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Research Article
Assessment of Water Stress Tolerance in Wheat Genotypes Based on Half Diallel Analysis and DNA Fingerprinting

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Abstract

Background and Objective: Deficit or scarcity of water resources are considering as one of the most serious environmental phenomenon that hinder agricultural production in many countries and the present study evaluated some wheat accessions for water stress tolerance under Egyptian conditions. **Materials and Methods:** Five wheat genotypes and their ten F1 crosses from half diallel analysis were tested under both levels of irrigation (normal and drought stress conditions) through estimating some agro-morphological traits in addition, determining DNA fingerprinting meanwhile using five RAPD-PCR primers. **Results:** Final results detected that 4 parents and the best 5 F1 crosses were the most desirable genotypes for water stress tolerance depending on all results obtained for all calculated parameters under normal and water deficit treatments. **Conclusion:** Traditional breeding and DNA fingerprinting could be used to clarify and sort all genotypes to generate the best of them for water stress resistance which will be in the future as a nucleus for producing resistance wheat varieties for drought stress under Egyptian conditions.

Key words: Wheat, drought stress tolerance, DNA fingerprinting

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Data Availability: All relevant data are within the paper and its supporting information files.

INTRODUCTION

Wheat is one of the most important, widespread crops in the world and a strategic crop for the vast majority of the planet's population. Different varieties wheat are cultivating on a large scale in Egypt since ancient times. Water stress is coming at the forefront of the great problems faced by breeders and researchers alike because drought stress usually decreasing plant growth and improvement as well as the important agricultural traits involving the total production beside the destroying level obtained on final yield production which ranging from 35-57% at water stress taken as 40-45% of soil normal water content (NWC: 100%)[1]. Accordingly, thousands of researches and studies have been launched to solve this problem or attempt to reduce its severity and radical solutions have been proposed such as the development of sensitive varieties for drought stress resistance especially in the light of the intensification of water poverty crisis that hit the middle east which hampering wheat production required for feeding the vast majority of people in these countries.

Modern phenotyping percussion used for selecting the best genotypes in wheat and barley for water stress tolerance and presented the uses of utilizing stomatal conductance and paralleled it with photosynthetic average beside the rest indices of genetic variation for drought resistance, straight with the use of new phenomics techniques[2]. The enhancing methods using in improvement barley and wheat traits for water stress tolerance by breeding genetic resources and their potential utilization were revealed by Kosova *et al*.[3] and these results have supported the investigations obtained from Shavrukov *et al*.[4], who discussed reasons responsible for tolerance to adverse environmental factors, especially water deficit stress in wheat. In the same context[5] revealed water deficit resistance in some sorghum genotypes through studying some morphological traits under normal irrigation and the stress treatment besides studying RAPD and SRAP markers to determine some bands responsible for drought tolerance. Nine species of barley were evaluated for water deficit tolerance in different environmental zones in Tunisia using 6 SSR markers through stalling for 3 weeks and the results confirmed that the existence of a large genetic and geographical diversity of the genetic resources used for drought tolerance and indicated a relationship between some chemical compounds and water stress resistance[6]. El-Mouhamady *et al*.[7] presented some mechanisms for water stress tolerance and some negative effects on the final yield due to water deficit in wheat genotypes through estimated some tolerance indices based on half diallel analysis and genetic fingerprinting. Ramadan *et al*.[8] showed the impact of water stress on some barley genotypes through estimated some agro-morphological traits reflected water deficit resistance and confirmed the importance of drought tolerance indices for screening barley accessions for drought tolerance. Eldessouky *et al*.[9] exhibited the effect of water deficit stress on some rice entries through using half diallel analysis and ISSR markers and showed highly significant variation for water stress resistance among all studied materials.

As mentioned before, it is possible to clarify the purpose of this study, which was evaluating a group of local wheat varieties and their hybrids under two levels of irrigation (natural and water stress treatment) as well as testing of these genotypes through studying yield and its components traits beside root traits as a significant physiological indicator related to resistance of wheat plants to water deficit conditions.

MATERIALS AND METHODS

Sowing: The present investigation was carried out in the farm of agricultural Research Centre (ARC) in Sakha Research Station, Sakha city (Kafrel-sheikh governorate), Department of Genetics and Cytology, Division of Genetic Engineering and Biotechnology, National Research Centre, Dokki, Giza, Egypt during the period from the first of March, 2017 to the first of April, 2018 where the hybridization among parents was done in the first of March, 2017. The parental genotypes were grown in a randomized complete block design through three planting dates with 10 days interval in order to overcome the differences in flowering time between parents in the first of March, 2017 season. In November, 2018 season all genotypes (parents and their F1 crosses) were grown in two experiments isolated from each other (normal and water stress conditions) in the farm of sakha research station. Each location was divided into 3 replicates and the package of all other recommendations of wheat planting be followed in the same season (2018) and harvesting was done in the first of April, 2018.

Plant materials: Three Egyptian wheat germplasm namely, (Masr 1, Masr 2 and Gimeza 7) beside two imported lines from morocco as follows, L1 (Arrehane) and L2 (JALNHIR-8/GITMILL-3) were used in this investigation where the five accessions have different response for drought tolerance and all genotypes were evaluated under normal and water stress conditions.

Table 1: Identification of the selected five Accessions of wheat used in a half diallel analysis

Serial No.	Names of genotypes	Origin	Duration	Drought response	Stripe (yellow) rust reaction
1	Masr 1	Egypt	165	Tolerance	Resistance
2	Masr 2	Egypt	168	Moderately	Resistance
3	Gimeza 7	Egypt	166	Sensitive	Resistance
4	L1	Morocco (gene bank)	169	Tolerance	Resistance
5	L2	Morocco (gene bank)	170	Tolerance	Resistance

The two treatments of irrigation were isolated from each other with 15 m distance between them to prevent nominated water from normal irrigation to drought treatment and the previous varieties were kindly supplemented from Agriculture Research Centre, Wheat Research Department

Treatments: The normal treatment was the normal irrigation of wheat crop at winter season, where it was divided into five irrigates, the first one was at agriculture time, while the other four irrigates were with one month intervals. Water stress treatment was divided into two irrigates only the first one was at sown time and the second irrigate was after 45 days from agriculture, no irrigation was done till harvesting (Low input system). The two experiments (normal and water stress treatment) were isolated from each other one.

