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SOURCES OF RESISTANCE FOR WHEAT(*TRITICUM AESTIVUM*) LOOSE SMUT, CAUSED BY (*USTILAGO TRITICI* (PERS.)).

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Abstract :*A total of three - hundred and ninety nine genotypes of wheat (Triticum aestivum L.) were evaluated for resistance to loose smut disease , caused by the seed borne fungus, Ustilago tritici (Pers.) Rostr., by artificial inoculation with a mixture of the local strains of the fungus under field conditions. The evaluation was based on the percentage of smutted heads .*

Results revealed that, forty- seven genotypes showed highly resistance to loose smut disease, exhibiting zero infection incidence. Moreover, eighty-four genotypes showed infection incidence category (0 - 10%) that were considered resistant.

It is worth mentioning that, excellent resistance to loose smut disease has been identified and should be incorporated into the local cultivars.

Introduction

Loose smut disease of wheat, caused by the seed borne fungus *Ustilago tritici* (Pers.) Rost.r is a contemporary wheat disease after rusts in Egypt. The smut problem is overcome by different aspects including fungicidal seed treatments, manual collection of smutted heads and selection of resistant strains and /or varieties (Bassiouni *et al.*, 1988; Youssef, 1990; Mehair *et al.*, 1990 and Sherif *et al.*, 1991).

The major deterrent in the development of smut resistant wheat cultivars is the lack of knowledge on genetic variability of smut pathogens, as well as lack of resistance resources. This may be due to intense labor and large amounts of time required for determining races and the assumption that the smuts can be easily managed by resistant cultivars and seed treatments. Breeding for resistance is of great value. Therefore, the objective of the present work is to evaluate and screen for a source of resistance to loose smut disease under the Egyptian conditions.

Materials and Methods

A total of three hundred and ninety nine wheat genotypes (Table 1) were sown in 1 -m rows, 25 cm apart in the field at Zarzora Agricultural Research Station, Behera governorate, during 1995/96

(113 genotypes), 1996/97 (129 genotypes) and 1997/98 (157 genotypes) growing seasons. For screening against loose smut , five spikes of each genotype were artificially inoculated at the mid-anthesis (Large, 1954) with a mixture of the local strains of loose smut pathogen using the method adopted by Oort (1939). The inoculated spikes were covered with paper bags and clipped to maintain high humidity for susceptible infection. After repining, they were collected and threshed by hand. Seeds of each line were counted and stored until the next growing season.

In the following season (1996/97, 1997/98 and 1998/99) the inoculated seeds were sown on November, 15th in the field , at Zarazora Station. Seeds were planted separately 30-33 / row, 3-m long. Seedlings were counted after emergence to determine the absence resulting from hypersensitive reaction and / or retard effect of the environment. All plants were grown under net- house conditions to reduce the contamination from the surrounding environment.

At ear emergence, smutted heads were counted as a percentage of the total. Scoring data and disease severity were computed according to the method adopted by Nielsen (1987), in which the plants having 0-10 % smutted heads are considered to be resistant, and that having more than 10% smutted heads are considered susceptible. But, for economic view, the following classes were adapted :

Infection incidence	**Reaction class**
0-10%	(R) Resistant
11-30%	(MR) Moderately resistant
31-50%	(MS) Moderately susceptible
51-70%	(S) Susceptible
over 70%	(HS) Highly susceptible

Table (1) : List of the lines tested against infection to loose smut, *Ustilago tritici* (Pers.) Rostr. during 1995/96, 1996/97 and 1997/98 growing seasons.

No	Experiment*	No of lines / growing season		
		1995/96	1996/97	1997/98
1	A-Yield Trial	76	90	84
2	A-Yield Trial Introduced	-	-	44
3	B-Yield Trial	21	21	14
4	D-Yield Trial	16	18	15
Total		113	129	157

* Supplied by Wheat Research Section, Field Crop Res. Instit., ARC, Giza.

Results and Discussion

The most feasible approach for managing the smut diseases of wheat is to use of resistant cultivars. Development of such cultivars is costly by assuring production. The first step in a resistance breeding programs is the collection of natural variability followed by finding out the source of resistance.

