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PHYSIOLOGICAL RACES AND VIRULENCE DIVERSITY OF *PUCCINIA GRAMINIS PERS. F. SP. TRITICI* ERIKS. & E. HENN. DURING 2011/2012 AND 2012/2013 GROWING SEASONS IN EGYPT

Nabila A. El-Sherif, Gamalat A. Hermas, M. A. Hasan and Somaya Tohamey

Wheat Dis. Res. Division, Plant Path. Res. Inst., ARC, Giza, Egypt.

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ABSTRACT: ***Stem rust of wheat caused by Puccinia graminis Pers. f. sp. tritici Eriks. & E. Henn., is the most destructive disease of wheat worldwide as well as in Egypt. It can causes high sever losses of wheat crops over wide areas during epidemic years. Hence, this study was carried out to detect the virulence dynamic and diversity of P. graminis f. sp. tritici in different locations and studying the efficacy of stem rust resistant genes in Egypt seedling stage. Stem rust collections were obtained from infected wheat stems throughout the survey of wheat fields and nurseries in three locations (Sids, El Sharkia and El Nubaria) during 2011/2012 growin g season. Whereas during 2012/2013 growing season the samples collected from six locations (Giza, Sids, Tag El Aiz, Sakha, El Sharkia and El Nubaria). Based on race analysis of stem rust populations, and race determination by inoculating stem rust differential hosts, the phenotypic characterization of P. graminis f. sp. tritici during 2011/2012 growing season resulted in identification of 86 races from 22 successful samples, all of them showed 1.16% frequency. Race BBBBC was a virulent on all the tested Sr genes, except Sr MCN, whereas race TTTTK was virulent on all the tested Sr except Sr 24. On the other hand, analysis during the next growing season revealed that, 123 races with a frequency ranged from 0.81% to 2.43% were identified. Race groups BB---, LG---, BJ---and TT--- were common at the tested locations during the two growing seasons. Regarding stem rust resistant gene efficacy during the study Sr24, Sr38 and Sr31 exhibit the highest efficacy% (95.34, 91.86 and 87.21 respectively) during the two seasons. Thus, deployment of effective Sr genes such as Sr24, Sr38 and Sr31 in single cultivar through gene pyramiding has paramount importance as the additive effects of several genes gives the cultivar a wider base stem rust resistance along with periodic race survey.***

Key words: ***Wheat stem rust, race analysis, gene efficacy.***

INTRODUCTION

Wheat is the most important food grain crops grown in Egypt. It is among the cereal crops that contribute significantly to food security in the country. Stem rust of wheat caused by *Puccinia graminis* Pers. f. sp. *tritici* Eriks. & E. Henn. is the most destructive disease of wheat worldwide. Successful control of the disease over three decades through the use of genetic resistance has resulted in a sharp decline in research activity in recent years. The previous studies of (Wamishe and Milus 2004) reported that, many cases of genetic resistance become ineffective because the population of rust pathogen respond to selective pressure of resistant host cultivars and produced more virulent phenotypes that overcome the resistant genes newly deployed in the commercials wheat cultivars.

Occurrence of new races in a geographic/ epidemiologic regions can be attributed to the migration from an

outside countries which considered a great threat to our cultivars. Detection and spread of race TTKS, in East Africa commonly known as Ug99, and its migration path i.e. to North Africa through Arabian Peninsula and then to Middle East and Asia. Identifying/developing adapted resistant cultivars in a relatively short time and replacing the susceptible cultivars before rust migrates out of East Africa is the strategy to mitigate potential losses (Singh, *et al*., 2008). So, the panel recommends that breeding strategy could be implemented to incorporate diverse genetic resistance to such race into germplasme before the migration to other areas. , Brennan and Marray (1988) stated that a breeding program should develop rust resistant cultivars conditioned with resistance genes(both race- specific and race- non specific resistance) exist in wheat should be used. The inheritance of adult plant resistance has often been considered as a complex, but there is also an evidence that it is oligogenic (Barcellos *et al*.,2000). The identification of genes conferring stem rust adult plant resistance would be a significant step towards a good control of such disease (Manninger *et al*.,1998; Nazim *et al*., 2001; Hermas, 2003; Mousa *et al*., 2004 and EL-Shamy *et al*., 2011).

MATERIALS AND METHODS

Collection of wheat stem rust samples:

The collected samples from the different locations during 2011/2012 and 2012/2013 included wheat stems having the symptoms of stem rust disease caused by *Puccinia graminis* Pers. f. sp. *tritici* Eriks. & Henn., were used to identify physiologic races. The collected samples (rusted stems) were kept in glassine envelopes (8 x 15 cm) and left at room temperature for 24 hours to remove the humidity in the samples. After that the samples were preserved in dissector in fridge till usage or re inoculate on highly susceptible wheat cultivars Morocco which don't carry any pustules to known stem rust resistance genes Roelfs and Martens 1988.

Isolation and multiplication of pure isolates:

Eight days old seedlings were sprayed with an atomizer in the inoculation chambers with water then inoculated by shaking and brushing rusted materials over the plants and sprayed gently again with water in order to induce "dew" on the plant. Finally, the inoculated plants were kept in damp chambers for 24 hours to allow the rust spore to germinate and cause infection for 18 hours dark at 18-22ºC followed by exposure to light for 3-4 hours to provide condition for infection and seedlings were allowed to dry their dew for about 1-2 hours. Then, the seedlings were transferred from the dew chamber to glass compartments in the greenhouse where conditions was regulated at 12 hours photoperiod at temperature of 18–25ºC and relative humidity (RH) of 60-70%. After developing the rust, three to five single pustules were separately isolated from each sample for spore increase on susceptible wheat cultivar Morocco seedlings to obtain enough urediospores for inoculating the differential sets. Seedling reaction was recorded as low (L) or high (H)infection type depending on the infection type produced according to the method adopted by Stakman *et al*., (1962). Infection types were categorized as either being Low (incompatible or resistant; ITs of 0, 0;, 1, and 2) or High (compatible or susceptible; ITs of 3 & 4).

