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GENE-POSTULATION FOR STEM RUST RESISTANCE IN TWENTY CERTAIN EGYPTIAN WHEAT VARIETIES

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ABSTRACT

Matching of sixteen monogenic lines and twenty wheat (*Triticum aestivum* L.) varieties representing the Egyptian germplasm inoculated with thirty different stem rust isolates to postulate stem rust resistance gene (*Sr*). Genes were determined according to the infection types (IT) to different *Puccinia graminis* f. sp. *tritici* isolates for seedling resistance in wheat varieties. All of the tested varieties were probably present in *Sr7b* and *Sr8a*, with the exception of Giza 160 and Sohag-3, whereas, *Sr9e* gene were detected in Gemmeiza-7 but it was not detected in the rest of tested varieties. Thirteen genes were probably present in Gemmeiza-7 (the highest), however Sakha 61, Sohag-3 and Sakha 160 wee included the least genes (*Sr's*). *Sr29, Sr30, Sr36* followed by *Sr7b* and *Sr8a* were most commonly postulated and having the highest frequency, while *Sr9e, Sr21, Sr26* SrT_{t-1} appeared in lower frequencies within the used Egyptian wheat varieties.

Keywords: stem rust, *Sr's* genes, postulation, infection type.

INTRODUCTION

Wheat stem rust caused by *Puccinia graminis* f. sp. *tritici* Eriks & Henn. Play an important role in wheat production in Egypt with rust diseases of wheat (*Triticum aestivum* L.). Stem rust can attack all of the above ground parts of the plant, damage to plants results from the loss of photosynthetic area. Severe losses have been Roelfs (1978) and Statler, (1971). Gene(s) conditioning resistance to *Pgt*. in these varieties are largely unknown. Therefore previously studies reported that *Sr9g, Sr9b,Sr25* and *Sr36* were common and having the highest frequency, while, *Sr5, Sr9e, Sr24, Sr26, Sr29 and* $SrGt^{+}$ were not detected and may be absent in the some Egyptian wheat varieties Imbaby *et al.,* (1997). Genes conditioning resistance to stem rust in Egypt and Neighbouring countries seem to be *Sr9e, Sr22, Sr24, Sr26* and *Sr27*, since they were effectively resistant to most isolated virulences Abd El-Hak *et al.,* (1982). Resistance in this wheat to Australian pathotypes was determined by combination of known and unknown genes more recently, Singh and McIntosh (1986) reported that Kenya plume possessed eight genes *Sr2, Sr5, Sr6, Sr7a, Sr8a, Sr9b, Sr12* and *Sr17*. Shahin (2002) indicated that resistance genes *i.e. Sr36*, *Sr30*, *Sr29* followed by *Sr7b*, *Sr8a* were present in 20 Egyptian cultivars, however SrT_{t-1}, *Sr26*, *Sr21*, *Sr9e* were

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less frequent, in another term the local cultivars lacked these genes to be incorporated.

The main objectives of present investigation had been to study was conducted to determine probable gene (*Sr*) resistance in twenty Egyptian wheat varieties share genes for resistance to *Pgt*.

MATERIAL AND METHODS

Twenty wheat varieties representing the Egyptian germplasm indicated in Table (1) in addition to known stem rust resistance genes *i.e*. *Sr's* Table (2) were tested for stem rust resistance using 30 cultures of stem rust *Puccinia graminis tritici* obtained from collected samples of 2005/2006.The materials were tested obtained from Cereal Dis. Res. Dept., Plant Pathology Research Institute., Agricultural Research Center, Giza, Egypt.

These varieties were grown in the greenhouse at Giza Agric. Res. Stn., during 2007/2008. Rust data were recorded as infection types according to the method of Stakman *et al.* (1962). All wheat materials were grown in plastic pots, with 10 cm. diam. each pot contained four varieties in each corner clockwise.

Table (1). List of Egyptian wheat entries and their pedigree which were evaluated through out the present study.

