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GENETIC ANALYSIS AND ISSR BASED MARKERS FOR LEAF RUST RESISTANCE IN BREAD WHEAT (*Triticum aestivum* L.)

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ABSTRACT: The present study aimed to investigate the genetic behavior of leaf rust resistance in bread wheat (*Triticum aestivum* L.), in a population of five parents and ten F_1 hybrids under field conditions with artificial inoculation. Wide variations among parents and their F_1 hybrids were detected for the five characters under study, *i.e.* incubation period (IP), disease severity (DS), infection response (IR), average co infection (ACI) and area under disease progress curve (AUDPC). The average means of criteria related to resistant varieties showed that Giza 168 and Sakha 93 wheat cultivars have good response for resistance as long time of incubation period, as well as little amount of disease severity, the same performance of both varieties for infection response, average co infection and AUDPC= D [1/2 (Y_1 + Y_k) + (Y_2 + Y_3 + …….. Y_{k-1})] criteria. The behaviour of F_1's for studied criteria appeared to be different among and within five criteria. Gemmiza 11 × Giza 168 possessed complete dominance of long period, high (DS) and (ACI). In contrast, it was low value of AUDPC. The analysis of variance for five criteria were recorded highly significant differences among parents and their hybrids. The regression of (Wr/Vr) was insignificantly different from unity for all criteria except disease severity (DS). Significant differences of H_1 and H_2 estimates were obtained for incubation period (IP), disease severity (DS) criteria. While, AUDPC criteria possessed significant differences of D estimate. Mean degree of dominance $(H_1/D)^{1/2}$ indicated the presence of over dominance for all studied criteria. The proportion of genes with positive and negative effects in the parents ($H_2/4H_1$) indicated un equal frequances of positive and negative among the parents for DS and AUDPC criteria, except IP possessed nearly equal positive and negative gene among the parents. F_1 graphic analysis revealed that cultivars G.168 and Sakha 93 had most dominant genes for resistance but cultivars Gemmiza 11 and Gemmiza 9 had most recessive genes for susceptibility. Bulked Segrigant Analysis were used by eight ISSR primers, the results confirmed the importance of Giza 168 may be as doner of resistant gene's, as well as Gemmiza 9. These confirmed the importance of Giza 168 considered as in late genotypes for using it to transport leaf rust resistant genes to other genotypes, Gemmiza 9 followed Giza 168 in the importance of leaf rust resistance, these results confirmed also the susciptability of Gemmiza 11 variety for leaf rust disease in bread wheat.

Key words: Hybridization, artificial inoculation, diallel analysis, molecular markers.

INTRODUCTION

Leaf rust, caused by the fungal pathogen *Puccinia triticina* Eriks. The wheat leaf rust disease fungus is adapted to a range of different climates, and the disease can be found in diverse wheat growing areas throughout the world. Wheat cultivars that are susceptible to leaf rust regularly suffer yield reductions of 5–15% according to **Samborki (1985)** or greater, depending on the stage of crop development when the initial rust infections occur according to **Chester (1946)**. The nature and pre-vention of the cereal rusts as exemplified in the leaf rust of wheat. Genetic resistance is the most economical and preferable method of reducing yield losses due to leaf rust. Various wheat breeding programs throughout the world had

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multi results in producing cultivars with long-lasting, effective resistance to leaf rust. Genetic resistance to leaf rust can be most fully utilized by knowledge of the identity of resistance genes in commonly used parental germplasm and released cultivars. Depending on the severity and duration of infection, leaf rust, caused by the fungal pathogen *Puccinia triticina* Eriks., has been the most prevalent disease in wheat-producing areas (**Kolmer, 2005**). The greater is the area under the cultivars since ancient times, leaf rust, caused by an obligate parasitic fungus *Puccinia triticina* Erikss., has been a challenge for wheat growing and, which continues to cause annual losses and to be an important disease of wheat worldwide (**Huerta-Espino *et al.*, 2011; Kolmer, 2013**). Due to a wide variability of the pathogen, there are continuously emerging new virulent races which overcome resistant genes of a host. Because of the airborne nature of urediniospores, the pathogen can be transferred by wind to adjacent and distant wheat growing areas (**Kolmer, 2005**). Disease resistance genes, transferred from wild species, support wheat production on a global level (**Davoyan A.N.E.R 2011**). The present study aimed to study the genetic behavior and ISSR molecular markers for leaf rust resistance in bread wheat (*Triticum aestivum* L.) under field conditions by using artificial inoculation according to **Guha *et al.* (1996)**.

MATERIALS AND METHODES

The present investigation was carried out at the Experimental Farm and Molecular Genetics Lab, Faculty of Agriculture, Zagazig University, Egypt, during the three growing seasons (2014 to 2016). Five bread wheat varieties namely (Giza 168, Gemmiza 9, Gemmiza 11, Sids 13 and Sakha, 93) and their F_1 hybrids were used in this experiment.

