

Validation of Simple Sequence Repeats (SSRs) Linked to Drought Susceptibility Index in Diallel Cross Wheat

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Abstract

Wheat (*Triticum aestivum* L.) is one of the most crucial staple food crops in Egypt and worldwide it is adversely affected by water stress. The study aims at examine the genetic characterization of nine bread wheat genotypes, Sahel-1 (P1), Gemmiza-9 (P2), Sakha-94 (P3), Misr-1 (P4), Giza-168 (P5), L146 (P6), L133 (P7), L142 (P8) and L147 (P9) using microsatellite (SSR) markers. A total number of 48 scorable bands were amplified by five SSR primers. Thirty-four out of 48 fragments were monomorphic bands (70.83%), thus 14 loci were polymorphic (29.17% polymorphasim). PIC value of the five SSR primers ranged from 0.863 to 0.881 with an average of 0.870. The Nei genetic identity index ranged from 0.81 to 0.95. The genetic similarity among nine parents of wheat fell into three main clusters.

Key words: wheat (*Triticum aestivum* L.), Drought, SSR.

Introduction

Global changes will impact food security and a decrease of rain as a result of it has severely affected food security. An increase of the heat has direct effect on farming practices, and agricultural production, leading to more severe drought (Mickelbart *et al.*, 2015). When plants are exposed to abiotic stress conditions e.g. high temperature, salinity, drought and exaggerated rainfall, this affects the plant growth adversely and it induces physiological and metabolic alterations in the plants (Bita and Gerats 2013). Drought is the main abiotic stress factor which negatively affects the quantity and quality of wheat crop (Shao *et al.*, 2005; Kirigwiet *et al.*, 2007; Huseynova and Rustamova, 2010; El-Hosary and Gehan El Deen 2015). To reduce the effects of drought-induced by the weather changes, scientific research to generate plants tolerant of drought should be continued. The effect of abiotic stress on plants has quite complex properties, and subsequently, several reports are being performed to get a better comprehension. In spite of limitations induced by the environment in terms of polygenic characterization, morphological markers have been applied for the breeding researches. Molecular markers overcome the biochemical and morphological markers limitations (Gupta *et al.*, 1999; Dodig *et al.*, 2010). To illustrate the genotypic mechanisms of drought-tolerant lines; conventional breeding studies, genetic engineering approaches, and molecular markers must be applied together. Most crops, increased in yield by classical breeding ways, grow under suitable conditions. For this reason, most of the cultivars of crops applied for agricultural generation are not tolerant to water stress (Öztörk, 2015). So, it is very important that biotechnological approaches must continue at a rapid speed to develop lines tolerant drought which can acclimate under local conditions. The first phase of

drought-tolerant cultivar breeding starts with approaches focusing on different aspects like decrease the effects of drought, biochemical and molecular properties and classification of wheat cultivars and putting them in terms of tolerance to drought.

Recent advances in molecular and genomic techniques have enabled the development of molecular markers which can be applied for several crops and the QTLs identification. These improvements have led to the crop development which is tolerant to drought stress in future (Salvi and Tuberosa, 2015). To fulfill this, many molecular markers are applied. Among these markers, Simple sequence repeats (SSR) markers are frequently applied for molecular studies of wheat because it has a big number in genomes, co-dominant kind of inheritance, loci specificity, reproducibility, and high informational content (Yıldırım *et al.*, 2009).

The study aims at examine the genetic characterization of nine bread wheat genotypes using microsatellite (SSR) marker for drought tolerant. In additions determinate the genetic diversity among them.

Materials and Methods

Plant materials

Nine genotypes of bread wheat (*Triticum aestivum* L.), Sahel-1, Gemmiza-9, Sakha-94, Misr-1, Giza-168, L146, L133, L142 and L147 representing a wide range of diversity for several agronomic characters and drought resistance measurements were used in the present study. Name, pedigree of origin of these genotypes are presented in Table (1). For each genotype drought susceptibility index (DSI) was calculated for yield and yield compound traits using the formula given by Saulescu *et al.* (1995)

$$DSI = S/NS$$

Where: Ns and S character with normal irrigated and stress conditions, respectively.

Genomic DNA isolation

A sample of 0.5 g of young leaves from each of nine wheat genotypes were collected and soaked in liquid nitrogen for DNA extraction using the 2% Cetyl trimethyl ammonium bromide (CTAB)-based procedure as described by **Doyle and Doyle, (1990)**.

SSR fingerprints

A total of six SSR primers Table (2) were used to amplify DNA from nine genotypes under study. Each 25 µl amplification reaction contained 1X PCR reaction buffer, 2.0 mM MgCl₂, 0.2 mM dNTPs mix, 0.4 µM of each primer set, 1.5 U TaqDNA polymerase and adjusted to 25 µl using double-distilled water (ddH₂O). Amplifications were carried out in a DNA thermocycler (Biometra, Germany) with the following temperature profile: 1 initial denaturation step at 94°C for 5 minutes, followed by 35 cycles at 94°C for 30 seconds, 55°C for 1 minute and 72°C for 90 seconds and a final extension cycle of 72°C for 10 minutes.

Gel electrophoresis

The amplified DNA (15 µl) for all samples was electrophoresed on a 1% agarose gel containing Ethidium Bromide (0.5 µg/ml) in 1X TBE buffer (89 mM Tris-HCl, 89 mM Boric acid, 2.5 mM EDTA, pH 8.3) at 75 constant volts, and visualized using a UV transilluminator (UVI Geltec version 12.4, 1999-2005 (USA)). The size of each fragment was estimated with reference to a 10 Kb DNA ladder (BioRoN, Germany).

Data analysis

A matrix was generated for SSR marker by scoring reproducible bands as 1 for their presence and as 0 for their absence across the accessions. Genetic similarity coefficients were computed following **Nei and Li, (1979)** as follows:

$$\text{Similarity} = \frac{2N_{xy}}{N_x + N_y}$$

where 'N_x' and 'N_y' are the number of bands present in accessions 'x' and 'y', respectively, and N_{xy} is the number of bands shared by the accessions 'x' and 'y'. The data were subsequently used to construct a dendrogram using the unweighted pair group method of arithmetic averages (UPGMA) (**Sneath and Sokal, 1973**) employing sequential, agglomerative hierarchy and non-overlapping clustering (SAHN). All the computations were carried out using the software NTSYS-PC (Numerical Taxonomy and Multivariate Analysis System), version 2.1 (**Rohlf, 2000**). Correlation coefficients were calculated using similarity coefficients obtained from SSR marker.