No.	Vars.	Pedigree
1	Sids-1	HD2172/Pavon "S"//1158.57/Maya74"S".
2	Sids-6	Maya "S"/Mon "S"//CMH74A.592/3/Sakha8*2SD/10002.
3	Sids-7	Maya "S"/Man "S"//CMH74A592/3/Sakha8*2SD/10002
4	Sids-8	Maya "S" /Man "S"//CMH74A592/3/Sakha8*2S D/10002.
5	Sids-9	Maya"S"/Man"S"/4/CMH72.428/MRC//JUP/3/CMH74A582/5/Giza 157*2SD10003.
6	Giza 160	(Regent 975-11 × Giza 139^2) × Mida Cadet × Hindi 62.
7	Giza 164	KVS – BUHO "S" × KAL - B.B (VEERY "S").
8	Giza 165	CNO / MFD /MAN "S".
9	Giza 167	Au/up301//GLL/SX/Pew"s"141Mai"S"/May"S"//Pew"S".
10	Giza 168	MRL/BUC//Seri.
11	Sakha 8	INDUS / NORTENO.
12	Sakha 61	INIA – RL 4220 ×7$_C$ / YR "S"
13	Sakha 69	INIA – RL4220 × 7$_C$ / YR "S"
14	Sakha 202	BL1133/3/CMH79A.955*2/CNO79//CMH79A.955/Bow"S".
15	Gemmeiza-3	BB/7C*2//Y50/KAL*3×Sakha8/4/PRV/WW/5/3/BJ/"S"// ON * 3/ BON.
16	Gemmeiza-5	Vee"S"/SWM6525Gm.4017-1Gm.7Gm.-3Gm.-0Gm.
17	Gemmeiza-7	CMH74A.630/SX//SER182/AGENTC'Gm.4611-2Gm.-3GM.-1Gm.-0Gm.
18	Sohag-1	Gdovz 469/3/Ja"s"//bi-30/Lds.
19	Sohag-3	Mexi."s"/MGHA*51792//Durum 6.
20	Beni Sweif-1	Jo"s"/AA"s"//Fg"s".

Inoculation and incubation were performed in moist chambers at 20-24°C. Inoculated plants were held at approximately 100% relative humidity for 24 hr., plants were returned to the greenhouse bench at 22 - 24°C till disease on set. Rust reaction on the first leaf was recorded (22 days after sowing) following the method adopted by Stakman, *et al.* (1962).

The infection type on each cultivar or near isogenic line was classified at the scale of (0 - 4). 12 days after inoculation, where infection types (IT) *i.e*. R= (0, 0;, 1 and 2) were classified as low infection type (LIT) or resistant and S= (3 and 4) were considered as high infection types (HIT), or susceptible using a method similar to those of Browder, (1973) and Statler (1984) to determine the probable resistance genotypes of the cultivars for each pair of tested hosts.

Table (2). Cultivars and lines of wheat carrying single genes for resistance used to identify stem rust cultures in Canada. (Green 1981).

Genes for resistance	Typical resistant infection type		Cultivar or line
	Seedling [a]	Adult [b]	
Sr5	**0**	**I**	**Prelude*6/Reliance**
Sr6	0;, X	R	Mida-McMurachy-Echange/6*Perlude
Sr7b	2+-	MS	Chinese Spring/Hope (C.I. 14165)
Sr8a	2+-	MS	Chinese Spring/Red Egyptian (C.I. 14165)
Sr9b	2, 2, 3	MR	Prelude*4// Marquis*6/Kenya 117A
Sr9d	;2-	MR	H-44-24/6*Marquis
Sr9e	;, ;1+, 2	R	Vernstein W3196
Sr9g	2-	MR	Lee
Sr11	1+, ;2	R-MR	Chinese Spring/Timstein C.I.14171
Sr17	0;1	R	Prelude/8*Marquis*2//Esp 518/9
Sr21	0;	R	*Tricticum monococcum*
Sr25	2	MS-S	*Agropyron elongatum*
Sr26	;2-	MR	*Agropyron elongatum*
Sr27	0;	I	WRT 238-5
Sr29	2-	MS	Prelude/8*Marquis//Etoil de Choisy
Sr30	2	MS	Webster
Sr36	0;, X	I, Tr S	Prelude*4/NHLII.64.62.1
$SrGt^{+}$	2+	MS	Gamut
SrT_{t-1}	2	R	$W269LSrT_{t-1}$

[a] Low infection types at 18 °C, may vary at other temperature.
[b] I = immune, R = resistant, MR = moderately resistant, MS = moderately susceptible, S = susceptible, Tr S = trace susceptible.
[c] Cited after Green (1981).