Artificial inoculation used in this experiment was done by using a mixture strains of leaf rust spores, (PKDCH - IKCGC - IBHBD) during 2015-2016 and (NKTSS - PHTTT - PKTTT) during 2016-2017. These varites were obtained from Crop Research Institute, ARC, Giza, Egypt.

Source of freshly collected urediospores of *Puccinia triticina*. Strains were kindly provided by wheat, Dis. Res. Dept., Pl. Pathol. Res. Inst., ARC, were used as artificial inoculation. Moreover Morrocco, *Triticum spelta* saharensis and thatcher wheat cvs, were used as a surrounding spreeder border.

To study the inheritance of wheat leaf rust resistance some wheat cultivars were choosen as fowllos, two resistant parents (Giza 168, Sakha 93) and three susceptible ones (Gemmiza 11, Gemmiza 9 and Sids 13) Each entry was sown in a plot of ten rows, it's area was $2m^2$, distance between each two rows was 20 cm, each row was planted by 5 gm of seeds. Leaf rust resistance components were calculated as follows:

1-Incubation period (IP).

2- Disease severity (DS) according to (**Peterson *et al.*, 1948**).

3-Infection response (IR).

4-Average Co Infection as outlined by **Das *et al.* (1993)**.

5-Area under disease progress curve (AUDPC), as calculated by **Pandy *et al.* (1989**).

In the first winter season 2014 - 2015, the five cultivars were sown for hybridization between them, 10 F_1 hybrids were obtained as diallel cross.

In the second winter season 2015-2016, five cultivars and their F_1 hybrids were sown in experimental farm in 20/11/2015. Artificial inoculation for leaf rust disease was carried out with uredospores of leaf rust mixed with baby powder in the late day while there was water film on the leaves blades to allow spores germination, grow and appear the leaf rust postules (Artificial inoculation) according to **Tervet and Cassel (1951)**.

In the third winter season 2016-2017, G.168, Gemmiza 9, Gemmiza 11,F_1 and F_2 hybrids of these cultivars were sown in experimental farm in 20/11/2016, artificial inoculation for leaf rust disease was carried out as previously mentioned for application of Bulked segregant analysis (BSA) according to **Guha *et al.* (1996)**.

Molecular Genetics

Bulked segregant analysis (BSA) was used in the present study. Three parents, two F_1 hybrids and four F_2 generations were investigated by using ISSR markers technique (Tables 2 and 3).

Table 1. List of five different bread wheat cultivars and their pedigree which were evaluated throughout the present study

Cultivar	Pedigree
- Gemmiza 9	-Ald "S"/Huac "S"//CMH74A.630/5Xcgm4583-5GM-OGM.
- Gemmiza 11	-BOW"S"//KVZ"S"//7C/SER182/3/GIZA168/SKHA61.
- Giza 168	-MIL/BUC//SeriCM93046-8M-OY-OM-2Y-OB.
- Sids 13	-AMAZ19=KAUZ"S".
- Sakha 93	-Sakha92/TR810328 S8871-IS-25-OS.

Table 2. The nine genotypes that were used in bulked segregant analysis (BSA) by ISSR technique with eight primers

Parents	F_1 hybrids	F_2 hybrids
1- Giza 168	4-Giza 168xGemmiza 11	6-30 (R) Giza 168xGemmiza 11*
2- Gemmiza 9	5-Gemmiza 9xGemmiza 11	7-30 (S)Giza 168xGemmiza 11
3- Gemmiza 11		8-30 (R) Gemmiza 9xGemmiza 11
		9-30 (S)Gemmiza 9xGemmiza 11

* The thirty plant for F_2 resistants (R) and suscibtability (S) were collected for F_2 generation.

Table 3. Sequance and codes of ISSR primers used for leaf rust resistance in bread wheat (*Triticum aestivum* L.)

Sr. No.	Primer	Sequance (5'-3')	Primer code
1	844A	5' CTC TCT CTC TCT CTC TGC 3'	RSW-1000
2	844B	5' CTC TCT CTC TCT CTA 3'	RSW-1001
3	HB12	5' CAG CAG CAG GC 3'	RSW-1002
4	HBS10	5' GAG AGA GAG AGA CC 3'	RSW-1003
5	HBS11	5' GTG TGT GTG TGT CC 3'	RSW-1004
6	17889A	5' CAC ACA CAC ACA AC 3'	RSW-1005
7	17889B	5' CAC ACA CAC ACA GT 3'	RSW-1006
8	17899A	5' CAC ACA CAC ACA AG 3'	RSW-1007

Statistical Analysis

Means and their least significant differences for each studied character were calculated according to **Gomez and Gomez (1984)**. Diallel F1analysis was applied to estimate the genetic parameters as described by **Hayman (1954 a and b)**. Illustration of **Singh and Chaudhary (1977)** was adopted to estimate the components of genetic variance and heritability in broad and narrow sense.