Results and Discussion

SSR analysis

Five SSR primers were used to amplify nine wheat genotypes. **Table (3)**. A total number of 48 scorable bands were amplified by five SSR primers (9.6 bands per primer), ranging from 95 (SSR-162 and SSR-603) to 1500 bp (SSR-162) **Table (3)**. Thirty-four out of 48 fragments were monomorphic bands (70.83%), 14 loci were polymorphic (29.17%). The number of fragments per primer varied from nine (SSR-C9 and SSR-603) to 10 (SSR-108, SSR-C596, and SSR-162). Primer SSR-C596 recorded the highest number of polymorphism (50%), followed by primer SSR-603 (44.44%). However, Primer SSR-108 scored the lowest number of polymorphism (10%). Six bands were unique markers (12.50%) **Table (3)**. The level of polymorphism among the nine wheat genotypes was estimated by calculating polymorphic information content (PIC) values for each of the five SSR markers. The PIC values varied greatly for all the SSR primers tested. PIC value of the five SSR primers ranged from 0.863 (SSR-C596) to 0.881 (SSR-108) with an average of 0.870 **Table (3)**. Sahel-1 recorded one marker of 600 bp. Misr-1 and L147 appeared the maximum number of markers (two) with molecular sizes (-95 and -550 bp) and (+200 and +400 bp), respectively. However, Giza 168 displayed one negative marker of -510 bp. In contrast, Gemmiza 9, Sakha 94, L146, L133 and L142 have not any markers **Table (3)**.

Triticum aestivum L. is one of the most crucial staple food crops in Egypt and worldwide is adversely affected by water stress. Comprehension of its genetics and genome organization by SSR-PCR is of big impact for wheat breeding programs. In the current study, the percentage of polymorphism among nine wheat genotypes was low 29.17%, using SSR technique. Six bands were unique markers (12.50%) **Table (3)**. Sahel 1 recorded one marker of 600 bp. Misr 1 and L147 appeared the maximum number of markers (two) with molecular sizes (-95 and -550 bp) and (+400 and +200 bp), respectively. However, Giza 168 displayed one negative marker of -510 bp. In contrast, Gemmiza 9, Sakha 94, L146, L133 and L142 have not any markers. These results were an agreement with **Hammer, (2000)**; **Dreisigacker et al., (2004)** mentioned that SSR analysis acts the most suitable markers in wheat genotypes and have been successfully applied to identify genetic variability in advanced wheat breeding programs. **Iqbal et al., (2016)** found that the relationship between pattern of drought-responsive biochemical characters and molecular markers in the selected wheat genotypes was identified to screen drought-tolerant wheat cultivars for cultivation in drought-affected areas of the country.

Table 1. Pedigree and source of the studied wheat genotypes.

NO	Entry name	Pedigree	Source
1	Sahel 1	N.S.732/Pim/Vee"S"	Egypt
2	Gemmiza 9	Ald"S"/Huac"S"/CMH74A.630/5x CGM4583-5GM-1GM-0GM	Egypt
3	Sakha 94	Opata/Rayon//Kauz	Egypt
4	Misr 1	OASIS/SKAUZ//4*BCN/3/2*PASTOR. CMSS00Y01881T -050M-030Y-030M-030WGY-33M0Y--0EGY	Egypt
5	Giza 168	MIL/BUC//Seri CM93046-8M-0Y-0M-2Y-0B	Egypt
6	L 146	CMH.S87.146\ ELVIRA	CIMMYT
7	L 133	MILAN \ S7133\ \ Hall //(Ne700011)	CIMMYT
8	L 142	MILAN \ S7142\ \ OAPYMex	CIMMYT
9	L 147	MILAN \ S87147 \ \ BABAX	CIMMYT

Table 2. SSR primers sequences used in this study.

No	Primer name	Sequence (5'-3')	Annealing Temperature
1	BARC108-f27	5' GCG GGT CGT TTC CTG GAA ATT CAT CTA A '3	50
	BARC108-r27	5'GCG AAA TGA TTG GCG TTA CAC CTG TTG '3	50
2	Wmc603-f27	5' ACA AAC GGT GAC AAT GCA AGG A'3	61
	Wmc603-r27	5CGC CTC TCT CGT AAG CCT CAA C'3	61
3	Wmc596-f27	5' TCA GCA ACA AAC ATG CTC GG'3	61
	Wmc596-r27	5'CCC GTG TAG GCG GTA GCT CTT '3	61
4	Xgwm162-f27	5'AGT GGA TCG ACA AGG CTC TG '3	61
	Xgwm162-r27	5'AGA AGA AGC AAA GCC TTC CC '3	61
5	Wmc9-f27	5'AAC TAG TCA AAT AGT CGT GTC CG '3	61
	Wmc9-r27	5'GTC AAG TCA TCT VGAC TTA ACC CG '3	61

Table 3. SSR-PCR analysis, a total number of bands, monomorphic, polymorphic, unique bands for nine genotypes of wheat.

Prime r Code No.	Size range of the scorable loci (bp)	Total loci	No. of monomorphic loci	No. of polymorphic loci	% Polymorphism	PIC	Unique loci	Molecular size of markers (bp)
SSR-	175-850	10	9	1	10	0.881	1	+400
SSR-	130-600	9	9	0	0	0.878	0	-
SSR-	95-550	9	5	4	44.44	0.864	2	-550, -95
SSR-	160-1461	10	5	5	50	0.863	2	+600, -510
SSR-	95-1500	10	6	4	40	0.864	1	+200
Total	95-1500	48	34	14	29.17%	-	6	12.50%

Table 4. Genetic similarity and for nine wheat genotypes.

Parents	Sahel 1	Gemmiza 9	Sakha 94	Misr1	Giza 168	L146	L133	L142	L147
Sahel 1	1.00								
Gemmiza 9	0.95	1.00							
Sakha 94	0.90	0.90	1.00						
Misr1	0.83	0.83	0.88	1.00					
Giza 168	0.85	0.85	0.85	0.87	1.00				
L146	0.84	0.88	.88	.85	.88	1.00			
L133	0.86	0.90	0.86	0.83	0.85	0.93	1.00		
L142	0.88	0.88	0.88	0.89	0.92	0.86	0.93	.00	
L147	0.84	0.84	0.88	.81	.83	0.82	0.88	0.90	1.00