Phenotyping differential sets and designation of races:

Race designation and nomenclatural was done by grouping the differentials into five subsets: (i) *Sr5, Sr21, Sr9e,*

***Sr7b*, (ii) *Sr11, Sr6, Sr8a, Sr9g*, (iii) *Sr36, Sr9b, Sr30, Sr17*, (iv) *Sr9a, Sr9d, Sr10, SrTmp*, (v) *Sr24, Sr31, Sr38* and *SrMcN* (Roelfs and Martens, 1988; Jin *et al*., 2008). The differential host series consisted of wheat rust monogenic lines, arranged in five subsets Table (1). Races were assigned using the international Pgt-code as suggested by Roelfs and Martens (1988). The frequency of each race was calculated as a percentage from the total number of isolates analyzed.**

RESULTS AND DISCUSSION

Surveillance data from the two growing seasons revealed that, eighty six isolates were identified during the first season from three locations, Sids, Sharkia and Nubaria. The highest number of isolates and frequency was obtained from Sids location (45 and 52.32%). During 2012/2013 season the survey covered six locations and race analysis revealed that one hundred twenty three isolates were identified. The highest number of isolates and frequency obtained from Tag El Aiz location, whereas the lowest number obtained from Sids location. In these districts, large numbers of samples were collected but most of the samples were unable to germinate in the greenhouse race analysis Teklay, *et al*., (2013) as shown in (Table 2).

Table (1). A key for identification and nomenclature of Pgt races of *Puccinia graminis* f. sp. *tritici.*

	Infection types produced on host lines with Sr				
subset	1	5	21	9e	7b
	2	11	6	8a	9g
	3	36	9b	30	17
	4	9a	9d	10	TmP
	5	24	31	38	MCN
Pgt-code	B	Low	Low	Low	Low
	C	Low	Low	Low	High
	D	Low	Low	High	Low
	F	Low	Low	High	High
	G	Low	High	Low	Low
	H	Low	High	Low	High
	J	Low	High	High	Low
	K	Low	High	High	High
	L	High	Low	Low	Low
	M	High	Low	Low	High
	N	High	Low	High	Low
	P	High	Low	High	High
	Q	High	High	Low	Low
	R	High	High	Low	High
	S	High	High	High	Low
	T	High	High	High	High

Roelfs and Martens 1988

Table (2): No. of isolates and their frequency collected from different location in Egypt during 2011/ 2012 and 2012/2013 seasons.

No.	Locations	2011/2012 season		2012/2013 season	
		No. of isolatets	Frequency %	No. of isolatets	Frequency %
1	Sids	45	52.32	3	1.62
2	Sharkia	30	34.32	19	15.44
3	Nubaria	11	12.74	22	17.88
4	Tag El Aiz	-	-	44	36.58
5	Sakha	-	-	19	16.26
6	Giza	-	-	16	12.19
Total		86		123	

Physiological races of *P. graminis* f. sp. *tritici.:*

Wheat stem rust is a re-emerging disease, posing a new threat to wheat production worldwide, which is highlighted by the occurrence and spread of Sr31-virulent races in the Ug99 race group (Singh *et al.,* 2015). Since first reported in Uganda (Pretorius *et al.,* 2000), the TTKS (or Ug99) race group has been rapidly evolving and expanding its geographical range. Race analysis of the collected samples during 2011/2012 season (Table 3) revealed that 86 races were identified based on their reaction on 20 differential sets. Most of the identified races showed the same virulence frequency (1.16) on stem rust resistance genes; this indicated a high level of variation both in quantity and virulence spectrum. The obtained data gave evidence that, races BBBBC, BBBJB, BBBLB and BBFBB were less aggressive on stem rust resistant genes, which overcome *Sr* MCN, 9a, 9d, 30 and 17respectively. On the other hand the broadest virulence spectra were recorded for races TTTTK, TTKTF and TSPSK making most of the tested *Sr* stem rust resistance genes ineffective. The rest identified races varied in their virulence on stem rust resistance genes; this indicated a high level of variation both in quantity and virulence spectrum. Similar results were recorded by Mousa *et al*., (2004), Najeeb *et al*., (2004) and Youssef, *et al*., (2012). During 2012/2013 season 123 races were identified from the collected samples, all of them showed frequency 0.81%. Race BBBBB was a virulent on all the tested *Sr*, while race TTTTF was virulent on most of the tested *Sr* Table (4). The rest identified races showed different infection types on stem rust resistance genes. Infection type and genotypic data confirmed that none of these races belonged to the TTKS (Ug99) race group. Similar was reported by Similar results were registered in different countries, Olivera *et al.,* (2015) identified JRCQC, TRTTF and TTKSK from 34 isolates, both races JRCQC and TRTTF possess virulence on stem rust resistance genes Sr13 and Sr9e. In addition, race TRTTF was virulent to three stem rust resistance genes that were effective to race TTKSK, including Sr 36, Sr Tmp, and resistance conferred by the 1AL.1RS rye translocation.

Table (3): Pathotypes of *Puccinia graminis f.sp.tritici* (Pgt-code) identifiedin Egypt during 2011/2012 and their frequencies using the 20 American differential hosts and their localities.

