percentage of heritability (h^2 %) for FRS (%), AUDPC and rAUDPC (Miller *et al*., 1958):

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

Where:

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

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

Genetic advance (GA) was calculated for each of the three disease parameters according to the following formula (Miller *et al*., 1958):

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

Where:

k = constant equal 2.06 at 5% selection intensity.

Statistical analysis:

MSTAT-C software was use to perform combined analysis of variance. The least significant difference (L.S.D.) at 5% level of significant was utilized to compare genotype means. Moreover, correlation and regression coefficient "SPSS Regression Modeling" was performed to evaluate the relationship between each of the three stem rust parameters, *i.e.* FRS (%), AUDPC and rAUDPC and the two yield components; 1000 kernel weight (g) and yield/plot (kg) of the tested wheat lines.

RESULTS AND DISCUSSION

Disease parameters as well as yield components were estimated to evaluate 51 wheat advanced lines, at Sakha, Kafr El-Hamam and Nubaria locations, during 2019/2020 growing season. These lines were selected from a total of 190 wheat genotypes introduced from CIMMYT nurseries to accurately characterize their field resistance to stem rust infection at three hot-spot locations, in order to facilitate the future use of them as the new sources of stem rust resistance.

Analysis of variance:

The level of adult plant resistance (APR) was estimated by combined analysis of variance of the three locations. The relationship between disease response of the tested wheat lines and environmental conditions was previously investigated (Niks *et al*., 2011). However, in the current study highly Significant differences were found in the interaction between locations (L) and the tested wheat genotypes (G), concerning with FRS (%), AUDPC and rAUDPC (Table 2), as affected by the slight changes in environmental conditions, between different environments (Qamar *et al*., 2007 and Omara *et al*., 2018).

Additionally, the interaction between locations (L) and genotypes (G) was significantly in 1000 kernel weight and yield/plot (Table 3). Due to the highly significant of this interaction, values of L.S.D. were used to compare the variances in the studied traits of any two lines under study within each environment (location). This result was supported by the previous findings of Singh and Narayanan (2000), as they showed that the interaction between genotypes and environments (GE) was significant.

Table 2. Combined analysis of variance for three disease parameters over three locations of 51 wheat lines, in addition to check variety, during 2019/2020 growing season.

S.O.V.	D.F.	Disease parameters					
		M.S.			F value		
		FRS[a] (%)	AUDPC[b]	rAUDPC[c]	FRS[a] (%)	AUDPC[b]	rAUDPC[c]
Locations (L)	2	8676.984	2674527.925	5903.709	117.363**	15407.366**	267.157**
Error	6	73.933	173.588	22.098	-	-	-
Genotypes (G)	51	3276.474	1120883.066	4156.598	179.796**	15492.014**	7007.161**
Interaction (L×G)	102	138.184	49999.548	130.545	7.582**	691.0567**	220.071**
Error	306	18.223	72.352	0.593	-	-	-

FRS[a] (%) = Final rust severity (%), AUDPC[b] = Area under disease progress curve and rAUDPC[c] = Relative area under disease progress curve.
**** = high significant.**

Table 3. Combined analysis of variance for 1000 kernel weight and yield/plot over three locations of 51 wheat lines, in addition to check variety, during 2019/2020 growing season.

S.O.V.	D.F.	Yield components			
		M.S.		F value	
		1000 kernel weight (g)	Yield/plot (kg)	1000 kernel weight (g)	Yield/plot (kg)
Locations (L)	2	365.019	6.241	127.961**	4.946*
Error	6	2.853	1.262	-	-
Genotypes (G)	51	152.330	6.325	140.027**	180.834**
Interaction (L×G)	102	15.736	2.282	14.465**	65.251**
Error	306	1.088	0.035	-	-

*** = significant and ** = high significant.**

Evaluation of the tested wheat lines for adult plant resistance to stem rust and yield potentiality under field conditions:

a) Characterization of stem rust resistance in the tested lines:

The stem rust severity (%) of 51 promising lines was evaluated initiating from symptoms appearance up to reaching the maximum disease severity on the check variety (Misr-1). Final rust severity (FRS %), AUDPC and rAUDPC were accurately estimated to evaluate stem rust resistance in the tested wheat lines at three hot-spot locations; Sakha, Kafr El-Hamam and Nubaria, during 2019/2020 growing season. Data presented in Table (4) show, in general, that eight wheat lines; no's 1, 9, 12, 14, 20, 25, 47 and 49 have exhibited high levels of APR to stem rust infection at all the three locations, under study. Wherein, no disease symptoms (flecks or pustules) were noticed on these lines. So, they should be described as the completely resistant lines. However, several or numerous reports showed that this type of resistance is the most important for genetic improvement in wheat. It is also useful to avoid sudden disease epidemics in the future and reduces the annual losses in grain yield of crop production, worldwide (Rahmatov *et al*., 2011 and Singh *et al*., 2011).

