PATHOGENIC SPECIALIZATION AND PATHOTYPE DISTRIBUTION OF *PUCINIA GRAMINIS TRITICI* IN EGYPT IN 2005/2006 AND POSTULATED GENES OF RESISTANCE IN SOME WHEAT GENOTYPES

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Abstract

Wheat stem rust surveys gave evidence to the presence of nine and sixteen physiologic races in 2005 and 2006 growing season, respectively. In the first season, race 34 was the predominant (51.98%) followed by race 11 (25.25%). Two-hundred and two virulence phenotypes were detected among these races. The most effective resistance genes *were Sr 26, 29, 11, 31, 35,* and *9e.* In the second season, race 15 was the predominant (27.26%) followed by race 11 (24.23%). Sixty-six virulence phenotypes were detected under these races. *Sr26* was the most effective gene. Most of these genes were postulated to be present, either alone or in combinations, in the genotypes tested.

INTRODUCTION

Stem rust of wheat caused by *Puccinia graminis* f. sp. *tritici*, is one of the major diseases of wheat and barley and, therefore, a potential threat to the world food supply.

Surveys of pathogenic variability in the *Pgt* have been conducted in most of the major wheat growing regions of the world. Such surveys have monitored the pathogenicity of *Pgt* with respect to resistance genes effective through the entire growth cycles of the host (seedling resistance genes). Studies of pathogenic variability in *Pgt* were the first to demonstrate the existence of physiologic races in a rust fungus (Stakman and Piemeisel 1917). Isolates of the pathogen were found to differ in ability to infect a set of wheat genotypes, known as differentials, and those isolates with the same pathogenic attributes on the set of differentials were referred to as a physiologic race. Such races, also referred to as strains or pathotypes, are now known to exist in all cereal rust fungi, and monitoring their occurrence and distribution in annual surveys is an important part of many efforts to develop cultivars with rust resistance.

The gene- for –gene relationship (Flor, 1971) makes it possible to postulate the gene(s) for resistance to rusts in host lines of unknown genotypes. Data for infection types (ITs) of the host: pathogen interaction have been used to postulate the genes present in wheat cultivars for leaf rust and stem rust resistance (McVey, 1992, McVey and long 1993 and Singh *et al.,* 1999).

The main objectives of the present work were to characterize the virulences using the *Pgt* populations in Egypt in 2004/2005 and 2005/2006 growing seasons, to the North American *Pgt* Differentials (Roelfs and Martens, 1988) and other selected monogenic lines of wheat to provide information on the frequency of virulence for these *Sr* genes and to postulate the stem rust resistance genes in some genotypes of wheat which can frequently be used as donors of other agronomic and quality characteristics.

MATERIALS AND METHODS

This investigation was carried out at Wheat Diseases Dept., Plant Pathol. Res. Institute, ARC, Giza, Egypt during 2004/2005 and 2005/2006 growing seasons.

Sample collection and storage:

Samples of stem rust were collected from experimental plots, rust trap nurseries, and from farmers fields during regular surveys that involved random crop inspection every 20-30 km along predetermined routes. Rust samples were stored in paper envelopes and dried at room temperature overnight. The samples were then placed in glycine envelops and stored in a desicator in the refrigerator at 3°C. Rust isolates maintained good viability under these conditions for up to 6 month.

Differential genotypes and pathotype nomenclature:

Urediospores from each sample were transferred, purified, and increased onto the primary leaves of the highly susceptible variety *Triticum spelta* wheat seedlings, in 10-cm diameter pots. The seedlings were inoculated by transferring the inoculum from dried leaves samples to primary leaves with a spatula and incubated overnight in a chamber at 100% RH and 20 to 25°C. The plants were then placed in the greenhouse where daily temperature varied between 20 and 25°C. One single- uredinial isolate per sample collection was evaluated for virulence phenotype. A mixture of urediospore-talcum powder (1: 20 v/v) of each pure isolate was dusted onto the primary leaves of 7- day old seedlings of the near-isogenic series of stem rust differentials (Tables 1 and 2), by using a baby cyclone (Tervet and Cassell, 1951). As previously described, the inoculated plants were set in a darkened dew chamber overnight and then transferred to the greenhouse benches. After 12 days, infection types (ITs) of each near- isogenic line were recorded as either low (o, ,, 1, 2 and x) or high (2 and 3). For the pathotype identification, both the standard method and *Pgt* –code nomenclature for *Puccinia graminis* f.sp. *tritici* were followed using the standard differential varieties and set of 20 monogenic lines with single stem rust resistance genes (Roelfs and Martens, 1988), shown in Table (1). The isolates were used for virulence analysis, using 37 monogenic lines (Table 2). The avirulence /virulence formula suggested by Green

(1966) was used to describe the tested isolates. The efficacy of the *Sr* genes were determined according to their virulence frequency as follows:

$$\text{Gene efficacy\%} = \frac{\text{Total No. of tested isolates-No of virulent isolates}}{100}$$

Gene postulation:

The method adapted by Statler (1984) was applied to determine the probable resistance genes of 11 commercial wheat cultivars. The infection types (ITs) of the 11 wheat cultivars with unknown resistance genes were compared to the infection types of the 37 monogenic lines each carrying a single known gene for resistance to stem rust.

Table 1. *Pgt*-code for the 20 *Pgt* differential hosts for *Puccinia graminis* f. sp. *tritici* in ordered subsets of five.

