

PROBABLE GENES FOR YELLOW RUST RESISTANCE IN SOME EGYPTIAN WHEAT CULTIVARS

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ABSTRACT

The present work gave evidence to the presence of 11 physiological races of *Puccinia striiformis* West., the causal agent of stripe rust of wheat in Egypt during 2005/2006. These races were identified as: 4E0, 4E2, 4E16, 64E4, 76E4, 134E18, 196E18, 198E150, 198E86, 206E30 and 230E186. These races were identified according to their virulence to both the world and European set of wheat differentials. They showed a wide range of virulence. The obtained results indicated the efficacy of Yr4^r, YrSP, Yr1, Yr5 and Yr10.

It was recommended to incorporate such genes within the local wheat cultivars aiming to increase their level of resistance against stripe rust.

Matching between cultivars and lines indicated that the wheat cultivar Sakha 61 was postulated to have 9Yr's. Also, the obtained results indicated that matching amongst cultivars clarified the presence of common resistance genes against stripe rust. This may be the reason behind the considerable level of resistance to stripe rust *i.e.*, Yr6 and Yr2 and this would indicate the genetic approximation of such cultivars (Gemmeza 5, Gemmeza 7, Giza 168, Sakha 61 and Sakha 93). This report is considered a primitive indicator to the presence of resistance genes, it could be confirmed by studying the pedigree of each cultivar and/or making crosses to observe the segregation. Consequently, the present work is considered an effective tool in the breeding program of wheat against rust diseases in general.

INTRODUCTION

Wheat (*Triticum aestivum*, L.) stripe rust incited by (*Puccinia striiformis* West.) is an important disease worldwide (Stubbs, 1985 and 1988 and Roelfs *et al.*, 1992). Cool and high humidity are suitable factors to the wide distribution of the disease (Stubbs, 1988, Johnson, 1988 and Danial, 1994). Since the discovery of genetic resistance in stripe rust that reported by Biffen (1905), many papers were reported *i.e.*, Flor (1955) suggested the gene- for gene theory, the occurrence of pyramiding resistance (accumulating multiple genes) as a term was suggested by Watson (1970). In Egypt, a lot of papers were published in the same trend *i.e.*, physiological specialization and varietal resistance (Abdel-Hak *et al.*, 1972; El-Daoudi *et al.*, 1977; Abu El-Naga *et al.*, 1997, 1998, 1999 and 2001, and Youssef *et al.*, 2003; 2006a and 2006b).

The main objective of the present work is the identification of stripe rust physiologic races in some of the northern governorates in Egypt and determining the postulated and common stripe rust genes involved in some Egyptian wheat cultivars.

MATERIALS AND METHODS

The present work was carried out at Sakha Agricultural Research Station, Wheat Disease Research Section in 2005/2006 growing season.

Stripe rust samples were collected from the different susceptible wheat cultivars showing the symptoms of stripe rust disease on leaves and/or

spikes (Hendrix, 1967, Hendrix and Fuchus, 1970; Manners, 1971 and Shaner and Powelson, 1973).

The general survey included certain governorates *i.e.*, Dakahlia, Dumyitta and Kafrel-Sheikh in areas grown to wheat cultivars *i.e.*, Sakha 8, Sakha 69, Giza 163 and Rust trap nursery. Samples were left to dry over envelopes at room temperature overnight and preserved at a fridge in disseccator containing calcium chloride till usage

Purification: single pustules were picked from each sample and used in the inoculation of eight days old seedlings from the susceptible wheat cultivar *i.e.*, Morocco, Little club or *Triticum spelta saharensis* following the method adopted by (Stubbs, 1988), in which seedlings were rubbed gently between fingers using sterile distilled water plus adhesive material (Tween 20), then inoculated with spore powder from each samples, preserved in humid apparatus at 9-10°C overnight in darkness. Transferred to the benches in controlled cadges at 15-18°C for 8 hrs. at night, and 16 hrs. at 15-18°C at light density of 7500 lux. This diurnal system was applied for 8-10 days. The developed uredial sori were immediately picked and transferred to complete pots of susceptible wheat cvs. to be used.

