VIRULENCE AND DIVERSITY OF *PUCCINIA TRITICINA* IN EGYPT IN 2005/2006

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Abstract

One hundred and eight isolates of P. triticina , causing wheat leaf rust, were collected across eight governorates i.e. Alexandria, Ismailia, Dakhlia, Beheira, Demietta, Beni-Swief, Sharkia and Fayoum during 2005/2006 and analyzed for virulence to 47 'Thatcher' near-isogenic wheat lines, each carrying a single gene for resistance to leaf rust. Of the 68 virulence phenotypes identified among 108 isolates,39% were collected from Alexandria, 37% from Ismailia, 6% from Dakhlia, 5% from each of Beheira, Demietta, and Beni-Swief, 4% from Sharkia and 1% from Fayoum. The most frequent were T- virulence phenotype groups (40% of the total isolates), P-virulence phenotype groups (18%), F-virulence phenotype groups (11%) and M-virulence phenotype groups (6%). Moreover, the most virulent isolates were TTTT, TTST, and TTTS (91.5% of the tested genes were susceptible), followed by isolates FSTT, PMTT, TRTT AND TTKT (89.4% Virulence) . The frequency of virulence was greater than 90% to Lr3, Lr22b, Lr46, less than 50% to Lr2a, Lr36, Lr39, Lr45 and between 50 and 90% to the rest Lr genes. Moreover, the Lr37 was the most effective gene (85.2% efficacy) followed by Lr39 and Lr45 (66.7% efficacy, each) then Lr2a and Lr 36 (53.7%, each). The lowest isolates with virulence to these genes and the high level of resistance that they confer indicate that genes Lr37 and Lr39 would provide effective resistance in a breeding program

INTRODUCTION

Wheat leaf rust, caused by *Puccinia triticina (=Puccinia recondita* f. sp. *tritici)*, occur annually through most wheat growing areas of Egypt. Virulence survey of cereal rust fungi have traditionally used differential host lines that express resistance in the primary leaves of seedling plants.

Johnson and Mains in 1932 and Mains and Jackson in 1926 were the first to report the physiological specialization of *P. triticina*. They initially used the wheat cultivars Kanred and Malakof to separate *P. triticina* isolates, and then later used a series of 11 cultivars to differentiate physiological races. Their differential series was later reduced to eight cultivars (Malakof, *Lr1*,Webster, *Lr2a*, Carina, *Lr2b*, Brivt, *Lr2*and *LrB*, Loros, *Lr2c*, Mediterranean, *Lr3a*, Democrat, *Lr3*a and Hussar, *Lr11*)(Mians and Jackson, 1926, Johson and Mains, 1932 and Dyck and Samborski, 1968). This set was further reduced to Malakof, Webster, Loros, Democrat, and Hussar, and virulence pathotypes of *P. triticina*, based on those five remaining genes were classified into Unified Numeration (UN) races. Currently, the identification of virulence phenotypes is

based on infection types expressed on seedling of Thatcher wheat lines that are near-isogenic for 16 different leaf rust resistance genes (Long and Kolmer, 1989).

Surveys on the physiological specialization of wheat pathogens have been used to estimate the relative prevalence and distribution of pathotypes, to monitor the spread of new virulence phenotypes and the loss of previously virulent phenotypes, and to identify which resistance genes are ineffective (Kolmer, 1999, Long *et al.*, 1998 and Niewoehner and Leath 1998). These surveys provide information needed in breeding for leaf rust resistance.

So, the main objectives of this study were to characterize the virulence of the *P. triticina* populations in Egypt in 2005/2006 growing season, to the North America *Pt* differentials (Long and Kolmer, 1989) and other selected monogenic –lines of wheat and to compare these results with those of previous survey.