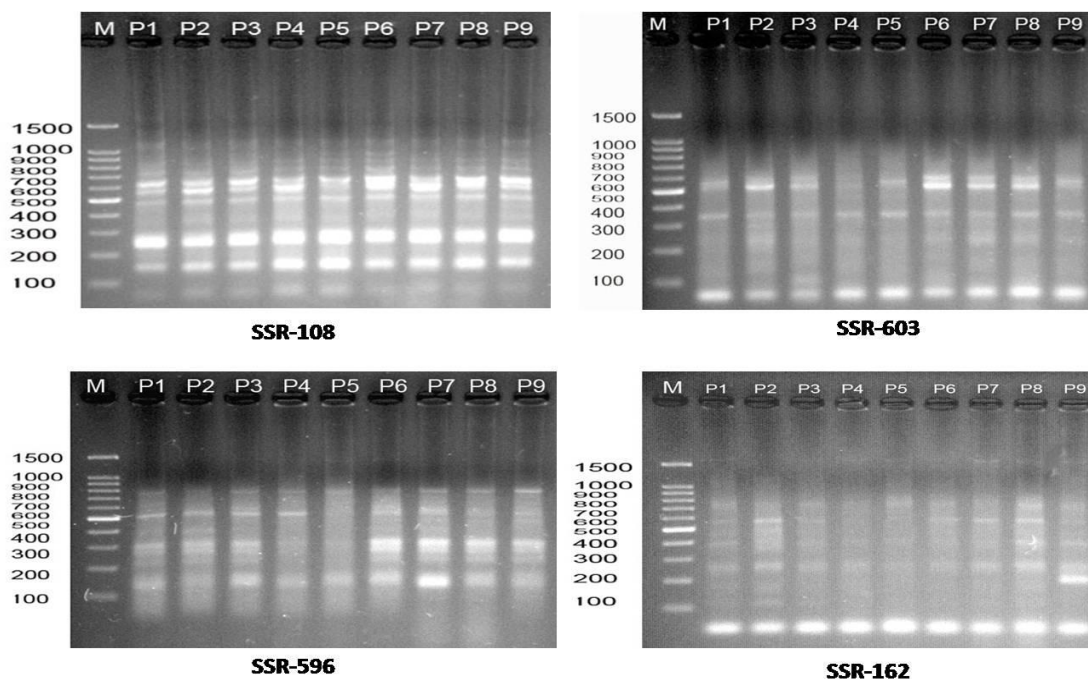


Fig (1). Amplified products of SSR-PCR using of primers SSR-108, SSR-603, SSR-596 and SSR-162 for analyzed nine parents of wheat. Lane M= DNA ladder 100 bp.

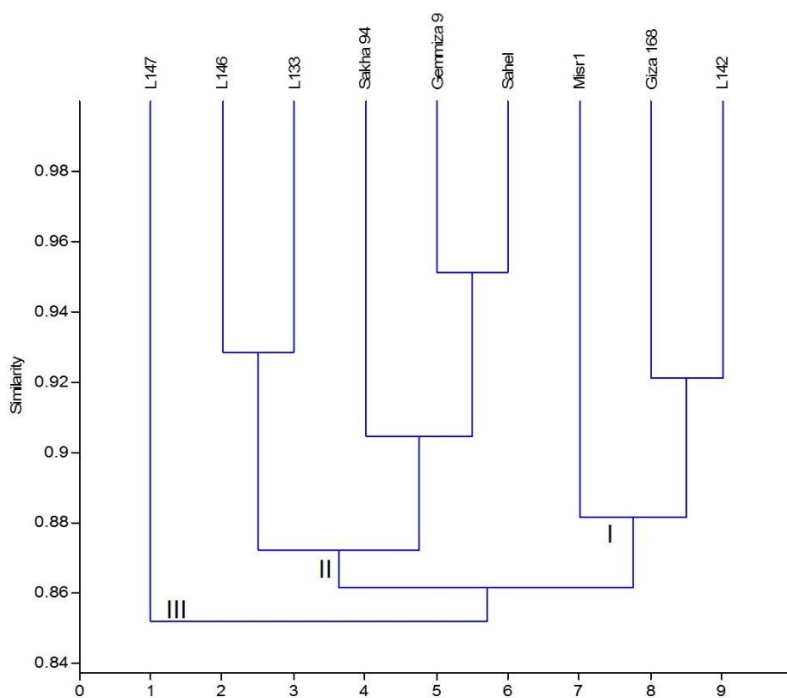


Fig (2). UPGMA dendrogram of nine genotypes of wheat depend on Jaccard's similarity coefficient.

Cluster analysis

The dendrogram resulting from cluster analysis appeared three major clusters for wheat genotypes. The genetic similarity among nine wheat genotype fell into three main clusters. The Nei genetic identity

index ranged from 0.81 between (Misr 1 and L147) to 0.95 between (Sahel 1 and Gemmiza 9) (**Fig 2. and Table 4**). The genetic similarity among nine parents of wheat fell into three main clusters was recorded. The first cluster (I) contained on parents Misr1, Giza

168 and L142. The second cluster (II) composed of Sahel 1, Gemmiza 9, Sakha 94, L133 and L146. The third cluster (III) has L147. Similar studies were conducted by different investigators using SSR markers (Chakravarthy and Naravani, 2006; Panaud *et al.*, 2016 and El-Hosary a and b 2019).

2. Susceptibility index experiment:

2.1 Analysis of Variance and mean performance

The analysis of variance for susceptibility index (SI) of yield and yield components are presented in Table 5. Highly significant mean squares due to genotypes, parents and crosses were detected for all studied traits except plant height was only significant for crosses. Meanwhile, the crosses have significant values in plant height. Such results indicate the wide diversity among all wheat genotypes of this study.

Mean performance of the nine parents along with their crosses of wheat of SI are presented in Table (6). Results indicated that Parent (P₂) was the best parent for No. of kernels/spike, straw yield (g) per plant and biological yield (g)/ plant. Parent (P₅) seemed to be the best parent for plant height and spike length. Parent (P₆) gave the desirable SI for 1000 kernel weight (g), grain yield (g) per plant, harvest index. Parent (P₉) seemed to be the best parent for number of spikes/plants, regarding plant height and spike length, the cross P₃ x P₇ had the best susceptibility index of stress irrigation. Results also indicated that the most desirable susceptibility index were detected for the crosses P₂ x P₆ and P₃ x P₅ for No. of spikes /plant; P₂ x P₄ and P₂ x P₈ for No. of kernels/spike, P₆ x P₈ for 1000 kernel weight (g) and grain yield (g) per plant, P₂ x P₇ for Straw yield (g) per plant and Biological yield (g)/ plant. Most of tested cross gave desirable susceptibility index for harvest index Table (6).

2.2. Heterosis:

Mean squares for parents vs. crosses as an indication to average heterosis overall crosses were significant ($P \leq 0.05$ or 0.01) for all studied traits, except for straw yield per plant and biological Yield Table(5).

Heterosis expressed as the percentage deviation of F₁ mean performance relative to mid parent and better parent values for SI for yield and yield components is presented in Table (7,8).

Regarding to plant height, the cross P₅ x P₆ exhibited significant and negative heterosis for mid parent and better parent. For spike length, the four crosses P₂ x P₉, P₃ x P₇, P₆ x P₉ and P₈ x P₉ gave the best heterotic effects relative to mid parent. For No. of spikes /plant, the two crosses; P₄xP₆ and P₄xP₇ exhibited significant and positive heterotic effects relative to mid parent and better parent. For number of kernels/spike, nine and two crosses exhibited significant and positive heterotic effects relative to mid parent and better parent, respectively. Regarding 1000 kernel weight, the cross namely, P₂ x P₉ gave significant and positive

heterotic effects relative to mid parent and better parent. However, P₆ x P₈ gave significant and positive heterotic effects relative to mid parent. For Straw yield / plant(g), four crosses expressed significant and positive heterotic effects relative to mid parent. However, the cross P₇xP₉ gave the most desirable recorded 33.74*.