No.	Pathotype (Pgt)	Locality	No. of isolates	Frequency %	No.	Pathotype (Pgt)	Locality	No. of isolates	Frequency %
1-	BBBBC	N	1	1.16	44-	KTMSB	Sh	1	1.16
2-	BBBJB	Sh	1	1.16	45-	L JTSJ	S	1	1.16
3-	BBBLB	S	1	1.16	46-	LBCQB	Sh	1	1.16
4-	BBBLF	Sh	1	1.16	47-	LBDGB	Sh	1	1.16
5-	BBFBB	S	1	1.16	48-	LBKQD	Sh	1	1.16
6-	BBHSB	N	1	1.16	49-	LGGLB	Sh	1	1.16
7-	BBQLB	Sh	1	1.16	50-	LGHQB	S	1	1.16
8-	BCBFC	S	1	1.16	51-	LGQNF	Sh	1	1.16
9-	BCMTC	S	1	1.16	52-	LKSSF	Sh	1	1.16
10-	BDFBD	Sh	1	1.16	53-	LLHDB	Sh	1	1.16
11-	BGMDB	Sh	1	1.16	54-	LTHNC	Sh	1	1.16
12-	BJBDB	S	1	1.16	55-	LTKTD	S	1	1.16
13-	BJHSD	S	1	1.16	56-	NGRBB	S	1	1.16
14-	BKCSD	S	1	1.16	57-	NKMPB	N	1	1.16
15-	BKTLK	Sh	1	1.16	58-	NKRLB	S	1	1.16
16-	BMSLP	Sh	1	1.16	59-	NRGQC	S	1	1.16
17--	BNKGF	S	1	1.16	60-	PDTSF	Sh	1	1.16
18-	BQBLB	Sh	1	1.16	61-	QBGLB	S	1	1.16
19-	CFCJC	S	1	1.16	62-	QBHGB	Sh	1	1.16
20-	CLBBB	Sh	1	1.16	63-	QCDNC	S	1	1.16
21-	DBBBC	N	1	1.16	64-	QFTHC	S	1	1.16
22-	DBJGF	S	1	1.16	65-	QHTHC	S	1	1.16
23-	DBKBD	N	1	1.16	66-	QKSDK	Sh	1	1.16
24-	DCRTF	S	1	1.16	67-	RCSND	N	1	1.16
25-	DDDBD	N	1	1.16	68-	RGKSD	S	1	1.16
26-	DFKRC	N	1	1.16	69-	RSMLD	Sh	1	1.16
27-	DKTSB	S	1	1.16	70-	RTTTF	S	1	1.16
28-	FBHQB	Sh	1	1.16	71-	SCHDC	Sh	1	1.16
29-	FRRLD	S	1	1.16	72-	SCTTB	S	1	1.16
30-	GCFBC	S	1	1.16	73-	SJRBD	S	1	1.16
31-	GHBGD	N	1	1.16	74-	SKKQD	N	1	1.16
32-	GHTPB	S	1	1.16	75-	SNHQF	S	1	1.16
33-	GJBGB	S	1	1.16	76-	SRKQB	S	1	1.16
34-	GJQLC	S	1	1.16	77-	STFTD	Sh	1	1.16
35-	GNQMF	S	1	1.16	78-	STJNP	S	1	1.16
36-	GTGBF	Sh	1	1.16	79-	STKSB	S	1	1.16
37-	GTTST	Sh	1	1.16	80-	STMTF	Sh	1	1.16
38-	JCKSF	S	1	1.16	81-	STSSF	S	1	1.16
39-	JFHPC	S	1	1.16	82-	TCDST	Sh	1	1.16
40-	JMKTD	S	1	1.16	83-	TCTDC	S	1	1.16
41-	KBSDB	n	1	1.16	84-	TSPSK	S	1	1.16
42-	KKPDF	S	1	1.16	85-	TTKTF	Sh	1	1.16

43-	KLTTF	S	1	1.16	86-	TTTTK	S	1	1.16

S(sids) N(Nubaria) Sh (Sharkia)

Table (4): Pathotypes of *Puccinia graminis* f.sp.*tritici* (Pgt-code) identified in Egypt during 2012/2013 and their frequencies using the 20 American differential hosts and their localities.

No.	Pathotype (Pgt)	Locality	No. of isolates	Frequency %	No.	Pathotype (Pgt)	Locality	No. of isolates	Frequency %
1-	BBBBB	Tag	1	0.81	43-	FCTTC	Tag	1	0.81
2-	BBBBC		1	0.81	44-	FDBDB	Sid	1	0.81
3-	BBBGC		1	0.81	45-	GBBLC	Noub.	1	0.81
4-	BBBGC	K	1	0.81	46-	GBLFC	G	1	0.81
5-	BBBGC	SK	1	0.81	47-	GCLQC		1	0.81
6-	BBBLC	Tag	1	0.81	48-	GCTTC	Tag	1	0.81
7-	BBBPC	Noub.	1	0.81	49-	GDBBC		1	0.81
8-	BBBQB		1	0.81	50-	GDQRM	G	1	0.81
9-	BBBQF		1	0.81	51-	GHLQD	K	1	0.81
10-	BBBSC	Tag	1	0.81	52-	GJBBC	G	1	0.81
11-	BBGGC		1	0.81	53-	HGLDC	Noub.	1	0.81
12-	BBLRB	G	1	0.81	54-	HTCTC	SK	1	0.81
13-	BBLTC	Tag	1	0.81	55-	KFKTC	Tag	1	0.81
14-	BBMRC		1	0.81	56-	KKTTC	Noub.	1	0.81
15-	BCHRB	K	1	0.81	57-	LCBQC	SK	1	0.81
16-	BDLBC	Tag	1	0.81	58-	LCQHC		1	0.81
17--	BGBBB		1	0.81	59-	LCRNC		1	0.81
18-	BGLRC		1	0.81	60-	LFDMC	Tag	1	0.81
19-	BHBSC	Giz	1	0.81	61-	LFNTC	K	1	0.81
20-	BHNDC	K	1	0.81	62-	LFQRB		1	0.81
21-	BDQHB	Giz	1	0.81	63-	LFQRB	SK	1	0.81
22-	BHCTC	Tag	1	0.81	64-	LGDBC	Noub.	1	0.81
23-	BJMPC		1	0.81	65-	LGLHC	Giz	1	0.81
24-	BJMRC	Noub.	1	0.81	66-	LHTTC	Noub.	1	0.81
25-	BJQGC	Tag	1	0.81	67-	LJCBC	Tag	1	0.81
26-	BKDRB		1	0.81	68-	LJGMC	Noub.	1	0.81
27-	BKQLB		1	0.81	69-	LKMFB	SK	1	0.81
28-	BLBSC		1	0.81	70-	LTQGC		1	0.81
29-	BLDCC		1	0.81	71-	MBKRC	Noub.	1	0.81
30-	BLLBC	GIZ	1	0.81	72-	MQLSC		1	0.81
31-	BRLLC	Tag	1	0.81	73-	MHJRC	SK	1	0.81
32-	BRQCB		1	0.81	74-	MHMRC	Tag	1	0.81

No.	Pathotype (Pgt)	Locality	No. of isolates	Frequency %	No.	Pathotype (Pgt)	Locality	No. of isolates	Frequency %
33-	BRRPC	Giz	1	0.81	75-	MHSTC	Noub.	1	0.81
34-	BNBBC	Tag	1	0.81	76-	NBLGC		1	0.81

Table (4): Cont.