Studied traits: This investigation aimed to study genetic behavior responsible for drought tolerance in wheat genotypes through testing yield traits such as spike length, number of spikes/plant, number of filled grains/spike, 1000-grain weight and grain yield/plant in addition, some root traits for example, maximum root length, root volume, number of roots/plant, root xylem vessel number and root dry weight under the two conditions of irrigation beside estimating random amplified polymorphic DNA (RAPD) analysis through using five primers (Table 1). All root traits were determined according to the method of Passioura[10] as follows:

- **Spike length (cm):** It was recorded using the main spike length of each plant
- **Number of spikes/plant:** These were determined by counting the number of spikes per plant, when all plants were at the ripening stage
- **Number of filled grains/spike:** Filled grains of the main spike with separated and counted
- **1000-grain weight (g):** It was recorded as the weight of 1000 random filled grains per plant
- **Grain yield/plant (g):** It was recorded as the weight of grain yield of each individual plant and adjusted to 14% moisture content
- **Maximum root length (cm):** It was measured (in centimeters) from the tillering plateau to the longest root tip
- **Root volume:** Volume of all root system was determined in cubic centimeters using standard column
- **Number of roots per plant:** The total number of secondary and tertiary roots of each single plant was counted 2 cm below the tillering plateau
- **Root xylem vessel number:** The average xylem vessel number of roots of the same plant was counted under the light microscope
- **Root dry weight:** All roots of each single plant were collected and oven-dried at 55°C for 5 days and weighted (g)

Statistical analysis: All calculated data performed from the studied traits under the two experiments were analyzed using half diallel analysis[11] mode 1, method 2 for estimating heterosis over better-parent and also general and specific combining ability effects, respectively.

Estimation of tolerance indices: All tolerance indices were estimated by Fischer and Maurer[12], Bouslama and Schapaugh[13], Lin *et al.*[14], Hossain *et al.*[15], Fernandez[16], Gavuzzi *et al.*[17] and Golestani and Assad[18] as follows:

MS = YS+YP/2
STI = YP+YS/mean of YP^2
GMP = $(YP \times YS)^{0.5}$
YI = YS/ mean of YS
YSI = YS/YP
(YR) = 1-YS/YP
DSI = (1-YD/YW)/D

Molecular markers

DNA Isolation: The genomic DNA was extracted from fresh leaves of 10 wheat genotypes, five parents which have different reaction for drought tolerance and the best five crosses resulting from these parents using half diallel analysis and revealed highly tolerance of drought stress according to the data of all studied traits beside results of genetic parameters under drought stress treatment compared with the control experiment as follows: P1: (Parent 1), P2: (Parent 2), P3: (Parent 3), P4: (Parent 4), P5: (Parent 5) and the best five hybrids were H1: (P1×P2), H3: (P1×P4), H6: (P2×P4), H8: (P3×P4) and H10: (P4×P5) according to the protocol of Biospin plant genomic DNA extraction Kit (Bio basic), respectively.

Polymerase chain reaction (PCR) procedure: A set of five random 10-mer primers were used in the detection of polymorphism among 10 wheat genotypes. These primers were synthesized at RAPD-PCR and carried out according to the procedure given by Williams *et al.*[19] with minor modifications.

Amplification reaction was carried out in 25 µL reaction mixture contained 2 µL of genomic DNA, 3 µL of the primer, 2.5 µL of 10x *Taq* DNA polymerase reaction buffer, 1.5 units of *Taq* DNA polymerase and 200 µL of each dNTPs. The following PCR program was used in a DNA Thermocycler (PTC-100 PCR version 9.0-USA). Initial denaturation at 94°C for 5 min, followed by 35 cycles of 94°C for 30 sec, 42°C for 90 sec. For annealing temperature, 72°C for 90 sec and final extension at 72°C for 2 min. Products by RAPD-PCR were separated on 1.5% agarose gels in 1x TAE buffer and detected by staining with ethidium bromide[20].

DNA ladder (50-1500 bp) including 17 bands was used and PCR products were visualized by UV-trans illuminator and photographed by gel documentation system, Biometra-Bio documentations, the amplified bands were scored as (1) for presence and (0) for the absence of all wheat materials under studying according to gel analyzer protocol.

Data handling and cluster analysis (phylogenetic tree): Data was scored for computer analysis on the basis of the presence or absence for the amplified products of each primer. Pairwise components of the 10 genotypes based on the presence or absence of unique and shared polymorphic products were used to determine similarity coefficients[21]. This formula used for analysis the similarity coefficients construct dendrograms, then using the un weighted pair group method with arithmetic averages (UPGMA) employing the SAHN (Sequential, Agglomerative, Hierarchical and Nested clustering) from the NTSYS-PC (Numerical Taxonomy and Multivariate Analysis System), version 1.80 (Applied Biostatistics Program).

RESULTS

Mean performance: Mean values of all studied traits of wheat genotypes under normal irrigation and water stress conditions were revealed in Table 2. It was found that the parents number (1, 2, 4 and 5) beside the crosses (H1, H3, H6, H8 and H10) recorded the highest mean values and revealed the best wheat genotypes for water stress tolerance for all studied traits under both treatments and for example the mean values ranged from 9.54-28.77 and 7.04-25.0 cm for panicle length trait, 24.51-89.45 and 9.78-73.56 g for grain yield/plant trait, 49.27-115.43 and 33.56-95.19 cm for maximum root length trait and 10.02-57.14 and 4.0-44.88 for root xylem vessel number trait under normal and water deficit conditions, respectively.

Analysis of variance: Data viewing in Table 3 cleared that mean squares of all studied traits of wheat genotypes recorded highly significant variances under both treatments of irrigation and the same results were detected for mean squares for GCA and SCA for all traits under the previous conditions. The ratio of GCA/SCA was less than the unity for all characters studied under both treatments of irrigation.

Heterosis over better-parent: The data detected in Table 4 revealed that five crosses out of 10 hybrids showed highly significant and positively percentages of heterosis over better-parent for all studied traits under normal and stress and these desirable crosses were (H1, H3, H6, H8 and H10), respectively. The rest crosses presented the negative direction for this parameter under all conditions for all studied traits and as example not limited the mean values ranged from 13.26 to -56.49 and 15.88 to -59.48% for panicle length, 9.41 to -65.90 and 8.49 to -85.02% for grain yield/plant, 13.61 to 31.64 and 12.35 to -53.64% for maximum root length and 23.26-121.64 and 30.69-99.20% for root xylem vessel number under both treatments, respectively.