RESULTS AND DISCUSSION

Mean performance of studied wheat genotypes for leaf rust criteria is presented in Table 4. Wide variations among parents and their F_1 hybrids were detected for the five characters under study, *i.e.,* 8.65 -11 for (IP), 2.4-8.26 for (DS), S-MR for (IR), 0.96-8.26 for (ACI) and 43.33-86.3 for AUDPC . The average means of criteria related to varieties resistance showed that the two varieties Giza 168 and Sakha 93 had a good response for leaf rust resistance. In contrast Gemmiza 9, Gemmiza 11 and seds 13 can consider as a susceptable varieties for leaf rust disease. Similar results show. These results may the importance of the four criteria, IP, DS, IR and ACI than the genetic mechanism of area under disease progress curve (AUDPC). These results agreed with the findings obtained by **Penthus (1959) and Oury *et al.* (1993)**.

The analysis of variance for the five criteria showed high significant differences among parents and their hybrids (Table 5). The major assumption postulated for diallel analysis (**Hayman, 1954a**) was found to be valid as the t^2 value was insignificant for all characters. The regression of (Wr/Vr) was insignifican different from unity for all criteria except disease severity (DS).

Estimates of the genetic components of variations and their proportions are presented in Table 6. Significant differences of H_1 and H_2 estimates were obtained for incubation period (IP), disease severity (DS) criteria indicating the importance of dominance gene effects in the genetic control of them. While, AUDPC criteria possessed significant differences of D estimate, indicating the importance of additive gene effects in it's genetic control. These results confirm with the previous conclusion about the behavior of F_1 hybrids for these criteria. Mean degree of dominance $(H_1/D)^{1/2}$ indicated the presence of over dominance for all studied criteria. The proportion of genes with positive and negative effective effects in the parents $(H_2/4H_1)$ indicated unequal frequances of positive and negative among the parents for DS and AUDPC criteria, except IP possessed nearly equal positive and negative gene among the parents. Also unequal frequancies of dominance and recessive genes were observed between parents for all the three criteria with more dominant than recessive genes. By comparing (Wr+Vr) values for each array with the mean of common parents, comparing (Wri+Vri) correlation coefficient (r) between them is negative, it means that parents containing the most increasing genes and having the lowest values of (Wri+Vri) and thus containing most dominant genes, these are conclude whether or not the increasing or decreasing genes are the dominant over (**Singh and Chaudhaly, 1977**). Long period dominant over short period for incubation period for negative disease severity, the lower values dominant over higher value of disease severity. As well as, lower AUDPC value dominant over higher value. These results agree with the findings from Wr/Vr graph, whereas the parent Seds 13 possess most dominant genes. In contrast, Gemmiza 11 possess most recessive genes. Disease severity from Wr/Vr graph, indicated that the seds 13 possess most dominant genes and sakha 93 has most recessive genes, these results explained the susceptibility of dominant over resistance. In the same trend for AUDPC-Y_D Y_R , values indicate the previous conclusion in the direction of dominance. Whereas the heritability in broad and narrow sense indicate the lower values of narrow sense and the broad sense. These results confirm the importance of non additive gene effects which play an important role for the inheritance of leaf rust disease resistance, which be selected at late generations to improve the resistance of leaf rust.

Table 4. Average mean of incubation period (IP), disease severity (DS), infection responses (IR) and area under disease progress curve (AUDPC) of wheat genotypes to leaf rust disease under field conditions with artificial inoculation

Genotype	Incubation period (IP)	Disease severity (%)	Infection response (IR)	Average co Infection (ACI)	AUDPC
Gem.9	9.33	5.866	S	5.866	66.5
Gem.11	8.65	5.866	S	5.867	71.166
G.168	11	2.4	MR	0.96	52.5
Sids 13	11	8.266	S	8.267	72.33
Sakha 93	10	2.4	MR	0.96	43.33
P1×P2	8.	5.866	S	5.867	71.16
P1×P3	10	3.466	MS	2.733	61.83
P1×P4	10	6.933	S	6.933	73.5
P1×P5	11	7.6	S	7.6	58.33
P2×P3	8	5.866	S	5.866	38.5
P2×P4	10	6.933	S	6.933	58.33
P2×P5	8	2.933	MR	1.173	70
P3×P4	9	6.933	S	6.933	77
P3×P5	10	8.266	S	8.266	78.16
P4×P5	11	6.933	S	6.933	86.33

Table 5. Analysis of variance, t^2 values, regression coefficients for validity and their test of significant for incubation period (IP), disease severity (DS) and area under disease progress curve (AUDPC)