No.	Pathotype (Pgt)	Locality	No. of isolates	Frequency %	No.	Pathotype (Pgt)	Locality	No. of isolates	Frequency %
35-	BSBQC		1	0.81	77-	NDGKC		1	0.81
36-	CBRSC	K	1	0.81	78-	NDLTC	K	1	0.81
37-	CCBHC	Tag	1	0.81	79-	NFHRB	Tag	1	0.81
38-	CDTMC		1	0.81	80-	NT SSB		1	0.81
39-	CGBTC		1	0.81	81-	NTSTF	SK	1	0.81
40-	CQGTC		1	0.81	82-	PJQSC	SK	1	0.81
41-	DPPQC	SK	1	0.81	83-	QBLBB	Noub.	1	0.81
42	DTRPM	Giz	1	0.81	84-	QCLBC	K	1	0.81
85-	QCLDC	K	1	0.81	105-	STPSC	Sid	1	0.81
86-	QCMCC	Noub.	1	0.81	106-	TBBRC		1	0.81
87-	QDBMC	K	1	0.81	107-	TBTTC	Tag	1	0.81
88-	QDLNC	Giz	1	0.81	108-	TCRKF	K	1	0.81
89-	QFJHB	K	1	0.81	109-	TCSTC	SK	1	0.81
90-	QKBTC		1	0.81	110-	TCSTC	K	1	0.81
91-	QMTTC		1	0.81	111-	TDLGM	Giz	1	0.81
92-	QRLGB	Tag	1	0.81	112-	TFTHC	Tag	1	0.81
93-	QSQHF	SK	1	0.81	113-	THRTC		1	0.81
94-	RFTTC	Tag	1	0.81	114-	TJPTC	Sk	1	0.81
95-	RHCTB	K	1	0.81	115-	TKRTC	Tag	1	0.81
96-	RHTTC	Tag	1	0.81	116-	TKTPC	Sk	1	0.81
97-	RJRTC		1	0.81	117-	TKTTC	Noub.	1	0.81
98-	RSHRC	Noub.	1	0.81	118-	TTRTC	G	1	0.81
99-	RSPCB	Tag	1	0.81	119-	TTSGC	Noub.	1	0.81
100-	SBTPN	Giz	1	0.81	120-	TTTPB	Sk	1	0.81
101-	SHQTC	SK	1	0.81	121-	TTTTC	Noub.	1	0.81
102-	SKQQB	G	1	0.81	122-	TTTTC	Sk	1	0.81
103-	SKTTC	K	1	0.81	123-	TTTTF	Noub.	1	0.81
104-	SPNTC		1	0.81					

S(sids) K(Kafer Elshak) G(Giza) Tag(Tagelize) N(Nuobaria) Sh (Sharkia)

To simplify and facilitate the handling of race analysis results, data in Table (5) showed that, the most common race groups were BB---,LG---,BJ---and TT---,

which were common and the most frequent during the two growing seasons (8.13, 4.41, 2 and %) at 2011/2012, and (11.38, 2, 3 and 7%) at 2012/2013, respectively. Whereas the rest race groups were in between. Similar results were reported by Hasan (2006), he found that, race groups TT and BB were the most frequent race groups during 2003 and 2004 seasons.

Table (5): Race group of *Puccinia graminis tritici,* no. of isolates and their frequencies of during 2011/ 2012 and 2012/2013 season.

No.	2011/ 2012 season			2012/ 2013 season		
	Race group	No. of isolates	Frequency %	Race group	No. of isolates	Frequency %
1	BB	7	8.13	BB	14	11,38
2	ST	5	5.61	TT	7	4,88
3	DB	3	4.41	LF	4	3,52
4	LB	3	4.41	BH	3	2,44
5	LG	3	4.41	BJ	3	2,44
6	BC	2	2.32	BL	3	2,44
7	BJ	2	2.32	BR	3	2,44
8	BK	2	2.32	GB	3	2,44
9	GH	2	2.32	GC	3	2,44
10	GJ	2	2.32	GD	3	2,44
11	GT	2	2.32	LC	3	2,44
12	LT	2	2.32	MH	3	2,44
13	NK	2	2.32	QC	3	2,44
14	QB	2	2.32	TC	3	2,44
15	SC	2	2.32	TK	3	2,44
16	TC	2	2.32	LG	2	1,63
17	TT	2	2.32	LJ	2	1,63
18				NT	2	1,63
19				QD	2	1,63
20				RH	2	1,63
21				RS	2	1,63
22				SK	2	1,63
23				TB	2	1,63
Total	45			65		
Others	41			58		
Total	86			123		

Virulence frequencies:

virulence frequencies of identified races indicated that the stem rust resistance genes *Sr 5,21,9e,7b,8a,9g,36,9b,17,9a,9d,10,Tmp* and *MCN* were susceptible against the tested race during the two seasons of study (Tables 6 and 7). While, the stem rust resistance genes *Sr24, 36,38* and *31* were resistant against the tested races. They proved to be important genes for breed resistant wheat varieties. On the other hand, race TTTTK was the most virulent pathotype to stem rust *Sr31*.Race BBBBB was a virulent for all tested Sr genes. Belayneh *et al.,* (2009), reported

similar finding, McNair 701 (SrMcN) was susceptible to all of the races identified. In the same way, according to the same authors seven stem rust resistance genes; Sr9a, Sr9g, Sr10, Sr7b, Sr9b, Sr9d and Sr8b were ineffective for more than 96% of the collected isolates.