For grain yield per plant, fourteen and seven crosses gave positive and significant heterosis relative to mid and better parent, respectively. For biological yield/plant(g), five crosses expressed significant and positive heterotic effects relative to mid parent. Sixteen and seven crosses recorded significant and positive heterotic effects relative to mid parent and better parent, respectively for harvest index.

3.2. Combining ability analysis:

Analysis of variance for combining ability for SI in plant height, yield and yield components is presented in Table 5. The variances associated with general and specific combining ability were highly significant for SI in all studied traits. Such results indicated that both types gene action namely additive and non-additive are important in the inheritance of susceptibility index for plant height, yield and yield components.

The ratio between GCA and SCA were more than one for all traits except SI for spike length and No of spikes / plant which low GCA/ SCA ratio were detected indicating the predominance of additive type of gene action in controlling such traits. For the exceptional traits, non-additive type of gene action seemed to be more important than additive gene action in the inheritance of such traits. Similar results were reported by Wafaa, Hassan (2007) and Uzair *et al.*(2016).

A-General combining ability effects (\hat{g}_i):

Estimations of G.C.A effects (\hat{g}_i) for individual parental genotypes for SI in plant height yield and yield components are presented in Table 9.

The parental variety P1 expressed the highest significant and positive (\hat{g}_i) effects for No. of spikes /plant, No. of kernels/spike, straw yield / plant, grain yield / plant and biological yield/ plant.

The parental variety P2 exhibited significant undesirable (\hat{g}_i) effects for No. of spikes /plant, No. of kernels/spike, straw yield / plant, and biological yield/ plant.

The parental variety P3 exhibited significant undesirable (\hat{g}_i) effects for 1000 kernel weight (g) and harvest index.

The parental variety P5 expressed significant and positive (\hat{g}_i) effects for No. of spikes /plant, straw yield / plant, and biological yield/ plant.

The parental variety P6 had desirable significant (\hat{g}_i) effects for No. of spikes /plant, No. of kernels/spike, 1000 kernel weight, Grain yield / plant, Biological yield/ plant and harvest index.

The parent P7 expressed significant and positive (\hat{g}_i) effects for 1000 kernel weight.

The parent P8 was the best general combiner for plant height while gave negative and high significant (\hat{g}_i) effects and expressed significant and positive (\hat{g}_i) effects No. of kernels/spike, straw yield / plant and biological yield/ plant.

The parent P7 expressed significant and positive (\hat{g}_i) effects for harvest index.

B-Specific combining ability effects (\hat{s}_{ij}):

Specific combining effects for SI in yield and yield components are presented in Table (10,11). For susceptibility index. six, twelve, thirteen, seven, five, twelve, four, and ten crosses expressed significant and positive \hat{s}_{ij} effects for spike length, No. of spikes /plant, No. of kernels/spike, 1000 kernel weight, Straw

yield / plant, Grain yield / plant, Biological yield)/ plant and harvest index, respectively. And three crosses expressed significant and negative \hat{s}_{ij} effects for plant height.

However, the most desirable \hat{s}_{ij} effects were detected for the cross combination $P_2 \times P_9$ for spike length; the cross $P_3 \times P_5$ and $P_4 \times P_6$ for number of spikes/ plant, $P_7 \times P_9$ for No. of kernels/spike, $P_2 \times P_9$ for 1000 kernel weight, $P_2 \times P_7$ for straw yield / plant, $P_6 \times P_8$ for grain yield / plant, $P_2 \times P_4$ and $P_2 \times P_7$ for biological yield/ plant and $P_4 \times P_7$ for harvest index (Table 10,11). It could be concluded that stress tolerant genotypes, as defined by SI values, need not have a high yield potential since SI provides a measure of tolerance based on minimization of yield loss under stress rather than non- stress yield.

Table 5. Observed mean squares from ordinary analysis of variance for susceptibility index (SI) of yield and its components.

S.O.V.	d.f.	Plant height	spike length	No. of Spikes/plant	No. of kernels/plant	1000 kernel weight	Straw yield	Grain yield	Biological yield	Harvest index
Rep/E	2	0.00	0.00	0.00	0.00*	0.00	0.02	0.01	0.02	0.00
Genotypes	44	0.00**	0.01**	0.03**	0.02**	0.01**	0.06**	0.09**	0.05**	0.12**
Parent	8	0.01**	0.01**	0.07**	0.01**	0.01**	0.09**	0.19**	0.07**	0.21**
Cross	35	0.00*	0.02**	0.02**	0.02**	0.01**	0.05**	0.07**	0.04**	0.09**
Par.vs.cr.	1	0.00*	0.01*	0.03**	0.06**	0.02**	0.01	0.23**	0.01	0.47**
Error	88	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.01	0.02
GCA	8	0.00**	0.00**	0.01**	0.01**	0.01**	0.05**	0.04**	0.03**	0.05**
SCA	36	0.00**	0.01**	0.01**	0.01**	0.00**	0.01**	0.03**	0.01**	0.04**
Error	88	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
GCA/SCA		2.15	0.48	1.13	0.89	2.36	3.23	1.34	2.82	1.32

* and ** significant at 0.05 and 0.01 levels of probability, respectively.

Table 6. Mean performance for susceptibility index (SI) of plant height, spike length, number of spikes/plant, No. of kernels/spike, 1000 kernel weight (g), straw yield (g) / plant, grain yield (g) /plant, biological yield (g)/ plant and harvest index .

Genotypes	plant height	spike length	No. of spikes /plant	No. of kernels/ spike	1000 kernel weight (g)	Straw yield (g) /plant	Grain yield (g) per plant	Biological yield (g)/ plant	Harvest index
Sahel-1(P1)	0.90	0.93	0.88	0.91	0.94	0.80	0.83	0.80	1.04
Gemmiza9(P2)	0.91	0.95	0.84	0.95	0.88	1.00	0.51	0.86	0.59
Sakha94(P3)	0.95	0.91	0.89	0.94	0.95	0.68	0.86	0.71	1.21
Misir1(P4)	0.88	0.92	0.47	0.80	0.98	0.47	0.26	0.41	0.63