MATERIALS AND METHODS

Leaf rust uredinial collections were made from farm fields through Alexandria, Ismailia, Dakhlia, Baheira, Demietta, Beni-Swief, Sharkia, and Fayoum governorates and from wheat nurseries during 2005/2006 growing season. A sample collection consisted of leaves bearing uredinia from each of five to 10 plants per field. Uredinia –bearing leaves were placed in glycine bags and stored in a cooler on ice until transported to the laboratory. In the lab. they were dried overnight at room temperature and then placed in glycine envelops and stored in a dessicator in the refrigerator at 3°C until October 2006.

Urediospores from each collection were transferred, purified, and increased onto primary leaves of Giza 139 wheat seedlings, in 10-cm –diameter pots. The plants were inoculated after the first leaves had fully formed by using the spatula method. After inoculation, the seedling plants were placed in a darkened dew chamber at 98% relative humidity maintained at 15°C overnight. 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) for each pure isolate, was dusted onto the primary leaves of 7-day-old seedlings of the near-isogenic series of leaf rust differentials, 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 onto the greenhouse benches. After 12 days, infection types (ITs) of each near-isogenic line were recorded as either low (,, 1, or 2) or high (3 or 4). The isolates were assigned four-letter race designations based on low and

high IT to the 16 Thatcher differential lines (Long and Kolmer, 1989) (Table 1). The isolates were used for virulence analysis, using 47 monogenic lines (Table 5).

The avirulence/virulence combinations suggested by Green (1966) was used to describe the tested isolates. The efficacy of the *Lr* genes were determined according to their virulence frequency.

Table 1. Code (Pt) for the 16 North American differential hosts for *Puccinia triticina* in ordered sets of four and an additional set four.

		Infection type[b] produced on near isogenic *Lr* lines:			
	Host set 1:	1	2a	2c	3a
	Host set 2:	9	16	24	26
	Host set 3:	3ka	11	17	30
Pt code[a]	Host set 4:	10	18	21	2b
B		Low	Low	Low	Low
C		Low	Low	Low	H
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]Pt code consists of the designation for set I followed by that for set 2, etc. For example, race MGB: set 1 (M) - virulent to Lr1, 3a, set 2 (G) - virulent to Lrl6, set 3 (B) - avirulent.

[b]Low infection type (avirulent pathogen), Hgh infection type (virulent pathogen), see Table 2.

Table 2. Description of infection types and symptoms

Infection type		Symptoms
0	Low	No uredinia or other macroscopic sign of infectiton
0,	Low	Few faint flecks
,	Low	No uredinia, but hypersensitive necrotic or chlorotic flecks present
1	Low	Small uredinia often surrounded by a necrosis
2	Low	Small to medium uredinia often surrounded by chlorosis
Y	Low	Ordered distibution of variable-sized uredinia with largest at leaf tip
X	Low	Random distibution of variable-sized uredinia
3	High	Medium-sized uredinia without chlorosis or necrosis
4	High	Large uredinia without chlorosis or necrosis

RESULTS AND DISCUSSION

In 2005/2006, a total of 108 single uredinial isolates of *Puccinia triticia* were characterized. Sixty- eight virulence phenotypes were identified (Table 3) on the basis of the 16 differential host lines(Long and Kolmer, 1989) which are isogenic for leaf rust resistance genes. Virulence phenotypes are arranged in Table (3) by Pt code (Long and Kolmer, 1989) and results are presented as percentage of isolates for each phenotype and as number of isolates for each geographic area. About 40% of the isolates had the T- (virulent to *Lr's 2c, 12, 14a, 29, 35, 36, 42, 46,* and *47*) phenotypes. The most frequently identified phenotype was TTTT, comprising 13% of the total isolates. Moreover, it was the most widespread phenotype (75% geographic distribution) representing 7% phenotype frequency in Demietta and Beni- Swief areas, and was the most frequent phenotype in Alexandria (13.3% phenotype frequency), Ismailia (4.0%), and in Sharkia (2%).Three other T- phenotypes, TTST, TTTS, TRTT, together comprised 8.3% of the population nationwide. Phenotype TTST was common in Ismailia (7.5% frequency), whereas. Phenotypes TTTS and TRTT were also common in Alexandria (4.8%, each).

