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Molecular Identification of Some Stem Rust and Yellow Rust Resistance Genes in Egyptian Wheat and Some Exotic Genotypes

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Abstract

Wheat stem rust, caused by *Puccinia graminis* f. sp. *tritici*, and yellow rust, caused by *Puccinia striiformis* Westend. f. sp. *tritici Erikss*. (*Pst*), are the most important wheat diseases. The study used molecular characterization and identification of candidate lines and cultivars for predicting stem rust and yellow rust resistance genes (*Sr2, Sr28, Sr35, Sr40*; *Yr10, Yr15* and *Yr18*), respectively. The result of this study showed that the analysis of four Egyptian cultivars and three Libyan local cultivars and three advanced breeding lines from CIMMYT and ICARDA for a marker linked to individual gene, *Sr2* was present in all test genotypes, *Sr28* was present in six genotypes, *Sr35* was present in four genotypes,*Sr40* was present in two genotypes. Likewise, *Yr10* was present in two genotypes, *Yr15* in six genotypes and *Yr18* wasn't found in any of the tested genotypes. These markers should be useful in marker-assisted pyramiding of stem rust and yellow rust resistance genes to develop new cultivars with multiple gene resistance against stem rust, yellow rust races in Egyptian wheat.

Keywords: *Wheat, Stem Rust, Yellow Rust, ISSR, Molecular Characterization, Sr Genes, Yr Genes, Resistance Genes, Molecular Markers, SSRs , Egyptian Wheat, Exotic Genotypes*

Introduction

Wheat (*Triticum aestivum* L.), is the largest cultivated crop in both cultivated areas and total production in the world and Egypt. In the last 50 years, many epidemics of rusts have occurred in Egypt. In recent years, stem rust caused by *Puccinia graminis* Pers. f. sp. *tritici* Eriks. and E. Henn., has become one of the major diseases of wheat throughout the world. New *Pgt* strain Ug99 was detected by Pretorius *et al*. (2000) and was designated by Wanyera *et al*. (2006) as TTKS pathotype. It showed a virulence to *Sr*31 and its variants, TTKST and TTTSK which were detected in Kenya in 2006 and 2007 with virulence to genes *Sr24* and *Sr*36, respectively (Jin *et al*., 2008).Also, yellow rust (*Puccinia striiformis* f. sp. *tritici*) epidemic has occurred in 1958(Hasssebrauk,1959); 1967 (Abdel-Hak *et al.,*1972); 1995 (El-Daoudi *et al.,*1996) and sever infection was present in 1997 causing high losses estimated by 14 – 26 % in Delta Egypt and 10 % all over the country. Controlling the disease through usage of chemicals besides

being costly to the farmer is also harmful to the environment. Utilization of resistant cultivars is the most economical and environmental-friendly approach to control the diseases, enabling reductions in fungicide use. A diversified and effective resistant gene resource must be the basis of breeding wheat cultivars with rust resistance. Incorporation of the resistance genes is eco-friendly system which does not place any cost burden on the growers . Nowadays, various molecular markers have been widely used in plant genetic mapping and marker-assisted selection (MAS), such as random amplified polymorphic DNA (RAPD), amplified fragment length polymorphism (AFLP), restriction fragment length polymorphism (RFLP), sequence tagged site (STS), simple sequence repeats (SSRs), inter-simple sequence repeats (ISSRs). Currently, microsatellites (simple sequence repeats, SSRs) are the preferred type of molecular marker for marker-assisted selection (MAS) in wheat breeding.

There is limited information on the presence/absence of major stem rust resistance genes in local Egyptian genotypes. This information will aid wheat breeders in selecting markers to use in MAS and gene pyramiding to enhance durability of stem rust resistance.

In this study our objectives were to check whether the stem rust resistance genes, *Sr*2, *Sr*28, *Sr*32, *Sr*35 and *Sr*40 monogenic lines, as well as yellow rust genes *Yr*10, *Yr*15and *Yr*18 are presented in some wheat genotypes and four Egyptian wheat cultivars.

Materials and Methods

1. Plant materials

The plant material used in this study comprised of four Egyptian wheat old and new commercial cultivars, three Libyan local cultivars and three advanced breeding lines from CIMMYT and ICARDA and monogenic lines carrying stem rust resistance genes *Sr2*, *Sr28, Sr35andSr40 as well as* monogenic lines carrying stripe rust resistance genes *Yr10, Yr15, Yr18*. Details of the cultivars and their pedigree are present in (Table 1).