Table 6 cont.									
Giza168 (P5)	0.98	0.99	0.85	0.81	0.93	0.90	0.56	0.80	0.71
LineM1 146(P6)	0.94	0.89	0.87	0.93	0.99	0.75	0.97	0.80	1.22
LineM1 133(P7)	0.96	0.87	0.72	0.77	0.96	0.51	0.42	0.50	0.86
LineM1 142(P8)	0.85	0.90	0.66	0.84	0.91	0.75	0.46	0.67	0.69
LineM1 147(P9)	0.95	0.76	0.97	0.82	0.82	0.70	0.88	0.73	1.21
P1×P2	0.93	0.74	0.82	0.67	0.95	0.72	0.58	0.68	0.86
P1×P3	0.94	0.84	0.82	0.76	0.93	0.67	0.86	0.70	1.23
P1×P4	0.93	0.94	0.92	0.90	0.95	0.69	0.86	0.73	1.19
P1×P5	0.93	0.95	0.87	0.66	0.79	0.80	0.79	0.79	1.01
P1×P6	0.96	0.91	0.83	0.86	0.89	0.63	0.9	0.69	1.29
P1×P7	0.96	0.93	0.91	0.82	0.86	0.70	0.88	0.75	1.18
P1×P8	0.94	0.90	0.85	0.90	0.89	0.88	0.76	0.85	0.89
P1×P9	0.88	0.83	0.69	0.92	0.85	0.91	0.46	0.82	0.56
P2×P3	0.94	0.85	0.71	0.80	0.93	0.56	0.56	0.56	1.01
P2×P4	0.91	0.83	0.84	0.94	0.87	0.86	0.77	0.83	0.92
P2×P5	0.93	0.88	0.77	0.90	0.81	0.57	0.53	0.56	0.94
P2×P6	0.94	0.92	0.98	0.91	0.94	0.71	0.91	0.75	1.21
P2×P7	0.95	0.94	0.80	0.70	0.87	0.98	0.61	0.89	0.69
P2×P8	0.93	0.91	0.92	0.94	0.85	0.88	0.84	0.87	0.98
P2×P9	0.92	0.98	0.95	0.86	0.95	0.81	0.88	0.82	1.08
P3×P4	0.97	0.90	0.71	0.74	0.94	0.41	0.56	0.45	1.25
P3×P5	0.94	0.70	0.98	0.74	0.84	0.63	0.66	0.64	1.10
P3×P6	0.95	0.92	0.73	0.82	0.98	0.68	0.65	0.67	0.96
P3×P7	0.99	0.98	0.72	0.63	0.98	0.54	0.49	0.53	0.94
P3×P8	0.92	0.91	0.82	0.69	0.90	0.77	0.59	0.73	0.80
P3×P9	0.93	0.85	0.79	0.85	0.91	0.40	0.41	0.40	1.04
P4×P5	0.94	0.94	0.93	0.81	0.88	0.74	0.82	0.76	1.09
P4×P6	0.91	0.93	0.95	0.80	0.90	0.80	0.86	0.82	1.05
P4×P7	0.93	0.95	0.87	0.77	0.88	0.56	0.84	0.63	1.40
P4×P8	0.93	0.83	0.63	0.74	0.83	0.56	0.64	0.58	1.11
P4×P9	0.97	0.77	0.89	0.73	0.82	0.63	0.84	0.67	1.25
P5×P6	0.91	0.74	0.97	0.76	0.96	0.87	0.83	0.86	0.97
P5×P7	0.96	0.82	0.82	0.78	0.89	0.75	0.83	0.77	1.11
P5×P8	0.98	0.84	0.78	0.78	0.87	0.86	0.72	0.82	0.88
P5×P9	0.95	0.79	0.75	0.85	0.90	0.62	0.79	0.66	1.20
P6×P7	0.94	0.85	0.82	0.93	0.96	0.59	0.75	0.63	1.19
P6×P8	0.98	0.87	0.91	0.91	1.00	0.73	1.06	0.80	1.29
P6×P9	0.94	0.96	0.79	0.71	0.89	0.70	0.69	0.70	0.99
P7×P8	0.93	0.90	0.81	0.87	0.93	0.75	0.82	0.76	1.07
P7×P9	0.94	0.81	0.80	0.91	0.92	0.81	0.81	0.81	1.01
P8×P9	0.87	0.96	0.82	0.78	0.90	0.68	0.84	0.71	1.20
average parent	0.92	0.90	0.79	0.86	0.93	0.73	0.64	0.70	0.91
average crosses	0.94	0.88	0.83	0.81	0.90	0.71	0.74	0.71	1.05
average genotypes	0.94	0.88	0.83	0.82	0.91	0.71	0.72	0.71	1.02

Table 7. Heterosis over both mid – parent and better – parent of plant height, spike length, number of spikes/plant, number of kernels/spike and 1000 kernel weight for susceptibility index (SI).

Genotypes	Plant height		spike length		No. of spikes /plant		number of kernels/spike		1000 kernel weight	
	M.P	B.P	M.P	B.P	M.P	B.P	M.P	B.P	M.P	B.P
P1×P2	3.15	2.27	-20.51**	-21.31**	-4.22	-6.69	-28.15**	-29.60**	4.76*	1.6
P1×P3	1.77	-1.23	-8.73*	-9.76*	-7.56	-7.96	-17.59**	-18.64**	-1.27	-2.14
P1×P4	4.91	3.81	2.17	1.92	36.59**	4.91	5.50**	-1.37	-0.94	-3.07
P1×P5	-0.67	-4.93	-0.35	-3.33	0.02	-1.72	-23.49**	-28.02**	-15.40**	-15.59**
P1×P6	4.84	2.3	-0.32	-2.18	-5.02	-5.64	-6.64**	-7.39**	-7.50**	-9.78**
P1×P7	3.2	-0.42	3.72	0.8	13.65**	3.15	-2.53	-9.98**	-8.73**	-9.74**
P1×P8	7.58**	4.9	-1.49	-2.63	10.69*	-2.97	2.45	-1.51	-4.32*	-5.51**
P1×P9	-4.63	-7.28*	-1.95	-10.91*	-25.31**	-28.83**	5.83**	0.32	-2.95	-8.80**
P2×P3	0.78	-1.35	-8.14*	-10.09*	-17.64**	-20.09**	-14.94**	-15.59**	1.73	-2.18
P2×P4	1.73	-0.19	-11.12**	-12.23**	27.72**	-0.04	8.01**	-0.92	-6.96**	-11.64**
P2×P5	-1.11	-4.56	-8.68*	-10.52*	-8.06	-8.86	2.84*	-5.07**	-10.23**	-12.74**
P2×P6	1.98	0.35	0.06	-2.78	15.14**	12.89**	-3.57**	-4.76**	1.26	-4.14*
P2×P7	0.95	-1.77	3.83	-0.08	2.77	-4.45	-19.25**	-26.80**	-5.17**	-9.02**
P2×P8	5.29	1.82	-1.76	-3.87	22.81**	10.18*	4.22**	-1.74	-5.69**	-7.40**
P2×P9	-1.09	-3.02	15.50**	4	4.96	-2.45	-2.94*	-9.74**	12.04**	8.44**
P3×P4	6.58*	2.4	-1.83	-2.7	4.59	-19.91**	-14.51**	-21.03**	-2.61	-3.86
P3×P5	-2.68	-4.07	-26.10**	-29.10**	12.53**	10.11*	-15.68**	-21.62**	-10.72**	-11.70**
P3×P6	0.83	0.28	2.45	1.68	-16.43**	-17.33**	-12.05**	-12.47**	1.42	-0.21
P3×P7	3.58	2.97	10.10*	8.2	-9.78*	-18.43**	-25.90**	-32.37**	2.57	2.34
P3×P8	1.79	-3.58	0.51	0.48	5.52	-7.83	-23.03**	-26.91**	-3.11	-5.16*
P3×P9	-2	-2.17	2.51	-5.88	-14.58**	-18.28**	-2.76	-8.93**	1.99	-4.95*
P4×P5	1.11	-4.19	-1.71	-4.88	40.61**	9.35	1.4	0.71	-7.84**	-10.01**
P4×P6	0.25	-3.17	2.94	1.26	42.23**	9.75*	-6.75**	-13.48**	-8.24**	-8.54**
P4×P7	1.19	-3.34	5.46	2.75	46.55**	21.47**	-1.9	-3.18	-9.51**	-10.47**
P4×P8	7.96**	6.37*	-8.60*	-9.44*	10.81	-5.16	-9.37**	-11.97**	-12.11**	-15.05**
P4×P9	5.93*	1.94	-8.01	-16.22**	22.72**	-8.85*	-10.08**	-11.40**	-9.56**	-16.72**
P5×P6	-5.05*	-6.91*	-20.80**	-24.56**	13.30**	12.05*	-12.25**	-18.06**	0.59	-2.1
P5×P7	-0.86	-1.7	-11.44**	-16.42**	5.17	-3.01	-1.54	-3.47	-5.47**	-6.73**
P5×P8	7.33**	0.29	-10.60**	-14.25**	3.72	-7.67	-5.88**	-7.98**	-5.42**	-6.39**
P5×P9	-1.35	-2.93	-9.13*	-19.65**	-17.95**	-23.12**	4.40**	3.57*	2.72	-3.27
P6×P7	-1.16	-2.28	-4.16	-5.1	3.27	-5.72	8.97**	-0.1	-1.68	-3.04
P6×P8	9.34**	4.11	-3	-3.71	18.37**	4.36	2.48	-2.23	5.09**	1.25
P6×P9	-0.06	-0.43	16.10**	7.34	-14.71**	-19.24**	-19.27**	-24.06**	-1.19	-9.29**
P7×P8	3.01	-2.97	1.3	-0.42	17.15**	12.71*	7.44**	3.03	-0.43	-2.76
P7×P9	-1.61	-0.84	-0.63	-10.05*	-5.82	-18.15**	14.34**	4.80**	3.07	-1.44
P8×P9	-2.99	-7.96**	15.95**	6.48	0.61	-15.38**	-5.92**	-7.29**	3.13	-1.93