Pgt Code	Subset[a]	Infection type produced on host lines with *Sr* genes			
	1	5	21	9e	7b
	2	11	6	8a	9g
	3	36	9b	30	17
	4	9a	9d	10	TMP
	5	7a	8d	13	15
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

[a] *Pgt*-code consists of the designation for subset 1 followed by that for subset 2, etc. For example, race TTTTT is virulent (high infection type) on all 20 differential hosts and race DCLGS is virulent on differential hosts with *Sr9e, 9g, , 36,*and *9d,* and is avirulent on *Sr15* . Low and high infection types indicate an incompatible and a compatible host-pathogen interaction, respectively (Roelfs and Martens 1988).

Table 2. Wheat Stem Rust Resistance Genes#: Source, Gene Location, and Tester Lines (Roelfs *et al.*, 1992)

No	*Sr* gene	Genome location	Original source	Tester
1	5	6DS	Reliance	ISr5-Ra
2	6	2DS	Red Egyptian	ISr6Ra
3	7a	4BL	Kenya117A	Line G sel
4	7b	4BL	Marquis	ISr7b-Ra
6	8a	6AS	Red Egyptian	ISr8-Ra
7	8b	6AS	Barleta Benvenuto	Barleta Benvenuto
8	9a	2BL	Red Egyptian	ISr9a-Ra
9	9b	2BL	Kenya117A	W2691Sr9b
10	9d	2BL	*T. turgidum* (Yaroslav emmer)	ISr9d Ra
11	9e	2BL	*T. turgidum* (Vernal emmer)	Vernstein
12	9g	2BL	Lee	CnSSr9g
13	10		Egypt NA95	W2691Sr10
14	11	6BL	Lee	ISrl1-Ra
15	13	6AL	*T. turgidum* (Kaphli emmer)	W2691Srl3
16	15	7AL	Norka	W2691Srl5
17	16	2BL	Thatcher	ISr16-Ra
18	17	7BL	*T. turgidum*? (Yaroslav emmer)	CS (Hope7B)
19	21	2AL	*T. monococcum*	Einkorn
20	22	7AL	*T. monococcum*	SwSr22T.B.
21	23	2BS	Exchange	Exchange
22	24	3DL	*Thinopyron ponticum*	BtSr24Agt
23	26	6AL	*Thinopyron ponticum*	Eagle (Australian)
24	28	2BL	Kota	W2691Sr28Kt
25	29	6DL	Etiole de Choisy	PusaSr29Edch
26	30	5DL	Webster	BtSr30Wst
27	31	1BL	Secalis cereale (Imperial rye)	Line ESr31Kvz
28	32	2A, 2B	*T. aestivum speltoides*	ER5155
29	33	1DL	*T. tauschii*	TetraCanthatch/T. tauschii
30	34	2A,2B	*T. comosa*	Compair
31	35	3AL	*T. monococcum*	Mq(2)5xG2919
32	36	2BS	*T. timopheevi*	W2691SrTt-1
33	37	4AL	*T. timopheevi*	W2691SrTt-2
34	Dp-2		*T. turgidum* (Golden Ball)	Media Ap9d
35	Tmp	4B	Triumph 64	Triumph 64
36	Tt-3		*T. timopheevi*	Fed *2/SrTt-3
37	Wld 1		Waldron	BtSrWldWld

Roelfs *et al.*, 1992

RESULTS

Race identification:

Data in Tables (3, 4 & 5) present the prevalent physiologic races in Egypt during 2004/2005 and 2005/2006 growing seasons expressed in both traditional and *Pgt* – code Nomenclature System. Data in Table (3) indicated that 202 isolates represented 9 physiologic races in the first season, whereas 66 isolates belonging to 16 physiologic races were identified in the second season. Races 34 and 11 in the first season, and 15, 11, and 189 in the second season, were the most frequent representing 51.89%, 25.25% and 27.26%, 24.23% and 22.72%, respectively (Table 3). In the two seasons, race 11 was the most dominant. Table (4) showed that, 177 virulence phenotypes of *Pgt* were identified from 202 isolates collected in 2004/2005. Out of them, the virulence phenotypes RKTTS (3.38% frequency), RKTTT (2.25%) were the most frequent followed by virulence phenotypes RKTTP, RKSTT, and TKTSS (1.96%, each). Virulence phenotypes RKSSS, RKTFT, RKTHN, RKTIS, RKTSN, RKTSP, RKTTN, RTTCS, TKTIQ, TKTKS, TKTKT, and TKTTN were found twice (1.12%, each), while the least virulence phenotypes (0.56%, each) occurred most frequently. In 2005/2006, 53 virulence phenotypes were identified among 66 collected isolates (Table, 5). The most frequent virulence phenotype was TTTTT (13.65%), followed by virulence phenotypes TKKTT, TKTTT, TTRTT, and TTTTR (3.03%, each). The rest of pathotypes occurred at 1.52%frequency each.

Table 3. No. of isolates and frequency % of *Puccinia graminis* f. sp. *tritici* physiologic races identified in Egypt during 2004/2005 and 2005/2006 growing seasons.