Moreover, the phenotypes TTTTT, TTST, TTTS were the most virulent phenotypes (91.5% virulence frequency), followed by phenotype TRTT (89.4% virulence frequency) (Table 4).Eighteen other T- phenotypes made up 18.5% of the total isolates.

Isolates in the P- virulence phenotypes group (virulent to *Lr's 2b, 2c,* and *3*) comprised 18.0% of the total characterized isolates (Table 3).The present data categorized 6.5% of the isolates into the PTTT phenotype and 2.8% into PRST

phenotype. Phenotype PTTT was the most common in Ismailia (10.0%phenotype frequency), and was also common in Alexandria (7.14% frequency).Moreover, phenotype PRST occurred at 0.9% frequency in Fayoum and was common in Ismailia (1.8% frequency). Phenotypes PQTT (1.8% frequency) and PRTJ (1.8% frequency were common in Ismailia and Beheira, respectively. Fifteen other P- phenotypes made up of 13% the populations (Table 3).

Data in Table 3 shows that, phenotype PMTT in Alexandria (0.9% phenotype frequency) was the most virulent phenotype (89.4% virulence frequency), followed by phenotypes PRST (87.4%), and PTTT (85.1%). The wide distribution of T- and P-phenotypes through Alexandria (40% phenotype frequency), Ismailia (28%) Beheira (33.3%), Dakhlia (50.0%), Demietta (50.0%), Fayoum (100%), and Sharkia (100%) through the wheat producing areas show that Lower and Middle Egypt comprise the suitable environmental conditions for leaf rust disease development.

The F-virulence phenotypes group (virulent to *Lr's2c, 3, 9, 10 14a, 15, 19 22a, 22b, 23, 42, 44* and *B*) made up only 11% of the leaf rust populations (Table 3). The most common phenotype FTTT, comprised 6% frequency of the total isolates (3.0% in Demeietta, 1.0% in each of Alexandria, Ismailia, and Dakhlia), followed by phenotype FSTT (2.0% phenotype frequency) in Ismailia (1.0%) and in Beheira (1.0%). On the other hand, Table (4) show that phenotype FSTT was the most virulent (89.4% virulence frequency) followed by phenotype FTTT (85.1%). Four other F-Phenotypes comprised up to 4% of the total populations (Table 3).

The phenotype M-group (virulent to *Lr's 3, 42,B*) were found in only 6% of the total isolates, without dominance for any of them (Table 3). The most virulence phenotype was MTTS (80.9% virulence) (Table 4). On the other hand, the B-virulence phenotypes group repeated four times (3.7% phenotype frequency). The common phenotype BBBM comprised 2.8% of the total isolates (1.9% in Alexandria, and 0.9% in Beheira and Beni-Swief) (Table 3).

The C-groups repeated three times (2.8% phenotype frequency) and 67% of them were identified in Ismailia. The G-, D-, and K- groups were repeated twice only (1.9% phenotype frequency, each).Also, the groups H-, N-, and J- individually were less than 1.0% of the total isolates. Most of the C-, G-, D-, K-, H-, N-, and J-phenotypes were found in lower Egypt, except for phenotype BBBM which was the only phenotype in Beni-Swief (Table 3).

Table 3. Races of *Puccinia triticina*, Their geographical distribution, No. of isolates, and frequencies, identified in leaf rust collections from farm fields and nurseries in Egypt in 2005/2006 growing season.