Meanwhile, wheat lines; no's 2, 5, 6, 7, 8, 11, 13, 16, 17, 19, 21, 22, 28, 29, 30, 31, 33, 34, 35, 38, 39, 42, 43, 44, 45, 46, 48, 50 and 51, showed susceptible disease reaction ("S" infection type) to stem rust, but in the same time they were delayed disease development at the three locations of the study and ultimately showed low to moderate levels of final rust severity (less than 30.6%). Also, their AUDPC and rAUDPC estimated values not exceeded up to 475.6 and 26.4, respectively (Table 4). Therefore, these lines could be considered as the partially resistant (PR) lines, as they proved to have an adequate level of slow-rusting resistance to stem rust, under field conditions (Singh *et al.*, 2011 and Qamar *et al.*, 2012). However, limited deployment of partial resistance genes (PR genes) in the national breeding program in Egypt, and the good application or full utilization of this type of resistance has remained little, and it perhaps less appreciated than it should be (Boulot *et al.*, 2015).

Breeding strategies includes the major gene (s) for resistance (MGR), or the complete resistance and the exploitation of partial resistance (Rahmatov *et al.*, 2011). The first strategy could be used by the farmer's, but it quickly loses its effectiveness by the rapid changes in pathogen population. While, the latter is similarly effective against all races (race-non-specific resistance or polygenic resistance), and supposed to be more durable than the first strategy (Rahmatov *et al*., 2011 and Omara *et al*., 2017).

The lines no's 3, 4, 10, 15, 18, 23, 24, 26, 27, 32, 36, 37, 40 and 41 showed, in general, high susceptible reaction (HS) to stem rust, under field conditions at the three locations. Thus, these genotypes should be classified as the fast-rusting group of wheat lines. Highest values of AUDPC could be estimated for this group of lines (ranged from 925.3 to 1050.6 at Sakha, from 625.3 to 900.6 at Kafr El-Hamam and from 1375.3 to 1450.6 at Nubaria). In comparison AUDPC, was reached its maximum and high estimates in the check variety, Misr-1, *i.e.* 1450.6, 1550.6 and 1800.0 in the above three locations, respectively. Moreover, slight decrement in the level of stem rust resistance, expressed as the higher estimates of the three parameters, *i.e.* FRS %, AUDPC and rAUDPC of Nubaria location rather than those at the other locations; Sakha and Kafr El-Hamam. This could be due to the slight differences in environmental conditions among the three locations (Shah *et al*., 2010). Moreover, the variety of the prevalent rust races within the pathogen populations from one location to another (Singh *et al*., 2008 and Wan and Chen 2012).

Table 4. Final rust severity (FRS %), AUDPC and rAUDPC of 51 wheat lines, in addition to the check variety at the three locations, during 2019/2020 growing season.