2. Molecular marker analyses

DNA isolation:

Fresh leaf samples from 10 to 15 day old seedlings were ground into fine powder in liquid nitrogen and 20 - 50 mg of powdered tissue was used for isolation of total genomic DNA using the following CTAB (Cetyl trimethyl ammonium bromide) method as modified by (Allen *et al*., 2006). The DNA was diluted to a final concentration of 10 ng/µl and quantified in 1% agarose gel for marker analysis.

PCR amplification and marker analysis:

Four SSR markers linked to stem rust resistance genes as well as, two SSR and one STS markers linked to yellow rust resistance genes (Table 2) were used for detecting the presence of stem rust resistance genes in Egyptian wheat.

The PCR reaction was carried out in a 20 ml reaction volume containing 3.0 µl of template DNA (10ng/µl stock), 3.0 µl of 5X PCR buffer (Promega , USA), 1.5 µl of 25 mM MgCl2 (total 1.5 to 2.5 mM $MgCl_2$ per reaction), 3.0 µl of each dNTP (Promega, USA), 0.2 µl of Taq

DNA polymerase (GoTaq® Flexi DNA Polymerase, Promega, USA), 1.5 µl of each SSR marker (5mM) stock and 6.3 µl distilled H_2O.

Amplification was carried out in a PTC-200 Peltier thermal cycler programmed at one cycle of 4 min at 94°C, 94°C for 1 min, 50-61°C (depending on marker) for 1 min. and 72°C for 1 min (35 cycles) and a final extension step of 72°C for 7 min (one cycle). PCR products were resolved on 1.5 to 3% agarose (SIGMA, USA) gel at 100v for 3 to 4h. Gels were stained in ethidium bromide and photographed on a digital gel documentation system (ChemiDoc MP system, BIO-RAD, USA).

The DNA ladder (100 bp DNA) was used (3 µl) for determining the molecular size of the DNA bands.

Table 1. Cross/pedigree of wheat cultivars and genotypes

Sr. No	Plant materials	Pedigree	Origin
1	**Kafra**	Local variety	Libya
2	**Mergawe**	Local variety	Libya
3	**Kassy**	Local variety	Libya
4	**Line1**	CHEWINK #1/FRNCLN CMSS08Y00486S-099Y-099M-099NJ-13WGY-0B	CIMMYT-MXI12-3\M47IBWSN\191 (8^{TH}STEMRUST/2013)
5	**Line 2**	WEEBILL-1/2*QAFZAH-21 ICW02-20182-10AP/0TS-0AP-0AP-8AP-0AP-0DZ/0AP-0DZ-0KUL/0SIN/0AP-0NJ/0AP-0ALK/0AP	ICARDA-DSBWYT-12 (2013)
6	**Line 3**	KACHU//KIRITATI/2*TRCH CMSS08Y00152S-099Y-099M-099Y-2M-0WGY	CIMMYT-MXI12-13 /M8EBWYT/15/(8^{TH}EBWYT/2013)
7	**GIZA168**	MRL/BUC//SERI CM93046-8M-0Y-0M-2Y-0B-0GZ	Agricultural Research Center ,Egypt
8	**GIZA171**	Sakha 93/Gemmeiza 9 Gz 2003-101-1Gz-4Gz-1Gz-2Gz-0Gz	Agricultural Research Center
9	**GEMMEIZA9**	ALD"S"/HUAC"S"//CMH74A.630/SX CGM45835-GM-1GM-0GM	Agricultural Research Center
10	**GEMMEIZA11**	BOW"S"/KVZ"S"//7C/SERI82/3/GIZA186/SAKHA61 CGM78922-GM-1GM-2GM-1GM-0GM	Agricultural Research Center

3. Evaluation for stripe and stem rust resistance under field condition:

Stripe rust severity was recorded on individual plants following modified Cobb's scale (Peterson *et al.,* 1948) that includes disease severity (percentage of leaf area covered with rust urediospores) as well as disease response (infection type). The infection types were recorded as zero (immune); TR (traces of severity); MR (moderately resistant), MS (moderately susceptible); S (susceptible) and disease severity was recorded as percent leaf area infected. Adult plant resistance was evaluated on the same set of materials during 2015/2016 in the experimental farm, Faculty of Agriculture, Mansoura University; the recommended agricultural practices were applied.