Source of variation	MS			
	df	IP	DS	AUDPS
Replication	2	38.6**	33.60**	281.10**
Genotypes	14	3.86*	12.285*	520.2**
Error	28	0.123	1.451	148.51
T^2		2.494	1.209	0.118
b		0.410	0.745	0.052
±SE (b)		0.544	0.068	0.964
H0: b=0		0.754	10.92**	0.053
H0: b=1		1.083	3.480*	0.981

Table 6. Mean estimates of components of genetic variation and their proportions of the studied criteria under artificial inoculation with leaf rust strains

Component of variation and proportion	IP	DS	AUDPC
D±SE (D)	0.470±0.537	-0.856±2.067	272.447±94.89**
F±SE(F)	0.4261.341	-2.638±5.164	212.906±237.05
H1±SE(H1)	3.165±0.364**	12.039±1.402**	369.190±256.28
H2±SE(H2)	3.234±1.315*	8.766±5.063	301.521±232.45
h^2±SE(h^2)	1.499±0.888	0.817±3.418	6.374±156.94
E±SE(E)	0.896±0.219**	1.198±0.843	52.45±38.74
$(H1/D)^{1/2}$	2.594	1.59	1.164
H2/4H1	0.238	0.179	0.204
Dom/Res	1.423	1.131	2.011
r	0.265	-0.019	-0.136
r^2	0.701	0.001	0.0185
Y^D	8.650	6.070	53.75
Y^R	10.88	5.940	148.36
$H^2_{(ns)}$	0.007	0.433	0.332
$H^2_{(bs)}$	0.470	0.798	0.726

Table 7. Mean value of Wr, Vr of the arrays under study for incubation period, disease severity, average co infection and area under disease progress curve

Array	IP			DS			AUDPC		
	Wr	**Vr**	**Yr**	**Wr**	**Vr**	**Yr**	**Wr**	**Vr**	**Yr**
1	0.272	1.477	9.333	0.199	6.421	5.866	13.22	161.56	66.5
2	1.261	1.966	8.633	0.704	2.467	5.866	14.76	44.64	71.16
3	-0.505	1.588	11.00	0.327	3.889	2.40	204.43	138.42	52.5
4	0.072	0.323	11.00	0.071	0.533	8.266	141.35	63.019	72.3
5	0.438	1.366	10.00	0.152	7.559	2.40	93.65	285.60	43.33
Total	1.538	6.710	47.333	2.353	20.87	24.798	467.43	693.26	339.5
Mean	0.307	1.340	9.466	0.470	4.174	4.959	93.486	138.65	67.9