No.	*Pt* code*	Alexandria	Ismailia	Dakhlia	Beheira	Demietta	Beni-Sweif	Sharkia	Fayoum	No.of isolates	Frequency %
1	BBBM	++					+			3	2.7
2	BBHB				+					1	0.9
3	CCKN		+							1	0.9
4	CSJT		+							1	0.9
5	CTTS		+							1	0.9
6	DLKG	+								1	0.9
7	DTTP			+						1	0.9
8	FQSM	+								1	0.9
9	FLRT	+								1	0.9
10	FPMS		+							1	0.9
11	FSTT		+		+					2	1.8
12	FTKT		+							1	0.9
13	FTTT	+	+	+		+++				6	5.4
14	GBCG	+								1	0.9
15	GPFJ	+								1	0.9
16	HRMT		+							1	0.9
17	JTHS	+								1	0.9
18	KTTT		+	+						2	1.8
19	MBGB	+								1	0.9
20	MBQB	+								1	0.9
21	MRPT		+							1	0.9
22	MNRQ		+							1	0.9
23	MTTT	+								1	0.9

*= *Pt* code or virulence phenotype is based on high/low infection type on 16 near- isogenic lines of Thatcher wheat each with a different gene for leaf rust resistance (Long and Kolmer, 1989).

Table 3. Cont.

No.	Pt code*	Alexandria	Ismailia	Dakhlia	Beheira	Demietta	Beni-Sweif	Sharkia	Fayoum	No of isolates	Frequency%
24	MTTS	+								1	0.9
25	NBBT				+					1	0.9
26	PMTT	+								1	0.9
27	PQTT		++							2	1.8
28	PQQT		+							1	0.9
29	PRSN		+							1	0.9
30	PRST		++						+	3	2.7
24	MTTS	+								1	0.9
25	NBBT				+					1	0.9
32	PRTJ				++					2	1.8
33	PRRP		+							1	0.9
34	PRRS		+							1	0.9
35	PRTT					+				1	0.9
36	PSTP		+							1	0.9
37	PSTT			+						1	0.9
38	PTTT	+++	++++							7	6.3
39	PTMT	+								1	0.9
40	PTRT	+								1	0.9
41	PTST		+							1	0.9
42	PTTS	+								1	0.9
43	PTTP	+								1	0.9
44	PTRS			+						1	0.9
45	PPTT	+								1	0.9
46	SKTT	+								1	0.9

*= *Pt* code or virulence phenotype is based on high/low infection type on 16 near- isogenic lines of Thatcher wheat each with a different gene for leaf rust resistance (Long and Kolmer, 1989).

Table 3. Cont.

No.	Pt code*	Alexandria	Ismailia	Dakhlia	Beheira	Demietta	Beni-Sweif	Sharkia	Fayoum	No.of isolates	Frequency%
47	TKRN			+						1	0.9
48	TQTT		+							1	0.9
49	TRST	+								1	0.9
50	TRRF		+							1	0.9
51	TRTS		+							1	0.9
52	TRTT	++								2	1.8
53	TRMT		+							1	0.9
54	TPPS							+		1	0.9
55	TSSB						+			1	0.9
56	TSSM		+							1	0.9
57	TSST	+								1	0.9
58	TSTT							+		1	0.9
59	TSJP						+			1	0.9
60	TSKT	+								1	0.9
61	TTTQ	+	+							2	1.9
62	TTTT	++++++	++++			+	+	++		14	13.0
63	TTTC	+								1	0.9
64	TTST	+	+++							4	3.6
65	TTKT	+								1	0.9
66	TTTP	+								1	0.9
67	TTTS	++	+							3	2.7
68	TTRT	+						+		2	1.8
Total		42	40	6	5	5	5	4	1	108	

*= *Pt* code or virulence phenotype is based on high/low infection type on 16 near- isogenic lines of Thatcher wheat each with a different gene for leaf rust resistance (Long and Kolmer, 1989).

Table 4. Virulence phenotypes of *Puccinia triticina* isolates collected in Egypt in 2005/2006 growing season.