Wheat line	Final rust severity (FRS %)			Area under disease progress curve (AUDPC)			Relative area under disease progress curve (rAUDPC)		
	Sakha	Kafr El-Hamam	Nubaria	Sakha	Kafr El-Hamam	Nubaria	Sakha	Kafr El-Hamam	Nubaria
Line 1	0.0	0.0	0.0	0.0	0.0	0.0	0	0.0	0.0
Line 2	20.3	10.3	30.3	240.0	140.0	475.6	16.6	9.0	26.4
Line 3	30.0	10.0	40.6	375.3	160.3	625.6	25.9	10.3	34.8
Line 4	50.6	20.3	60.6	775.6	270.6	1150.6	53.5	17.5	63.9
Line 5	10.0	0.0	10.3	143.3	0.0	155.6	9.9	0.0	8.64
Line 6	10.3	5.3	20.3	140.6	105.3	265.3	9.7	6.7	14.7
Line 7	10.6	0.0	10.3	150.6	0.0	152.3	10.4	0.0	8.4
Line 8	10.0	0.0	10.6	145.6	0.0	162.3	10.1	0.0	9.0
Line 9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Line 10	60.6	40.3	70.3	1025.0	625.3	1375.3	70.7	40.3	76.4
Line 11	20.3	10.6	30.6	256.0	146.3	475.6	17.7	9.4	26.4
Line 12	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Line 13	10.0	0.0	10.3	148.3	0.0	152.3	10.2	0.0	8.4
Line 14	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Line 15	20.3	10.3	40.3	262.3	143.3	725.6	18.1	9.2	40.3
Line 16	10.0	5.0	10.6	142.3	98.6	152.3	9.9	6.3	8.4
Line 17	0.0	0.0	20.3	0.0	0.0	235.6	0.0	0.0	13.1
Line 18	20.6	30.6	40.6	295.6	475.3	525.6	20.4	30.7	29.2
Line 19	5.0	0.0	10.3	46.3	0.0	146.6	3.2	0.0	8.1
Line 20	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Line 21	10.0	10.3	20.3	146.3	133.6	242.3	10.1	8.6	13.5
Line 22	10.3	5.0	10.3	156.6	101.3	186.3	10.8	6.5	10.4
Line 23	40.6	30.6	50.6	625.3	475.6	775.3	43.11	30.7	43.1
Line 24	60.6	50.6	80.3	925.3	775.3	1425.3	63.8	50.0	79.2
Line 25	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Line 26	20.3	20.3	40.3	265.0	245.6	725.6	18.3	15.8	40.3
Line 27	30.6	20.3	50.6	465.3	265.6	975.6	32.1	17.1	54.2
Line 28	0.0	0.0	20.3	0.0	0.0	245.6	0.0	0.0	13.6
Line 29	0.0	0.0	30.6	0.0	0.0	422.6	0.0	0.0	23.5
Line 30	20.3	10.6	20.3	265.3	146.3	295.3	18.3	9.4	16.4
Line 31	10.6	5.3	20.6	155.6	98.6	265.6	10.8	6.3	14.8
Line 32	30.6	20.6	40.3	475.3	265.6	625.3	32.8	17.1	34.7
Line 33	10.0	0.0	20.3	146.3	0.0	265.6	10.1	0.0	14.8
Line 34	20.0	0.0	30.6	262.3	0.0	426.3	18.1	0.0	23.7
Line 35	10.3	5.0	10.3	162.3	91.3	192.3	11.2	5.8	10.7
Line 36	60.3	40.6	80.6	1050.6	725.3	1450.6	72.4	46.8	80.6
Line 37	40.6	30.3	60.3	725.6	475.6	1125.3	50.0	30.7	62.5
Line 38	10.0	5.0	20.6	155.6	101.6	265.3	10.7	6.5	14.7
Line 39	5.0	3.0	10.3	98.3	54.3	133.3	6.8	3.5	7.4
Line 40	30.0	20.6	50.6	470.3	265.6	775.3	32.4	17.1	43.1
Line 41	60.6	50.6	70.3	1025.6	900.6	1450.6	70.7	58.1	80.6
Line 42	0.0	0.0	16.3	0.0	0.0	235.6	0.0	0.0	13.1
Line 43	20.0	10.3	20.0	262.6	155.6	265.0	18.1	10.0	14.7
Line 44	20.6	10.3	30.0	265.6	215.3	475.0	18.3	13.9	26.4
Line 45	5.3	3.6	10.0	88.3	54.3	183.0	6.1	3.5	10.2
Line 46	5.3	0.0	5.0	91.0	0.0	101.0	6.3	0.0	5.6
Line 47	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Line 48	0.0	0.0	10.0	0.0	0.0	136.0	0.0	0.0	7.5
Line 49	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0
Line 50	5.0	0.0	10.0	50.0	0.0	88.0	3.5	0.0	4.8
Line 51	10.3	0.0	20.0	156.3	0.0	236.0	10.8	0.0	13.1
Misr-1 (check)	80.6	80.3	90.0	1450.6	1550.6	1800.0	100.0	100.0	100.0
LSD$_{0.05}$ of interaction (lines × locations)		6.83			13.61			2.13	

b) Yield potentiality in the tested wheat genotypes:

Any successful wheat breeding program must be planned to combine a high and an adequate level of resistance to the major diseases (three rusts), especially stem rust with high grain yield potentiality in the breeding materials produced. The obtained results in this study relevant to 1000 kernel weight and yield/plot showed significant differences among the tested lines, as affected by stem rust infection, under field conditions (Table 5). The highest values of 1000 kernel weight (more than 43.5 gm), as well as the highest estimated of yield/plot (more than 7.2 kg) were recorded with the highly resistant or completely resistance wheat lines; no's 1, 9, 12, 14, 20, 25, 47 and 49, followed by the partially resistant (PR) lines; no's 2, 5, 6, 7, 8, 11, 13, 16, 17, 19, 21, 22, 28, 29, 30, 31, 33, 34, 35, 38, 39, 42, 43, 44, 45, 46, 48, 50 and 51. While, the lowest values of each 1000 kernel weight and yield/plot were recorded in wheat lines no's 3, 4, 10, 15, 18, 23, 24, 26, 27, 32, 36, 37, 40 and 41. Similar results were previously reported under the Egyptian field conditions by Ashmmawy *et al*. (2013) and Abdelaal *et al*. (2018) who reported that there are significant negative correlation relationships between the studied disease parameters and yield.

Table 5. Yield components of 51 wheat genotypes, in addition to the check variety; Misr-1 as affected by stem rust at the three locations, during 2019/2020 growing season.