It should be taken into consideration that, new races of *Ustilago tritici*, appear to arise infrequently and to spread slowly and nearly excessively on cultivated wheat varieties. New races may result either from recombination of pre-existing virulence genes or mutation from avirulence to virulence of some genes. The first possibility is greatest in a field of mixture of land races of the host, carrying a mixture of races of the pathogen (Nielsen, 1987).

A few attempts were made to identify the physiological races of *Ustilago tritici*. Abu El-Naga *et al.* (1990) identified 4 physiologic races of *U. tritici* from 13 field collections, representing the northern governorates of Egypt during 1986/87 and 1987/ 88 growing seasons. These races designated as race T34, which was the most frequent (77.5%, frequency), followed by races T1, T17, and T38 at 7.5% frequency, each . The results obtained by Youssef (1995), gave evidence to the existence of three physiologic races viz. T34, T38 and T41 in 1990/91 growing season. Race T34 was the most frequent and consequently the most prevalent, representing 77.8% frequency, followed by the the two races T38 and T41 (11.1% frequency, each). In 1991/92, only race T34 was identified from eighteen smutted samples collected and tested. Moreover, from the perspective of genetic make-up of the virulence genes the author concluded that, virulence in race T34 is controlled by single gene, i.e. Utv_2 , while race T38 exhibited two genes for virulence, i.e. Utv_1 and Utv_2 as it infects of the two differentials Florence x Aurora and Little Club, respectively.

On the other hand, the literature concerned with competition between strains of plant pathogens has been considered by different scientists. Flor, (1956), working with *Melampsors lini*, proposed a hypothesis that races with wide host ranges lack fitness to survive in the field. Watson (1958) concluded that races of *Puccinia graminis* f. sp. *tritici* with wide host ranges were unable to maintain themselves in mixtures with races of narrow host ranges when grown on susceptible seedling in the greenhouse. Van der Plank (1968) proposed a concept of stabilizing selection in which unnecessary virulence genes reduce fitness and prevent widely virulent races from predominating on simple varieties.

The obtained data (Tables, 2,3, 5, 6, 7, 8, and 9) revealed that, forty- three genotypes (13 genotypes A-YT, in 1996; 2 genotypes, B-YT, in 1996; 2 genotypes, A-YT in 1997; 15 genotypes, A-YT in 1998; 9 genotypes, A-YT, long spikes, in 1998; 1 genotype B-YT, in 1998 and 1 genotype D-YT, in 1998) showed complete resistance to loose smut (zero infection incidence).

Moreover, eighty genotypes including, 33 genotypes (A-YT, 1996), 2 genotypes (B-YT, 1996), 2 genotypes (D-YT, 1996), 14 genotypes (A-YT, 1998), 21 genotypes (A-YT, long spikes, 1998), 5 genotypes (B-YT, 1998), and 3 genotypes (D-YT, 1998) showed infection incidence (0-10%) which are considered resistant genotypes.

On the other hand, the remaining genotypes showed different reaction to the disease ranging from moderately resistance (infection incidence, 11-30 %) to moderately susceptible (infection incidence, 31-50 %) to susceptible reaction (infection incidence, 51-70 %) , to completely susceptible (over 70% disease incidence).

It is worth mentioning that, loose smut disease, in Egypt, received no attention by cereal pathologists as well as wheat breeders, since the early 1997's, after introducing the resistant variety Giza 155 in 1967/68. Therefore, using the genotypes (43 genotypes) that are entirely resistant as a source of resistance to loose smut disease must be taken into consideration in our breeding programs for successful long-term loose smut resistance of wheat.