No	Standard physiologic race	2004/2005		2005/2006	
		No of isolates	Frequency%	No of isolates	Frequency%
1	11	51	25.25	16	24.23
2	15	3	1.49	18	27.26
3	17	6	2.96	-	-
4	19	7	3.47	3	4.55
5	20	-	-	1	1.52
6	21	6	2.96	-	-
7	22	-	-	2	3.02
8	34	105	51.98	-	-
9	39	11	5.45	1	1.52
10	40	-	-	1	1.52
11	42	5	2.48	-	-
12	59	-	-	1	1.52
13	60	-	-	1	1.52
14	88	-	-	1	-
15	89	-	-	1	1.52
16	98	-	-	1	1.52
17	111	-	-	2	1.52
18	122	-	-	1	1.52
19	158	-	-	1	1.52
20	189	8	3.96	15	22.72
Total		202	100	66	100

Table 4. Virulence phenotypes of *Puccinia graminis* f. sp. *tritici* (*Pgt*- code) identified in Egypt during 2004/2005 and their frequencies using the 20 North American Differential hosts

No	Pathotype(*Pgt*#)	No of isolates	Freq.%	No	Pathotype(Pgt)	No of isolates	Freq. %	No	Pathotype (*Pgt*)	No of isolates	Freq. %
1	CIBFF	1	0.56	60	RISSS	1	0.56	119	RMSSQ	1	0.56
2	CCLBC	1	0.56	61	RISTL	1	0.56	120	RSSTS	1	0.56
3	CHTID	1	0.56	62	RISTN	1	0.56	121	RTISN	1	0.56
4	CKKIG	1	0.56	63	RISTT	1	0.56	122	RTKKP	1	0.56
5	CCKTN	1	0.56	64	RITFS	1	0.56	123	RTRPN	1	0.56
6	CKRKS	1	0.56	65	RITTT	1	0.56	124	RTSKS	1	0.56
7	CKTIR	1	0.56	66	RKBDC	1	0.56	125	RTSQI	1	0.56
8	FKTQD	1	0.56	67	RKBKS	1	0.56	126	RTSRS	1	0.56
9	GKBBC	1	0.56	68	RKBNP	1	0.56	127	RTSST	1	0.56
10	GMTKS	1	0.56	69	RKFKD	1	0.56	128	RTSTN	1	0.56
11	HBBBB	1	0.56	70	RKFST	1	0.56	129	RTTCS	2	1.12
12	HCCIS	1	0.56	71	RKIIS	1	0.56	130	RTTNF	1	0.56
13	HCPSB	1	0.56	72	RKISN	1	0.56	131	RTTRS	1	0.56
14	HCTSS	1	0.56	73	RKITN	1	0.56	132	RTTST	1	0.56
15	HHTID	1	0.56	74	RKLTL	1	0.56	133	RTTTN	1	0.56
16	HHTTN	1	0.56	75	RKPKS	1	0.56	134	RTTTS	1	0.56
17	HITKI	1	0.56	76	RKQDI	1	0.56	135	TCTCI	1	0.56
18	HKHKN	1	0.56	77	RKRDD	1	0.56	136	TISTS	1	0.56
19	HKIDN	1	0.56	78	RKRSP	1	0.56	137	TITTP	1	0.56
20	HKISF	1	0.56	79	RKSFT	1	0.56	138	TKFRC	1	0.56
21	HKKTN	1	0.56	80	RKSGS	1	0.56	139	TKGST	1	0.56
22	HKQKN	1	0.56	81	RKSIS	1	0.56	140	RTTTS	1	0.56
23	HKRSP	1	0.56	82	RKSKD	1	0.56	141	TKITT	1	0.56
24	HKTIK	1	0.56	83	RKSKI	1	0.56	142	TKKST	1	0.56
25	HKTRS	1	0.56	84	RKSKP	1	0.56	143	TKSDN	1	0.56
26	HKTTB	1	0.56	85	RKSKS	1	0.56	144	TKSFS	1	0.56
27	HRTRF	1	0.56	86	RKSSN	1	0.56	145	TKSGN	1	0.56
28	HTRIN	1	0.56	87	RKSSS	2	1.12	146	TKSGT	1	0.56
29	IGSQL	1	0.56	88	RKSTT	3	1.69	147	TKSII	1	0.56
30	ITSKT	1	0.56	89	RKTDN	1	0.56	148	TKSIK	1	0.56
31	KINIP	1	0.56	90	RKTFT	2	1.12	149	TKSIS	1	0.56
32	KKSKN	1	0.56	91	RKTGS	1	0.56	150	TKSSN	1	0.56
33	LBBBC	1	0.56	92	RKTHN	2	1.12	151	TKSSS	1	0.56
34	LKSID	1	0.56	93	RKTHS	1	0.56	152	TKSTK	1	0.56
35	MIKDT	1	0.56	94	RKTIG	1	0.56	153	TKTDN	1	0.56
36	MKTST	1	0.56	95	RKTIN	1	0.56	154	TKTIQ	2	1.12
37	MKTTF	1	0.56	96	RKTIS	2	1.12	155	TKTIT	1	0.56
38	MKTTS	1	0.56	97	RKTKB	1	0.56	156	TKTKF	1	0.56
39	PKKPS	1	0.56	98	RKTKP	1	0.56	157	TKTKS	2	1.12
40	PKKSQ	1	0.56	99	RKTKP	1	0.56	158	TKTKT	2	1.12
41	PKTSS	1	0.56	100	RKTKR	1	0.56	159	TKTND	1	0.56
42	QHSHS	1	0.56	101	RKTKS	1	0.56	160	TKTSN	1	0.56
43	QKRPQ	1	0.56	102	RKTQD	1	0.56	161	TKTSS	3	1.69
44	QKSTP	1	0.56	103	RKTQT	1	0.56	162	TKTST	1	0.56
45	QKTGS	1	0.56	104	RKTRN	1	0.56	163	TKTTD	1	0.56
46	QTSIP	1	0.56	105	RKTSD	1	0.56	164	TKTTF	1	0.56
47	QTTQI	1	0.56	106	RKTSF	1	0.56	165	TKTTI	1	0.56
48	RBBBD	1	0.56	107	RKTSN	2	1.12	166	TKTTN	2	1.12
49	RBDDD	1	0.56	108	RKTSP	2	1.12	167	TKTTP	1	0.56
50	RCRTT	1	0.56	109	RKTSS	1	0.56	168	TKTTS	1	0.56
51	RCTTS	1	0.56	110	RKTST	1	0.56	169	TNCKK	1	0.56
52	RCTTT	1	0.56	111	RKTTD	1	0.56	170	TRSTQ	1	0.56
53	RFRSD	1	0.56	112	RKTTF	1	0.56	171	TTRNE	1	0.56
54	RHFII	1	0.56	113	RKTTI	1	0.56	172	TTSTS	1	0.56
55	RHIKP	1	0.56	114	RKTTL	1	0.56	173	TTTKI	1	0.56
56	RHTKF	1	0.56	115	RKTTN	2	1.12	174	TTTSP	1	0.56
57	RHTKI	1	0.56	116	RKTTP	3	1.69	175	TTTSS	1	0.56
58	RHTST	1	0.56	117	RKTTS	6	3.38	176	TTTTD	1	0.56
59	RISKS	1	0.56	118	RKTTT	4	2.25	177	TTTTP	1	0.56