Matching or comparing the cultivars with unknown resistance genes (host B) to the isogenic lines each carrying single known gene for resistance to stem rest (host A) was performed. The infection types of tested cultivars were classified into four categories according to the following scheme.

		Host B	
Host A		Resistant	Susceptible
	Resistant	LIT:LIT	LIT:HIT
	Susceptible	HIT:LIT	HIT:HIT

The HIT:LIT and LIT:HIT infection types are most critical to determine probable resistance genotypes. The four categories were based on whether or not each of these infection types occurred.

Category 0: absence of LIT:LIT isolates indicating that host B has the same gene(s) as in host A, however host B may have additional resistance genes.

Category -: no of HIT:LIT isolates but some LIT:HIT isolates indicating that host B does not contain the resistance genes in host A.

Category -0: no of HIT:LIT isolates and no LIT:HIT isolates indicating that both hosts carry the same resistance genes at least for resistance to the isolates used.

Category +: some HIT:LIT isolates and no LIT:HIT isolates indicating that both hosts do not carry the same resistance gene (s).

The infection types (IT) of the twenty wheat varieties with unknown resistance genes (host B) were compared to the infection types of the sixteen monogenic lines each carrying a single, known gene for deduce Sr genes account for the resistance to stem rust (host A).

RESULTS

Data presented in Table (3) revealed the matching of 16 monogenic lines and 20 commercial wheat varieties against 30 isolates of stem rust pathogen (*P. graminis tritici*). These data indicated the presence of low infection type: high infection type in the (commercials : monogenic) indicating the inclusion of the *Sr* within the genetic make up of the commercial cultivar. This was assigned by the symbol (0).

Other group of comparisons showed the presence of low infection type: high infection type and high infection type: low infection types between the commercials and monogenics against the tested isolates and this would indicate that each of the vars. may have gene(s) not involved in the other. It was assigned by the symbol (+). Certain group showed low infection types within the monogenics, however the commercials exhibited high infection type in the matching against the isolates. This would indicate the absence of such gene (s) within the commercials, and would assigned by the symbol (-).

Data in Table (4) revealed the probable resistance genes may be presented in the genetic back ground of certain commercial varieties as derived from the last table. These data indicated that cultivar Sakha 61 included the least number of stem rust resistant genes *i.e*. (3) followed by Giza 160 (4). On the other hand, Gemmeiza-7 exhibited the highest number of genes *i.e*. 13 followed by Giza 167 (11) and Giza 165, Sohag-1 (10). The rest of cultivars included between 5 and 9 resistant genes.

As regard to the distribution of stem rust resistant genes within commercial cultivars, data presented in Table (5) revealed that Sr 36 is the most common gene within the Egyptian commercials, *i.e*. (20 var.) followed by *Sr29* and *Sr30* (95%), *Sr8a* (80%) and *Sr7b* (80%). The rest of resistance genes ranged between 5% and 30%.

Table (3). Incidence of low infection type : high infection type (R:S) comparisons of monogenic lines and varieties inoculated with 30 isolates of *Puccini graminis* f. sp. *tritici*.