Race identification: The differential varieties listed in Table (1) in addition to 9 local vars. were artificially inoculated with the purified samples using the technique of Stubbs (1988). Records of stripe rust were recognized as high infection type (HIT) and low infection type (LIT). the high infection for each race was expressed as the decenary value for each differential of both world and European sets.

Postulation of resistance genes within local wheat cvs.

After the record of stripe rust, data on cvs. *versus* physiological races, a matching was performed between cvs. (unknown genes) and wheat stripe rust differentials (known genes) to reach to the gene presence (whether it probably present or may be present) the method suggested by Statler (1984) was followed in this regard. This suggested method omitted the races that characterized by complete virulence or avirulence to test cvs. or Yr's.

Likewise, the host lines and /or cvs. Having complete resistance or susceptibility were also omitted from matching. So, the reaction (LIT):(HIT) or (HIT):(LIT) were adequately selected for the matching. The four categories (+, -, - 0, and 0) were belt on the following basis:

- 0 : absence of (LIT): (HIT) cultures this means that cultivars involved the same gene(s).
- : the absence of (HIT) : (LIT), indicating that the hosts (Yr's) or (cv.), does not contain the same gene(s).
- 0 : the absence of H : L or L : H cultures indicating that both hosts carry the same resistance gene(s) at least for the used culture.
- + : the occurrence of some H : L cultures and some L : H cultures indicating that hosts do not carry the same resistant gene(s).

Compared 9 cultivars with unknown resistance genes (host B) to 17 isogenic lines each carrying a single known gene for resistance to stripe rust (host A). Because host A carries only a single gene, infection type in categories "0" and "- 0" *i.e.*, no LIT : HIT cultures indicates that cultivars carries the gene present in the isogenic line. Category "- 0" indicated that it

carries only that gene. Category "-" and "+" (i.e., some cultures in the LIT : HIT infection type) indicate that the tested cultivar does not possess the gene carried in the isogenic line. Category "-" means that the cultivar does not carry the gene for resistance in the comparison. While category "+" indicates that there is a different gene for resistance.

Table (1): Identification of 11 physiologic races of stripe rust (*Puccinia striiformis* West.) on 17 wheat differential cultivars and their specifications in Egypt (2005/2006).

Differential cultivar	Triticum aestivum L. ssp. album SPYr5										World Set										European Set	Race											
	Clement Yr9		Suwong2XOmmar Yrau		Strubs Dikopf YrSD		Moro Yr10		Vilmorin 23 Yr3V		Heinsoeben Yr6		Lee Yr7		Chinese 166 Yr1		Heins VII Yr2*		Spalding prolific YrSP				Carsten V Yrcv		Compaire Yr8		Nord Desperz Yr3N		Heins Peko Yr6*		Reichersberg 42Y17		Hybride 48 Yr4*
Abbreviation	SP	CL	SU	SD	Mo	V23	HK	Lee	Ch							VII	SP	cv	Com	ND	Pe	R42	H46										
Yrs	5'	9'	SU	SD	10	3V	6	7	1							2'	5'	Q2	8	3N	6'	7'	4'										
Decenary value	(2)	(2)	(2)	(2)	(2)	(2)	(2)	(2)	(2)							(2)	(2)	(2)	(2)	(2)	(2)	(2)	(2)										
	256	128	64	32	16	8	4	2	1							128	64	32	16	8	4	2	1										
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Virulence percentage was computed by dividing the susceptible responses by the total number of responses.