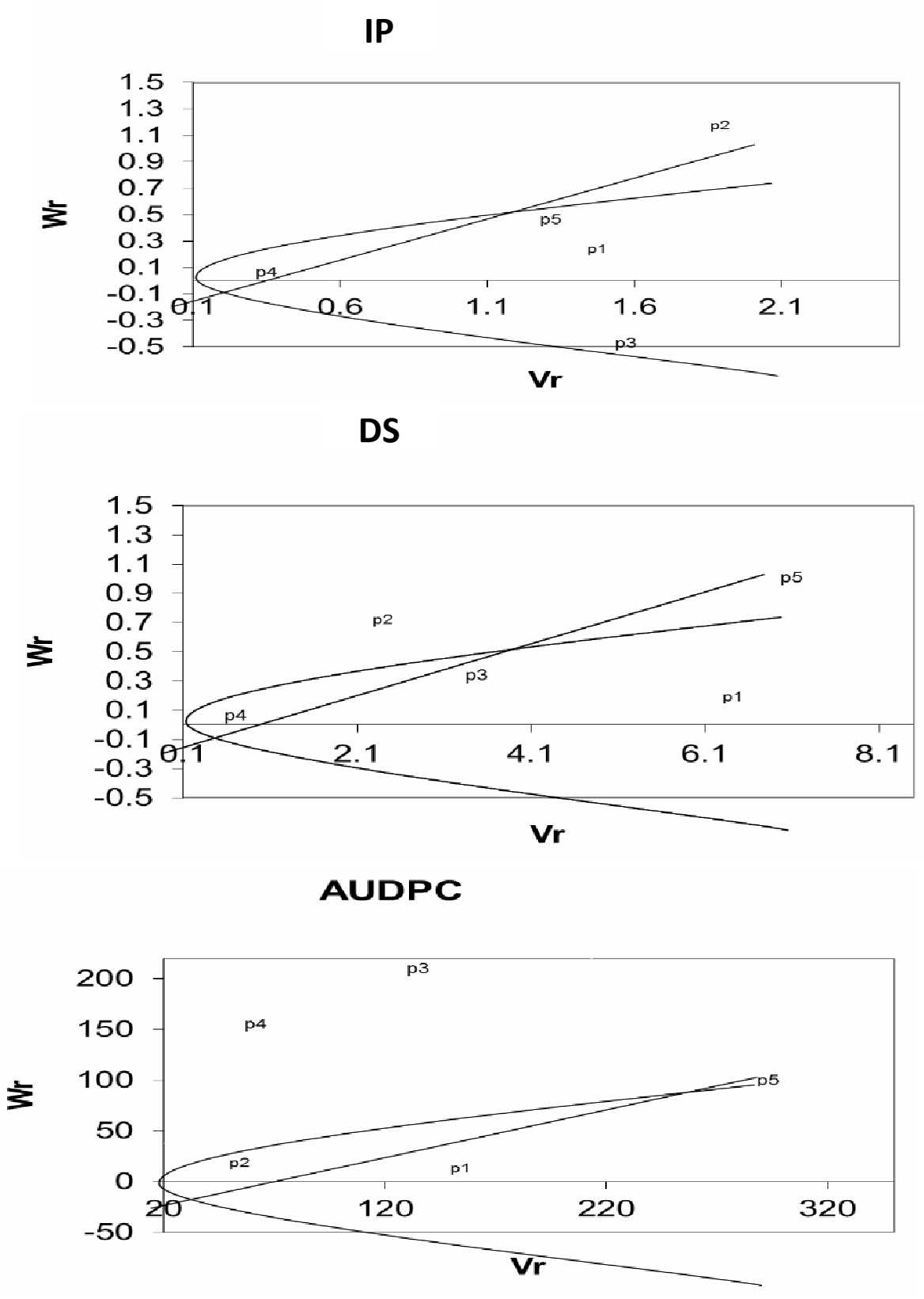


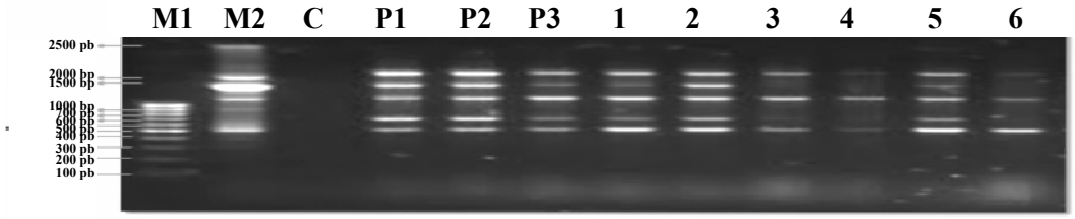
Fig. 1. Graphic analysis for F $_1$ Wr/Vr of incubation period (IP), disease severity (DS) and area under disease progress curve (AUDPC)

Graphic analysis of these criteria showed that these varieties have over dominance for area under disease progress curve, incubation period and disease severity. The F_1 graphic analysis confirmed the above results on the mean degree of dominance, in addition most dominance gene effects play an important role in genetic control of leaf rust, the regression line passed below the point of origin for disease severity (DS), incubation period (IP) and area under disease progress curve (AUDPC) suggesting over dominance. These findings confirmed the previous results from $(H_1/D)^{1/2}$ proportions.

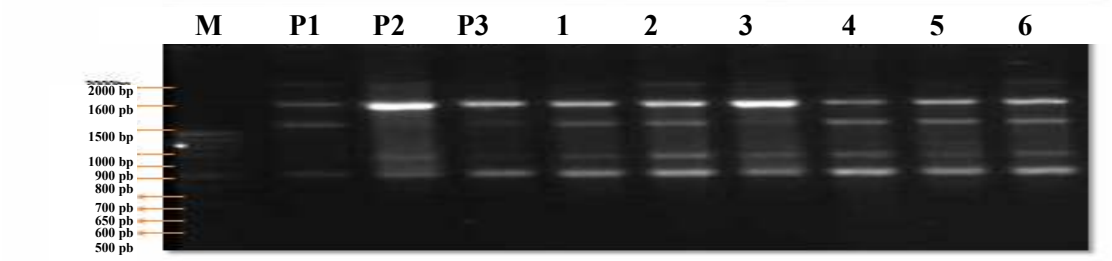
Molecular Analysis

In this ISSR investigation, eight ISSR primers were used. Bulked segregant analysis technique were applied in two hybrids ,each hybrid included two parents (resistant and susceptible), F_1 's and two extreme of F_2 (plant resistant group and other plant susceptible group).The results confirmed the importance of Giza 168 cultivar, whereas possessed one band (2000bp) in primer 844A at the parent and more resistant F_2 group. As well as, Gemmiza 9 cultivar had one 400bp band with (844A), and their most resistant F_2 group. In contrast Gemmiza 11 had one band (1500bp) with (HBS10) primer and the more susceptible of their F_2 group, as well as ,this cultivar Gemmiza 9 had also one band (1000bp) with (HBS10) primer and more susceptible for their F_2 group . For confirming of the important results were obtained from (17889A) primers, whereas 1500bp band appeared at Giza 168 parent, their F_1 's and more resistant F_2 group. More remark confirmed the important of Giza 168 as a doner for leaf rust resistant gene's. This cultivar had17889B primer, on two bands *i,e.*, 1200bp and 700bp at the mother cultivar (Giza 168), their F_1's and more resistant F_2 group. The conclusion of these results confirmed the importance of Giza 168 wheat cultivars which considered as illate genotype for using of it to transport it leaf rust resistant genes to other genotypes , Gemmiza 9 followed Giza 168 in the importance of leaf rust resistance, these results confirmed also the susciptability of Gemmiza 11 cultivar for leaf rust disease.