General and specific combining ability effects: The parents number (1, 2 and 5) for the traits, spike length, number of filled grains/spike, root volume, number of roots /plant, root xylem vessel number and root dry weight were showed highly significant and positively values of general combining ability effects under both types of irrigation, while the other parents (P3 and P4) were exhibited highly significant and negatively values of GCA effects for the previous traits under the same conditions (Table 5). On the same track the parents number (1, 4 and 5) for the traits, number of spikes/plant and grain yield/plant in addition, the parents number (1 and 4) only for maximum root length trait were revealed highly significant positively values of GCA effects under normal and drought conditions, while the rest parents (P2 and P3) for number of spikes/plant and grain yield/plant beside the entries number (2, 3 and 5) for maximum root length trait were detected highly significant and negatively results for this parameter under all conditions, respectively. In the same regard, the data showed in Table 6 presented that five crosses(H1, H3, H6, H8 and H10) out of 10 hybrids obtained from 5×5 half diallel analysis were exhibited highly

Table 2: Mean performance of all studied traits in wheat genotypes under both levels of irrigation

	Studied traits									
	P.L (cm)		No. of. P/P		No. of F. G/P		1000-G.W (m)		G.Y/P (g)	
Genotypes	N	D	N	D	N	D	N	D	N	D
P1	15.45	12.80	8.32	6.15	108.35	93.57	53.36	48.44	63.12	59.03
P2	20.03	16.33	14.70	12.35	97.83	89.30	42.66	39.17	71.88	65.33
P3	12.50	8.63	5.13	3.08	46.98	34.50	27.55	19.87	33.14	12.75
P4	21.89	18.70	17.87	15.00	111.57	90.52	57.25	49.60	59.67	55.43
P5	25.40	20.09	18.47	16.70	105.64	95.48	48.35	38.49	60.21	54.63
H1	24.80	19.78	19.32	15.80	125.49	107.37	60.13	52.66	78.65	72.34
H2	11.80	7.04	4.60	2.78	44.70	29.76	21.60	14.40	31.00	11.74
H3	26.68	23.50	20.29	18.60	117.85	105.00	63.89	60.05	69.86	64.50
H4	14.00	10.37	8.11	5.77	77.23	54.06	28.57	22.12	43.49	39.37
H5	9.54	7.13	4.15	2.68	41.81	26.52	25.30	17.48	24.51	9.78
H6	28.53	22.60	23.70	19.31	119.58	107.35	66.86	51.43	81.98	73.56
H7	16.48	11.70	10.45	7.33	73.79	51.40	37.21	28.59	48.04	26.72
H8	25.46	21.67	19.40	17.59	126.48	114.83	65.07	53.42	68.35	60.14
H9	11.05	8.14	3.96	2.72	39.53	24.00	24.88	15.92	31.98	10.06
H10	28.77	25.00	24.28	20.06	117.38	112.06	59.48	54.42	89.45	69.18
LSD at 0.05	0.48	1.11	0.89	1.51	1.03	1.25	1.19	0.58	0.91	1.75
LSD at 0.01	0.69	1.61	1.30	2.19	1.49	1.82	1.73	0.85	1.32	2.54
	Studied traits									
	M.R.L (cm)		R.V		No. of. R/P		R. X. V. No		R.D.W (g)	
Genotypes	N	D	N	D	N	D	N	D	N	D
P1	78.45	72.40	48.17	42.06	581.22	533.38	19.34	17.02	12.17	9.88
P2	71.13	66.05	54.34	49.18	456.87	420.68	23.34	19.48	10.57	7.13
P3	65.55	42.18	31.50	22.14	266.12	150.45	11.56	4.17	6.47	2.97
P4	87.68	81.04	62.00	58.30	389.00	370.50	25.78	22.36	17.58	14.83
P5	82.15	75.61	71.14	67.88	631.57	570.23	24.05	22.53	15.33	11.84
H1	89.13	88.05	69.55	61.76	745.89	680.30	28.77	25.46	15.60	13.78
H2	61.67	33.56	21.60	17.74	250.43	142.18	10.02	3.09	4.65	2.50
H3	104.56	91.06	70.44	69.00	719.38	705.40	34.72	30.88	19.58	15.96
H4	69.88	58.34	32.78	19.47	500.30	371.47	17.22	14.60	9.43	5.32
H5	49.27	36.12	30.00	16.89	243.78	125.09	10.36	3.59	5.12	2.78
H6	107.44	93.03	89.33	80.06	490.83	477.00	46.71	40.03	20.18	17.83
H7	56.77	41.39	50.53	39.18	236.36	220.75	18.35	16.20	7.54	4.08
H8	115.43	92.04	71.88	64.78	755.90	622.45	51.42	37.24	21.47	17.35
H9	60.49	37.30	21.20	18.34	157.80	121.40	10.03	4.00	6.22	2.14
H10	106.08	95.19	94.45	87.32	853.20	633.67	57.14	44.88	23.46	18.00
LSD at 0.05	1.05	1.68	0.53	0.84	0.95	0.74	1.76	1.21	1.11	0.82
LSD at 0.01	1.53	2.45	0.77	1.22	1.37	1.08	2.56	1.76	1.61	1.14

P.L: Plant height, No. of F.G/P: Number of filled grains/plant, G.W.: Grain weight, G.Y/P: Grains yield/plant, M.R.L: Maximum root length, R.V: Root volume, No. of R/P: Number of root/plant, R.X.V. No.: Root xylem vessel number, R-D.W: Root dry weight, N: Normal irrigation, D: Drought conditions

significance and positive values of SCA effects for all studied traits under both treatments of irrigation. On the other hand, the rest crosses namely (H2, H4, H5, H7 and H9) revealed highly significant and negative results of SCA effects for all traits under both treatments of irrigation.

Tolerance indices: The calculated data and presented in Table 7 exhibited that parents genotypes (P1, P2, P4 and P5) beside hybrids (H1, H3, H4, H6, H8 and H10) were recorded the highest mean values of YSI, MP and GMP. The previous genotypes (except the cross H4) revealed mean values higher than the unity for YI and DTI. On the other hand, it was found that the genotypes (P1, P2, P4, P5, H1, H3 and H4) for the tolerance indices YR and DSI and H6 and H8 for DSI only were recording mean values lower than the unity.