Line	1000 kernel weight (g)			Yield/plot (kg)		
	Sakha	Kafr El-Hamam	Nubaria	Sakha	Kafr El-Hamam	Nubaria
Line 1	43.8	44.9	44.8	7.2	7.5	8.2
Line 2	39.6	40.1	38.6	5.3	5.4	4.9
Line 3	37.5	40.0	36.5	5.1	5.4	4.7
Line 4	34.4	38.4	31.0	4.5	5.3	4.1
Line 5	41.5	44.9	42.1	6.2	7.3	6.4
Line 6	42.7	42.8	40.7	6.1	6.3	6.0
Line 7	42.6	44.4	42.6	6.3	6.4	6.2
Line 8	42.8	43.4	42.8	6.0	6.5	6.2
Line 9	44.9	43.8	44.9	7.2	7.0	7.6
Line 10	31.6	34.4	30.6	4.0	4.2	4.1
Line 11	39.2	40.6	38.2	5.7	5.9	5.8
Line 12	43.3	44.0	44.1	7.5	7.4	8.1
Line 13	35.6	42.8	35.6	5.1	6.3	4.9
Line 14	44.6	43.8	45.8	7.8	7.4	7.9
Line 15	38.8	41.7	35.8	5.6	6.0	4.9
Line 16	41.2	42.4	41.2	6.3	6.5	6.2
Line 17	43.8	44.6	39.8	6.7	7.6	5.4
Line 18	38.9	37.8	34.9	5.8	5.6	4.8
Line 19	42.6	43.9	42.6	6.3	6.7	6.3
Line 20	43.8	43.6	44.8	7.8	7.9	8.8
Line 21	41.5	41.4	40.5	6.2	6.2	6.1
Line 22	42.6	43.5	41.6	6.3	6.4	6.2
Line 23	34.1	35.2	33.1	4.6	4.7	4.3
Line 24	31.8	30.9	28.8	4.1	4.0	3.8
Line 25	44.5	43.5	43.5	8.2	8.5	9.1
Line 26	40.1	40.0	38.2	5.9	6.2	5.8
Line 27	37.6	39.5	31.65	5.4	5.8	4.4
Line 28	43.8	43.0	41.8	6.3	6.7	6.2
Line 29	43.2	42.0	40.2	6.4	6.7	6.3
Line 30	40.5	42.1	40.57	5.9	6.4	6.3
Line 31	41.6	43	41.6	6.0	6.8	6.3
Line 32	39.1	40	37.1	5.7	5.9	5.6
Line 33	41.7	43.1	40.7	6.2	6.5	6.3
Line 34	40.6	43.3	39.6	5.8	6.2	5.7
Line 35	42.8	42.2	41.8	6.3	6.4	6.5
Line 36	31.2	34.6	28.2	4.6	4.5	3.7
Line 37	33.6	36.6	31.6	4.2	4.1	3.9
Line 38	42.8	42.5	40.8	6.3	6.7	6.4
Line 39	42.7	42.6	41.7	6.5	6.3	6.0
Line 40	35.6	39.5	33.6	4.6	5.8	4.2
Line 41	30.2	34.8	29.2	3.9	4.1	3.8
Line 42	43.7	41.6	44.7	6.7	6.1	7.5
Line 43	40.7	42.5	39.7	6.4	6.3	5.9
Line 44	39.8	41.9	37.8	5.8	5.9	5.4
Line 45	42.3	43.0	41.3	6.4	7.3	6.3
Line 46	42.5	43.0	42.5	6.8	6.9	6.7
Line 47	44.9	44.2	44.9	7.6	7.9	8.2
Line 48	42.7	42.1	41.7	6.5	6.7	6.4
Line 49	44.3	43.3	44.3	9.1	8.9	9.3
Line 50	42.3	43.8	42.3	6.9	6.8	6.5
Line 51	41.5	43.8	40.5	6.3	6.7	6.2
Misr-1 (check)	29.0	28.6	27.0	3.4	3.3	3.1
LSD$_{0.05}$ of interaction (lines × locations)		1.66			0.29	

Several studies were done at CIMMYT, in order to improve stem rust resistance in wheat genotypes based on utilization of additive interaction of slow-rusting genes or using a number of minor genes with additive effects for achieving the PR resistance in their wheat breeding materials. High levels of resistance to stem rust were successfully combined with high potentiality of grain yield in the advanced wheat lines. CIMMYT and ICARDA materials are new and good sources of resistance to rust diseases, in particular stem rust with high grain yield potentiality and other traits for possible use in crossing blocks, is the main objective of the national breeding program in Egypt. Future studies are needed to confirm and emphasize the effectiveness and stability of the evaluated genotypes for stem rust resistance under different climatic conditions or wide range of environmental conditions as useful or profitable advanced lines (Rahmatov *et al.*, 2011).

c) Genetic components:

High estimates of heritability were 99.81, 99.99 and 99.99% for FRS (%), AUDPC and rAUDPC at the three locations under study, respectively (Table 6). This result indicates that the phenotypic variations were due to genetic structure of the studied wheat lines. Moreover, the variation in disease response of stem rust reaction of the tested lines was less affected by the climate changes from location to another (Xiaowen *et al*., 2008 and Hermas and El-Sawi 2015). The results could also be used to recover the most effective and desirable genes for stem rust resistance in the future early generations (Boulot *et al.,* 2015 and Omara *et al*., 2017).