Table (6): Virulence spectrum (based on ineffective Sr genes) of races of *Puccinia graminis f. sp. tritici* identified in Egypt during 2011/2012

No.	Pathotype (Pgt)	Virulance	Vir. Fre. %	No.	Pathotype (Pgt)	Virulance	Vir. Frey. %
1-	BBBBC	MCN	1.16	44-	KTMSB	21,9e,7b,11,6,8a,9g,36,17,a,9d,10, MCN	1.16
2-	BBBJB	9a	1.16	45-	L JTSJ	5,6,8A,8B,9B,30,17,9D,,10,31,38	1.16
3-	BBBLB	9d,10	1.16	46-	LBCQB	5,17,9A,9B	1.16
4-	BBBLF	30,17	1.16	47-	LBDGB	5,30,9D	1.16
5-	BBFBB	9a,38,MCN	1.16	48-	LBKQD	5,9b,30,17,9A,9D,38	1.16
6-	BBHSB	36,9b,9a	1.16	49-	LGGLB	5,6,9a,8d	1.16
7-	BBQLB	6,8a.10	1.16	50-	LGHQB	5,6,9a,17,9a,8d	1.16
8-	BCBFC	11,6a,9a	1.16	51-	LGQNF	5,6,36,9b,9a,10,38,MCN	1.16
9-	BCMTC	9g,10,Tmp.MCN	1.16	52-	LKSSF	5,6,8A,9G,36,9B,30,9A,9,D,10,38, mcn	1.16
10-	BDFBD	8a,30,17,38	1.16	53-	LLHDB	5,11,9B,17,10	1.16
11-	BGMDB	6,36,17,10	1.16	54-	LTHNC	5,11,6,8A,9G,9b,17,9a,10, MCN	1.16
12-	BJBDB	9b,17,9a,9d,10	1.16	55-	LTKTD	5,6,11,8a,9g,9b,30,17,9a,9d,10,Tmp,38	1.16
13-	BJHSD	9g,36,17,9a,9d,10,Tmp,MCN	1.16	56-	NGRBB	5,9e,6,36,9b,17	1.16
14-	BKCSD	6,8a,9b,17,9a,9d,10,38	1.16	57-	NKMPB	5,9e,6,8a,9g,36,17,9a,10,Tmp	1.16
15-	BKTLK	6,8a,9g,17,9a,8d,10,38	1.16	58-	NKRLB	5,9e,6,8a,9f,36,9b,17,9a	1.16
16-	BMSLP	11,9g,36,9b,30,9a,24,MCN	1.16	59-	NRGQC	5,9e,11,9g,9b,9a,9d,MCN	1.16
17--	BNKGF	11,8a,9b,30,17,9d,38,MCN	1.16	60-	PDTSF	5,9e,6,36,9b,36	1.16
18-	BQBLB	6,8a,9g,36,9b,30,17,9a,31,38 ,MCN	1.16	61-	QBGLB	5,21,9b,9a	1.16
19-	CFCJC	7b,11	1.16	62-	QBHGB	5,21,9b,17,9d	1.16
20-	CLBBB	7b,8a,9g,17,9d,10,MCN	1.16	63-	QCDNC	5,21,9g,30,9a,10,MCN	1.16
21-	DBBBC	9e,MCN	1.16	64-	QFTHC	5,21,8a,9g,8b,9b,30,17,9d,Tmp,MCN	1.16
22-	DBJGF	9e,8a,,30,38	1.16	65-	QHTHC	5,21,6,9g,8b,9b,30,17,9d,MCN	1.16
23-	DBKBD	9c,9b,30,17,36	1.16	66-	QKSDK	5,21,6,8a,9g,36,9b,30,10,30,38,MCN	1.16
24-	DCRTF	9e,9b,30,9d,38,MCN	1.16	67-	RCSND	5,21,7b,8b,30,9a,10,38	1.16
25	DFKRC	9e,8a,9g,9b,30,17,9a,9d,Tmp,MCN	1.16	68-	RGKSD	5,21,7b,6,9b,30,9a,9d,38	1.16
26	DCRTF	9e,9g,36,9b,30,17,9a,9d,38	1.16	69-	RSMLD	5,21,7b,11,6,8a,36,17,9a,38	1.16
27	DKTSB	9c,6,8a,9g,36,9b,30,17,9a,9d ,10	1.16	70-	RTTTF	5,21,7b,11,6,8a,9g,8b,9b,30,17,9a, 9d,10,Tmp,38,MCN	1.16
28	FBHQB	9e,7b,9b,17,9a,9d	1.16	71-	SCHDC	5,21,9e,9g,9b,17,10,MCN	1.16
29	FRRLD	9e,7b,11,6,9g,36,9b,17,9a,38	1.16	72-	SCTTB	5,21,9e,9g,36,9b,30,17,9a,9d,10,Tmp	1.16
30	GCFBC	21,6,8a,9d	1.16	73-	SJRBD	5,21,7b,6,8a,36,9b,17,38	1.16
31	GHBGD	21,9g,30,17,MCN	1.16	74-	SKKQD	5,21,9e,6,8a,9g,9b,30,17,9a,9d,38	1.16
32	GHTPB	21,6,9g,9d,38	1.16	75-	SNHQF	5,21,11,9e,8a,9b,17,9a,9d,38,MCN	1.16
33	GJBGB	21,6,8a,8b,9b,9a,MCN	1.16	76-	SRKQB	5,21,9a,11,6,9g,9b,30,17,9a,9d	1.16
34	GJQLC	21,11,6,8a,9g,9b,38,MCN	1.16	77-	STFTD	5,21,9e,11,6,8a,9g,30,17,9d,9b,10, Tmp,38	1.16
35	GNQMF	21,11, ,8a,8B,9b,Tmp,38,MCN	1.16	78-	STJNP	5,21,9e,11,6,8a,9g,9b,30,9a,10,24, 38,MCN	1.16
36	GTGBF	21,6,9g,8b,9,30,17,9a,10,Tmp	1.16	79-	STKSB	5,21,9e,11,6,8a,9g,9b,30,17,9a,9d,10	1.16
37	GTTST	21,11,6,8a,9g8b,9b,30,17,9a, 9d,10,31,38	1.16	80-	STMTF	5,21,9e,116,8a,9g,36,17,9a,9b,10,Tmp,38,MCN	1.16
38	JFHPC	21,9e,8a,9g,9b,17,9a,10,Tmp,MCN	1.16	81-	STSSF	5,21,9E,11,68a,9g,8b,9b,30,9a,9d,10,38,MCN	1.16
39	JCKSF	21,9e,9g,9b,30,17,9a,9d,10,38,MCN	1.16	82-	TCDSJ	5,21,9E,7b,9g,30,9a,9d,10,31,38,	1.16
40	JMKTD	21,9e,11,9g,9b,30,17,9a,9d,10,Tmp,38	1.16	83-	TCTDC	5,21,9e,7b,9g,8b,9b,30,17,10,MCN	1.16