Histological studies showed that, resistance can occur at several points in the infection cycle, including, ovary resistance, embryo exclusion, inhibition of penetration of the growing point, reduction of growing point infection during plant development, differential inter node elongation, and seedling or embryo death that eliminates the infected plants(Gaskin and Schafer, 1962). Golik *et al.* (1982)in field trials, using artificial inoculation, selected three cultivars (Khar'kovskaya 2, Khar'kovskaya 4 and Khar'kovskaya 6) having high resistance to loose smut (*Ustilago tritici*).Moreover, they reported that, the durum wheat cvs. Khar'kovskaya 3, Khar'kovskaya 7 and Khar'kovskaya 9 were particularly resistant to *U. nuda*. Turbin *et al.* (1982) found that, the spring triticale cvs. GL-24, GL-27, GL-29 and the cvs. Minskaya 2 and Moskovskaya 35 were resistant to loose smut (*Ustlago nuda*).

As a future work, the completely resistant lines identified herein can be subject to a histological studies to

...rcentage % of infection of the preliminary screening yield trial (P.Y.T, B.W) genotypes exhibiting the highest level of resistance to *Ustilago tritici* in 1995/96 growing season.

Genotype No.	Pedigree	No of plants /genotype		% of infection
		Smutted	Healthy	
1	Inia/RL4220//7C/YR"S" CM15430-25-65-05.	24	316	7.06
7	Giza 144//PJN"S"/BOW"S" S.9216-1S-8S-3S-OS.	2	101	1.94
8	Giza144//PJN"S"BOW"S" S.9216-2S-2S-3S-0S.	4	155	2.52
9	Giza144//PJN"S"BOW"S" S.9216-2S-2S-3S-0S.	9	144	5.88
10	Giza 164/Sakha 61 S.9243-2S-4S-5S-0S.	1	101	0.98
11	Giza 164/Sakha 61 S.9243-2S-9S-1S-0S.	5	54	8.47
12	Giza 164/Sakha 61 S.9243-2S-9S-4S-0S.	4	76	5.00
13	Giza 164/3/WRM/PTM//Coc S.9244-23S-4S-5S-0S.	0	145	0.00
14	Fink"S"/Sakha 61 S.9401-3S-1S-4S-0S.	7	92	7.07
15	SPRW"S"/8/zz"S"/6/REN*2/908//FN/4/4777/3/Rei//Y/KT/5/COFEN/7/S227/SON1. S9413-5S-2S-4S-0S.	4	122	3.17
16	SPRW"S"/8/zz"S"/6/REN*2/908//FN/4/4777/3/Rei//Y/KT/5/COFEN/7/S227/SON1. S9413-5S-2S-5S-0S.	0	286	0.00
17	SPRW"S"/8/zz"S"/6/REN*2/908//FN/4/4777/3/Rei//Y/KT/5/COFEN/7/S227/SON1. S9413-5S-2S-6S-0S.	0	184	0.00
18	CFN/Con"S"/RON/3BB/NOR67/4/TL/3/FN/TH/2*NAR59/5/PEW"S" S.9471-3S-1S-3S-0S.	6	96	5.88
19	KVZ/4/CC/INIA//ELGAU/SON64/5/CNO79/PRL"S" S.8917-5S-1S-3S-0S.	9	120	6.98
20	SPRW"S"/PVN"S"//ALD"S"/5/BCH"S"/4/PATO"B"/3/LR64/INIA//INIA/BB S.89776S-7S-3S-2S-0S.	5	70	6.67
21	CNO"S"/GLL/3/SON64/KLRE//BB/4/UP301/5/TL//FN.TH/2*NAR59/6/(BB**CNO*TOTA/JAR)2F5/2F2**(1N*TGLR**CNO"S"PJ62*JAR"S")2F1 S.9070-5S-1S-5S-1S-0S.	0	133	0.00
22	CHIL/RRL CM.92803-25Y-0M-0Y-4M-0RES.	8	87	8.42
23	PIK/OPTATA CM94950-34Y-0M-0Y-3M-0RES.	8	102	7.27
24	BUC/CHRC//PRL/VEE#6 CM.94699-3Y-0M-0Y-6M-0RES.	20	210	8.70
26	BOW"S"/CROW"S"	0	74	0.00
28	V.1287-GLL//71STS2959/Crow"S" CGM4622-7GM-4GM-2GM-1GM-0GM.	0	80	0.00
29	GIZA165Xmaya74"s"-Sakha69//Sham#4 CGM4673-6GM-4GM-3GM-1GM-0GM.	1	109	0.91
30	Vee"S"//GV/Ald"S" CGM4744-10GM-6GM-2GM-1GM-0GM.	0	129	0.00
31	Cc//Cal/Cc/3/KalBb//Ser82 CGM5509-8M-3GM-3GM-1GM-0GM.	4	70	5.41
32	WW33/Vee"S"//BOW"S" CGM5536-9GM-6GM-3GM-1M-0GM.	1	243	0.41
33	Era-Sx3/Kal-BbxCJ"S"/Hork/PVN"S"//Pavon76/Coc/BTT"S"/Nac-Buc"S" CGM4132-1GM-1GM-1GM-1GM-0GM	3	133	2.12
35	PRLIII/CM65531 TE82-0026Y-05M-0Y-8M-0Y.	8	99	7.48
39	A115.57/MAYA74"S"//GIZA157/3/HD2172/PAVON"S"//1158.57/MAYA74"S" SD2431-1SD-4SD-1SD.	7	80	8.05