Pgt–code according to Roelfs and Martens, 1988.

Table 5. Virulence phenotypes of *Puccinia graminis* f. sp. *tritici* (*Pgt*- code) identified in Egypt during 2005/2006 and their frequencies using the 20 North American differential hosts

No	Pathotype (*Pgt#*)	No of isolates	Freq. %	No	Pathotype (*Pgt*)	No of isolates	Freq. %	No	Pathotype (*Pgt*)	No of isolates	Freq. %
1	BHRRR	1	1.52	19	RKKSB	1	1.52	37	TKTKT	1	1.52
2	BHBFC	1	1.52	20	RKPTT	1	1.52	38	TKTKR	1	1.52
3	BPRRD	1	1.52	21	RKRTT	1	1.52	39	TKTTT	2	3.03
4	CDJFD	1	1.52	22	RTPTT	1	1.52	40	TKTTR	1	1.52
5	HJIKI	1	1.52	23	RTTST	1	1.52	41	TMSPT	1	1.52
6	JTRTP	1	1.52	24	RTTTT	1	1.52	42	TPKTG	1	1.52
7	KTPRD	1	1.52	25	SCTTD	1	1.52	43	TPTTT	1	1.52
8	NBTCQ	1	1.52	26	SJKKT	1	1.52	44	TRTTP	1	1.52
9	PKTKK	1	1.52	27	SJTKC	1	1.52	45	TTFTT	1	1.52
10	PKTKT	1	1.52	28	STTTT	1	1.52	46	TTHJK	1	1.52
11	PKTTT	1	1.52	29	TDDTB	1	1.52	47	TTKTR	2	3.03
12	PTKKR	1	1.52	30	TFTTK	1	1.52	48	TTRRL	1	1.52
13	QHHTQ	1	1.52	31	TJTTT	1	1.52	49	TTRTP	1	1.52
14	QKTTG	1	1.52	32	TKCKM	1	1.52	50	TTRTT	2	3.03
15	QSTTT	1	1.52	33	TKJTT	1	1.52	51	TTTTP	1	1.52
16	RJRTH	1	1.52	34	TKKTT	2	1.52	52	TTTTR	2	3.03
17	RJTRT	1	1.52	35	TKKFT	1	1.52	53	TTTTT	9	13.65
18	RKKJB	1	1.52	36	TKTFR	1		Total		66	100

#Pgt-code according to Roelfs and Martens, 1988.

Geographic distribution:

The geographical distribution of the identified races in 2005/2006 are shown in Table (6). Race 11 had the highest dominance occurring in all sampled governorates followed by race 189 , then race 15 and race 19 . Races 22 and 111 had intermediate dominance, while the rest races had the least dominance each showing in one governorate only. The present data also, ravealed that, Beheira and Sharkia have the highest frequencies of isolates, being 33% and 26% of the total isolates, respectively. Kafr El-Sheikh has 21%, while Beni-Suief has 14% of the total identified isolates. Moreover, the highest number of physiologic races was identified in Beheira (50% of the total races), Beni-Suief (44%), and Kafr El-Sheikh (31%), then Alexandria and Sharkia (25%, each).

Table 6. Geographical distribution of *Puccinia graminis* f. sp. *tritici* physiologic races in Egypt during 2005/2006 growing season.