41	KBSDB	21,9e,7b,8b,9b,30,10	1.16	84-	TSPSK	5,21,9e,7b,11,8a,8b,30,17,9e,8d,10 ,31,38,MCN	1.16
42	KKPDF	21,9e,7b,6,8a,9g,8b,30,17,10 ,38,MCN	1.16	85-	TTKTF	5,21,9e,7a,11,6,8a,9g,9b,30,17,9a, 9d,10,Tmp,38,MCN	1.16
43	KTMSB	21,9e,7b,11, 36,9b,30,17,9a,9d,10, Tmp,38,MCN	1.16	86-	TTTTK	5,21,9e,7b,11,6,8a,9g,8b,9b,30,17, 9a,10,Tmp,31,38,MCN	1.16

Table (7): Virulence spectrum (based on ineffective Sr genes) of races of *Puccinia graminis f. sp. tritici* dentified in Egypt 2012/2013

No.	Pathotype (Pgt)	Virulance	Vir. Fre. %	No.	Pathotype (Pgt)	Virulance	Vir. Fre. %
1-	BBBBB	-	0.81	61-	LGLHC	5,6,369d,MCN	0.81
2-	BBBBC	MCN	0.81	62-	LHTTC	5,6,36,9b,30,17,9a,9d,10,Tmp	0.81
3-	BBBGC	10,Tmp, MCN	2.43	63-	LJCBC	5,6,8a,9b,MCN	0.81
4-	BBBLC	9d, Tmp, MCN	0.81	64-	LJGMC	5,6,8a,9b,9a,Tmp,MCN	0.81
5-	BBBPC	36,30,17, MCN	0.81	65-	LKMFB	5,6,8a,9g,36,17,10,Tmp	0.81
6-	BBBQB	9a,9d, MCN	0.81	66-	LTQGC	5,11,6,8a,9g,36,9b,17,10,MCN	0.81
7-	BBBQF	9a,9d,38	0.81	67-	MBKRC	5,7b,9b,30,17,9a,9d,Tmp,MCN	0.81
8-	BBBSC	9a,9d,10,35,MCN	0.81	68-	MQLSC	5,7a,11,6,9g,36,9a,9d,10,MCN	0.81
9-	BBGGC	30,10,MCN	0.81	69-	MHJRC	5,7a,6,9b,30,9a,9d,Tmp,MCN	0.81
10-	BBLRB	36,9a,9d,17,24,31,M CN	0.81	70-	MHMRC	5,7a,6,36,9a,9d,Tmp,MCN	0.81
11-	BBLTC	36,9a,9d,10,Tmp,MCN	0.81	71-	MHSTC	5,7a,36,9b,30,9a,9d,10,Tmp,MCN	0.81
12-	BBMRC	36,17,9a,9d,Tmp,MCN	0.81	72-	NBLGC	5,36,9d,MCN	0.81
13-	BCHRB	9g,9b,9a,9d,Tmp,	0.81	73-	NDGKC	5,9e,8a,9d,,10,Tmp,MCN	0.81
14-	BDLBC	8a,36,MCN	0.81	74-	NDLTC	5,9d,36,9a,9d,10,Tmp,MCN	0.81
15-	BGBBB	6	0.81	75-	NFHRB	5,9e,9G,9B,9a,9d,Tmp,	0.81
16-	BGLRC	6,36,9a,9d,Tmp,MCN	0.81	76-	NT SSB	5,9e,11,6,8a,9g,9a,9d,30,	0.81
17--	BHBSC	6,9a,9d,10,MCN	0.81	77-	NTSTF	5,9e,,11,6,8a,9g,9a,9d,10,Tmp,38,M CN	0.81
18-	BHNDC	6,36,30,10,MCN	0.81	78-	PJQSC	5,9e,7b,6,8a,36,9b,17,9a,9d,10,MCN	0.81
19-	BDQHB	8a,36,9b,17,10	0.81	79-	LGDBC	5,6,30,MCN	0.81
20-	BHCTC	6,17,9a,9d,10,17,MCN	0.81	80-	QBLBB	5,21,7b,36	0.81
21-	BJMPC	6,8a,36,17,9a,10,Tm p,MCN	1.62	81-	QCLBC	5,21,7b,9g,36,MCN	0.81
22-	BJQGC	6,36,9b,17,9d,MCN	0.81	82-	QDBMC	5,21,7b,8a,9a,Tmp,MCN	1.62
23-	BKDRB	6,8a,9g,30,9a,9d,Tmp	0.81	83-	QFJHB	5,21,7b,8a,9g,,9b,30,9d,	0.81
24-	BKQLB	6,8A,9g,36,9b,17,9a,	0.81	84-	QKBTC	5,21,7b,6,8a,9g,9a,9d,10,Tmp,MCN	0.81
25	BLBSC	11,9a,9d,10,MCN	0.81	85-	QMTTC	5,21,7b,11,9g,36,9b,30,17,9a,9d,10, Tmp,MCN	0.81
26	BLDCC	11,30,Tmp,MCN	0.81	86-	QRLGB	5,21,7b,11,6,9g,36,9d,	0.81
27	BLLBC	11,36,MCN	0.81	87	QSQHF	5,21,7b,11,6,8a,36,9b,17,9d,38,MCN	0.81
28	BRLLC	11,6,9g,36,9a,MCN	0.81	88	RFTTC	5,21,7b,8a,9g,36,9b,30,17,9a,9d,10, Tmp,MCN	0.81
29	BRQCB	11,6,9g,36,9b,17,Tmp,	0.81	89	RHCTB	5,21,7b,6,17,9a,9d,10,Tmp,	0.81
30	BRRPC	11,6,9g,36,9b,17,9a, 10,Tmp,MCN	0.81	90	RHTTC	5,21,7b,6, 36,9b,30,17,9a,9d,10,Tmp, MCN	0.81
31	BNBBC	11,8a,MCN	0.81	91	RJRTC	5,21,7b,6,8a,36,9b,17,9a,9d,Tmp,M CN	0.81
32	BSBQC	11,6,8a,9a,9d,17,MCN	0.81	92	RSHRC	5,21,7b,11,6,8a,9b,9a,9d,Tmp,MCN	0.81
33	CBRSC	7b,36,9b,17,MCN	0.81	93	RSPCB	5,21,7b,11,6,8a,36,30,17,Tmp,	0.81