* and ** significant at 0.05 and 0.01 levels of probability, respectively.

Table 8. Heterosis over both mid – parent and better – parent of straw yield per plant(g) , grain yield / plant(g), biological yield / plant(g), number of kernels/spike and harvest index for susceptibility index (SI).

Genotypes	Straw yield / plant(g)		Grain yield / plant(g)		Biological yield / plant(g)		Harvest index	
	M.P	B.P	M.P	B.P	M.P	B.P	M.P	B.P
P1×P2	-19.42*	-27.53**	-13.24	-30.04*	-17.65*	-20.37*	5.28	-17.33
P1×P3	-9.19	-16.05	1.73	-0.16	-7.53	-12.72	9.37	1.47
P1×P4	9.62	-13.07	58.34**	3.86	19.85	-9.38	43.13**	15.04
P1×P5	-6.02	-11.67	14.24	-4.34	-0.96	-1.04	16.13	-2.18
P1×P6	-19.16	-21.43	-0.43	-7.62	-13.36	-13.54	14.16	5.52
P1×P7	7.63	-11.44	40.11**	5.89	15.02	-6.9	24.55*	13.69
P1×P8	13.69	10.51	18.09	-8.26	15.99	6.52	3.72	-13.83
P1×P9	21.60*	14.04	-46.21**	-47.68**	6.68	2.06	-49.99**	-53.61**
P2×P3	-33.48**	-44.19**	-18.06	-34.86**	-29.05**	-35.11**	11.76	-16.85
P2×P4	17.57	-13.7	100.49**	51.27**	31.42**	-2.86	50.19**	45.61*
P2×P5	-39.96**	-42.73**	-1.15	-5.7	-32.61**	-34.79**	45.03**	32.92*
P2×P6	-19.03*	-28.99**	22.83*	-6.39	-9.22	-12.4	33.69**	-0.79
P2×P7	29.78**	-1.65	30.29	19.53	30.69**	3.1	-5.2	-19.85
P2×P8	0.89	-11.53	72.54**	64.25**	13.13	0.77	53.62**	43.05*
P2×P9	-4.54	-18.89*	26.84*	0.16	3.06	-4.52	19.83	-10.85
P3×P4	-28.10*	-39.24**	0.59	-34.60**	-20.72	-37.49**	36.06**	3.39
P3×P5	-19.63*	-29.79**	-7.21	-23.46*	-15.64	-20.43*	14.02	-9.59
P3×P6	-4.65	-9.45	-29.23**	-33.17**	-10.9	-15.73	-21.08*	-21.41*
P3×P7	-8.76	-19.68	-23.71	-43.07**	-12.82	-26.04*	-9.47	-22.76*
P3×P8	8.08	2.65	-10.92	-31.71**	6.17	3.11	-15.63	-33.94**
P3×P9	-41.91**	-42.79**	-53.06**	-53.48**	-44.54**	-45.31**	-14.51	-14.53
P4×P5	8.24	-17.97	100.23**	46.38**	25.10*	-5.46	62.11**	52.96**
P4×P6	31.58*	6.64	40.46**	-11.03	35.34**	2.48	13.89	-13.7
P4×P7	14.32	9.03	144.34**	96.65**	39.30*	27.31	88.26**	63.38**
P4×P8	-8.06	-25.49*	78.66**	39.63	6.58	-14.09	68.73**	61.84**
P4×P9	8.32	-9.59	47.93	-4.23	17.56	-8.26	35.40**	2.87
P5×P6	5.48	-3.45	8.7	-14.27	7.29	6.98	0.26	-20.74*
P5×P7	5.97	-16.91	69.18**	48.71**	18.28	-4.33	42.23**	30.09*
P5×P8	4.03	-4.78	41.36*	28.69	11.19	2.05	26.04	23.9
P5×P9	-22.27*	-31.19**	10.14	-9.79	-13.72	-17.52	24.47*	-1.32
P6×P7	-7.03	-21.71	7.34	-22.84*	-2.24	-20.75*	14.29	-2.81
P6×P8	-2.78	-2.78	47.84**	8.95	8.71	0.03	35.04**	5.42
P6×P9	-2.9	-6.41	-25.23**	-28.78**	-8.65	-12.43	-18.81*	-19.12*
P7×P8	18.95	0.16	86.25**	79.14**	31.01**	13.93	39.10**	25.27
P7×P9	33.74*	7.6	24.24	-7.84	31.25**	5.46	-2.4	-16.74
P8×P9	-6.53	-9.91	26.04*	-3.98	1.1	-3.14	26.12*	-1.27

* and ** significant at 0.05 and 0.01 levels of probability, respectively.