Variety (A)	Host monogenic lines *Sr's* (B)															
	Sr5	*Sr6*	*Sr7b*	*Sr8a*	*Sr9e*	*Sr9g*	*Sr11*	*Sr17*	*Sr21*	*Sr26*	*Sr27*	*Sr29*	*Sr30*	*Sr36*	*SrGt*$^{+}$	*SrT*$_{t-1}$
Sids-1	+	+	+	+	+	+	+	+	+	-	0	0	0	0	+	+
Sids-6	+	+	0	0	+	+	+	+	+	+	+	0	0	0	+	+
Sids-7	0	0	0	0	+	+	+	+	+	+	+	0	0	0	+	+
Sids-8	+	+	0	0	+	+	+	+	+	+	+	0	0	0	+	+
Sids-9	+	+	0	0	+	+	+	+	+	-	+	0	0	0	+	+
Giza 160	+	+	+	+	+	+	+	+	+	+	+	0	0	0	+	+
Giza 164	+	0	0	0	+	+	+	+	+	+	+	0	0	0	+	+
Giza 165	0	+	0	0	+	0	0	+	0	+	0	0	0	0	+	+
Giza 167	0	0	0	0	+	0	+	0	+	+	0	0	0	0	0	+
Giza 168	+	0	0	0	+	+	+	+	+	-	+	0	0	0	+	+
Sakha 8	+	+	0	0	+	+	+	+	-	-	+	0	0	0	+	+
Sakha 61	+	+	+	0	+	+	+	+	+	+	+	+	+	0	0	+
Sakha 69	+	+	0	0	+	+	+	+	+	+	+	0	0	0	+	+
Sakha 202	+	+	0	0	+	+	+	+	+	+	+	0	0	0	0	+
Gemmeiza-3	+	+	0	0	+	+	+	+	+	+	+	0	0	0	0	+
Gemmiza-5	+	+	0	0	+	+	+	+	+	+	+	0	0	0	+	+
Gemmeiza-7	0	+	0	0	+	0	+	0	+	+	0	0	0	0	0	+
Sohag-1	0	+	0	0	+	0	+	0	+	+	0	0	0	0	0	+
Sohag-3	+	+	+	+	+	+	+	+	+	+	+	0	0	0	+	+
Bani Sweif-1	+	+	0	0	+	+	+	+	+	-	+	0	0	0	+	+

0 = Host B has the same gene (s) as in the host A and additional genes.
+ = Hosts A and B do not carry the same resistance genes.
- = Host B does not contain the resistance gene in host A.

Table (4). Probable resistance genes for stem rust in some Egyptian wheat entries.

No.	Wheat entries	Probable *Sr* genes
1	Gemmeiza-3	*7b, 8a, 29, 30, 36, Gt*$^{+}$
2	Gemmeiza-7	*5, 6, 7b, 8a, 9e, 9g, 11, 26, 29, 30, 36, Gt*$^{+}$*, T*$_{t-1}$
3	Gemmeiza-5	*7b, 8a, 29, 30, 36*
4	Giza 160	*27, 29, 30, 36*
5	Giza 164	*6, 7b, 8a, 29, 30, 36*
6	Giza 165	*5, 7b, 8a, 9, 11, 21, 27, 29, 30, 36*
7	Giza 167	*5, 6, 7b, 8a, 9g, 17, 27, 29, 30, 36, Gt*$^{+}$
8	Giza 168	*6, 7b, 8a, 29, 30, 36*
9	Sakha 202	*7b, 8a, 29, 30, 36, Gt*$^{+}$
10	Sakha 61	*8a, 36, Gt*$^{+}$
11	Sakha 69	*7b, 8a, 29, 30, 36*
12	Sakha 8	*7b, 8a, 29, 30, 36*
13	Sids-1	*27, 29, 30, 36*
14	Sids-6	*7b, 8a, 29, 30, 36*
15	Sids-7	*5, 6, 7, 8a, 29, 30, 36*
16	Sids-8	*7b, 8a, 29, 30, 36*
17	Sids-9	*7b, 8a, 29, 30, 36*
18	Beni Sweif-1	*7b, 8a, 29, 30, 36*
19	Sohag-1	*5, 7b, 8a, 9g, 17, 27, 29, 30, 36, Gt*$^{+}$
20	Sohag-3	*29, 30, 36*

Table (5). Probable resistance genes for stem rust in some Egyptian wheat entries.