Molecular detection using RAPD markers: The profile of RAPD-PCR analysis was presented in Table 8 and Fig. 1, the data revealed that 66 amplicons were generated from the five primers, 19 of them were monomorphic and the rest (47) were polymorphic with 71.21% polymorphism including 13 unique bands with range size 174-2357 bp. The first primer OPC-1 detected 13 fragments (4 monomorphic and 9 polymorphic) with 69.23% polymorphism with sizes from 192-1143 bp. While, OPC-10 primer generated 13 fragments

Table 3: Mean squares of the half diallel analysis for all studied traits under both levels of irrigation

		P.L (cm)		No. of P/P		No. of F.G/P		1000-G.W (g)		G.Y/P (g)	
S.O.V	DF	N	D	N	D	N	D	N	D	N	D
Reps	2	0.78	1.54	4.33	7.18	13.05	8.11	13.77	6.36	0.48	0.82
Genotypes	14	44.36**	27.30**	37.50**	60.12**	38.44**	64.22**	24.50**	12.40**	112.40**	42.63**
GCA	4	123.45**	228.14**	357.24**	165.08**	206.44**	180.44**	417.33**	100.20**	233.78**	188.36**
SCA	10	67.45**	89.45**	111.31**	78.04**	73.32**	56.03**	125.41**	33.70**	78.26**	53.12**
Error	28	0.12	0.64	0.42	1.19	0.55	0.82	0.74	0.18	0.43	1.59
Error term		0.04	0.21	0.14	0.39	0.18	0.27	0.24	0.06	0.14	0.53
GCA/SCA		0.26	0.36	0.45	0.3	0.4	0.46	0.47	0.42	0.43	0.51
		M.R.L (cm)		R.V		No. of. R/P		R. X. V. No		R.D.W (g)	
S.O.V	DF	N	D	N	D	N	D	N	D	N	D
Reps	2	0.11	0.29	1.54	2.37	0.93	1.45	5.2	1.12	3.59	0.84
Genotypes	14	109.40**	255.68**	79.33**	112.55**	543.33**	419.77**	318.35**	228.06**	14.57**	11.80**
GCA	4	85.34**	104.22**	714.45**	804.78**	155.29**	115.88**	466.39**	735.19**	288.94**	178.38**
SCA	10	26.59**	44.84**	213.51**	194.67**	127.73**	45.32**	352.14**	179.50**	86.67**	34.78**
Error	28	0.58	1.48	0.15	0.37	0.47	0.29	1.63	0.77	0.64	0.32
Error term		0.19	0.49	0.05	0.12	0.15	0.09	0.54	0.25	0.21	0.10
GCA/SCA		0.46	0.33	0.48	0.59	0.17	0.36	0.19	0.58	0.47	0.73

P.L: Plant height, No. of F.G/P: Number of filled grains/plant, G.W.: Grain weight, G.Y/P: Grains yield/plant, M.R.L: Maximum root length, R.V: Root volume, No. of R/P: Number of root/plant, R.X.V. No.: Root xylem vessel number, R-D.W: Root dry weight, N: Normal irrigation, D: Drought conditions

Table 4: Estimation of heterosis over better-parent in the 10 wheat crosses for all studied traits under normal and drought conditions

	P.L (cm)		No. of P/P		No. of F.G/P		1000-G.W (g)		G.Y/P (g)	
Crosses	N	D	N	D	N	D	N	D	N	D
H1	23.81**	21.12**	31.42**	27.93**	15.81**	14.74**	12.68**	8.71**	9.41**	10.73**
H2	-23.62**	-45.0**	-44.71**	-54.79**	-58.74**	-68.19**	-59.52**	-70.27**	-50.88**	-80.11**
H3	21.88**	25.66**	13.54**	24.0**	5.62**	12.21**	11.59**	21.06**	10.67**	9.26**
H4	-44.88**	-48.38**	-56.09**	-65.44**	-28.72**	-43.38**	-46.45**	-54.33**	-31.09**	-33.30**
H5	-52.37**	-56.33**	-71.76**	-78.29**	-57.26**	-70.30**	-40.69**	-55.37**	-65.90**	-85.02**
H6	30.33**	20.85**	32.62**	28.73**	7.17**	18.59**	16.78**	3.68**	14.05**	12.59**
H7	-35.11**	-41.76**	-43.42**	-56.10**	-30.14**	-46.16**	-23.04**	-27.01**	-33.16**	-59.09**
H8	16.30**	15.88**	8.56**	17.62**	13.36**	26.85**	13.65**	7.70**	14.54**	8.49**
H9	-56.49**	-59.48**	-78.55**	-83.71**	-62.58**	-74.86**	-48.54**	-58.63**	-46.88**	-81.58**
H10	13.26**	24.44**	31.45**	20.11**	5.20**	17.36**	9.13**	9.71**	48.56**	24.80**
LSD at 0.05	0.48	1.11	0.89	1.51	1.03	1.25	1.19	0.58	0.91	1.75
LSD at 0.01	0.69	1.61	1.3	2.19	1.49	1.82	1.73	0.85	1.32	2.54
	M.R.L (cm)		R.V.		No. of R/P		R.X.V. No		D.W (g)	
Genotypes	N	D	N	D	N	D	N	D	N	D
H1	13.61**	21.61**	27.99**	25.57**	28.33**	27.54**	23.26**	30.69**	28.18**	39.47**
H2	-21.38**	-53.64**	-55.15**	-57.82	-56.91**	-73.34**	-48.19**	-81.84**	-61.79**	-74.69**
H3	19.25**	12.36**	13.61**	18.35**	23.77**	32.25**	34.67**	38.10**	11.37**	7.61*
H4	-14.93**	-22.84**	-53.92**	-71.31**	-20.78**	-34.85**	-28.39**	-35.19**	-66.60**	-76.52**
H5	-30.73**	-45.31**	-44.79**	-65.65**	-46.64**	-70.26**	-55.61**	-81.57**	-51.56**	-61.01**
H6	22.53**	14.79**	44.08**	37.32**	7.43**	13.38**	81.18**	79.02**	14.78**	20.22**
H7	-30.89**	-45.25**	-28.97**	-42.28**	-62.57**	-61.28**	-23.70**	-28.09**	-50.81**	-65.54**
H8	31.64**	13.57**	15.93**	11.11**	94.31**	68.0**	99.45**	66.54**	22.12**	16.99**
H9	-26.36**	-50.66**	-70.19**	-72.98**	-75.01**	-78.71**	-58.29**	-82.24**	-59.42**	-81.92**
H10	20.98**	17.46**	32.76**	28.63**	35.09**	11.12**	121.64**	99.20**	33.44**	21.37**
LSD at 0.05	1.05	1.68	0.53	0.84	0.95	0.74	1.76	1.21	1.11	0.82
LSD at 0.01	1.53	2.45	0.77	1.22	1.37	1.08	2.56	1.76	1.61	1.14