Table 2. Primers, sequences, product size and the reference of 4 markers linked to *Sr*2, *Sr*28, *Sr35* and 3 markers linked *to Yr10, Yr15,* and *Yr18.*

S.No	Marker name	Primer sequence	Amp.size	Reference
Sr2	*Xgwm533*	F-5' AAGGCGAATCAAACGGAATA 3'	120bp	Spielmeyer *et al.,* 2003
		R-5' GTTGCTTTAGGGGAAAAGCC 3'		
Sr28	*Xwmc332*	F-5'CATTTACAAAGCGCATGAAGCC3'	196bp	Rouse *et al.,*2012
		R-5'GAAAACTTTGGGAACAAGAGCA3'		
Sr35	*Xwmc559*	F-5'ACACCACGAATGATGTGCCA3'	338bp	Zhang *et al.,*2010
		R-5' ACGACGCCATGTATGCAGAA3'		
Sr40	*Xwmc661*	F-5'CCACCATGGTGCTAATAGTGTC3'	190bp	Wu *et al.,*2009
		R- 5'AGCTCGTAACGTAATGCAACTG3'		
Yr10	*Xpsp3000*	F-5' GCAGACCTGTGTCATTGGTC3'	260	Wang *et al.,*2002
		R-5' GATATAGTGGCAGCAGGATACG3'		
Yr15	*Xgwm413*	F-5' TGCTTGTCTAGATTGCTTGGG 3'	96bp	Peng *et al.,*2000
		R-5' GATCGTCTCGTCCTTGGCA 3'		
Yr18	*csLV34*	F-5'GTT GGT TAA GAC TGG TGA TGG3`	150bp	Lagudah *et al.,* 2006
		R-5'TGC TTG CTA TTG CTG AAT AGT3`		

Results

The objective of this study was to identify *Sr* resistance genes (*Sr2*, *Sr28, Sr35* and *40*) and *Yr* resistance genes (*Yr10, Yr15, Yr18*) in four Egyptian bread wheat cultivars and in two lines from CIMMYT, one line from ICARDA and three local Libyan cultivars to exploit these genes in breeding program through Marker Assisted Selection (MAS).

1. Molecular marker analysis:

Four Egyptian bread wheat cultivars (Giza168, Giza171, Gemmeiza9 and Gemmeiza11) and two lines from CIMMYT, one line from ICARDA and 3 local Libyan cultivars (Kafra, Mergawe and Kassy) and seven monogenic lines for individual gene were used at positive resistant control to detect the presence of stem rust resistance genes (*Sr2, Sr28, Sr35 and Sr40*) and three *Yr* genes (*Yr10*,*Yr15* and *Yr18*) using molecular markers linked to individual gene.

Stem rust marker data:

Microsatellitemarkers or SSR markers *Xgwm533* linked to *sr2* was used to detect the presence of *Sr2* gene in current materials. *Xgwm533* linked to *sr2* with a DNA fragment 120bp, was identified in all four Egyptian cultivars, three Libyan local cultivars and tested line (Fig 1, Table 3).

Likewise, Microsatellites marker*Xwmc332*amplified a DNA fragment of 196-bp known to be linked to *Sr*28 indicates the presence of *Sr*28 in present samples. Mergawe, Lines 1, 2, 3, Giza168, Giza171 and Gemmeiza11 showed the presence of *Sr28* introgression while 3 Libyan local cultivars and Gmmeiza9 did not show the *Sr28* introgression (Fig 2, Table 3).

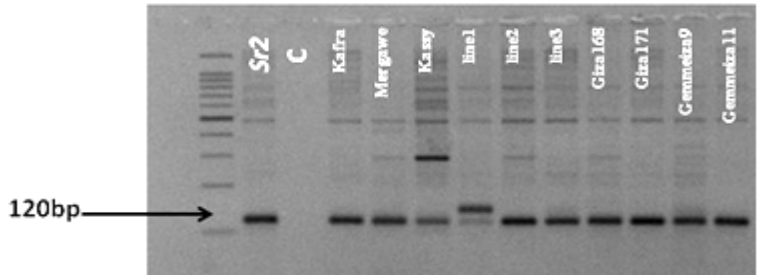

Figure 1: Amplification profile of SSR marker *Xgwm533* marker linked to *Sr2*. The arrow showed the fragment which is associated with *Sr2*.