No.	*Pt* code*	Virulence combination#	No. of susceptible genes	No. of resistant genes	Virulence%
1	TTTT	37,39,40,45/	4	43	91.5
2	TTST	25,30,37,39/	4	43	91.5
3	TTTS	2b,23,36,37/	4	43	91.5
4	FSTT	1,2a,23,26,28/	5	42	89.4
5	PMTT	2a,16,24,38,39/	5	42	89.4
6	TRTT	24,25,36,37,45/	5	42	89.4
7	TTKT	3ka,36,37,38,45/	5	42	89.4
8	PRST	2a,24,27,30,40,45/	6	41	87.2
9	KTTT	1,23,25,37,44,45/	6	41	87.2
10	FTTT	1,2a,34,36,37,43,45/	7	40	85.1
11	TRTS	2b,23,24,34,36,37,45/	7	40	85.1
12	PTTT	2a,18,37,39,41,45,46/	7	40	85.1
13	TTTP	18,33,34,36,37,39,40/	7	40	85.1
14	TTTQ	13,16,34,37,39,41,43,44/	8	39	83.0
15	TPPS	2b,16,27,36,37,38,39,40/	8	39	83.0
16	TSTT	23,24,25,26,34,35,37,45/	8	39	83.0
17	TRMT	3bg,11,17,24,35,36,37,39/	8	39	83.0
18	TRRF	10,14b,17,18,22a,24,27,36/	8	39	83.0
19	TRST	23,24,25,30,34,36,39,47/	8	39	83.0
20	TQTT	24,26,34,35,36,37,38,40,45/	9	38	80.9
21	PTTP	2a,18,21,23,25,27,37,39,45/	9	38	80.9
22	MTTS	11,14a,17,26,32,34,37,40,46/	9	38	80.9

*=*Pt* code or virulence phenotype is based on high/low infection type on 16 near- isogenic lines of Thatcher wheat each with a different gene for leaf rust resistance (Long and Kolmer, 1989).

#= *Lr* genes on which the isolate is virulent.

Table 4. cont.

No.	*Pt* code*	Vrrulence combinations#	No. of susceptible genes	No. of resistance genes	Virulence%
23	MRPT	2a,2c,11,24,34,36,37,39,45/	9	38	80.9
24	PTST	2a,25,30,34,36,37,43,44,45/	9	38	80.9
25	PQTT	2a,3bg,15,23,24,26,34,35,45/	9	38	80.9
26	PSTT	2a,23,25,26,34,36,37,43,45/	9	38	80.9
27	PRTT	2a,23,24,33,36,37,39,42,45/	9	38	80.9
28	TTRT	3,17,23,28,36,37,39,43,45,B/	10	37	78.7
29	FTKT	1,2a,3ka,14b,23,25,32,35,37,45/	10	37	78.7
30	PPTT	2a,16,32,33,34,37,39,40,42,44/	10	37	78.7
31	PTRT	2a,15,17,36,37,38,39,40,41,43,44,45/	10	37	78.7
32	TTTC	3BG,10,12,14A,18,21,23,25,29,37/	10	37	78.7
33	MTTT	2a,2c,14b,25,27,34,36,37,39,40,45/	11	36	76.6
34	PTRS	2a,11,14a,22b,25,33,34,36,37,39,45/	11	36	76.6
35	PRRS	2a,2b,14b,17,24,34,36,37,39,43,45/	11	36	76.6
36	PTMT	2a,3bg,11,17,23,25,29,37,39,44,45/	11	36	76.6
37	PTTS	1,2a,2b,3bg,25,32,33,34,35,37,39,40/	12	35	74.5
38	TSST	3bg,23,26,30,33,34,37,38,40,43,44,45/	12	35	74.5
39	GPFJ	1,3ka,11,14b,15,16,27,36,37,39,45,B/	12	35	74.5
40	TSSM	2b,3bg,14b,18,21,26,27,30,36,37,39,43,45/	13	34	72.3
41	PRRP	2a,17,18,19,22a,23,24,37,39,41,43,45,B/	13	34	72.3
42	SKTT	3,9,23,25,32,34,36,37,38,39,40,44,45/	13	34	72.3
43	FQSM	1,2a,13,14b,18,21,24,25,26,27,30,36,37,45/	14	33	70.2
44	HRMT	1,2c,3bg,11,13,17,22a,24,36,37,39,44,45,47/	14	33	70.2
45	PSTP	2a,3bg,18,23,25,26,27,35,37,39,40,43,45/	14	33	70.2
46	FLRT	1,2a,3bg,12,13,16,17,24,26,33,34,37,39,43,45/	15	32	68.1