P.L: Plant height, No. of F.G/P: Number of filled grains/plant, G.W.: Grain weight, G.Y/P: Grains yield/plant, M.R.L: Maximum root length, R.V: Root volume, No. of R/P: Number of root/plant, R.X.V. No.: Root xylem vessel number, R-D.W: Root dry weight, N: Normal irrigation, D: Drought conditions

(2 monomorphic and 11 polymorphic) including 5 unique bands with 84.61% polymorphism and the range size was from 174-1715 bp. Primer OPA-12 showed 16 fragments (7 monomorphic and 9 polymorphic) beside five fragments were unique bands, polymorphism percentage was 56.25% and the range size was 190-1696 bp. For OPA-4 primer, there were 14 fragments (3 monomorphic and 11 polymorphic) including 2 unique bands with 78.57% polymorphism percentage with sizes ranged from 214-792 bp. While, primer OPA-6 showed 10 fragments where

Table 5: Estimates of general combining ability effects for the 5-parent of wheat genotypes for all studied traits under normal and drought conditions

	P.L (cm)		No. of P/P		No. of F.G/P		1000-G.W (g)		G.Y/P (g)	
Parents	N	D	N	D	N	D	N	D	N	D
P1	19.56**	7.23**	11.67**	6.11**	38.77**	41.86**	10.32**	7.84**	5.68**	7.42**
P2	28.43**	15.04**	-28.57**	-8.78**	20.05**	16.57**	6.45**	8.90**	-10.0**	-13.59**
P3	-30.0**	-20.37**	-16.55**	-15.37**	-28.20**	-43.12**	-19.47**	-20.0**	-4.06**	-12.15**
P4	-29.77**	-35.04**	9.56**	9.88**	-39.76**	-27.64**	-11.07**	-10.16**	4.60**	11.89**
P5	11.78**	33.14**	23.89**	8.16**	9.14**	12.33**	13.77**	13.42**	3.78**	6.43**
LSD at 0.05(gi)	0.74	0.87	1.12	1.69	1.22	1.36	0.57	0.43	0.48	1.03
LSD at 0.01(gi)	1.18	1.33	2.19	2.45	1.75	1.88	0.84	0.71	0.63	1.22
	M.R.L (cm)		R.V		No. of R/P		R.X.V. No		R.D.W (g)	
Parents	N	D	N	D	N	D	N	D	N	D
P1	41.68**	22.89**	5.33**	20.55**	4.14**	1.33**	42.88**	28.45**	2.13**	1.18**
P2	-14.60**	-7.55**	7.38**	12.82**	2.86**	6.50**	32.29**	17.22**	0.79**	1.32**
P3	-20.14**	-20.61**	-14.15**	-18.57**	-5.18**	-4.47**	-36.55**	-29.64**	-1.54**	-1.53**
P4	18.70**	13.70**	-9.19**	-21.12**	-3.36**	-6.13**	-51.22**	-23.46**	-2.24**	-1.71**
P5	-25.64**	-8.43**	10.63**	6.32**	1.54**	2.77**	12.60**	7.43**	0.86**	0.74**
LSD at 0.05(gi)	3.77	2.55	1.53	1.64	0.62	0.39	2.15	1.79	0.23	0.19
LSD at 0.01(gi)	4.36	3.88	2.04	1.88	0.85	0.74	3.28	2.54	0.38	0.31

P.L: Plant height, No. of F.G/P: Number of filled grains/plant, G.W.: Grain weight, G.Y/P: Grains yield/plant, M.R.L: Maximum root length, R.V: Root volume, No. of R/P: Number of root/plant, R.X.V. No.: Root xylem vessel number, R-D.W: Root dry weight, N: Normal irrigation, D: Drought conditions

Table 6: Estimates of specific combining ability effects for the 10-crosses of wheat genotypes of all studied traits under normal and water deficit conditions

	P.L (cm)		No. of P/P		No. of F. G/P		1000-G.W (g)		G.Y/P (g)	
Crosses	N	D	N	D	N	D	N	D	N	D
H1	3.58**	2.77**	23.11**	14.38**	7.21**	4.33**	47.76**	36.80**	16.48**	27.39**
H2	-2.36**	-5.33**	-40.44**	-12.06**	-44.49**	-2.99**	-55.02**	-20.13**	-75.23**	-25.18**
H3	11.49**	10.38**	12.38**	3.76**	9.32**	12.50**	26.79**	19.41**	38.44**	11.99**
H4	-9.44**	-2.90**	-11.38**	-30.02**	-3.72**	-5.84**	-6.36**	-10.92**	-3.82**	-7.42**
H5	-12.86**	-5.53**	-5.32**	-4.17**	-4.60**	-6.08**	-5.33**	-12.70**	-14.27**	-4.13**
H6	15.90**	6.59**	62.17**	45.0**	17.38**	8.05**	7.26**	3.92**	19.70**	7.80**
H7	-5.70**	-2.73**	-36.07**	-2.85**	-10.0**	-15.30**	-4.60**	-15.49**	-20.0**	-10.50**
H8	7.60**	4.85**	14.26**	5.63**	22.72**	24.53**	14.79**	13.08**	52.42**	9.68**
H9	-11.07**	-9.66**	-22.76**	-22.68**	-7.48**	-24.63**	-34.47**	-25.44**	-19.32**	23.52**
H10	2.86**	1.56**	4.05**	3.01**	13.66**	5.43**	9.18**	11.47**	5.60**	13.89**
LSD at 0.05(Sij)	1.27	1.17	2.98	2.15	2.28	1.83	2.65	2.12	2.74	2.51
LSD at 0.01(Sij)	1.44	1.33	3.54	2.78	3.18	2.77	3.84	3.69	3.44	3.32
	M.R.L (cm)		R.V		No. of R/P		R.X.V. No		R.D.W (g)	
Genotypes	N	D	N	D	N	D	N	D	N	D
H1	12.03**	10.0**	3.53**	1.95**	14.92**	12.96**	3.87**	1.69**	6.58**	7.15**
H2	-3.0 NS	-1.54 NS	-15.60**	-0.63 NS	-22.37**	-6.18**	-2.74**	-1.58**	-8.66**	-17.40**
H3	4.77**	9.59**	4.88**	1.26**	7.80**	5.44**	14.66**	11.87**	33.77**	47.03**
H4	-2.12 NS	-0.47 NS	-2.33**	-0.55 NS	-29.04**	-20.0**	-7.80**	-10.02**	-24.80**	-6.49**
H5	-14.33**	-10.28**	-0.34NS	-0.61 NS	-13.80**	-8.79**	-4.82**	-7.53**	-26.07**	-5.79**
H6	6.93**	3.99**	7.22**	2.38**	23.63**	10.11**	5.80**	12.82**	14.11**	9.30**
H7	-8.77**	-2.98*	-0.73 NS	-0.78 NS	-48.86**	-44.58**	-12.60**	-1.49**	-10.17**	-8.25**
H8	17.28**	15.70**	10.04**	4.67**	52.12**	39.43**	9.32**	4.83**	12.26**	15.40**
H9	-18.51**	-30.05**	-18.98**	-14.80**	-3.95**	-2.47**	-8.04**	-12.51**	-15.29**	-62.45**
H10	5.72**	6.04**	12.31**	7.11**	19.55**	14.08**	2.35**	1.92**	18.27**	21.50**
LSD at 0.05(Sij)	3.28	2.61	0.74	0.87	1.93	1.7	1.32	1.18	4.32	3.12
LSD at 0.01(Sij)	4.38	3.54	1.02	1.13	2.81	2.24	1.67	1.44	5.88	4.89