No.	*Sr* genes	Frequency	%
1	*Sr5*	5	25
2	*Sr6*	5	25
3	*Sr7b*	16	80
4	*Sr8a*	16	80
5	*Sr9e*	1	5
6	*Sr9*	4	20
7	*Sr11*	2	10
8	*Sr17*	2	10
9	*Sr21*	1	5
10	*Sr26*	1	5
11	*Sr27*	4	20
12	*Sr29*	19	95
13	*Sr30*	19	95
14	*Sr36*	20	100
15	$SrGt^{+}$	6	30
16	SrT_{t-1}	1	5

DISCUSSION

In relation to the matching test performed between *Sr's* and commercials versus 30 isolates of *P. graminis tritici* at seedling stage, the obtained results indicated that the commercial varieties varied in their inclusion of postulated resistant genes. For example, Sakha 61 include 3 genes (the least), however, Gemmeiza-7 included 13 genes (the highest). On the other hand, the results gave evidence to the presence of *Sr's: 36, 30, 29* followed by *7b* and *8a*, as the more frequent and commonest genes. However, *Sr's: Tt-1, 26, 21, 9e* appeared in lower frequencies within the commercials.

If we put these results in comparison with the above mentioned ones, we would find that the common genes within cultivars are lacked as effective ones. However, those effective are less frequent or less common herein. This explanation seemed to be comprehensive and logical, because the basis of the first test *i.e.* virulence formulae depend upon the spore samples which were collected from the susceptible cultivars. However, the basis of the matching test "gene postulation" depends upon the matching of *Sr's* (known gene cultivars) and the commercials (unknown gene cultivars) versus high number of isolates.

This results seemed to be logical since the local commercials require *Sr's: Tt-1, 26, 21* and *9e* which are in turn effective in the virulence analysis results were reported by Claude *et al.* (1986); Hu and Roelfs (1986); Singh and McIntosh (1986); Hu (1988) and Imbaby *et al.,* (1997); Shahin, A.A. (2002).

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الاحتمال المتوقع لجينات المقاومة لمرض صدا الساق فى عشرين صنف تجارى من القمح مصرى

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****معهد بحوث امراض النباتات-مركز البحوث الزراعية-جيزة-مصر**

دلت نتائج دراسة التوقع الجينى المشتقاه من مقارنة الاصناف التجارية والاصناف الاحادية الجين Monogenic lines (*Sr's*) ضد ٣٠ عزلة فطرية داخل سلالات الفطر المسبب لصدأ الساق فى القمح ذلك للتعرف على العوامل الوراثية (جينات المقاومة) المتوقع وجودها فى طور البادرة فى بعض اصناف القمح التجارية فى مصر .

يمكن تلخيص أهم النتائج فى الاتى:

قد بينت نتائج الدراسة ان كل الاصناف التى تم اختبارها من المحتمل وجود تلك العوامل الوراثية *Sr7b* and *Sr8a*بها ماعدا صنفى جيزة ١٦٠ وسوهاج ٣ بينما كان العامل الوراثى *Sr9e* قد تم التعرف على احتمال وجودة فى صنف جميزة ٧ ولم تتمكن عزلات الفطر والاصناف الاختبارية من تعريف هذا العامل فى باقى الاصناف التجارية المختبرة كما دلت النتائج ايضاً على ان الصنف سخا ٦١ يحوى على اقل العوامل الوراثة ، حيث بينت الدراسة على احتمال احتواء (الصنف سخا ٦١) ٣ جينات مقاومة بينما احتوى الصنف (جميزة ٧)على ١٣ جين وتراوحت الاصناف الاخرى بين هذين الحدين وقد دلت نتائج التوقع الجينى على سيادة الجينات الآتية داخل الاصناف المصرية وهى : *Sr's: 36, 30, 29* ثم *Sr7b, Sr8a* بينما كان أقلها شيوعاً داخل الاصناف *SrTt-1, Sr26, Sr21, Sr9*e .