No	Standard physiologic race	No of isolates /Governorate				
		Beheira	Alexandria	Sharkia	Kafr El-sheikh	Beni-Suief
1	11	1	1	7	5	2
2	15	9	-	5	4	-
3	19	-	2	-	1	-
4	20	-	-	-	--	1
5	22	2	-	-	-	-
6	39	1	-	-	-	-
7	40	1	-	-	-	-
8	59	1	-	-	-	-
9	60	-	-	1	-	-
10	88	-	-	-	1	-
11	89	-	-	-	-	1
12	98	-	-	-	-	1
13	111	-	1	-	-	1
14	122	1	-	-	-	-
15	158	-	-	-	-	1
16	189	6	-	4	3	2
No of isolates		22	4	17	14	9
No of races		8	4	4	5	7

Virulence frequency:

Data in Table (7) show virulence frequency of the tested isolates as well as the efficacy of the 37 *sr* genes for these isolates. In 2004/2005, these data revealed that, four Sr genes had efficacy more than 80% *i.e.* Sr26 (92.08%), Sr29 (82.67%), Sr11 (82.18%), and Sr34 (82.18%). Four genes, Sr31 (77.72%), Sr35 (75.74%), Sr9e (74.26%), and Sr22 (70.79%), had efficacy of more than 70% against the tested isolates. In the second season, only Sr24 (87.88%) has efficacy of more than 80% and Sr26 (75.76%) has efficacy of more than 70%. If both seasons were considered, Sr26 could be regarded as the most effective gene of against the tested isolates.

Table 7. Virulence frequency% of *Puccinia graminis* f.sp.*tritici* isolates against 37 stem rust monogenic lines (*Sr's*) and gene efficacy% in Egypt during 2004/2005 and 2005/2006 growing seasons.

No	*Sr's*	2004/2005			2005/2006		
		No of virulent isolates	Virulence frequency%	Gene efficacy%	No of virulent isolates	Virulence frequency%	Gene efficacy%
1	*Sr5*	173	85.64	14.36	58	87.88	12.12
2	*Sr6*	194	96.04	3.96	54	81.82	18.18
3	*Sr7a*	149	73.76	26.24	51	77.27	22.73
4	*Sr7b*	189	93.56	6.44	50	75.76	24.24
5	*Sr8a*	183	90.59	9.41	57	86.36	13.64
6	*Sr8b*	111	54.95	45.05	52	78.79	21.21
7	*Sr9a*	119	58.91	41.09	50	75.76	24.24
8	*Sr9b*	186	92.08	7.92	57	86.36	13.64
9	*Sr9d*	176	87.13	12.87	60	90.91	9.09
10	*Sr9e*	52	25.74	74.26	47	71.21	28.79
11	*Sr9g*	180	89.11	10.89	57	86.36	13.64
12	*Sr10*	174	86.14	13.86	60	90.91	9.09
13	*Sr11*	36	17.82	82.18	24	36.36	63.64
14	*Sr13*	179	88.61	11.39	48	72.73	27.27
15	*Sr15*	63	32.19	68.81	51	77.27	22.73
16	*Sr16*	198	98.02	1.98	53	80.30	19.50
17	*Sr17*	136	67.33	32.67	60	90.91	9.09
18	*Sr21*	185	91.58	8.42	56	84.85	15.15
19	*Sr22*	59	29.21	70.79	27	40.91	59.09
20	*Sr23*	131	64.85	35.15	-	-	-
21	*Sr24*	121	59.90	40.10	8	12.12	87.88
22	*Sr26*	16	7.92	92.08	16	24.24	75.76
23	*Sr28*	170	84.16	15.84	51	77.27	22.73
24	*Sr29*	35	17.33	82.67	33	50.00	50.00
25	*Sr30*	176	87.13	12.87	53	80.00	20.00
26	*sr31*	45	22.28	77.72	27	41.00	59.00
27	*Sr32*	159	78.71	21.29	44	66.67	33.33
28	*Sr33*	121	59.90	40.10	-	-	-
29	*Sr34*	36	17.82	82.18	58	87.88	12.12
30	*Sr35*	49	24.26	75.74	25	37.88	62.12
31	*Sr36*	171	84.65	15.35	51	77.27	22.73
32	*Sr37*	-	-	-	58	87.88	12.12
33	*SrTmp*	111	54.95	45.05	63	95.45	4.55
34	*SrPl*	171	84.64	15.35	52	78.79	21.21
35	*SrWld*	161	79.70	20.30	40	60.61	39.39
36	*SrTt3+10*	174	86.14	13.86	53	80.30	19.7.
37	*Sr Dp2*	173	85.64	14.36	56	84.85	15.15

Table 8. Avirulenc/virulence, based on seedling reaction for 66 isolates of *Puccinia graminis* f.sp. *tritici* in Egypt during 2005/2006 growing season