P.L: Plant height, No. of F.G/P: Number of filled grains/plant, G.W.: Grain weight, G.Y/P: Grains yield/plant, M.R.L: Maximum root length, R.V: Root volume, No. of R/P: Number of root/plant, R.X.V. No.: Root xylem vessel number, R-D.W: Root dry weight, N: Normal irrigation, D: Drought conditions

(3 of them were monomorphic and 7 polymorphic) including one unique band with 70% polymorphism and the range sizes was ranged from 296-2357 bp. Results confirmed that, the highest number of fragments were observed in primer OPA-12 with 16 bands, but primer (OPA-06) revealed the lowest number of bands (10). The biggest percentage of polymorphism 84.61% was obtained with primer OPC-10 and the lowest percentage 56.25% was shown with OPA-12 primer. The results obtained in Table 9 revealed that P4 (the first morocco line Arrehane) recorded the highest

Table 7: Estimates of tolerance indices in wheat genotypes for grain yield trait under both levels of irrigation

Genotypes	GYP	GYD	YSI	YI	MP	DTI	GMP	YR	DSI
P1	63.12	59.03	0.93	1.29	61.07	1.14	61.04	0.065	0.35
P2	71.88	65.33	0.91	1.43	68.60	1.44	68.52	0.092	0.45
P3	33.14	12.75	0.38	0.27	22.94	0.12	20.55	0.616	3.11
P4	59.67	55.43	0.92	1.21	57.55	1.01	57.51	0.071	0.4
P5	60.21	54.63	0.90	1.19	57.42	1.01	57.35	0.092	0.5
H1	78.65	72.34	0.92	1.58	75.49	1.74	75.42	0.08	0.4
H2	31.00	11.74	0.37	0.25	21.37	0.11	19.07	0.621	3.16
H3	69.86	64.50	0.92	1.41	67.18	1.38	67.12	0.076	0.4
H4	43.49	39.37	0.90	0.86	41.43	0.52	41.37	0.094	0.5
H5	24.51	9.780	0.40	0.21	17.14	0.07	15.48	0.601	3.01
H6	81.98	73.56	0.89	1.61	77.77	1.85	77.65	0.102	0.55
H7	48.04	26.72	0.55	0.58	37.38	0.39	35.82	0.443	2.26
H8	68.35	60.14	0.87	1.31	64.24	1.26	64.11	0.12	0.65
H9	31.98	10.06	0.31	0.22	21.02	0.09	17.93	0.685	3.46
H10	89.45	69.18	0.77	1.51	79.31	1.90	78.66	0.226	1.15

GYP: Mean yield under normal conditions, GYD: Mean yield under drought conditions, YSI: Yield stability index, YI: Yield index, Mean productivity, DTI: Drought tolerance index, GMP: Geometrical mean productivity, YR: Yield reduction ratio, DSI: Drought susceptibility index

Table 8: Polymorphic loci amplified by the 5 RAPD primers and their sequences for the 10 wheat genotypes

Primer code	Total No. of generated bands	Monomorphic bands	Polymorphic bands	Unique band or positive marker	Polymorphism (%)	Sequences 5'-3'
OPC-1	13	4	9	0	69.23	TTCGAGCCAG
OPC-10	13	2	11	5	84.61	TGTCTGGGTG
OPA-12	16	7	9	5	56.25	TCGGCGATAG
OPA-4	14	3	11	2	78.57	AATCGGGCTG
OPA-6	10	3	7	1	70.0	GGTCCCTGAC
Total fragments	66	19	47	13	71.21	

number of amplified fragments (43), while that P5 (the second morocco line JALNHIR-8/GITMILL-3) exhibited the lowest number of amplified fragments (31), the other genotypes showed various numbers of amplified fragments. Primer OPA-12 recorded the highest number of bands (98) for the ten genotypes, while that primer OPC-10 displayed the lowest number of total bands (61) for the same genotypes.

Results are shown in Table 10 try to distinguish and classify with highly efficient form among all genotypes under studying, also attempt to draw map which included of positive and negative specific markers related with the most genotypes highly tolerance for water deficit conditions.

Primer OPC10 revealed five positive markers 3 of them with sizes 1715, 1339 and 1090 bp were showed for the cross H1 only, while two positive markers with molecular sizes 174 and 462 bp were observed for the genotypes H3 and H5 beside exhibited also 2 negative markers for H5 with sizes 448 and 742 bp. Also primer OPA12 recorded five positive specific markers with sizes 1009 and 743 bp for the cross H2, 839 and 190 bp for the cross H3 and 766 bp only for P4 beside one negative marker for P4 with size 208 bp, respectively.

Two positive specific markers were generated by primer OPA-04 at molecular sizes 418 bp for P5 and 724 bp for H3 and one negative marker was shown for P1 at size 249 bp by the same primer. While, one positive specific marker only was obtained by primer OPA-06 at molecular size of 886 bp for P4.