Table 2: Cont.

Genotype No.	Pedigree	No of plants /genotype		% of infection
		Smutted	Healthy	
41	K134(60)VEE*2/4/GULL"S"/MEXI"S"//USDA75/3/HUI"S"/5/K134(60)VEE"S" CM108334-2SD-4SD-2SD.	8	173	4.42
42	KOEL"S"/3/CNO6712*7C//CDL/4/DOVE"S"/BUC"S"/5/K134(60)/VEE"S" CM108413-1SD-4SD-1SD.	4	134	2.40
43	PRL"S"/PVN//PFAU"S"/3/K134(60)VEE"S" CM108414-1SD-3SD-1SD.	3	132	2.22
46	NINGNO.8308/BAU"S"//STAR"S" CM108432-1SD-1SD-3SD.	8	157	4.85
48	NINGNO.8308/BAU"S"//STAR"S" CM108432-1SD-1SD-5SD.	0	142	0.00
50	LURK/3CMH79A.(55x2/CNO79//79A.955/BOW"S' CM106551-1SD-2SD-0SD.	12	138	8.00
51	SERI82//VEE"S"/SNB"S" ICW88-0009-0L-1AP-OL-1AP-0AP.	3	47	6.00
53	OPATA*3/WULP CM100657-R-0B-OY.	0	147	0.00
56	BW154	0	155	0.00
57	Wa4767/39//56D18/14.53/1015-6410/3/W22/4/anxTUC"S"14/Tob/cc//Pato/HD832/Bb Sh87-74-0Sh-0Sh-0Sh-12Sh0Sh.	0	143	0.00
61	Cno-7CxKAL-Bb/PCI"S"Xveery"s" Sh87-84-0Sh-0Sh-0Sh-8Sh-Osh.	0	110	0.00
62	Cno-7CXKAL-Bb/PCI"S'Xveery"s" Sh87-84-0Sh-0Sh-0Sh-10Sh-0Sh.	3	78	3.70
64	JUP/ZP//COC/3/Pun/4/Gen CM93697-11M-0Y-0M-5Y-0B.	14	214	6.14
65	Bau/Pri CM92474-28Y-0M-0Y-8M-0RES.	3	121	2.42
71	Kal/Bb/Ald"S"/3/TR810328 S8919-3S-2S-1S-0S.	3	223	1.33
72	Banu/5/Inia"S"/CC/4/12300/Tib//Jar/3/pk20S9025-1S-7S-4S-0S	0	146	0.00
74	Cno"S"/G11/3/Son64/K1.Re//Bb/4/Up301/5TI/2'Nar59/6/(Bb*Cno**Cno*Tota/Jar)2F5/2F2**(1N *Tg1r**Cno"S"*Pj62*Jar"S")2F1.	3	37	7.50
76	ISR/16"S"7C750451-ZC-100R/H8RA"2F2/Inia66""BB/2F2/Sakha8.	1	197	0.51

Table (3): Percentage % of infection of the preliminary screening yield trial (B-YT, BW) genotypes exhibiting the highest level of resistance to *Ustilago tritici* in 1995/96 growing season.