Egyptian stem rust isolate(ES)	Standard race	Avirulence/virulence	Virulence frequency %
ES-11-1	11	13,24,35,36	88.89
ES-11-2	11	21,22,24, 26+9h/	88.89
ES-11-3	11	9e,24,26+9h,32,35/	86.11
ES-11-4	11	22,24,26+9h,29,31,35/	83.33
ES-11-5	11	9,11,24,26+9h,29,35,36/	80.58
ES-11-6	11	9a,9d,11,24,26+9h,35,36/	80.58
ES-11-7	11	9b,9e,11,22,24,26+9h,35/	80.56
ES-11-8	11	11,17,22,24,26+9h,29,35,36/	77.78
ES-11-9	11	7a,9a,11,21,22,24,26+9h,35/	77.78
ES-11-10	11	10,24,28,29,30,31,Pl,Wld,Tt3/	77.78
ES-11-11	11	6,8a,9b,17,22,24,26+9h,35/	77.78
ES-11-12	11	6,7a,10,11,24,26+9h,28,31,35,Tt3/	75.00
ES-11-13	11	6,7a,15,22,24,26+9h,28,31,35,36,Wld/	69.44
ES-11-14	11	5,9a,9e,10,11,22,24,26+9h,29,35,Tt3,Dp2/	69.44
ES-11-15	11	6,7a,7b,8a,8b,11,15,16,17,24,26+9h,28,31,34,36,Pl,Wld/	52.78
ES-11-16	11	6,7a8b,9a,10,11,13,15,16,17,22,24,26+9H,28,29,31,36,pL,wLD,Tt3,Dp2/	41.67
ES-15-1	15	24,30,35/	91.67
ES-15-2	15	22,29,31,Wld/	88.89
ES-15-3	15	11,22,26+9h,36/	88.89
ES-15-4	15	11,26+9h,29,32,35/	86.11
ES-15-5	15	9b,9e,22,26+9h,29/	86.11
ES-15-6	15	9b,22,32,35,36/	86.11
ES-15-7	15	9g,11,24,26+9h,28,35/	83.33
ES-15-8	15	9e,11,24,26+9h,29,30,35,36/	77.78
ES-15-9	15	11,24,26+9h,29,32,35,36,Wld/	77.78
ES-15-10	15	8a,15,16,22,24,30,31,36,Pl/	75.00
ES-15-11	15	9a,9b,11,13,24,26+9h,29,35,Pl/	75.00
ES-15-12	15	9a,11,13,22,24,26+9h,29,32,37/	75.00
ES-15-13	15	8a,8b,24,26+9h,28,29,31,35,37,Wld/	72.22
ES-15-14	15	9a,9b,13,21,22,24,26+9h,32,34,35,Dp2/	69.44
ES-15-15	15	7a,7b,9a,9g,11,13,15,22,24,26+9h,35/	69.44
ES-15-16	15	6,7a,8a,9e,9g,10,13,16,26+9h,28,30,Tt3,Dp2/	66.67
ES-15-17	15	8a,9a,9b,11,13,16,22,26+9h,29,30,32,35,36	61.11
ES-15-18	18	7a,9a,9b,10,16,17,22,24,26+9h,28,29,31,32,35,36,Tt3,Dp2/	55.56
ES-19-1	19	9e,9g,10,11,16,22,24,29,35,36	72.22
ES-19-2	19	5,7a,7b,8b,9a,10,15,16,21,24,26+9h,29,30,31,32,34,Pl,Wld,tt3/	44.44
ES-19-3	19	5,7b,8a,9b,9e,10,11,13,16,21,22,24,26+9h,29,31,32,35,36,Pl,Wld,Tt3,Dp2	38.89
ES-20-1	20	7a,8b,9a,9b,11,13,15,22,24,26+9h,28,29,31,32,34,35,36,Pl,Tmp,Wlp/	41.67
ES-22-1	22	24,31,32,Wld/	88.89
ES-22-2	22	6,10,24,26+9h,29,32,37,Wld,Tt3,Dp2/	72.22
ES-39-1	39	9a,11,22,24,26+9h,29,32,35/	77.78
ES-40-1	40	8b,24,32,Pl,Wld,Dp2/	86.33
ES-59-1	59	5,6,7a,8b,9a,9d,9e,9g,11,15,17,21,22,26+9h,28,29,30,31,32,34,35,36,Pl,Wld,Dp2	27.78

Table 8. Cont.

Egyptian stem rust isolate(ES)	Standard race	Avirulence/virulence	Virulence frequency %
ES-60-1	60	6,7b,8a,9a,9d,9g,10,11,13,15,16,21,24,26+9h,28,29,31,32,35/	47.22
ES-88-1	88	7e,8b,9e,11,13,15,16,24,29,31,34,35,36,Wld,Dp2/	52.78
ES-89-1	89	7b,8a,9e,11,13,15,24,26+9h,28,29,30,31,32,35/	58.33
ES-98-1	98	5,7a,8a,8b,9a,9b,9d,9e,11,13,21,22,24,26+9h,29,34,Pl/	52.78
ES-111-1	111	5,7b,8b,10,24,30,31,32,34,37,Tt3/	72.22
ES-111-2	111	5,7a,8b,10,15,24,26+9h,29,31,34,37,Pl,Wld,Tt3/	55.56
ES-122-1	122	8b,10,13,15,24,26+9h,Wld/	77.78
ES-158-1	158	9a,11,21,22,24,26+9h,32,35,37,Wlp/	69.44
ES-189-1	189	11,24/	94.44
ES-189-2	189	26+9h,Wld/	94.44
ES-189-3	189	9e,24,26+9h/	91.67
ES-189-4	189	13,24,35/	91.67
ES-189-5	189	7b,16,24/	91.67
ES-189-6	189	11,13,24,35/	88.89
ES-189-7	189	24,28,31,Wld/	88.89
ES-189-8	189	16,24,26+9h,35/	88.89
ES-189-9	189	24,31,Pl,Wld/	88.89
ES-189-10	189	13,24,35,36/	86.11
ES-189-11	189	22,24,26+9h,29,35/	86.11
ES-189-12	189	7b,9a,11,22,26+9h,35,36/	80.56
ES-189-13	189	8b,24,26+9h,29,30,31,35/	80.56
ES-189-14	189	7b,9e,9g,10,22,24,26+9h,31,Wld,Tt3/	75.00
ES-189-15	189	7a,7b,9e,10,11,24,26+9h,28,35,Wld,Tt3/	72.22

Postulation of resistance gene:

Data in Table (9) and summarized in Table (10) present the matching of 11 commercial wheat cultivars with 37 *Sr* genes both tested against 30 isolates of *P. graminis* f. sp. *tritici* at seedling stage to postulate resistance genes in the commercial cultivars. These data revealed that, Giza 168 contains 9 *Sr* genes, Giza 170 and Sakha8, each contain 2 genes, Gemmeiza7and Gemmeiza9 postulated to have 5 *Sr* genes, Gemmeiza 10 and Sakha 93 each contains 7 genes, Sakha 61 has 4 genes, Sakha69 has 8 genes, and Sids 1 and Sids 12 postulated to have 3 *Sr* genes.