EXPERIMENTAL RESULTS

As regard to the identification of stripe rust (*P. striiformis*) predominant in Egypt during 2005/2006, data presented in Table (1) revealed such characterization. These data revealed that 12 physiologic race could be identified on 17 universal differential varieties (included 9 European and 8 world sets). These identified races were; 4E0, 4E2, 4E16, 64E4, 76E4, 134 E18, 196E18, 198E150, 198E185, 206E30, and 230E186, respectively. The value relevant to each race was derived from the summation of the dicenary values for each of defeated cultivars in each set (for each high infection type). For example race *i.e.*, 4E0 indicated that the race attacked Heins Kolben (Yr6) only and was avirulent to either of the lines of the European Set. On this foundation the identification was accomplished with the rest of races. It must be remembered that race 230E186 was repeated twice. It is clear from the commulated data that vars. *i.e.*, *Triticum spelta album* (Yr5), Moro (Yr10), Chinese 166 (Yr1), Spalding prolific (YrSP) and Hybride 46 (Yr4*) were not attacked by either of the tested races. Consequently, these vars. were not represented in further matching to postulate gene in the commercials.

Data in Table (2) clarified the matching between 9 local commercial cvs., 16 stripe rust monogenic lines, when inoculated against 11 races of *P. striiformis* was singly used.

These data indicated that cv. Gemmeiza-5 may involve (Yr6 and Yr2), Gemmeiza-7 (Yr6 and Yr2), Gemmeiza-10 (Yr7 and Yr6), Giza 168 (Yr6, SU and 2), Sakha 8 (6 and 2), Sakha 61 (Yr1, 3N, 8, 7, 6, SU, 9, 2 and A*), Sakha 93 (8, 6 and 2). It was indicated that no tested Yr's could be detected with Gemmeiza-9 and Sakha-94.

Table (2): Revealed the incidence of cultivars in the LIT : HIT (Low infection type : High infection type) comparison of 16 near-isogenic lines of yellow rust (Yr's) and 9 commercial wheat cultivars inoculated with 11 races of *Puccinia striiformis* West. f.sp. *tritici* at seedling stage under greenhouse condition in 2005/2006 growing season.

Cultivars	Yr's															
	Yr7*	Yr6*	Yr3N	Yr8	Yrcv	Yr2*	Yr7	Yr6	Yr3V	YrSD	YrSU	Yr9*	Yr18	Yr2	Yr19	Yr(A*)
Gemmeiza5	+	+	-	-	-	-	-	0	-	-	+	-	-	0	+	-
Gemmeiza 7	+	+	-	-	-	-	-	0	-	-	+	-	-	0	+	-
Gemmeiza 9	-	-	-	-	-	-	-	+	-	-	-	-	-	+	-	-
Gemmeiza 10	0	+	-	+	-	+	+	0	+	+	+	+	+	+	+	+
Giza 168	+	+	+	+	+	+	+	0	-	+	0	+	+	0	+	+
Sakha 8	+	+	-	-	-	-	-	0	-	-	+	-	-	0	+	-
Sakha 61	0	+	0	0	+	+	0	0	+	+	0	0	+	0	+	0
Sakha 93	+	+	+	0	+	+	+	0	+	+	+	+	+	0	+	+
Sakha 94	+	+	-	-	-	-	-	+	+	-	+	-	+	+	+	-

Data in Table (2a) supported those recorded in table (2) since they indicated that Sakha 61 included ca., 9 Yr's. Both Giza 168 and Sakha 93 included 3 Yr's, *i.e.*, Gemmeiza-5, Gemmeiza-7, Gemmeiza-10 and Sakha 8 included 2 Yr's each conversely, no tested Yr's could be detected in either of Gemmeiza-9 or Sakha 94.

Table (2a): Probable resistance genes for yellow rust in some Egyptian commercial wheat cultivars in 2005/2006.