Genotype No.	Pedigree	No of plants /genotype		% of infection
		Smutted	Healthy	
9	Giza163/Pea"S" S8777-4S-1S-1S-0S.	7	109	6.03
11	Banu/5/Inia"S"/CC/4/12300/Tob//Jar/3/Pk20 S9025-1S-7S-3S-0S.	0	200	0.00
12	Hahn*2/pri CM90320-A-1B-5Y-0B-6M-0Y.	0	141	0.00
20	Mri/BUC//Seri CM93046-8M-OY-OM-2Y-0B.	10	171	9.17

Table (4): Percentage % of infection of the final national screening yield trial (D-YT, BW) genotypes exhibiting the highest level of resistance to *Ustilago tritici* in 1995/96 growing season.

Genotype No.	Pedigree	No of plants /genotype		% of infection
		Smutted	Healthy	
12	2CA542C/SHOROSPELKA/NEUZUCT/3/NAC76.SWM8943-1Y-1Y-0Y-4AP-3AP-0AP	1	138	0.72
13	55-1744/7C//5N/RD1/3/CROW"S"SWM12008-2AP-1AP-3AP-0AP	1	185	0.54

Table (5): Percentage % of infection of the preliminary screening yield trial (A-YT, BW) genotypes exhibiting the highest level of resistance to *Ustilago tritici* in 1996/97 growing season.

Genotype No.	Pedigree	No of plants /genotype		% o f infection
		Smutted	Healthy	
61	Psn"s"/Bow"s"//Kauz"s"CM/0/423-0AP-0L-4AP-0AP-1AP-0TS-0AP	0	203	0.00
89	Bb/6/Cnocher//om/3/gall/4/SA.42/5/Kal/HD 6485/7/gn/3/Pota//Bb/Cno/4/Emu"s"/Flicher CGZ91153-6gz-3gz-2gz-0gz	0	266	0.00

Table (6) : Percentage % of infection of the preliminary screening yield trial (A-YT, BW) genotypes exhibiting the highest level of resistance to *Ustilago tritici* in 1997/98 growing season.