Table 9. Incidence of low infection type (LIT) and high infection types (HIT) comparisons of monogenic lines and cultivars against 30 isolates of *Puccinia graminis* f. sp. *tritici* at seedling stage.

No	*Sr's*	1	2	3	4	5	6	7	8	9	10	11
1	*Sr5*	-	+	-	-	-	-	-	o	+	o	-
2	*Sr6*	o	+	+	+	o	o	+	o	o	-	+
3	*Sr7a*	-	+	+	+	+	+	o	-	+	+	+
4	*Sr7b*	+	+	+	o	+	+	+	o	+	o	+
5	*Sr8a*	+	-	+	+	+	+	o	+	+	+	+
6	*Sr8b*	+	+	+	+	o	-	o	+	+	+	+
7	*Sr9a*	+	+	+	+	+	+	+	+	o	+	o
8	*Sr9b*	+	+	+	+	o	+	+	+	+	-	+
9	*Sr9d*	+	+	+	+	+	+	+	+	+	+	+
10	*Sr9e*	o	+	-	o	o	-	+	+	+	-	+
11	*Sr9g*	-	+	+	+	-	+	+	+	+	o	+
12	*Sr10*	+	+	+	+	+	+	+	o	o	+	+
13	*Sr11*	o	o	+	+	-	+	+	+	+	+	+
14	*Sr13*	-	+	o	+	+	+	+	+	+	-	o
15	*Sr15*	-	+	+	o	+	-	+	-	+	-	+
16	*Sr16*	+	+	+	o	+	+	-	o	-	-	+
17	*Sr17*	-	+	-	+	+	o	+	+	-	-	+
18	*Sr21*	o	+	o	-	-	-	+	+	+	+	o
19	*Sr22*	+	+	-	-	+	-	+	-	+	+	+
20	*Sr23*	+	+	+	+	+	+	+	+	+	+	+
21	*Sr24*	o	+	-	+	o	-	+	+	+	+	+
22	*Sr26*	o	+	o	-	-	+	+	+	+	+	+
23	*Sr28*	+	+	o	+	-	+	+	o	o	+	-
24	*Sr29*	+	+	+	+	-	+	+	+	+	+	+
25	*Sr30*	o	+	+	+	-	+	+	+	-	+	+
26	*Sr31*	-	+	o	+	o	+	+	-	o	-	+
27	*Sr32*	+	+	+	+	+	+	+	+	+	+	+
28	*Sr33*	+	+	+	+	+	+	+	+	+	+	+
29	*Sr34*	+	+	+	+	+	+	+	o	+	+	+
30	*Sr35*	o	+	+	o	+	+	+	+	o	+	-
31	*Sr36*	o	o	+	+	+	+	o	o	o	-	+
32	*Sr37*	-	+	+	+	-	-	+	+	+	+	+
33	*SrTmp*	+	-	+	+	+	+	+	+	-	+	+
34	*SrPl*	+	+	+	+	o	+	+	+	+	+	+
35	*SrWld*	+	+	+	+	+	+	+	+	+	+	+
36	*SrTt3+10*	+	+	+	+	+	+	+	+	+	+	+
37	*Sr Dp2*	+	+	-	+	+	+	+	+	+	+	+

1= Giza 168,2= Giza 170,3= Gemmeiza 7,4= Gemmeiza 9, 5= Gemmeiza 10,6= Sakha 8,7= Sakha 61,8= Sakha 69,9= Sakha 93,10= Sids 1,11= Sids12

Table 10. Probable genes for resistance of 11 Commercial cultivars used to be determined by comparative infection type data

No	Cultivar	*Sr* gene
1	Giza168	*6,9e,11,21,24,26+9h,30,35,36*
2	Giza170	*11,36*
3	Gemmeiza7	*13,21,26+9h,28,31*
4	Gemmeiza9	*7b,9e,15,16,35*
5	Gemmeiza10	*6,7b,7e,8b,24,31,PL*
6	Sakha8	*6,17*
7	Sakha61	*7a,8a,8b,36*
8	Sakha69	*5,6,7b,10,16,28,34,36*
9	Sakha93	*6,9a,10,28,31,35,36*
10	Sids1	*5,7b,9g*
11	Sids12	*9a,13,21*