Cultivars	Probabililty Yr's genes	Efficacy of gene (%)
Gemmeiza5	Yr6 and Yr2	12.5
Gemmeiza 7	Yr6 and Yr2	12.5
Gemmeiza 9	0	0
Gemmeiza 10	Yr7* and Yr6	12.5
Giza 168	Yr6, YrSU and Yr2	18.75
Sakha 8	Yr6 and Yr2	12.5
Sakha 61	Yr7*, Yr3N, Yr8, Yr7, Yr6, YrSU, Yr9*, Yr2 and YrA*	56.25
Sakha 93	Yr8, Yr6 and Yr2	18.75
Sakha 94	0	0

* yellow rust resistance genes

Data in Table (2b) showed the efficacy of Yr genes against the tested stripe rust races during 2005/2006. These data indicated that Yr6 exhibited the highest rate of efficacy (77.7%) followed by Yr2 (66.6%), Yr's (7*, 8 and SU) were 22.2% each; Yr's (3N, 7, 9* and A*) represented by 11.1% each. finally no efficacy was detected with Yr's 6*, cv, 2*, 3V, SD, 18 and Yr14. ca. 0.0%.

Table (2b): The frequency of identified Yr's genes postulated in 9 commercial wheat cultivars in 2005/2006.

Yr's resistance genes	No. of cultivars carrying Yr's	Efficacy (%)
Yr7*	2	22.2
Yr6*	0	0.00
Yr3N	1	11.1
Yr8	2	22.1
Yrcv	0	0.00
Yr2*	0	0.00
Yr7	1	11.1
Yr6	7	77.7
Yr3V	0	0.00
YrSD	0	0.00
YrSU	2	22.2
Yr9*	1	11.1
Yr18	0	0.00
Yr2	6	66.6
Yr19	0	0.00
Yr(A*)	1	11.1

* yellow rust resistance genes

Data in Table (3) revealed the interrelationships amongst the commercials and its reciprocal reaction. These data indicated that a common stripe rust gene(s) may be presented between each of Gemmeiza-5 and Sakha 8 and between Sakha 8 and Gemmeiza-5 and Gemmeiza-7.

On the other hand, common genes probably present between Sakha 61 and each of Gemmeiza -5, -7, -9, -10, Giza 168, Sakha 8 and -94, however, Sakha 93 likely has common gene with Gemmeiza -5, -7, -9 Sakha

8 and Sakha 94, also, Giza 168 was postulated to have common gene with Gemmeiza 5, -7 -9 and Sakha 8. Likewise, Gemmeiza -9 probably has common genes with Gemmeiza -5 and -7. Finally, Sakha 8 likely has common gene with Giza 168.

DISCUSSION

Wheat stripe rust incited by *Puccinia striiformis* West., is considered to be one of the destructive diseases of wheat (*Triticum aestivum*, L.) all over the world due to the introduction of new cultivars and/or lines with new genetic make up (Stubbs, 1980 and 1985 and Zadoks, 1961).

It was reported that problem of stripe rust of wheat due to relatively olden period (Hendrix, 1967; Manners, 1971; Abdel-Hak et al., 1972; El-Daoudi, 1977 and Stubbs, 1980 and 1985), since the disease was known as a sporadic one, but its occurrence began to be continuous during 1990's (Abu- El-Naga et al., 2001).

The present work is considered an extension to the trend of stripe rust researchers established in the latter decades especially after the building of stripe rust greenhouse at Sakha, Kafr El-Sheikh governorate.

Table (3): Incidence of cultivars in the LIT : HIT (Low infection type : High infection type) comparison of cultivars inoculated with 11 physiologic races of *Puccinia striiformis* West. f.sp. *tritici*.

Cultivars	Gemmeiza5	Gemmeiza 7	Gemmeiza 9	Gemmeiza 10	Giza 168	Sakha 8	Sakha 61	Sakha 93	Sakha 94
Gemmeiza5		- 0	-	+	0	- 0	0	0	+
Gemmeiza 7	- 0		-	+	0	- 0	0	0	+
Gemmeiza 9	0	0		0	0	0	0	0	0
Gemmeiza 10	+	+	-		+	+	0	+	+
Giza 168	-	-	-	+		-	0	+	+
Sakha 8	-0	-0	-	+	0		0	0	+
Sakha 61	-	-	-	-	-	-		+	-
Sakha 93	-	-	-	+	+	-	+		-
Sakha 94	+	+	-	+	+	+	0	0	