Genotype No.	Pedigree	No of plants /genotype		% of infection
		Smutted	Healthy	
13	Sakha62/5/May"s"/Moncho"s"/4/Cno"s"/J62//Gallo/3/Pci"s"S.10251-1S-2S-1S-0S	8	78	9.30
15	Sakha62/5/May"s"/Moncho"s"/4/Cno"s"/J62//Gallo/3/Pci"s"S.10251-2S-2S-2S-0S	3	100	2.91
17	Bobwhite/HD2009 S.10342-1S-1S-1S-0S	12	186	6.06
21	Sannine/4/D6301/Nai//W/Rm/3/Cno"s"/Chr/5/May"s"/Moncho"s"/4/Cno"s"/Jb2//Gallo/3Pci"s"S.10469-2S-1S-2S-0S	9	96	8.57
22	Sannine/4/D6301/Nai//W/Rm/3/Cno"s"/Chr/5/Sonalika S.10470-6S-2S-3S-0S	0	53	0.00
23	Ti/3/Fn/Th//Nar59*2/4/Bal"s"/8/Zz"s"/6/Rfn2*908//Fn/4/4777/3/Rei//Y/Kt/5/Cofen/7/S.227/Son1 S.10525-10S-1S-1S-0S	0	241	0.00
24	Ti/3/Fn/Th//Nar59*2/4/Bal"s"/8/Zz"s"/6/Rfn2*908//Fn/4/4777/3/Rei//Y/Kt/5/Cofen/7/S.227/Son1 S.10525-10S-1S-2S-0S	0	109	0.00
31	Sakha73/5/Ias58/4/Kal/Bb//Cj"s"/3/Ald"s" S.9720-2S-3S-3S-2S-0S	0	208	0.00
32	Chil//Dwl5046/2*Celya S.9943-15S-8S-1S-3S-0S	3	105	2.78
47	KALLANSONA/5/CNO79/4/BB/SYG/3/RA/2F2//MO SD3550-8SD-3SD-0SD	16	146	9.88
50	4777//FKN/GB/3/VEE"S"/4/BUC"S"/PVN"S"/S/CMH74A.630/4*SX SD2847-2SD-2SD-2SD-0SD	3	50	9.64
52	MYNA"S"/VUL"S"/5/BUC"S"/4/IZPP//IRN46/CNO67/3/PRT SD2942-12SD-6SD-1SD-0SD	5	192	5.66
55	4777//FKN/GB/3/VEE"S"/4/BUC"S"/PVN"S"/5/KEA"S" SD3108-1SD-1SD-1SD-0SD	0	50	2.54
57	BAU"S"/ALPH105 SD2806-15SD-7SD-3SD-0SD	0	52	0.00
58	KAUZ"S"/5/BUC"S"/4/TZPP//IRN46/CNO67/3/PRT SD2809-7SD-3SD-2SD-0SD	0	98	0.00
63	VEE"S"/TSI//CMH79.959/2*CNO79 SD2919-1SD-2SD-2SD-0SD	0	59	0.00
64	MAYA"S"/SAP"S"//F134-71/CROW SD2922-2SD-3SD-5SD-0SD	7	261	2.61
65	SAKHA3/5/CNO79/4/BB/SYG/3/RA/2F2//MO SD2474-43SD-1SD-1SD-0SD	0	74	0.00
66	SAKHA79/3/AIFON*4//MAYA74/PVN"S" SD2534-69SD-2SD-1SD-0SD	0	94	0.00
70	MAYA74A"S"/ON//1160-147/3/BB/GLL/4/CHAT"S/5/CH"S"/BOW"S" SD3318-1SD-1SD-1SD-0SD	0	281	0.00
71	KAL//BB//MONCHO"S"/3/INIA/4/SON64/5/INIA KVZ/4/CC/INIA/3/CNO//ELGAU/SON64/6/SAKHA10 CR:5700-5GZ-4GZ-1GZ-1GZ-0GZ	0	198	0.00
72	KAL//BB//MONCHO"S"/3/INIA/4/SON64/5/INIAVEE"S"/CKR"S"CRGZ5701-3GZ-2GZ-2GZ-2GZ-0GZ	0	162	0.00
73	SAKHA8/5/PCI"S"MAYA74"S"/4TIRESEL/3/BBPC//SXCRGZ5711-4GZ-3GZ-2GZ-0GZ	0	147	0.00
74	SAKHA8/5/4777(2)//FKN/GB/3/VEE"S"/4/BUC"S"/PVN"S"CRGZ5724-3GZ-2GZ-1GZ-1GZ-OZ	5	139	3.47
75	NAC/VEE"S"/6/BCH"S"/HORKS/5/BCH"S"/4/7C/POT(B)/3/LR64/INIA//INIABB CRGZ5740-8GZ-5GZ-3GZ-3GZ-0GZ	8	158	4.82
78	AKHA8/5/K134/4/TOB/BMAN/BB/3/CALCRGZ91110-8GZ-6GZ-5GZ-3GZ-0GZ	22	240	8.40
79	SAKHA8/8CRESTA-F4(52078-R-81-82)CRGZ91111-6GZ-4GZ-3GZ-2GZ-0GZ	3	37	5.7
83	BUSH/AMIGOT105XS.69	0	235	0.00
84	BUSH/AMIGOT101XS.69	0	293	0.00