Proximity matrix analysis (genetic similarity): Data viewing in Table 11 showed 45 pairwise comparisons to debate the genetic relationships within the 10 wheat genotypes detected in terms of similarity. The genetic similarity ranged from 0.461 to 0.837 with an average of 0.649, where the highest value of genetic similarity 0.837 was among P2 and P3 and the lowest value (0.461) was between P2 and H3 in addition, some high trend of similarities were observed for example not limited among P1 and P2, P3 and P4, H1 and H2 and H4 and H5 and their values were 0.818, 0.822, 0.80 and 0.80, respectively.

Cluster analysis (Phylogenetic tree): Results of dendrogram obtained from UPGMA cluster analysis (Fig. 2) showed that all genotypes were divided into two main cluster where the first cluster included two sub-cluster, the first sub-cluster included P1 and two sub-sub cluster, where the first one included (P2 and P3), while that the second sub-sub cluster contained P4 only. The second sub-cluster included P5 only, respectively. The second cluster consists of two sub-cluster where, the first sub-cluster included (H1 and H2), while the second sub-cluster consisted of H3 and one set including (H4 and H5).

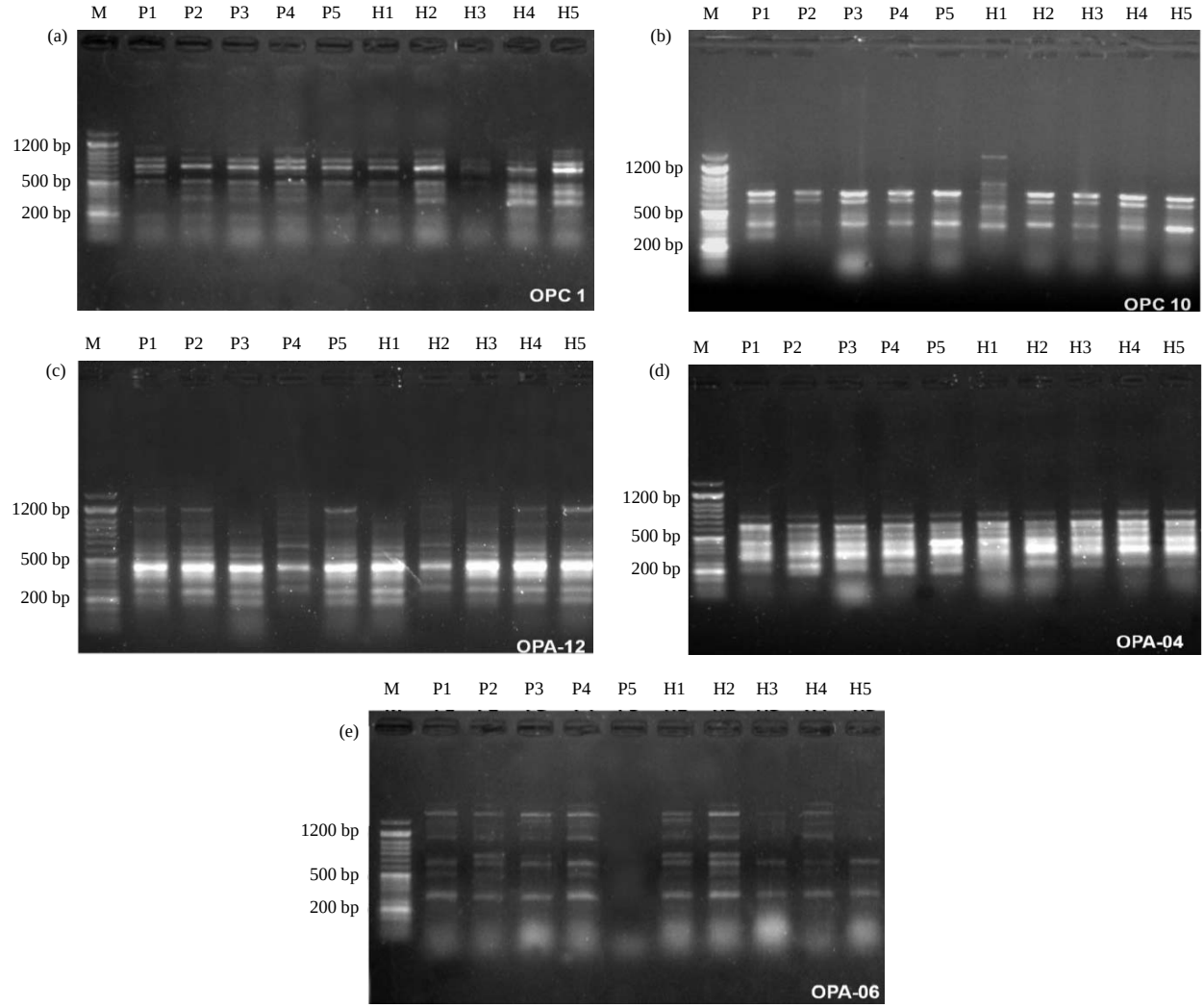

Fig. 1(a-e): PCR fragments with five RAPD primers (a) OPC-1, (b) OPC-10, (c) OPA-12, (d) OPA-04 and (e) OPA-06 of 10 wheat genotypes (1:10), M: DNA ladder (50-100-150-200-250-300-350-400-450-500-600-700-800-900-1000-1200-1500 bp) as marker, P1: Parent 1, P2: Parent 2, P3: Parent 3, P4: Parent 4, P5: Parent 5 and the best five hybrids were, H1: (P1×P2), H2: (P1×P4), H3: (P2×P4), H4: (P3×P4) and H5: (P4×P5)

Table 9: Total bands produced from each primer for the 10 wheat accessions and all amplified fragments in each genotype

	Primers					
Genotypes	OPC-1	OPC-10	OPA-12	OPA-04	OPA-06	Total bands*
P1	8	7	10	8	7	40
P2	7	5	10	9	9	40
P3	9	4	10	8	8	39
P4	9	4	11	9	10	43
P5	8	6	9	8	0	31
H1	8	10	9	6	8	41
H2	8	6	11	7	8	40
H3	7	7	10	8	4	36
H4	8	6	9	7	7	37
H5	9	6	9	7	4	35
Total bands	81	61	98	77	65	382