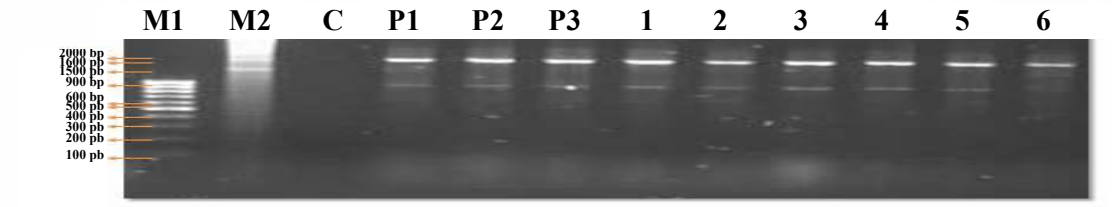
Primer 844A



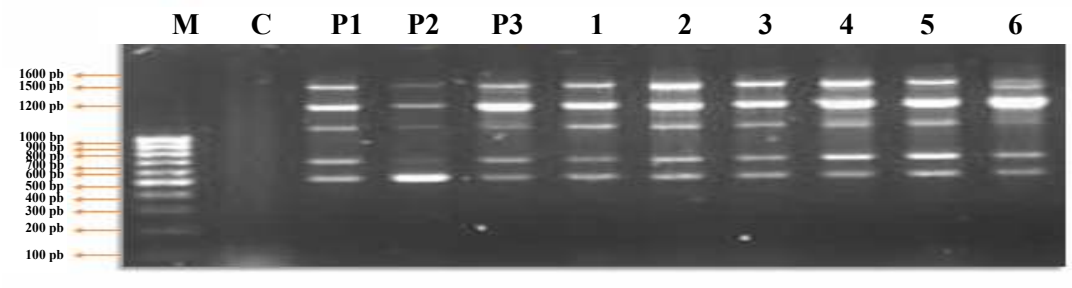
Primer 844B



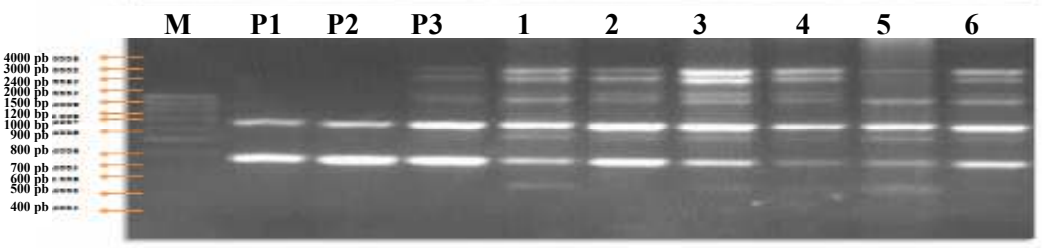
Primer HB12



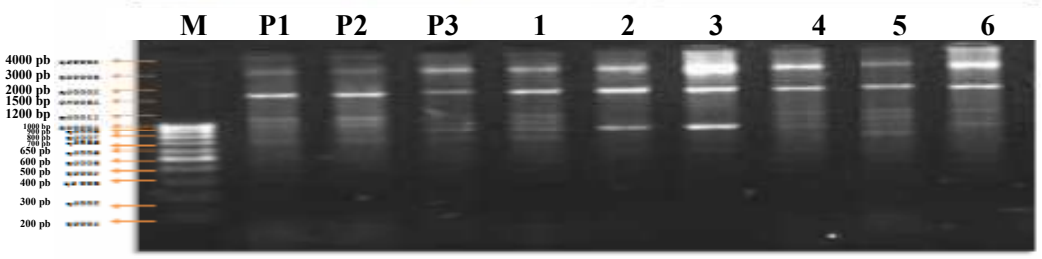
Primer HBS10



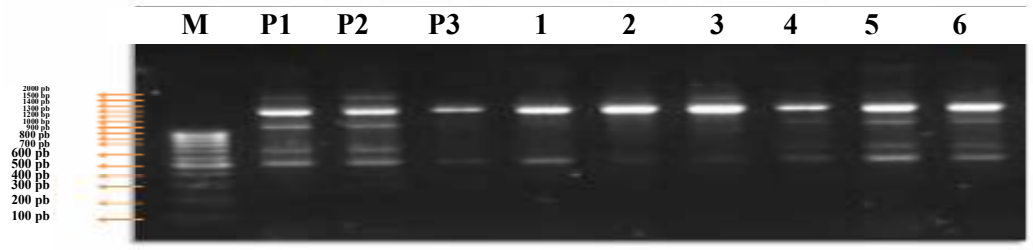
Primer HBS11



Primer 17889A



Primer 17889B



Primer 17899A

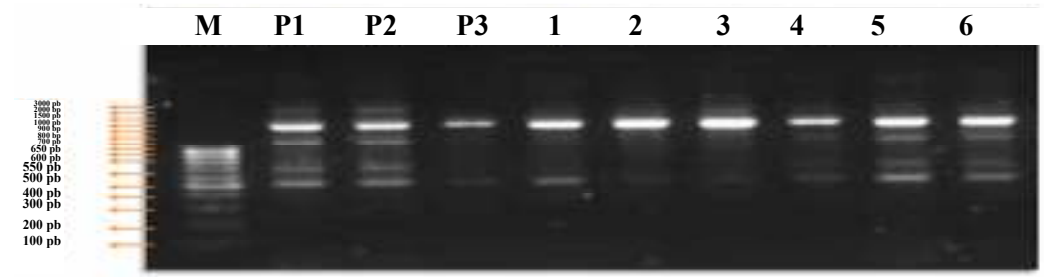


Fig. 2. Photos of gel electrophorasis for nine DNA bulks from wheat genotypes by using eight primers

Table 7. Survey of amplified ISSR bands in the studied leaf rust resistance in bread wheat (*Triticum aestivum* L.) after used primer

Amplified DNA fragment	Giza 168	Gem. 9	Gem. 11	1×3 F1	1×3® F2	1×3(s) F2	2×3 F1	2×3® F2	2×3(s) F2	
				844A						
2000bp	+	+	-	-	+	-	+	-	+	Polymorphic
1500bp	+	+	+	+	+	+	+	+	+	Monomorphic
1000bp	+	-	+	+	-	+	+	+	+	Polymorphic
700bp	-	-	-	-	-	-	-	+	-	Unique
600bp	-	+	+	+	+	+	+	+	+	Polymorphic
500bp	+	+	+	+	+	+	+	+	+	Monomorphic
400bp	-	+	-	-	-	-	-	+	-	Polymorphic
				844B						
2000bp	+	+	+	+	+	+	+	+	+	Monomorphic
1600bp	-	-	-	-	+	-	-	-	-	Unique
1500bp	+	+	+	+	-	-	+	+	-	Polymorphic
1000bp	+	+	+	+	+	+	+	+	+	Monomorphic
650bp	+	+	+	+	+	-	+	+	-	Polymorphic
500bp	+	+	+	+	+	+	+	+	+	Monomorphic
				HB12						
2000bp	+	+	+	+	+	+	+	+	+	Monomorphic
1600bp	-	-	-	-	-	-	-	-	+	Unique
1500bp	-	-	-	-	-	-	-	-	+	Unique
900bp	+	+	+	+	+	+	+	+	-	Polymorphic
				HBS10						
1600bp	+	+	+	+	+	+	+	+	+	Monomorphic