No.	Pedigree	No. of plants/genotype		% of infection
		Smutted	Healthy	
6	MAYA"S"/MON"S"//CMH74A.592/3/*2SAKHA8 SD10002-5SD-3SD-2SD-1SD-3SD-2SD	8	178	3.40
7	MAYA"S"/MON"S"//CMH74A.592/3/*2SAKHA8 SD10002-5SD-3SD-2SD-1SD-3SD-2SD	0	220	0.00
9	MAYA"S"/MON"S"//CMH74A.592/3/*2SAKHA8 SD10002-5SD-3SD-2SD-1SD-3SD-2SD	6	157	3.69
10	MAYA"S"/MON"S"//CMH74A.592/3/*2SAKHA8 SD10009-5SD-3SD-2SD-1SD-3SD-2SD	5	255	1.92
11	MAYA"S"/MON"S"//CMH74A.592/3/*2SAKHA8 SD10009-5SD-3SD-2SD-1SD-3SD-2SD	10	270	3.57
12	MAYA"S"/MON"S"//CMH74A.592/3/*2SAKHA8 SD10009-5SD-3SD-2SD-1SD-3SD-2SD	0	210	0.00
13	MAYA"S"/MON"S"//CMH74A.592/3/*2SAKHA8 SD100010-5SD-3SD-2SD-1SD-3SD-2SD	17	270	5.92
14	MAYA"S"/MON"S"//CMH74A.592/3/*2SAKHA8 SD100010-5SD-3SD-2SD-1SD-3SD-2SD	8	180	4.26
15	MAYA"S"/MON"S"//CMH74A.592/3/*2SAKHA8 SD100013-5SD-3SD-2SD-1SD-3SD-2SD	6	138	4.17
16	CMH77A.917/YAV79//CMH77A.917/3/BB/PATO(B)//COCCGM45282GM-3GM-1GM-0GM	0	133	0.00
17	CMH80A.768/3*CNO79/2/TR380-16.3A614/3/VHAT"S"CGM4540-5GM-3GM-2GM-0GM	2	148	1.33
18	CMH74A.630/SX/2/GV/D6301/3/ALD"S"CGM4543-6GM-2GM-1GM-0GM	3	255	1.16
19	CMH79A.955*2/CNO79//CMH79A.955/BOW"S"/3/TOW"S"/PEW"S"CGM4585-10GM-3GM-2GM-0GM	8	175	4.37
21	CMH83/BB/7C*2//Y50E/KAL*3CGM4592-6GM-3GM-1GM-0GM	0	230	0.00
22	CMH183/GENARO81CGM4531-4M-2GM-1GM-0GM	0	213	0.00
23	SERI82//SHI+4414/CROW"S"/3/CMH83CGM4552-4GM-3GM-2GM-0GM	2	275	0.72
24	GEMMEIZA3/CMH74A-630/4*SXCGM4539-5GM-3GM-1GM-0GM	3	240	1.24
25	BAU"S"/CMH83CGM4589-3GM-2GM-1GM-0GM	0	220	0.00
29	ISR//16ISR///6*TC750451-ZC100R/H8RA**ZF2/INID66**BB/2F2/3/CNO79*2/PRL"S"CRG91169-10GM-8GM-6GM-1GM-	1	207	0.48
30	ISR//16*TC750451-ZC100R/H8RA**ZF2/INID66**BB/2F2CRG91169-10GM-8GM-6GM-2GM-0GM	19	296	6.03
31	ISR//16*TC750451-ZC100R/H8RA**ZF2/INID66**BB/2F2CRG91169-10GM-8GM-6GM-3GM-0GM	28	276	9.21
32	ISR//16*TC750451-ZC100R/H8RA**ZF2/INID66**BB/2F2/4MAL"S"/BUC"S"CRGZ91174-4GM-3GM-2GM-0GM	25	277	8.28
33	ISR//16ISR///6*TC750451-ZC100R/H8RA**ZF2/INID66**BB/2F2/4/KALBB*CJ7/"S"/HORK(KVZT171/MAYD'S"BB-INID)55697CRGZ91175-8GM-4GM-3GM-3GM-0GM	8	156	4.88
35	ISR//16ISR///6*TC750451ZC100R/H8RA**ZF2/INID66**BB/2F2/5INID/NAPO//TOB66/3/SPRW"S"/4/SAKHA80CRGZ91179-8GM-6GM-4GM-1GM-0GM	1	160	0.62
37	CMH67.912/CMH7.6A769//BEE/2*CMH76.1084/3/CMH76.A.769//CMH.955/7/T.AESTIVUM/KAL/BB/6/CRGZ91181-8GM-6GM-4GM-0GM	0	238	0.00
38	CMH67.912/CMH7.6A769//BEE/2*CMH76.1084/5/GLL/BB/INI/A/4/NABO/TOB66/3/SPRW"S"CRGZ91182-6GM-4GM-3GM-1GM-0GM	7	143	4.67
39	CMH67.912/CMH7.6A769//BEE/2*CMH76.1084/3/CNO/GLL//BB/INIA/4/NABO/TOB66/3/SPRW"S"CRGZ91182-5GM-2GM-2GM-2GM-0GM	0	220	0.00
41	CMH7A.912/CMH76.A769//BB/2*CMH76.1084/3/CNO79*2/PRL"S"CRGZ91184-6GM-2GM-2GM-1GM-0GM	29	272	9.64
42	CMH7A.912/CMH76.A769//BB/2*CMH76.1084/3/CMH76A.CMH176A.769//CMH79A.955/4/DW15046/2*CELAYACRGZ91185-8GM-6GM-5GM-1GM-0GM	0	89	0.00
44	K134(60)/4/TOBBMAN/BB/3/CAL/5/MAYA"S"/MAN"S/4/CNO/J62//GALLO/3/CI"S"CRGZ91196-8GM-6GM-4GM-2GM-0GM	23	230	4.16