34	CCBHC	7b,9g,9d,MCN	0.81	94	SBTPN	5,21,9e,36,9b,30,17,9a,10,Tmp,24,38,	0.81
35	CDTMC	7b,8a,36,9b,30,17,9a ,Tmp,MCN	0.81	95	SHQTC	5,21,9e,6,36,9b,17,9a,9d,10,Tmp,M CN	0.81
36	CGBTC	7B,6,9A,9D,10,Tmp, MCN	0.81	96	SKQQB	5,21,9e,6,8a,9g,36,9b,17,9a,9b,Tm p	0.81

Table (7): Cont.

No.	Pathotype (Pgt)	Virulance	Vir. Fre. %	No.	Pathotype (Pgt)	Virulance	Vir. Fre. %
37	CQGTC	7b,11,6,9g,9b,9a,9d, 10,Tmp.MCN	0.81	97	SKTTC	5,21,9e,6,8a,9g,,36,9b,30,17,9g,9d, 10,Tmp, MCN	0.81
38	DPPQC	9e,11,8a,9g,36,9b,17 ,MCN	0.81	98	SPNTC	5,21,9e,11,8a,9g,36,30,9a,9d,10,Tm p,MCN	0.81
39	DTRPM	9e,11,6,8a,9g,36,9b, 17,24,MCN	0.81	99	TDLGM	5,21,9e,7b,8a,36,9d,24,MCN	0.81
40	FCTTC	9E,7B,9g,36,9b,30,1 7,9a,9d,10,Tmp,MCN	0.81	100	TFTHC	5,21,9e,7b,8a,7b,36,9b,30,17,9d,M CN	0.81
41	FCTTC	9E,7B,9g,36,9b,30,1 7,9a,9d,10,Tmp,MCN	0.81	101	THRTC	5,21,9e,7b,8a,9g,36,9b,17,9a,9d,10, Tmp,MCN	0.81
42	FDBDB	9e,7b,8a,Tmp	0.81	102	TJPTC	5,21,9e,7b,6,8a,36,30,17,9a,9d,10,T mp, MCN	0.81
43	GBBLC	21,9a,MCN	0.81	103	TKRTC	5,21,9e,7b,6,8a,9g,36,9b,17,9a,9d,9 10,Tmp,MCN	1.62
44-	GBLFC	21,36,10,Tmp,MCN	0.81	104	TKTPC	5,21,9e,7b,6,8a,9g,36,9b,30,17,9a,1 0,Tmp,MCN	0.81
45-	GCLQC	21,9g,36,9a,9b,17,M CN	0.81	105	TKTTC	5,21,9e,7b,6,8a,9g,36,9b,30,17,9a,9 d,10,Tmp,MCN	0.81
46-	GCTTC	21,9g,36,9b,30,17,9g ,9d,10,Tmp,MCN	0.81	106	TTRTC	5,21,9e,7b,11,6,8a,9g,36,9b,17,9a,9 d,10,Tmp,MCN	0.81
47-	GDBBC	21,8a,MCN	0.81	107	TTSGC	5,21,9e,7b,11,6,8a,9g,36,9b,30,9d, MCN	0.81
48-	GDQRM	21,8a,36,9b,17,9a,9d ,Tmp,24,MCN	0.81	108	TTTPB	5,21,9e,7b,11,6,8a,9g,36,9b,30,17,9 a,10,Tmp	0.81
49-	GHLQD	21,6,36,9a,9d,17,24, 38,MCN	0.81	109	TTTTC	5,21,9e,7b,11,6,8a,9g,36,9b,30,17,9 a,9d,10,Tmp,	1.62
50-	GJBBC	21,6,8a,MCN	0.81	110	TTTTF	5,21,9e,7b,11,6,8a,9g,36,9b,30,17,9 a,9d,10,Tmp,38,MCN	0.81
51-	HGLDC	21,6,36,10,MCN	0.81	111	TDLGM	5,21,9e,7b,8a,36,9d,24,MCN	0.81
52-	HTCTC	21,11,6,8a,9g,17,9a, 9d,10,Tmp,MCN	0.81	112	TFTHC	5,21,9e,7b,8a,9g, 36,9b,30,17,9d, MCN	0.81
53-	KFKTC	21,9e,7b.8a,9g,9b,30 ,17,9a,9d,10,Tmp,M CN	0.81	113	THRTC	5,21,9e,7b,6,36,9b,17,9a,9d,10,Tm p,MCN	0.81
54	KKTTC	21,9E,7B,6,8A,9G,36 ,9b,30,17,9a,9d,10,T mp,MCN	0.81	114	TJPTC	5,21,9e,7b,6,8a,36,30,17,9a,9d,10,T mp,MCN	1.62
55	LCBQC	5,9g,36,9b,17,MCN	0.81	115	TKRTC	5,21,9e,7b,6,8a,9g,36,9B,17, 9a,9d,10,Tmp,MCN	2.43
56	LCQHC	5,36,9b,17,9d,MCN	0.81	116	QFJHB	5,21,7b,8,a,9g,,9b,30,9d,	0.81
57	LCRNC	5,9g,36,9b,17,9a,10, MCN	0.81				
58	LFDMC	5,8a,9g,30,9g,Tmp,M	0.81				