Table 6. Heritability (h^2 %) and genetic advance (GA) for the three disease pramaters at the three locations, during 2019/2020 growing season.

S.O.V.	Disease parameters		
	FRS[a] (%)	AUDPC[b]	rAUDPC[c]
Heritability (h^2 %)	99.81	99.99	99.99
Genetic advance (GA %)	117.8	164.19	132.8

FRS[a] (%) = Final rust severity, AUDPC[b] = Area under disease progress curve and rAUDPC[c] = Relative area under disease progress curve.

Likewise, the genetic advance (GA) based on the use of either FRS (%), AUDPC or rAUDPC values, was also high at the three locations of the study (Table 6). The high environmental stability of the three disease parameters would greatly facilitate the effective use of such parameters to improve stem rust resistance through the selection process. Therefore, it seems reasonable from a genetic point of view to suggest that any of the three disease parameters, under study could be used as the good and more reliable estimator for screening wheat lines with adequate levels of stem rust resistance under field conditions. Moreover, FRS (%) is considered to be more appropriate rather than the other two parameters for screening large numbers of breeding materials, because it is more easily to be applied or handled. Also, it could safe time for effective selection of several genetic materials (Boulot *et al*., 2015).

d) Relative contribution of the environment (Location: L), genotype (G) and their interaction (L×G) of the studied disease parameters:

Relative contribution was determined for each disease parameter under study, *i.e.* FRS (%), AUDPC and rAUDPC. This was carried out in order to detect the effect of locations, genotypes and their interaction in the variation of these disease parameters expressed on the tested wheat lines. (Table 7).

Table 7. Relative contribution of final rust severity (FRS %), AUDPC and rAUDPC at the three locations, during 2019/2020 growing season.

S.O.V.	Disease parameters		
	FRS[a] (%)	AUDPC[b]	rAUDPC[c]
Genotypes (G)	81.68	86.54	84.51
Locations (L)	8.48	7.53	7.9
Interaction (L×G)	6.88	5.72	7.54

FRS[a] (%) = Final rust severity, AUDPC[b] = Area under disease progress curve and rAUDPC[c] = Relative area under disease progress curve.

The genetic structure of the tested lines relatively contributed by 81.68, 86.54 and 84.51 % on the variation found in FRS (%), AUDPC and rAUDPC, respectively (Table 7). While, the relative contribution of environments (locations) and the interaction between locations and genotypes (L×G) were very low (less than 8.48%).

Therefore, it seems reasonable to suggest that the variation in the studied disease parameters expressed on the tested lines is consistently attributed to their genetic structure or genetic make up of these lines. Similar results were in agreement with Abou-Zeid *et al.* (2019), who showed that the variation in the level of adult plant response to stem rust infection among stem rust monogenic lines (Sr,s) was mainly due to their genetic structure rather than changes in the environmental conditions over the three locations of the study.

Relationship between the three stem rust parameters and the two yield components, under study:

The relation between the three stem rust parameters and the two yield components was studied through correlation analysis over the three locations of the study. In general, high significant negative correlation was found among each of the three stem rust parameters and the two yield components under study (Figs. 1, 2 and 3).

At Sakha location, the correlation coefficient (R^2) between the aforementioned three disease parameters were (0.8888, 0.8342), (0.8807, 0.8052) and (8806, 0.8053) of 1000 kernel weight and yield/plot, respectively. As for Kafr El-Hamam location, these values were (0.7686, 7952), (0.7382, 0.7555) and (0.7383, 0.7555) for the above mentioned two yield components and the three disease parameters, respectively. Likewise, at Nubaria location these values were (0.8964, 0. 8283), (0.8932, 0.7857) and (0.8933, 0.7858) for the same two yield components and the three disease parameters, respectively. Similarly, statistics correlation was carried out between disease parameters and grain yield of wheat genotypes (Boulot *et al.*, 2015). Accordingly, it could be concluded that the relationship between FRS (%) and each of the two yield components; 1000 kernel weight and yield/plot, under study was more pronounced, and higher than the other relations, where the estimated values of R^2 were significantly high between FRS (%) and the two yield components of the study. As they were; 0.8888, 0.7686 and 0.8964 for 1000 kernel weight and 0.8342, 0.7952, 0.8285 of yield/plot, at Sakha, Kafr El-Hamam and Nubaria locations, respectively.