Table (8): Percentage % of infection of the preliminary screening yield trial (B-YT, BW) genotypes exhibiting the highest level of resistance to *Ustilago tritici* in 1997/98 growing season.

Genotype No.	Pedigree	No of plants /genotype		% of infection
		Smutted	Healthy	
5	S.9720-2S-4S-2S-0S	34	427	7.38
6	S.9720-2S-6S-1S-0S	25	237	9.54
7	CNO"S"/G11/3/SON64/KL.REND//BB/4/UP301/5/TI/3/FN/TH//2* NAR59/6/TI/3/FN/TH//NAR59*2/4/BAL"S"S.9751-3S-1S-2S-0S	2	90	2.17
9	CHIL//SNIN/ALD"S"S.9946-1S-3S-1S-0S	0	129	0.00
11	TLR"S"/JUM®MOR"S"/VEE"S"CGM4555-1GM-3GM-4GM-0GM	16	150	9.64
12	MAYA74A"S"/ON//1160-147/3/BB/GLL/4/CHAT"S"/5/GH"S"/BOW"S"SD3318-1SD-2SD-3SD-0SD	4	220	1.79

Table (9) : Percentage % of infection of the final national screening yield trial (D-YT, BW) genotypes exhibiting the highest level of resistance to *Ustilago tritici* in 1997/98 growing season.

Genotype No.	Pedigree	No of plants /genotype		% of infection
		Smutted	Healthy	
6	SAKHA92/TR810328S8871-1S-2S-1S-0S	19	245	7.20
7	ATTILACM85836-50Y-OM-0Y-3M-0Y	0	165	0.00
9	BOW"S"/CROW"S"CM69599-4AP-2AP-2AP-2AP-1AP-0AP	4	178	2.20
14	BUSH/AMIGO/T101XS.69	7	201	2.01

determine the type of resistance to serve the breeding program.

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مصادر المقاومه للتفحم السائب فى القمح المتسبب عن يوستيلاجو تريتيساى

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اجرى هذا البحث بغرض تقييم ٣٩٩ سلاله من قمح الخبز (تريتيكم سيتايفم) ضد الاصابه بمرض التفحم السائب ٠ اجرى هذا التقييم تحت ظروف الحقل بعمل عدوى صناعيه للسلالات المختبره باستخدام سلالات الفطر المحليه٠ وقد اعتمد التقييم على حساب النسبه المؤيه للسنابل المصابه الى العدد الكلى للسلاله النباتيه٠ هذا وقد اظهرت النتائج المتحصل عليها مايلى:-

١- وجود ٤٧ سلاله اظهرت مقاومه تامه للمرض حيث لم تظهر عليها اعراض ٠

٢- وجود ٨٤ سلاله اظهرت مقاومه للمرض حيث اعطت اصابه من صفر -١٠%٠

٣- امكن تعريف مصادر جيده للمقامه لمرض التفحم السائب والتى يجب ادخالها بكفاءه فى برامج التربيه لانتاج الاصناف المقاومه٠