Table 9. Estimates of general combining ability effects for susceptibility index (SI) of yield and its component.

Parent	plant height	Spike length	No. of spikes /plant	No. of kernels/spike	1000 kernel weight (g)	Straw yield / plant	Grain yield / plant	Biologic al yield)/ plant	Harvest index
Sahel-1 (P1)	-0.01	0.01	0.02*	0.01**	-0.01	0.04*	0.05*	0.05**	0.00
Gemmiza9 (P2)	-0.01	0.01	0.02*	0.04**	-0.01**	0.09**	-0.05*	0.05**	-0.12**
Sakha94 (P3)	0.01*	-0.01	-0.02*	-0.03**	0.02**	-0.10**	-0.06**	-0.09**	0.05*
Misir-1 (P4)	-0.01	0.01	-0.05**	-0.02**	0.00	-0.08**	-0.05*	-0.07**	0.03
Giza168 (P5)	0.01*	-0.02	0.03**	-0.03**	-0.02**	0.05**	-0.01	0.03*	-0.05*
LineM1146 (P6)	0.01	0.01	0.04**	0.03**	0.04**	0.01	0.12**	0.04*	0.10**
LineM1133 (P7)	0.02**	0.01	-0.02**	-0.02**	0.01**	-0.04*	-0.03	-0.03*	0.00
LineM114 (P8)	-0.02**	0.01	-0.03**	0.01**	-0.01	0.05*	0.00	0.03*	-0.06*
LineM1147 (P9)	-0.01	-0.03**	0.02	0.00	-0.03**	-0.01	0.02	0.00	0.05*
L.S.D gi 0.05	0.01	0.02	0.02	0.01	0.01	0.04	0.04	0.03	0.05
L.S.D gi 0.0	0.01	0.02	0.02	0.01	0.01	0.05	0.05	0.04	0.06
L.S.D gi-gj 0.05	0.02	0.03	0.02	0.01	0.01	0.05	0.06	0.05	0.07
L.S.D gi-gj 0.01	0.02	0.03	0.03	0.01	0.02	0.07	0.07	0.06	0.09

* and ** significant at 0.05 and 0.01 levels of probability, respectively.

Table 10 Estimates of specific combining ability effects for susceptibility index (SI) of plant height, spike length , number of spikes/plant, No. of kernels/spike and 1000 kernel weight (g).

cross	Plant height	spike length	No. of spikes /plant	No. of kernels/spike	1000 kernel weight (g)
P1xP2	0.01	-0.16**	-0.04	-0.20**	0.06**
P1xP3	0.00	-0.05	-0.01	-0.04**	0.01
P1xP4	0.01	0.04	0.13**	0.09**	0.05**
P1xP5	-0.01	0.08**	-0.01	-0.14**	-0.09**
P1xP6	0.03	0.01	-0.06*	0.00	-0.05**
P1xP7	0.02	0.03	0.09**	0.01	-0.05**
P1xP8	0.03	0.00	0.04	0.06**	-0.01
P1xP9	-0.04*	-0.03	-0.17**	0.08**	-0.02
P2xP3	0.00	-0.04	-0.12**	-0.03**	0.01
P2xP4	- 0.01	-0.07**	0.04	0.10**	-0.03*
P2xP5	-0.01	0.00	-0.10**	0.07**	-0.06**
P2xP6	0.01	0.02	0.09**	0.02	0.01
P2xP7	0.00	0.04	-0.02	-0.14**	-0.04**
P2xP8	0.02	0.00	0.11**	0.07**	-0.04**
P2xP9	0.00	0.12**	0.09**	0.00	0.08**
P3xP4	0.04*	0.01	-0.05	-0.04**	0.01
P3xP5	-0.02	-0.16**	0.14**	-0.03**	-0.07**
P3xP6	0.00	0.04	-0.12**	-0.01	0.01
P3xP7	0.03	0.09**	-0.06*	-0.14**	0.04**
P3xP8	-0.01	0.02	0.04	-0.12**	-0.02
P3xP9	-0.01	0.01	-0.03	0.06**	0.00
P4xP5	0.00	0.06*	0.13**	0.04**	0.00
P4xP6	-0.02	0.04	0.14**	-0.03**	-0.04**
P4xP7	-0.01	0.04	0.12**	-0.01	-0.04**
P4xP8	0.02	-0.07*	-0.11**	-0.07**	-0.06**
P4xP9	0.05**	-0.09**	0.10**	-0.08**	-0.06**
P5xP6	-0.04*	-0.13**	0.08**	-0.06**	0.04**
P5xP7	0.00	-0.05	-0.01	0.01	0.00
P5xP8	0.05**	-0.03	-0.04	-0.02*	-0.01
P5xP9	0.01	-0.04	-0.12**	0.05**	0.04**
P6xP7	-0.02	-0.05	-0.02	0.10**	0.00
P6xP8	0.05**	-0.03	0.07**	0.05**	0.06**
P6xP9	0.01	0.10**	-0.10**	-0.15**	-0.03*
P7xP8	0.00	0.00	0.04	0.06**	0.02
P7xP9	-0.01	-0.05	-0.02	0.11**	0.02

P8xP9	-0.04*	0.10**	0.02	-0.05**	0.02
LSD5%(sij)	0.03	0.06	0.05	0.02	0.02
LSD1%(sij)	0.05	0.07	0.07	0.02	0.03
LSD5%(sij-sik)	0.05	0.08	0.08	0.03	0.04
LSD1%(sij-sik)	0.07	0.11	0.10	0.04	0.05
LSD5%(sij-ski)	0.05	0.08	0.07	0.03	0.03
LSD1%(sij-ski)	0.06	0.10	0.09	0.03	0.05

* and ** significant at 0.05 and 0.01 levels of probability, respectively.

Table 11. Estimates of specific combining ability effects for susceptibility index (SI) of straw yield (g) /plant, grain yield (g) /plant, biological yield (g)/ plant, and harvest index.