*= *Pt* code or virulence phenotype is based on high/low infection type on 16 near- isogenic lines of Thatcher wheat each with a different gene for leaf rust resistance (Long and Kolmer, 1989).

#= *Lr* genes on which the isolate is virulent.

Table 4. Cont.

No.	*Pt* code	Virulence combinations#	No. of susceptible genes	No. of resistant genes	Virulence%
47	PQQT	2a,17,23,24,26,28,30,32,33,34,35,37,39,40,45/	15	32	68.1
48	CSJT	1,2a,2b,2c,25,26,29,34,36,37,38,39,40,43,45/	15	32	68.1
49	TSSB	2b,3bg,10,16,18,19,21,22b,23,26,30,37,38,41,45/	15	32	68.1
50	TSKT	2a,2b,10,14b,19,21,22a,22b,28,35,37,38,40,45,B/	16	31	66.0
51	DTTP	1,2a,3,16,19,23,29,36,37,39,40,41,43,45,47,B/	16	31	66.0
52	PRSN	2a,12,14b,15,16,18,21,23,24,26,28,30,35,39,42,45/	16	31	66.0
53	PRTJ	1,2a,2b,3bg,10,14b,23,24,25,26,28,38,39,41,46,B/	16	31	66.0
54	JTHS	1,2b,3,3bg,3ka,14a,14b,17,22a,22b,23,25,36,37,40,45/	16	31	66.0
55	TKRN	2b,9,17,18,22a,25,27,28,32,34,35,37,39,41,43,45/	16	31	66.0
56	CTTS	1,2a,2b,2c,14b,32,33,34,35,37,38,39,40,42,43,44,45/	17	30	63.8
57	MNRQ	2a,2b,2c,16,17,19,21,23,25,26,36,37,39,41,43,44,45/	18	29	61.7
58	FPMS	1,2a,2b,3bg,11,14b,16,17,25,28,32,33,34,35,37,40,41,45,46,47/	20	27	57.5
59	DLKG	1,2a,2b,3,3ka,10,12,16,21,24,25,26,33,34,37,39,45,46,47,B/	20	27	57.5
60	PRTM	1,2a,3ka,9,13,14a,14b,17,18,21,24,27,36,37,38,39,41,43,45,47/	20	27	57.5
61	TSJP	3ka,3bg,12,14b,15,18,22a,26,27,30,32,34,35,36,37,38,39,40,43,45,47/	21	26	44.7
62	CCKN	1,2a,2b,2c,3ka,3bg,9,13,14a,15,16,18,23,24,33,34,35,36,39,40,41,43,45,B/	24	23	48.9
63	NBBT	2a,3,3ka,9,11,12,13,14b,15,16,17,22a,23,24,25,26,27,29,30,36,37,38,40,42,43,47/	26	21	44.7
64	GBCG	1,2b,2c,3,3ka,9,10,11,14a,14b,15,16,19,21,23,25,26,27,29,30,32,34,35,36,37,38,39,40,43,44/	30	17	36.2
65	MBGB	2a,2b,2c,3ka,3bg,9,10,12,13,14a,14b,16,17,18,19,21,22a,22b,23,24,26,27,30,32,34,35,36,37,39,43,45/	31	16	34.0
66	BBHB	1,2a,2b,2c,3,3ka,9,10,12,14b,15,16,17,18,19,21,22b,23,24,25,26,28,29,34,35,36,37,38,39,40,42,44,45,47,B/	35	12	25.5
67	MBQB	1,2a,2b,2c,9,10,12,13,14a,14b,15,16,17,18,19,22a,23,24,25,26,27,28,29,30,32,33,34,35,36,37,38,39,40,41,43,44,45,46,47/	40	7	14.9
68	BBBM	1,2a,2c,3,3ka,9,11,12,13,14a,14b,15,16,17,18,19,21,22a,23,24,25,26,27,28,29,30,33,34,35,36,37,38,39,40,41,42,44,45,46,47,B/	40	7	14.9