Correlation analysis gave the great importance of FRS (%), as the good and more reliable indicators for an evaluation of field resistance of the promising lines against stem rust. Thus, the effective selection of a large number of wheat materials will be easier if used FRS (%). Similar results were previously noticed by Xiaowen *et al.* (2008), as they found, in general, the disease severity (%) is easily used for line screening, rather than AUDPC. Where, the correlation among DS (%) of the tested genotypes and their level of slow rusting resistance was high significant (R^2 = 0.91- 0.93).

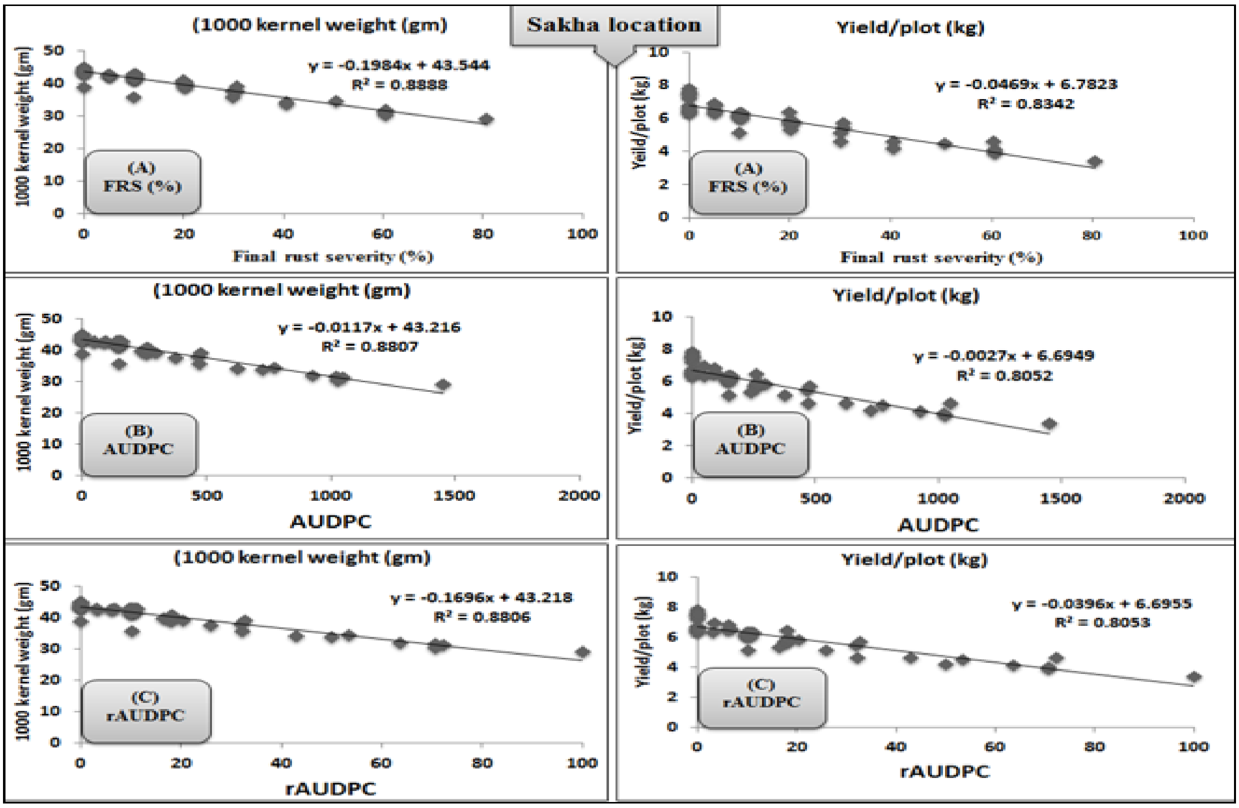

Fig. 1. Correlation coefficient between each of the three stem rust parameters; FRS (%) (A), AUDPC (B) and rAUDPC (C) and yield components; 1000 kernel weight (gm) and yield/plot (kg) of 51 wheat lines at Sakha location, during 2019/20 growing season.