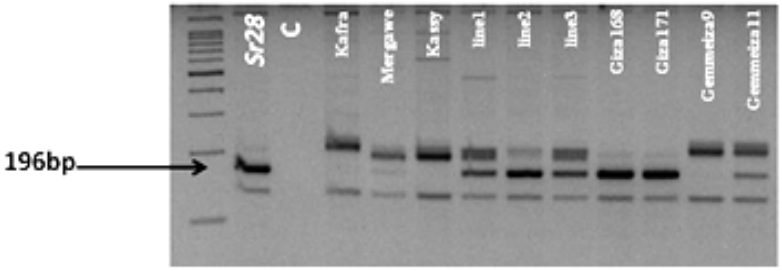

Figure 2: Amplification profile of SSR marker *Xwmc332* marker linked to *Sr28*. The arrow showed the fragment which is associated with *Sr28*.

For stem rust resistance gene *Sr35,* microsatellites marker *Xwmc559* amplified a DNA fragment of 225 bp known to be associated with *Sr*35. Four samples were positive with marker linked to *Sr35* (Kafra, Mergawe, Kassy and Gemmeiz11) while remain samples did not show the *Sr35* introgression (Fig 3, Table 3).

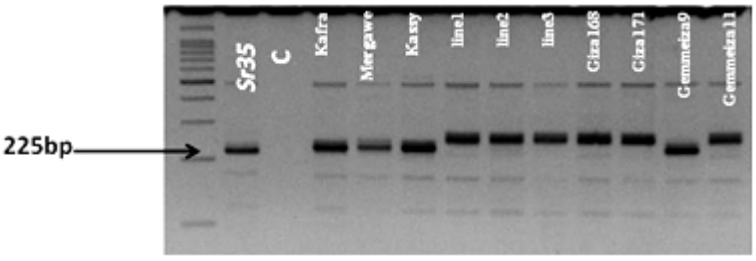

Figure 3: Amplification profile of SSR marker *Xwmc559* marker linked to *Sr35*. The arrow showed the fragment which is associated with *Sr35*.

The SSR marker, *Xwmc661* amplified a DNA fragment of 190-bp known to be associated with *Sr*40. Out of 10 samples, 2 samples were positive with the linked marker, *Xwmc661* (Mergawe, Line1 and Gemmeiza9) while remain samples did not show introgression of *Sr40* (Fig 4, Table 3).

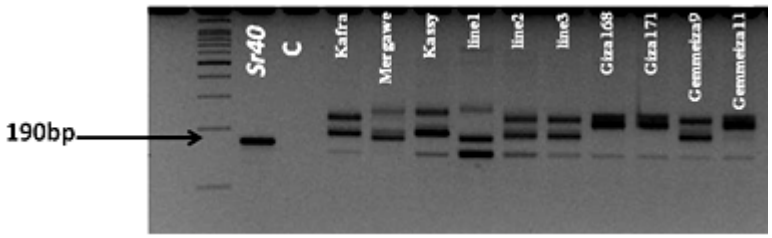

Figure 4: Amplification profile of SSR marker *Xwmc661* marker linked to *Sr40*. The arrow showed the fragment which is associated with *S40*.

Yellow rust marker data

Validation of *Yr10*

The stripe rust resistance gene *Yr10* was molecularly validated in present samples in current study. The molecular marker linked to *Yr10*, *Xpsp3000* amplified fragment size 260 bp in resistant plant. In present study *Yr10* was detected in Libyan cultivar Kassy and line 2 from CIM-MYT, while the remaining 8 samples were lacking of *Yr10* (Fig 5, Table 3).

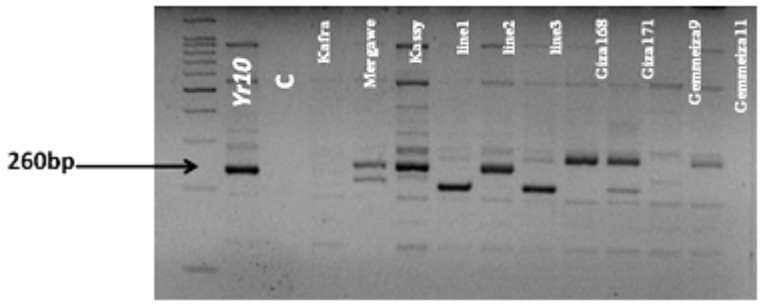

Figure 5: Amplification profile *of Xpsp3000* marker linked to*Yr10*. The arrow showed the fragment which is associated with *Yr10*.