Table 5. Virulence frequency* and gene efficacy for the 2005/2006 *Puccinia triticina* isolates to forty- seven near –isogenic lines

No.	*Lr* genes	No of virulent isolates	Virulence frequency%	Gene efficacy%	No.	*Lr* genes	No of virulent isolates	Virulence frequency%	Gene efficacy%
1	RL6003-Lr1	78	72.2	27.8	25	Transec-*Lr25*	64	59.3	40.7
2	RL6016-*Lr2a*	50	46.3	53.7	26	RL6078-*Lr26*	77	71.3	28.7
3	RL6019-*Lr2b*	83	76.8	23.2	27	Gatcher-*Lr27*	84	77.8	22.2
4	RL6047-*Lr2c*	95	88.0	12.0	28	RL6079-*Lr28*	91	84.3	15.7
5	RL6002-*Lr3*	98	90.7	9.3	29	RL6080-*Lr29*	97	89.8	10.2
6	RL6042-*L13bg*	82	75.9	24.1	30	RL6049-*Lr30*	85	78.7	21.3
7	RL6007-*Lr3*ka	92	82.2	14.8	31	RL5497-1-*Lr32*	83	76.9	23.2
8	RL6010-*Lr9*	94	87.8	12.2	32	RL6057-*Lr33*	81	75.0	25.0
9	RL6004-*Lr10*	96	88.9	11.1	33	RL6058-*Lr34*	56	51.9	48.2
10	RL6053-*Lr11*	91	84.3	15.7	34	RL5711-*Lr35*	76	70.4	29.6
11	RL6011-*Lr12*	84	77.8	22.2	35	E84018-*Lr36*	58	47.2	53.7
12	Manitou-*Lr1*3	96	88.9	11.1	36	RL6081-*Lr37*	16	14.8	85.2
13	RL6013-*Lr1*4a	93	86.1	13.9	37	KS86NGRC02-*Lr38*	79	73.1	26.9
14	RL6006-*Lr1*4b	89	82.4	26.9	38	KS89WGRC07-*Lr39*	36	33.3	66.7
15	RL6052-*Lr15*	91	84.3	15.7	39	KS90WGRC10-*Lr40*	60.0	55.6	44.5
16	RL6005-*Lr16*	87	80.6	19.4	40	TcLrT3-*Lr41*	87	80.6	19.4
17	RL6008-*Lr17*	84	77.8	22.2	41	RL6014-*Lr42*	95	88.0	12.0
18	RL6009-*Lr1*8	83	76.9	23.1	42	RL600-*Lr43*	72	66.7	33.3
19	RL6040-*Lr1*9	93	86.1	13.9	43	RL600-*Lr44*	90	83.3	16.7
20	RL6043-*Lr21*	90	83.3	16.7	44	RL600-*Lr45*	36	33.3	66.7
21	RL6044-*Lr22a*	87	80.6	19.4	45	RL600-*Lr46*	99	91.7	8.3
22	Thatcher-*Lr22b*	98	90.7	9.3	46	RL600-*Lr47*	93	86.1	13.9
23	RL6012-*Lr23*	63	58.3	41.7	47	RL6051-*LrB*	94	87.8	13.0
24	RL6064-*Lr24*	72	66.7	33.3					

*=Percentage of *P. triticina* isolates virulent to the near- isogenic lines tested.