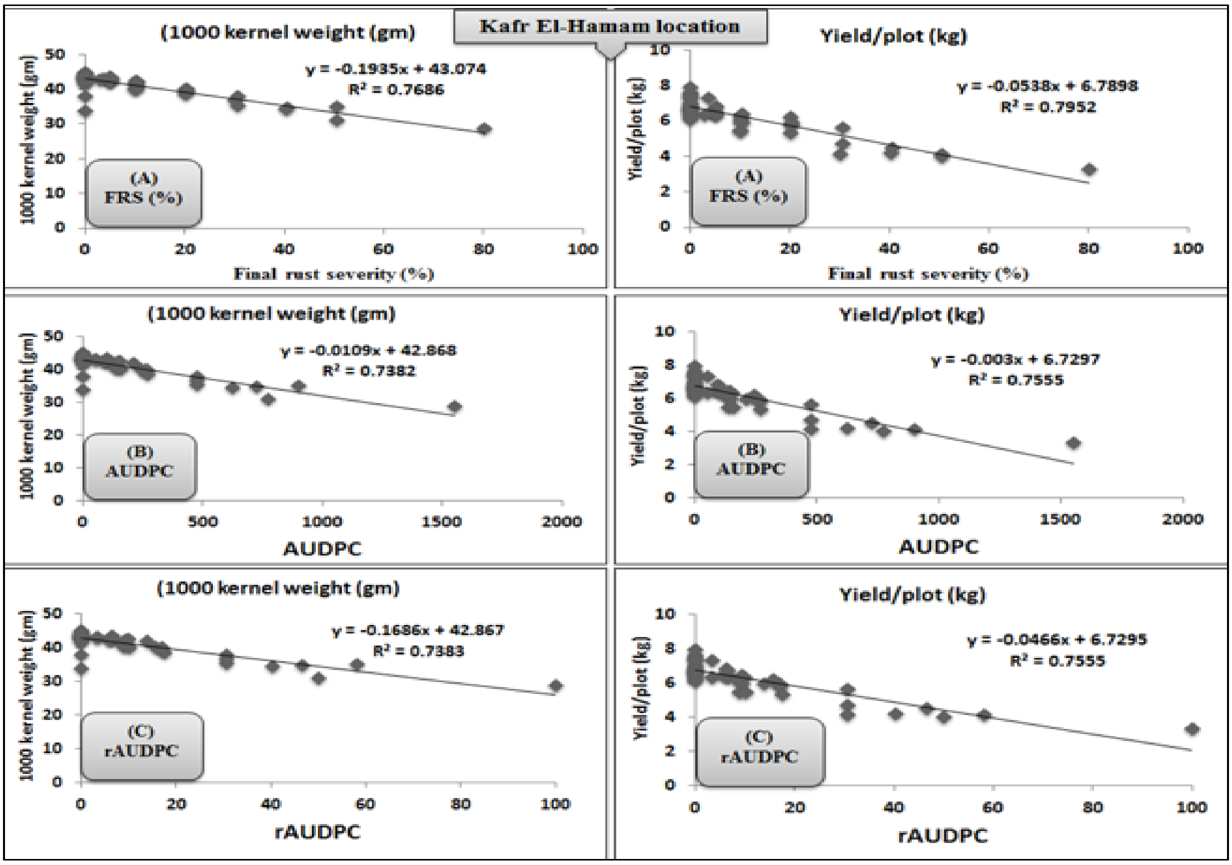

Fig. 2. Correlation coefficient between each of the three stem rust parameters ; FRS (%) (A), AUDPC (B) and rAUDPC (C) and yield components; 1000 kernel weight (gm) and yield/plot (kg) of 51 wheat lines at Kafr El-Hamam location, during 2019/20 growing season.