DISCUSSION

Ongoing surveys of the wheat rust pathotypes in Egypt have pointed a clear evidence of annual movement of the primary inoculum from the neighboring countries to Egypt. El-Daoudi *et al.* (1996) mentioned that, races 11, 15 and 122 were found allover the Nile Valley and Red Sea countries. The environmental conditions, especially wind plays an active role in urediospores dissemination and rust distribution. Mangistu *et al.*, (1991) suggested that, Ethiopia and Sudan are the foci of stem rust races from which active inocula attack wheat acreages in Egypt and Yemen. New pathotypes are derived by either mutation or exotic introduction of somatic hybridization. Therefore, annual surveys of the rust races is a continuous process to detect any shift in the pathogen populations to serve the national breeding program for rust resistance. Moreover, tracing rust movement between neighboring countries may explain the epidemiological aspects and helps in the advance of breeding program through the exchange of breeding materials in these countries. These observations stress the importance of maintaining a national strategy in breeding cereals for resistance to rusts. The present work revealed the existence of nine races of *P. graminis* f. sp. *tritici*, in 2005, with the predominance of race 34 (51.98%), followed by race 11 (25.25%). In 2006, the picture was different, where 16 races were determined and races 15, 11, and 189 were the most frequent having 27.26, 24.23, and 22.72% of the total isolates , respectively. Five races *i.e.* 11, 15, 189, 19, and 39 were found in both seasons, while eleven new races (races 20, 22, 40, 59, 60, 88, 89, 98, 111, 122, and 158) were detected in the second season.

On the other hand, race 11 was found allover the tested areas (distribution 100%), followed by race 189 (80%), then race 15 (60%). This provided a strong evidence of migration of rust races by wind among all wheat growing areas with periodic movement of isolates from North to South in Egypt. The occurrence of single races in a certain location could be, relevant to cultivation of certain cultivar (s) in such location. Similar results were reported by other workers (Sherif *et al.*, 1996, Imbaby and Ageeze, 1998 and Najeeb *et al.*, 2003&2005).

Using the *Pgt*-code for race identification gave evidence for heterogeneity of a physiologic race. In 2005, 202 isolates were identified among the 9 identified races The R-virulence phenotype group was the most frequent comprising 52%, followed by T-virulence phenotype group having 24% of the total isolates. In 2006, 66 virulence phenotypes, belong to 16 races, were detected, with the predominance of T-virulence phenotype group (56%).

As for the gene efficacy of the tested *Sr* genes, the results revealed the presence of high virulence among the isolates, with the exception of *Sr 26, 29, 11, 31, 9e,* and *35*, in 2005 and *Sr 24*, and *26*, in 2006. In a previous study, *Sr 35, 24,26 31, 21,* and *22* were the most effective genes tested against stem rust isolates having 97.64, 90.32, 89.66, 83.94, 81.75, 73.23% efficacy, respectively (Najeeb *et.al.*, 2005). Most of these genes were postulated to be present in the host genotypes tested, either alone or in combinations. This may be explain the resistance of these genotypes, at the seedling stage to the *P. graminis* isolates used.

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التخصص المرضى وتوزيع السلالات للفطر بكسينيا جيرامينيس فى مصر موسمى ٢٠٠٥ ,٢٠٠٦ وكذا الجينات المتوقعه فى بعض تراكيب القمح الوراثيه

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يعتبر مرض صدا الساق فى القمح المتسبب عن الفطر بكسينيا جيرامينيس من الامراض الهامه التى تهدد محصول القمح فى مصر والعالم. ونظرا لحدوث الاصابه بهذا المرض فى اخر موسم نمو القمح اصبح هذا المرض قليل الاهميه الاقتصاديه على القمح. الا ان برنامج التربيه للمقاومه لهذا المرض يجب ان يستمر لمواكبه التغير التى يمكن ان يحدث فى مجتمع الكائن الممرض حتى نتفادى الهزات الفجائيه والتى قد تحدث فى المحصول نتيجه ظهور سلاله فسيولوجيه جديده قد تكسر مقاومه الاصناف المنزرعه.

ولنجاح برنامج التربيه للمقاومه يجب ان تتوافر لدى المربى معلومات كافيه وواضحه سنويا عن السلالات الفسيولوجيه للمسبب المرضى - السائد منها وكذا قدرتها المرضيه وايضا الجينات الفعاله ضد هذه السلالات تحت الظروف المصريه. وهذه عمليه مستمره. ولذا تهدف هذه الدراسه الى حصر وتعريف السلالات الفسيولوجيه لفطر صدا الساق خلال الموسمين ٢٠٠٥و ٢٠٠٦ وكذا تعريف العوامل الوراثيه المسؤله عن المقاومه والمحتمل وجودها فى بعض التراكيب الوراثيه للقمح.

هذا وقد اوضحت الدراسه فى الموسم الاول ٢٠٠٥مايلى:-

١- وجود ٩ سلالات فسيولوجيه وكانت السلاله الفسيولوجيه ٣٤ هى الاكثر سياده (٩٨و٥١%) تليها السلاله ١١ (٢٥و٢٥%).

٢- اشتملت هذه السلالات على ٢٠٢ طراز مرضى.

٣- كانت الجينات *Sr26, 29, 11, 31, 35,* and *9e* هى الاكثر فاعليه ضد السلالات المختبره.

فى الموسم الثانى ٢٠٠٦:-

١- امكن تعريف ١٦ سلاله فسيولوجيه وكانت السلاله ١٥ هى الإكثر سياده (٢٦و٢٧%) تليها السلاله ١١ (٢٣و٢٤%).

٢- وجود ٦٦ طراز مرضى داخل هذه السلالات.

٣- كان العامل الوراثى *Sr26* الاكثر فاعليه .

٤- اغلب العوامل الوراثيه التى اثبتت مقاومه للسلالات المختبره امكن توقعها فى تراكيب القمح الوراثيه المستخدمه.