The obtained results indicated the presence of 11 physiologic races of *Puccinia striiformis* West. During the elapsed seasons, 2000-2005. These races were identified i.e., 4E0, 4E2, 4E16, 64E4, 76E4, 134 E18, 196E18, 198E150, 198E186, 206E30 and 230E186. Similar results were recorded by Abu- El-Naga et al. (2001), Youssef et al. (2003, 2006a and 2006b) who mentioned that the races 230E150, 4E0, 4E2 4E16, 198E186 and 198E150 in Egypt. On the other hand, in neighboring countries races; 134E150 230E150, 230E134 and 230E150 were recorded by Hakim et al. (2001), added to races 134E22, 2E16, 134E146, 134E150 and 6E16, 134E146 and 134E150 that also, recorded by Louwers et al. (1992). It is concluded that

specification of such races were similar in time and space since the simultaneous occurrence may be repeated each season due to the advance in both wheat breeding and disease programs as previously mentioned.

The obtained results also, indicated that Yr6 is considered a common gene amongst the tested cultivars followed by Yr2. So, the good performance of our cultivars may be due to the presence of such genes.

Conversely, the occurrence of Yr's i.e., 6*, cv, 2*, 3V, SD, 18 and 19 indicated inefficacy that may be noticed with only our cultivars, since cv having Yr18 are effective elsewhere, where Yr18 varied from 5R to 40MR in Kazakhstan to 100s in Tajikistan according to Absattarova *et al.* (2001).

As regard to comparison between cultivars and the Yr's (monogenic lines) followed by comparisons between cultivars and cultivars. The obtained results indicated that most of these cultivars exhibited common genes (Yr's). These findings are considered speculation or postulation and/or tentative generalization, and to confirm these results we must see their pedigree or make crosses to confirm the presence of such gene within cultivar depending on their segregations.

Finally, the present work would be an effective tool if it is exploited well in the program of breeding for disease resistance.

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جينات المقاومة المتوقعة للصدأ الأصفر في بعض أصناف القمح المصرية

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دلت نتائج هذا البحث علي وجود احدي عشر سلالة فسيولوجية من فطر الصدأ الأصفر علي أصناف القمح المصرية خلال موسم 2006/2005 ويتسبب هذا المرض عن فطر بكسينيا سترايفورمس *Puccinia striiformis* وهذه السلالات عرفت كالاتي: 4E0, 4E2, 4E16, 64E4, 76E4, 134E18, 196E18, 198E150, 198E86, 206E30 and 230E186

وقد تم تعريف هذه السلالات من منطلق عدوانيتها علي كل من مفرقات المجموعة العالمية والأوربية. وقد تراوحت هذه السلالات في مدى عدوانيتها علي هذه الأصناف المفرقة. وقد دلت النتائج علي كفاءة الجينات Yr4*, YrSP, Yr1, Yr5 and Yr10.

وقد أوصينا في هذا البحث بضرورة إدخال هذه الجينات في الأصناف المنزرعة بغية تحسينها من حيث المقاومة لهذا المرض والتصدي لحالات الوبائية التي قد تظهر فجأة. ومن ناحية أخرى دلت النتائج بأن الصنف سخا 61 من المحتمل أن يحتوي علي 9 جينات تقريبا. كما أن هناك جينات مشتركة بين أغلب الأصناف موضع الاختبار وهي Yr6 and Yr2 وهذه الجينات يعزى إليها المستوي العام للمقاومة للأصناف المختبرة ، ويدل أيضا على التقارب الوراثي بينها (جميزة 5، جميزة 7، جميزة 168، سخا 61، سخا 93).

وهذا البحث يعتبر مؤشر مبدئي علي نوعية جينات المقاومة في الأصناف السائدة ويتم تأكيد نتائج هذا البحث بدراسة نسب هذه الأصناف وكذلك بعمل تيجينات بين الأصناف ودراسة الانعزالات الناتجة عنها. ومن هنا نقول: أن هذا البحث يعتبر أداة فعالة في برامج التربية للمقاومة للأصناف في مصر.