Validation of *Yr15*

The SSR marker *Xgwm413* was used to identify the presence of *Yr15* introgression in present 10 entries. The SSR marker *Xgwm413*, linked to *Yr15*, with a DNA fragment 96 bp, was identified in six entries (Kassy, Mergawe, Lines1, 2, 3, Giza168 and Gemmeiza11) while 4 entries were lacking of *Yr15* (Fig 6, Table 3).

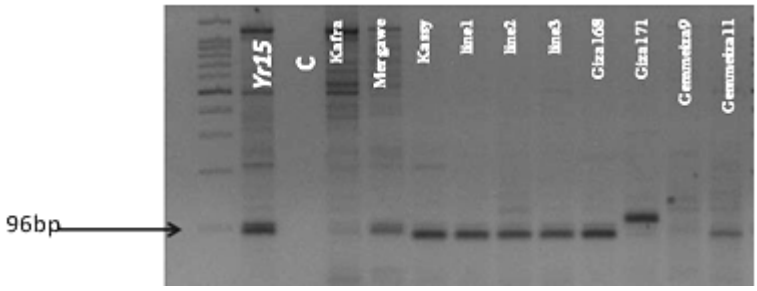

Figure 6: Amplification profile *of Xgwm413* marker linked to *Yr15*. The arrow showed the fragment which is associated with *Yr15*.

Validation of *Yr18*

The STS marker *csLV34*, linked to *Yr18*, with a DNA fragment 150 bp, was used to identify the presence of *Yr18* introgression in 10 entries. Our results showed that, the 10 samples did not show amplification fragment 150 bp neither the introgression of *Yr18* (Fig 7, Table 3).

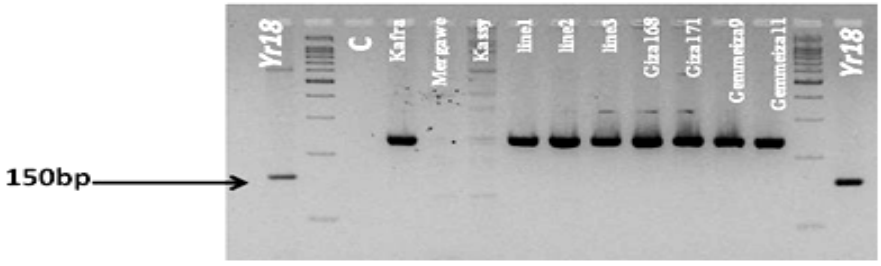

Figure 7: Amplification profile *of* STS marker csLV34 marker linked to *Yr18*. The arrow showed the fragment which is associated with *Yr18*.

Table 3. Disease reaction and Molecular marker data for present samples

Sr. No	Plant materials	Disease reaction		*Sr2*	*Sr28*	*Sr35*	*Sr40*	*Yr10*	*Yr15*	*Yr18*
		Yr	*Sr*	*Xgwm533*	*Xwmc332*	*Xwmc559*	*Xwmc661*	*XPSP3000*	*Xgwm413*	*csLV34*
1	Kafra	0	60S	+	-	+	-	-	-	-
2	Mergawe	0	50S	+	+	+	+	-	+	-
3	Kassy	0	40S	+	-	+	-	+	+	-
4	Line1	0	Tr R	+	+	-	+	-	+	-
5	Line 2	Tr MS	Tr MS	+	+	-	-	+	+	-
6	Line 3	0	0	+	+	-	-	-	+	-
7	GIZA 168	10S	10MS	+	+	-	-	-	+	-
8	GIZA 171	5S	5MR	+	+	-	-	-	-	-
9	GEMMEIZA 9	10MR	5MR	+	-	+	+	-	-	-
10	GEMMEIZA 11	10S	Tr R	+	+	-	-	-	+	-

2. Disease reaction

Yellow rust was recorded at adult plant stage, the first yellow rust disease scores were taken when disease severity of 50% based on the Modified Cobb's scale (Peterson *et al*., 1948). All the materials used in current study were screened at the experimental farm, Faculty of Agriculture, Mansoura University, season 2015/2016, under natural field condition. Stem rust was recorded at adult plant stage, under natural field condition. Our results (Table 3) showed that, three Libyan local cultivars were highly susceptible to stem rust, Line1, Line2 showed (Tr R) reaction, Line3 was (0) reaction while two Egyptian cultivars showed (5MR) reaction. Giza 168 showed (10Ms) and Gemmeiza11 was (Tr R). Likewise, stripe rust was recorded under field condition, three Libyan local cultivars showed good level of resistant under field condition, Line1, 3 showed (0) reaction, line (2) showed (TR MS) while Giza168was (10S), Giza171 was (5S), Gemmeiza9 showed (10MR) and Gemmeiza11 showed (10S) reaction.