1500bp	-	-	+	-	-	+	-	-	+	Polymorphic
1200bp	+	+	+	+	+	+	+	+	+	Monomorphic
1000bp	-	-	+	-	-	+	+	-	+	Polymorphic
900bp	+	+	+	+	+	+	+	+	+	Monomorphic
500bp	+	+	+	+	+	+	+	+	+	Monomorphic
400bp	+	+	+	+	+	+	+	+	+	Monomorphic
				HBS11						
4000bp	-	+	+	+	+	+	+	+	+	Polymorphic
3000bp	+	+	+	+	+	+	+	+	-	Polymorphic
2400bp	-	-	-	-	-	-	-	+	-	Unique
2000bp	-	-	-	-	-	-	-	+	-	Unique
1500bp	+	+	+	+	+	+	+	+	+	Monomorphic
				17889A						
4000bp	-	+	-	-	-	-	-	-	+	Polymorphic
3000bp	+	+	+	+	+	+	+	+	+	Monomorphic
2000bp	+	+	+	+	+	+	+	+	+	Monomorphic
1500bp	+	+	-	+	-	+	-	+	+	Polymorphic
1200bp	-	-	-	-	-	-	-	+	+	Polymorphic
1000bp	+	+	+	+	+	+	+	+	+	Monomorphic
800bp	-	-	-	+	-	-	-	-	-	Unique
700bp	-	+	-	+	-	-	-	-	-	Polymorphic
650bp	+	-	-	+	-	-	-	-	-	Polymorphic
400bp	+	-	-	-	-	-	-	-	-	Unique
300bp	+	-	-	-	-	-	-	-	-	Unique
100bp	-	-	-	+	-	-	-	-	-	Unique
				17889B						
2000bp	+	+	-	+	+	-	+	-	-	Polymorphic
1500bp	+	+	+	+	+	+	+	+	+	Monomorphic
1300bp	+	+	-	-	-	-	-	+	+	Polymorphic
1200bp	+	+	-	-	-	+	-	+	+	Polymorphic
900bp	+	+	-	-	-	-	-	-	+	Polymorphic
700bp	+	+	-	-	-	+	-	+	+	Polymorphic
500bp	+	+	+	+	+	+	+	+	+	Monomorphic
				17899A						
3000bp	-	-	+	+	+	+	+	+	+	Polymorphic
2000bp	-	-	-	-	+	+	+	-	+	Polymorphic
1500bp	-	+	+	+	+	+	+	+	+	Polymorphic
1000bp	+	+	+	+	+	+	+	+	+	Monomorphic
900bp	-	-	+	+	+	-	+	+	+	Polymorphic
700bp	-	-	+	-	-	-	-	-	-	Unique
500bp	+	+	+	+	+	+	+	+	+	Monomorphic
300bp	-	-	-	+	+	-	-	+	-	Polymorphic