Of the collected isolates, 39% were collected from Alexandria, 37% from Ismailia, 6% from Dakhlia, 5% from each of Beheira, Demietta, and Beni-Swief, 4% from Sharkia and 1% from Fayoum (table 3).

Table 5 summerizes the frequencies of virulence to each of the 47 near-isogenic lines among collections from the eight geographical areas. Virulence phenotypes were low to *Lr37* (85.2% efficacy), *Lr39* (66.7%) followed by *Lr36* and *Lr2a* (53.7%, each). Moderate (58.3%) to high virulence frequency (90.7%) were found for the remaining near- isogenic lines used. In 2004/2005,the most effective leaf rust resistant genes were *Lr's 37* (99.0%), *38* (95.41%), *9* (90.83%), *40* (88.79%), *45* (88.07%), *39* (86.24%), and *2c* (81.65%) (Najeeb *et al.*, 2005).

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القدرة المرضية والتنوع في الفطر بكسينيا تريتيسينا في الموسم ٢٠٠٥/٢٠٠٦

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يجرى على فطريات الأصداء في القمح حصرا سنويا بغرض دراسة القدرة المرضية وكذا التنوع في سلالات الكائن الممرض وأيضا التوزيع الجغرافي لها بالاضافه إلى اختبار كفاءه العوامل الوراثية (الجينات) المقاومة لتلك السلالات.

ومن خلال الحصر السنوي لموسم ٢٠٠٥/٢٠٠٦ على فطر صدا الأوراق في القمح (بكسينيا تريتيسينا) في ٨ محافظات هي الاسكندر يه ،الاسماعيليه ،الدقهليه ، البحيرة ، دمياط ، بنى سويف ، الشرقية ، وكذا الفيوم أمكن التوصل إلى النتائج التالية:

١- تعريف ١٠٨ عزله نقيه تمثل ٦٨ سلاله فسيولوجيه تقع في ١٣ مجموعه ممرضه (B-, C-, D-, F-, G-, H-, J-, K-, M-, N-, P-, S- and T-groups) .

٢- كانت المجموعات الممرضة T- and P-groups هي الأكثر تكرارا (٤٠% ، ١٨% تكرار على التوالي) تليهم المجموعات الممرضة F-group (١١%)، M-group (٦%) .

٣- كانت المجموعات الممرضة T- and P- groups أيضا هي الأكثر انتشارا (٧٥ % انتشار) على مستوى مناطق الدراسة حيث أمكن تعريف كل منها في ٦ محافظات هي الاسكندر يه ، الاسماعيليه ،الدقهليه ،البحيرة ، دمياط، والفيوم (مجموعه -P) و الاسكندر يه ، الاسماعيليه ، الدقهليه ،البحيره ، دمياط، الشرقية وبنى سويف للمجموعه T- group .

٤- كانت السلالات الفسيولوجيه BBBM, TTTS, TTST, FTTT, PTTT, TTTT هي الأكثر تكرارا من مجموع العزلات التي تم تعريفها (٨و٢%، ٨و٢%، ٧و٣%، ٥و٥%، ٥و٦%، ١٣% تكرار على التوالي).

٥- أظهرت الدراسة أيضا أن السلالات الفسيولوجيه TTTT, TTST, TTTS هي الأكثر قدره مرضيه (٩١,٥ قدره مرضيه لكل منها) تليها السلالات الفسيولوجيه FSTT, PMTT, TRTT, TTKT (٨٩,٤%).

٦- اظهر العامل الوراثي (الجين) *Lr 37* أعلى مقاومة ضد عزلات الكائن الممرض المختبرة (٨٥,٢% كفاءه) يليه العوامل الوراثيه *Lr 45* , *Lr 39* (٦٦,٧% كفاءه لكل منهما) ثم العوامل الوراثيه *Lr36, Lr2a* (كفاءه ٥٣,٧% لكل منهما) مما يشير إلى امكانيه استخدام تلك العوامل الوراثية في برامج التربية للمقاومة لمرض صدا الأوراق في القمح.