Discussion

Stem rust caused by *Puccinia graminis* Pers. *f. sp. tritici Eriks*. and *E. Henn.,* and stripe (yellow) rust, caused by *Puccinia striiformis* Westend. *f. sp. tritici Erikss*. (*Pst*), are the most destructive disease in all wheat growing area in Egypt. In order to

produce resistant cultivars, it is necessary to identify resistance genes in different germplasms. The objective of this study was to develop a set of public PCR assays for an efficient selection of resistance genes in wheat breeding programs.

Sr2 confers slow rusting adult plant resistance and is linked with the pseudo-black chaff (PBC) phenotype (Singh and Rajaram, 2002). It confers partial resistance to race TTKSK when homozygous and under low to moderate disease pressure (Mago *et al.,* 2010; Singh *et al.,* 2006).

Sr2 found in all tested genotypes with a diagnostic band of 120bp amplified and indicated the presence of *Sr2* gene. This was generally in agreement with previous study (Elkot *et al.,* 2016). Although this gene alone is capable of reducing the level of infection and slow rusting resistance gene reported by (Singh *et al*., 2011). The presence of *Sr2* in some of the land races (Haile *et al*., 2013) also strengthen this fact and showed that Ethiopian cultivated tetraploid wheat accessions are still good sources of stem rust resistance. *Sr2*, APR (Adult Plant Resistance) to Ug99 races conferred by *Sr2* on chromosome 3BS was validated in at least six recombinant inbred line populations characterized by CIMMYT (Bhavani *et al*., 2011), as well as in several other research efforts. An improved marker for *Sr2* is available (Mago *et al*., 2011), and continued efforts to develop "perfect" markers are underway. Significant interaction of markers linked to *Sr2* with markers linked to other resistance loci was detected in multiple association mapping panels (Yu *et al*., 2011 and 2012).

Gene *Sr28* was previously described as providing an intermediate level of resistance in a field nursery in Kenya to race TTKSK (Jin *et al.*, 2007). Microsatellite marker *Xwmc 332* was identified as linked to *Sr28* based on amplification of different alleles from the resistant and susceptible bulked DNAs (Rouse *et al*., 2012). The identification of flanking markers for the Ug99-effective resistance gene *Sr28* that will be selectable in Egypt spring wheat germplasm may facilitate the efficient introgression and selection of *Sr28*. In order to obtain highly effective and durable resistance, *Sr28* should only be used in combination with additional Ug99-effective resistance genes.

The *Sr35* resistance gene from *Triticum monococcum* L. was transferred to chromosome 3AL of Mq(2)5*G2919K (Zhang *et al.,* 2010). *Sr35* is effective against the TTKSK (Ug99) race of of *Puccinia graminis* sp. *tritici* and its variants, TTKST and TTTSK (Jin *et al.,* 2007). A number of polymorphic SSR and EST-derived markers were found on the *T. monococcum* fragment containing *Sr35* and transferred to hexaploid wheat. *Xwmc559* was used to identify in current study marker can be used in marker assisted selection for transferring *Sr35* into different materials.

Sr40 in RL6088 is located in chromosome 2BS and originated from *Triticum timopheevii* (Zhuk.) Zhuk. subsp. *armeniacum* (Jakubz.) *Slageren* (Dyck, 1992). The SSR marker *Xwmc661* flanked *Sr40* was used to detect the presence of *Sr40* in present study. Markers linked to *Sr40*

will be useful for marker-assisted integration and pyramiding of *Sr40* into elite wheat breeding lines, and reduction in the size of the *T. timopheevii* segment harboring this gene.

A microsatellite marker *Xpsp3000* located on the end of chromosome 1BS was linked with the yellow rust resistant gene *Yr10* with a distance 1.2 cM (Wang *et al.,* 2002). The microsatellite marker *Xpsp3000* is inherited in a co-dominant manner, and can be used to identify genotypes of individuals at any growth stage. The marker *Xpsp3000* was used in marker assisted identification of *Yr10* in present study and marker it could be used in marker assisted selection.