	Straw yield (g) /plant	Grain yield (g) /plant	Biological yield (g)/ plant	Harvest index
P1xP2	-0.12*	-0.14*	-0.13*	-0.05
P1xP3	0.01	0.15*	0.03	0.16*
P1xP4	0.02	0.14*	0.04	0.14
P1xP5	-0.01	0.03	0.00	0.03
P1xP6	-0.14*	0.00	-0.10*	0.16*
P1xP7	-0.01	0.14*	0.02	0.15*
P1xP8	0.08	-0.01	0.06	-0.08
P1xP9	0.17**	-0.34**	0.07	-0.51**
P2xP3	-0.14*	-0.05	-0.11*	0.06
P2xP4	0.14*	0.14*	0.15**	-0.01
P2xP5	-0.28**	-0.14*	-0.24**	0.09
P2xP6	-0.10	0.11	-0.05	0.21**
P2xP7	0.22**	-0.04	0.15**	-0.22**
P2xP8	0.04	0.16**	0.07	0.14
P2xP9	0.02	0.18**	0.06	0.14
P3xP4	-0.12*	-0.05	-0.10	0.16*
P3xP5	-0.03	0.01	-0.01	0.07
P3xP6	0.06	-0.13*	0.02	-0.21**
P3xP7	-0.03	-0.14*	-0.06	-0.14
P3xP8	0.11	-0.07	0.08	-0.21**
P3xP9	-0.20**	-0.27**	-0.21**	-0.08
P4xP5	0.06	0.15*	0.09	0.08
P4xP6	0.16**	0.06	0.14**	-0.10
P4xP7	-0.03	0.19**	0.03	0.34**
P4xP8	-0.11	-0.03	-0.09	0.12
P4xP9	0.02	0.14*	0.04	0.15*
P5xP6	0.10	0.00	0.08	-0.11
P5xP7	0.03	0.15*	0.06	0.13
P5xP8	0.05	0.01	0.04	-0.04
P5xP9	-0.12*	0.06	-0.08	0.17*
P6xP7	-0.10	-0.07	-0.08	0.05
P6xP8	-0.04	0.21**	0.02	0.22**
P6xP9	0.00	-0.18**	-0.04	-0.19*
P7xP8	0.03	0.13*	0.05	0.10
P7xP9	0.15*	0.09	0.13**	-0.07
P8xP9	-0.07	0.10	-0.03	0.19*
LSD5%(sij)	0.11	0.12	0.10	0.15
LSD1%(sij)	0.15	0.16	0.13	0.19
LSD5%(sij-sik)	0.17	0.18	0.15	0.21
LSD1%(sij-sik)	0.22	0.23	0.19	0.28
LSD5%(sij-ski)	0.16	0.17	0.14	0.20
LSD1%(sij-ski)	0.21	0.22	0.18	0.27

* and ** significant at 0.05 and 0.01 levels of probability, respectively.

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تقييم للتتابعات الجينية البسيطة المتكررة (SSR) ومدى ارتباطها بدليل الحساسية للجفاف في القمح

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1 قسم الوراثة و السيتولوجي -الهندسة الوراثية و البيوتكنولوجي-المركز القومي للبحوث-مصر
2 قسم المحاصيل -كلية الزراعة -جامعة بنها -مصر

1- استخدمت خمسة بوادى SSR على التسعة تراكيب وراثية (ساحل 1 ، حميزة 9 ، سخا 94 ، مصر 1 ، حميزة 168,146,133,142,L147) تحت التجربة. أظهرت النتائج وجود 48 باند بمتوسط 9.6 لكل بادئ و تراوحت اوزانها ما بين 95 bp (البادئ 162-603) الى 1500 bp (البادئ 162)

2- 34 شظية من 48 الـ DNA (Fragments) اظهرت اشكال احادية (monomorphic fragments) بنسبة 70.83% و كانت نسبة الشظايا المختلفة (Polymorphic fragments) 29.17% من خلال 14 موقع.

3- تراوح عدد الشظايا لكل بادئ ما بين 9 (البادئ 9-603) الى 10 (البادئات 108-596-162)

4- اظهر البادئ 596 على عدد من الاشكال المتعددة او المختلفة (Polymorphic fragments) بنسبة 50% ثم البادئ 603 بنسبة 44.44%

تراوح التماثل الوراثي ما بين 0.81% للباين P4 و P9 الى 0.95% للباين P1 و P2.

اوضح التحليل العنقودي Cluster analysis ان هناك علاقات وراثية للتقارب بين الاباء التسعة تحت الدراسة حيث تم تقسيم الاباء الى ثلاث اقسام رئيسية Three main clusters. أحتوى الاول على الاباء رقم p8,p5,p4 اما الثاني احتوى على الاباء p6,p7,p3,p2,p1 اما الثالث احتوى على الاب p9

اما بالنسبة لتقدير معالم الحساسية للجفاف للمحصول و مكوناته كانت كالآتي

التباين :

1. كان التباين الراجع للتراكيب الوراثية والأبء والهجن عالية المعنوية لكل الصفات تحت الدراسة ما عدا صفة طول النبات فكانت معنوية فقط
2. أظهرت النتائج ان الاب (p2) كان أفضل الابء بالنسبة لصفات عدد الحبوب / السنبله ومحصل القش /النبات و المحصول البيولوجي ، أعطي الاب P5 لصفة طول النبات و طول السنبله ، الاب P6 لصفة الالف حبة ومحصل الحبوب ، وكان الاب (P9) أفضل الأصناف بالنسبة لمعامل الحساسية للجفاف لصفة عدد السنابل .
3. كانت أفضل الهجن لمعامل الحساسية للجفاف هو الهجين P₆ x P₈ , P₂ x P₈ , P₂ x P₄ , P₂ x P₅ , P₃ x P₆ , P₂ x P₆ بالنسبة للمحصول وبعض مكوناته بالنسبة للاب الافضل و متوسط الابوين.

قوة الهجين :

أظهرت الهجن P₄×P₆ , P₄×P₇ , P₂×P₉ , P₆×P₈ و P₇×P₉ قوة هجين عالية ومعنوية لمعامل الحساسية للجفاف لمعظم الصفات تحت الدراسة.

3-3: القدرة علي التآلف :

1. كان التباين الراجع للقدرة العامة والخاصة علي التآلف عالية المعنوية لكل الصفات تحت الدراسة لمعامل الحساسية للجفاف.
2. كانت نسبة تباين القدرة العامة علي التآلف إلي تباين القدرة الخاصة علي التآلف لمعامل الحساسية للجفاف (GCA/SCA) ذات قيمة اعلى من الوحدة لكل الصفات تحت الدراسة فيما عدا طول السنبله و عدد السنابل / النبات .
3. أظهرت الدراسة أن أفضل الأبء هو P₅ , P₂ , P₆ , P₁ لمعامل الحساسية للجفاف حيث أظهرت قدرة عامة موجبة ومعنوية علي التآلف لصفات عدد السنابل / النبات ، عدد الحبوب / السنبله ، محصول القش ، محصول الحبوب والمحصل البيولوجي
4. أظهر الهجين P₆×P₈ لصفة محصول الحبوب ، P₁×P₆ لعدد السنبيلات/ السنبله ، P₄×P₆ بالنسبة لصفة عدد السنابل/النبات ، P₇×P₉ بالنسبة لعدد الحبوب/ السنبله و الهجين P₂×P₉ لصفة وزن الاف حبه و P₂×P₇ لمحصل القش والمحصل البيولوجي ، و P₆×P₈ لمحصل النبات الفردي و P₄×P₇ لمعامل الحصاد معنوية للقدرة الخاصة علي التآلف.

الكلمات المفتاحية : القمح -الجفاف -SSR