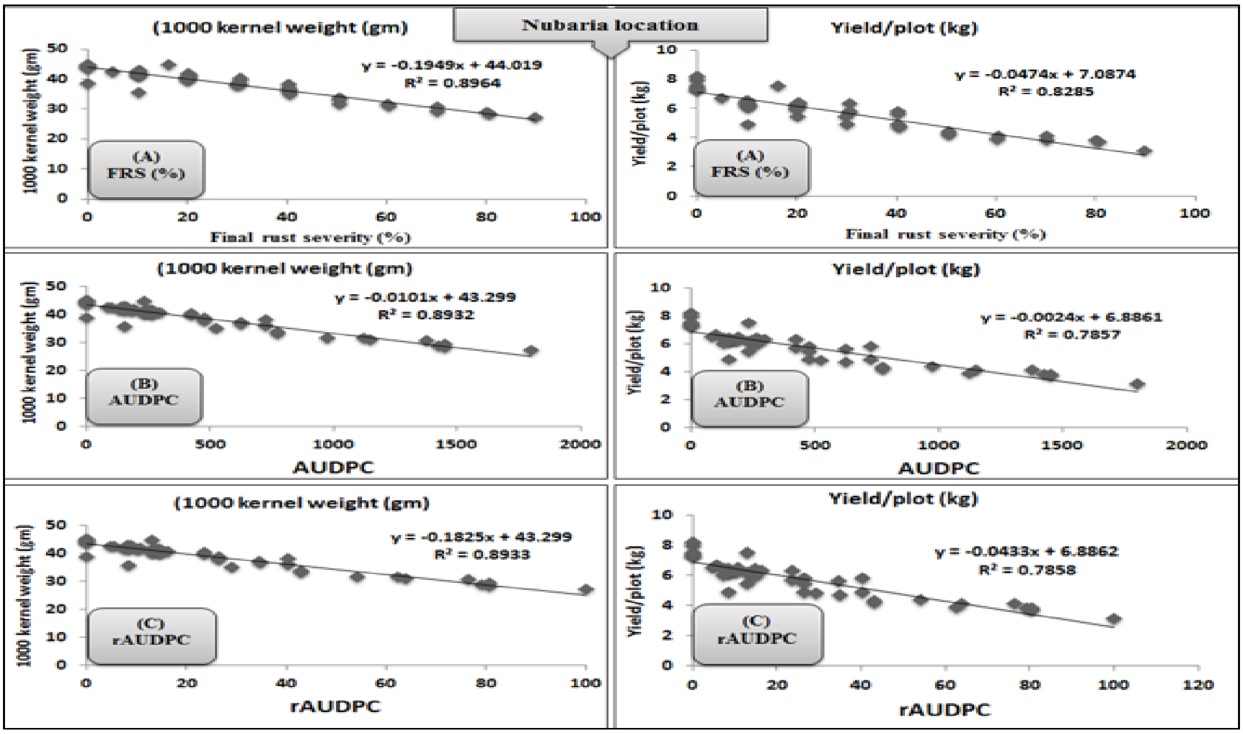

Fig. 3. Correlation coefficient between each of the three stem rust parameters ; FRS (%) (A), AUDPC (B) and rAUDPC (C) and yield components; 1000 kernel weight (gm) and yield/plot (kg) of 51 wheat lines at Nubaria location, during 2019/20 growing season.

CONCLUSION

Out of the tested wheat lines, eight promising lines; no's 1, 9, 12, 14, 20, 25, 47 and 49 proved to have a good performance at adult plant stage (adequate and completely resistant to stem rust), combined with high yield over the three locations. In addition to, 29 lines have the ability to delay stem rust increase or development of the three locations under study. Thus, these promising lines are characterized as partially resistant (PR) lines. Therefore, these promising lines should be used and utilized as the new sources of stem rust resistance in the future breeding programs for rust resistance in the country.

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غربلة التراكيب الوراثية لقمح السيميت ضد مرض صدأ الساق تحت ظروف الحقل في مصر

رضا إبراهيم عمارة ، عاطف عبد الفتاح شاهين و محمد إسماعيل محمد أحمد

معهد بحوث أمراض النباتات ، مركز البحوث الزراعية ، جيزة ، مصر

تم تقييم 51 سلالة قمح نباتية منتخبة من إجمالي 190 سلالة مستوردة من منظمة السميت في ثلاث مناطق مختلفة بمصر وهي سخا ، كفر الحمام ، النوبارية ، وذلك لتحديد مدي قدرتم علي المقاومة لمرض صدأ الساق في مرحلة النباتات البالغة كمصادر جديدة للمقاومة. حيث أظهرت نتائج تحليل التباين وجود فروق معنوية كبيرة بين السلالات النباتية المختبرة وذلك في الثلاث مناطق تحت الدراسة. وقد أسفرت تلك الدراسة عن وجود ثمانية سلالات نباتية مبشرة وهي 1 ، 9، 12 ، 14 ، 20 ، 25 ، 47 ، 49 ذات مقاومة عالية (كاملة) للمرض وبالتالي من الممكن إستخدامهم كمصادر جيدة للمقاومة ضد هذا المرض. وجد ايضاً 29 سلالة نباتية مبشرة تمتاز بصفة المقاومة الجزئية وذلك تحت ظروف الحقل في الثلاث مناطق تحت الدراسة. ومن ناحية أخري فقد ثبت من الدراسة وجود قيم عالية لمعامل التوريث (99٪) والتحسين الوراثي المتوقع من إجراء عملية الإنتخاب مما يدل دلالة واضحة علي أن الإختلافات الموجودة بين السلالات النباتية في رد فعلها للإصابة بالمرض تعد إختلافات وراثية إذ ترجع اساساً إلى التركيب الوراثي لتلك السلالات النباتية أكثر منها الي الظروف البيئية المحيطة.ومن خلال تحليل معامل الإرتباط تم التأكيد علي أهمية إستخدام الثلاثة مقاييس تحت الدراسة في تقييم الحالة المرضية للسلات المختبرة ، وخاصة النسبة المئوية لشدة المرض النهائية (FRS%) ، إذ تعتبر من الدلائل الجيدة والمناسبة أكثر من إستخدام المساحة الواقعة تحت منحني الأًصابة المرضي و المساحة النسبية الواقعة تحت منحني الإصابة المرضي ، لتقييم وإنتخاب أعداد كبيرة من السلالات النباتية (التراكيب الوراثية) لمرض صدأ الساق ، وذلك لسهولة إستخدامه في إجراء عملية الإنتخاب بنجاح في برامج التربية.