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التحليـــــل الـــــوراثي ومعلمـــات قـــواعد الـISSR لمقـــاومـــة صدأ الأوراق في قمـح الخبـــــز

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الدراسة الحالية هدفها دراسة وتوضيح السلوك الوراثى لمقاومة صدأ الأوراق فى قمح الخبز فى مجموعة من خمسة آباء وعشرة هجن تحت ظروف الحقل عن طريق إجراء العدوى الصناعية، التباين الواسع بين الآباء وهجن الجيل الأول تم اكتشافه فى خمس صفات تحت الدراسة هى فترة التحضين وشدة الإصابة والاستجابة للعدوى ومتوسط تأثير العدوى والمساحة تحت المنحنى المرضى، متوسط تلك الأصناف العائد إلى مقاومة هذه الأصناف أوضح أن جيزة ١٦٨وسخا ٩٣ تملك استجابة عالية للمقاومة كوقت طويل لفترة التحضين بالإضافة إلى قلة شدة الإصابة المرضية ونفس المعدل لكلا الصنفين فى الاستجابة للعدوى ومتوسط الإصابة والمساحة تحت المنحنى، تحليل التباين للخمس صفات سجل اختلافات غير معنوية لكل الصفات ماعدا شدة الإصابة، الاختلافات المعنوية لكل من H_1, H_2 المتحصل عليها لصفتى فترة التحضين وشدة الإصابة بينما صفة المساحة تحت المنحنى المرضى أوضحت اختلافات معنوية لتقدير الجين السائد، متوسط قيم السيادة أشارت إلى وجود السيادة الفائقة لكل الصفات المدروسة، نسبة تأثير الجينات الفعالة الموجبة والسالبة فى الأباء أشارت إلى تكرار موجب وسالب غير متساوى بين الأباء لصفتى شدة الإصابة والمساحة تحت المنحنى المرضى ماعدا فترة التحضين التى تملك جينات موجبة وسالبة متقاربة ومتساوية بين الأباء، تحليل الشكل البيانى أشار إلى أن الأصناف جيزة ١٦٨ وسخا ٩٣ تملك معظم جينات السيادة للمقاومة لكن الأصناف جميزة ١١ جميزة ٩ تملك معظم جينات التنحى لصفة الحساسية، المعلمات الجزيئية لتكنيك Bulk segregant analysis تم استخدامها عن طريق تكنيك ISSR الذى تم استخدامه عن طريق ثمانى بادئات، أكدت نتائج التحليل الجزيئى أن جيزة ١٦٨ تم اعتباره تركيب وراثى هام جدا لمقاومة مرض صدأ الأوراق، هذا الصنف امتلك اربعة قطع للوزن الجزيئى ٢٠٠٠ فى البادئ 844A و١٥٠٠فى البادئ 17889A و١٢٠٠و٧٠٠ فى البادئ 17889B هذه القطع ظهرت فى الاب جيزة ١٦٨ وهجن الجيل الأول وأكثر فى الجيل الثانى المقاوم، جيزة ١٦٨ ربما تملك معظم جينات المقاومة لمرض صدأ الأوراق، على العكس جميزة ١١ فى الوزن الجزيئى ١٥٠٠ فى البادئ HBS10 وأكثر فى مجموعة الجيل الثانى الحساس، أيضًا هى أكدت مدى حساسية الصنف جميزة ١١ لمرض صدأ الأوراق فى قمح الخبز.

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