		CN					
59	LFQRB	5,8a,36,9b,17,9a,9d, Tmp	1.62				
60	LGDBC	5,6,30,MCN	0.81				

Effectiveness of stem rust resistance gene(s) (*Sr,s*) at seedling stage.

It was evident that the majority of the resistance genes were found ineffective against most of the isolates tested in this study during the two seasons. Data in (Table 8) reveled that *Sr24, Sr31* and *Sr7b* were resistant to most races of *Puccinia graminis* f. sp. *tritici* which showed (95.34,87.21 and 81.40%) efficacy, whereas *sr 17* and *sr 9a* were the lowest efficacy during 2011/2012season. Meanwhile, *Sr31*, *Sr24* and *Sr38* posses a high level of resistance (100, 98.37 and 91.86%) efficacy in 2012/2013 season. On the other hand *Sr36* and *Sr9b* were ineffective. The rest of tested *Sr* genes were intermediate. Similar results were recorded by Youssef, *et al* (2012), he reported that *Sr31*, *Sr24* and *Sr38* were effective for most identified races. EL-Shamy *et al.,* 2012 found that *Sr*-genes *24, 31*and *36* had the highest mean efficacy percentage against all the identified isolates during the two growing seasons releasing 100.00% efficacy. Therefore, these resistance genes (*Sr24, Sr31, Sr38,* and *Sr7b* could be exploited in wheat breeding programs for producing new resistant cultivars.

Table (8): Virulence frequency percentage *of Puccinia graminis* f.sp.*tritici* isolates against Stem rust monogenic lines (Sr's) and gene efficacy during the two growing seasons.

No.	Sr's	2011/2012		2012/2013	
		No.of virulent isolates	Gene efficacy (%)	No.of virulent isolates	Gene efficacy (%)
1	5	38	55.81	57	46.34
2	21	42	51.17	65	52.84
3	9e	39	54.66	85	69.10
4	7b	16	81.40	75	60.97
5	11	27	68.61	94	76.42
6	6	45	47.68	61	49.59
7	8a	41	52.33	70	56.91
8	9g	46	46.52	47	38.21
9	36	39	54.66	37	30.08
10	9b	55	36.05	53	43.08
11	30	4	46.51	75	60.97
12	17	57	33.72	72	58.53
13	9a	57	33.72	39	31.70
14	9d	39	54.66	37	30.08
15	10	44	48.83	50	40.65

16	Tmp	21	75.59	51	41.46
17	24	4	95.34	121	98.37
18	31	11	87.21	123	100
19	38	42	51.17	113	91.86
20	Mcn	42	51.17	25	20.32

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السلالات الفسيولوجية والتنوع فى القدرة المرضيه لفطر صدا الساق فى القمح فى مصر خلال موسمى 2012/2011و 2013/2012

نبيلة امين الشريف وجمالات عبد العزيز هيرماس ومحمد عبد القادر حسن وسميه تهامى

قسم بحوث أمراض القمح . معهد بحوث أمراض النباتات مركز البحوث الزراعية . جيزة . مصر

الملخص العربي

يعد مرض صدا الساق على القمح المتسبب عن الفطر *بكسينيا جرامينيزتريتيسای* من اهم الامراض التى تدمر محصول القمح فى العالم وفى مصر. يمكن ان يحدث فقد كامل لمحصول القمح خاصة فى سنوات الوبائية. هذه الدراسة اجريت بهدف دراسة التنوع فى القدرة المرضية للفطر *بكسينيا جرامينيزتريتيسای* فى اماكن عديدة وكذلك دراسة كفاءة جينات المقاومة فى طور البادرة فى مصر.تم جمع عينات من صدا الساق من مناطق زراعة القمح وكذلك مصائد الاصداء من ثلاثة مواقع فى موسم 2012/2011 (سدس, الشرقية والنوبارية) بينما فى موسم 2013/2012 تم تجميع العينات من ستة مواقع وهى (سدس, الشرقية ,النوبارية, الجيزة , تاج العز وسخا). نتائج هذا البحث اعتمدت على تعريف السلالات من خلال عدوى عينات صدا الساق على مجموعة من الاصناف المفرقة, التوصيف المظهرى للفطر *بكسينيا جرامينيزتريتيسای* خلال موسم 2012/2011 نتج عنه تعريف 86 سلالالة ناتدة من 22 عينة ناجحه كلا منهم بنسبة تكرار 1.16% . السلالة (BBBBC) غير قادرة على كسر ايا من جينات المقاومة ما عدا (Sr24) على الجانب الاخر تحليل السلالات فى الموسم 2013/2012 نتج عنه تعريف 123 سلالة تراوح تكرار كلا منه من 0.81% وحتى 2.43%. كما أوضحت النتائج ان جين المقاومة *Sr 24* % كان الأكثر كفاءة متبوعاً ب *Sr 38* و*Sr 31* ولذلك فإن استخدام تلك الجينات وادخالها في اصناف القمح له اهمية كبيرة في اعطائها صفة المقاومة المستديمة ضد مرض صدأ الساق في مصر.

أسماء السادة المحكمين

أ.د/ محمد أمين زايـــــد كلية الزراعة – جامعة الزقازيق

أ.د/ مجدى السيد مهدى كلية الزراعة – جامعة المنوفية