Wild emmer wheat, *Triticum dicoccoides*, is an important source for novel stripe rust resistance (*Yr*) genes. *Yr15*, a major gene located on chromosome 1BS of *T. dicoccoides*, was previously reported to confer resistance to a broad spectrum of stripe rust isolates, at both seedling and adult plant stages (Yaniv *et al*., 2015). Introgressions of *Yr15* into cultivated *T. aestivum* bread wheat and *T. durum* pasta wheat that began in the 1980s are widely used. The SSR marker *Xgwm413* was used efficiently to identify *Yr15* and this marker can be used in marker assisted selection.

The adult plant resistance gene to stripe rust (*Yr18*) has also located on the same chromosome segment containing the *Lr34* gene and is tightly linked with it (McIntosh, 1992; Singh, 1992). Additionally, their co-segregation with other traits such as leaf tip necrosis (Ltn1), powdery mildew resistance gene (*Pm38*), and tolerance to barley yellow dwarf virus (Bdv1) has been reported (McIntosh 1992; Liang *et al.,* 2006; Singh, 1992; Spielmeyer *et al*., 2005). Therefore, this multi-pathogen resistance locus is a valuable source of resistance in wheat breeding (Urbanovich *et al*., 2006). The use of the slow rusting gene pair *Lr34/Yr18* in combination with other slow rusting genes has been suggested to contribute to near immunity to leaf and stripe rust infections (Singh *et al*., 2000). In our study *Yr18* wasn't present in all tested Egyptian, Libyan and CIMMYT materials.

The identification and knowledge of stem rust and stripe rust resistance genes commonly used parental germplasm to release cultivars importantly for utilizing them to control the rusts in full potential. The long term and economical status could thus be resistance breeding through deployment of effective rusts resistance genes over space and time. Under such circumstances, it has become imperative to characterize the set of germplasm, advanced breeding lines for identifying stem rust and yellow rust resistance genes.

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التوصيف الجزيئى لبعض جينات المقاومة لصدأ الساق والصدأ الأصفر فى القمح المصرى وبعض التراكيب الوراثية المستوردة

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الملخص:

يعتبر صدأ الساق(الصدأ الأسود) فى القمح الناجم عن *Puccinia graminis* والصدأ الأصفر الناجم عن *Puccinia striiformis* هي من أهم الأمراض التى تصيب القمح. تتمحور الدراسة فى التوصيف والتعريف الجزيئى لبعض التراكيب الوراثية وأصناف القمح المصرى لمجموعة جينات المقاومة لصدأ الساق والصدأ الأصفر *SR2*، *Sr28*، *SR35*، *Sr40* و*Yr10*، *Yr15*، *Yr18* على التوالي. وقد أظهرت نتائج هذه الدراسة من خلال تحليل أربعة أصناف مصرية وثلاثة تراكيب وراثية ليبية وثلاثة سلالات مستوردة من هيئات CIMMYT و ICARDA بواسطة واسمات جزيئية مرتبطة بجينات المقاومة المذكورة آنفاً. وبالتحليل الجزيئى وجد أن الواسمة المرتبطة بجين المقاومة *Sr2* كانت موجودة في جميع التراكيب الوراثية المختبرة، الواسمة المرتبطة بجين المقاومة *Sr28* ظهرت في ستة تراكيب وراثية ، الواسمة المرتبطة بجين المقاومة*SR35* ظهرت في أربعة تراكيب وراثية ، أما الواسمة المرتبطة بجين المقاومة*Sr40* فظهرت فى إثنين فقط من التراكيب الوراثية المختبرة. كذلك ظهرت الواسمة المرتبطة بجين المقاومة *Yr10* في اثنين من التراكيب الوراثية ، والواسمة المرتبطة بجين المقاومة *Yr15* في ستة تراكيب وراثية أما الواسمة المرتبطة بجين المقاومة *Yr18* فلم تظهر فى أى من التراكيب الوراثية المختبرة. هذه الواسمات الجزيئية يمكن أن تكون فعالة للإستعانة بها فى نقل جينات المقاومة لصدأ الساق والصدأ الأصفر لإنتاج أصناف جديدة تحتوى على أكثر من جين لمقاومة صدأ الساق والصدأ الأصفر في القمح المصرى.