*Refer to presence of all amplified fragments for each entry

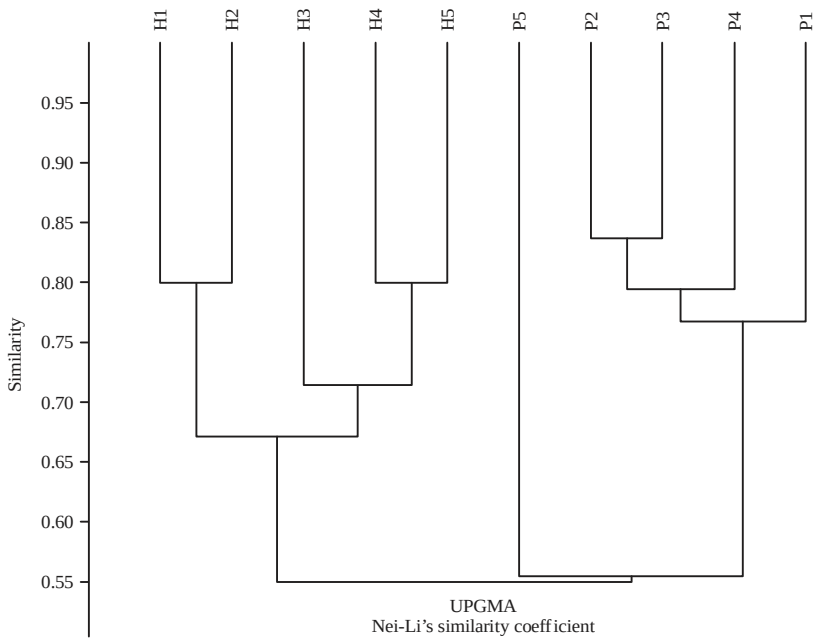

Fig. 2: Dendrogram representing the genetic relationship among the ten wheat genotypes, P1: Parent 1, P2: Parent 2, P3: Parent 3, P4: Parent 4, P5: Parent 5 and the best five hybrids were H1: P1×P2, H3: P1×P4, H6: P2×P4, H8: P3×P4 and H10: P4×P5 using UPGMA cluster analysis of Nei-Li's similarity coefficient generated from the five RAPD markers

Table 10: Mapping of positive (P) and negative (N) specific markers for the 10 wheat genotypes using five RAPD primers

RAPD-primers	MS (bp)	P1	P2	P3	P4	P5	H1	H2	H3	H4	H5	MT (P or N)
OPC- 10	1715	-	-	-	-	-	+	-	-	-	-	P (H1)
	1339	-	-	-	-	-	+	-	-	-	-	P (H1)
	1090	-	-	-	-	-	+	-	-	-	-	P (H1)
	742	+	+	+	+	+	+	+	+	+	-	N (H5)
	462	-	-	-	-	-	-	-	-	-	+	P (H5)
	448	+	+	+	+	+	+	+	+	+	-	N (H5)
	174	-	-	-	-	-	-	-	+	-	-	P (H3)
OPA-12	1009	-	-	-	-	-	-	+	-	-	-	P (H2)
	839	-	-	-	-	-	-	-	+	-	-	P (H3)
	766	-	-	-	+	-	-	-	-	-	-	P (P4)
	743	-	-	-	-	-	-	+	-	-	-	P (H2)
	208	+	+	+	-	+	+	+	+	+	+	N (P4)
	190	-	-	-	-	-	-	-	+	-	-	P (H3)
OPA-4	724	-	-	-	-	-	-	-	+	-	-	P (H3)
	418	-	-	-	-	+	-	-	-	-	-	P (P5)
	249	-	+	+	+	+	+	+	+	+	+	N (P1)
OPA-6	886	-	-	-	+	-	-	-	-	-	-	P (P4)
Range	174-1715	-	-	-	-	-	-	-	-	-	-	-
Total		3	4	4	5	5	7	6	8	4	3	17

Table 11: Genetic similarity percentages of the 10 wheat genotypes based on the five RAPD-PCR primers banding patterns

Parents	P1	P2	P3	P4	P5	H1	H2	H3	H4	H5
P1	1									
P2	0.818	1								
P3	0.755	0.837	1							
P4	0.729	0.765	0.822	1						
P5	0.577	0.543	0.555	0.541	1					
H1	0.588	0.557	0.6	0.584	0.531	1				
H2	0.568	0.568	0.612	0.627	0.51	0.8	1			
H3	0.52	0.461	0.53	0.462	0.522	0.604	0.617	1		
H4	0.604	0.571	0.617	0.568	0.581	0.772	0.75	0.738	1	
H5		0.47	0.51	0.471	0.571	0.652	0.63	0.69	0.8	1

DISCUSSION

All parameters obtained from half diallel analysis exhibited that the parents number (1, 2, 4 and 5) in addition, the crosses (H1, H3, H6, H8 and H10) were recorded highly mean performance, highly significant positively data of heterosis over better-parent beside both types of combining ability effects and revealed promising results related with drought tolerance indices under both limits of irrigation. There is no doubt that these previous superior accessions were considered a big important step for explaining mechanisms responsible for water deficit resistance in wheat crop under Egyptian conditions, since it has maintained the content of water necessary to complete the life cycle as well as it has penetrated deep layers in the soil to reach to water in the distant strata by deeply, a strong, thick and long root system. At the same time have a large of adventitious, occipital roots and root whiskers which were described as long and spaced trends in deep layers. It can be said that, these physiological changes taken by the plant to defense and keep his life at the time of water deficit conditions as the executive mechanism to water stress tolerance and were separated between the parents and their crosses used in this investigation in terms of resistance and tolerance to choose the best and strongest genotype for tolerance and resistance this environmental pressure. Accordingly, continuing cultivating these superior genotypes for several generations may have the tangible impact of access to the rate that genetic stability is very high and close to 100%, as well as access to a high degree of water stress tolerance (Table 2). Similar results were in agreement with those reported by Khatab *et al.*[5], El-Mouhamady *et al.*[22-27], El-Seidy *et al.*[28], Asifa *et al.*[29], Esmail *et al.*[30], Madhukar *et al.*[31] and Behboudi *et al.*[32]. Results obtained in Table 3 confirmed the effective of additive and non-additive types of gene action for dominating traits under studying. While that, non-additive type of gene action only was more fruitful in the inheritance and controlling the previous studied traits under both treatments of irrigation and enhanced water stress tolerance in wheat genotypes in the case of GCA/SCA ratio was less than one. Thus, the selection will be effective through using bulk method not pedigree method, respectively. Similar results were agreement with Khatab *et al.*[5], El-Mouhamady *et al.*[7], Ramadan *et al.*[8] and Esmail *et al.*[33]. For heterosis over better-parent, the previous superior wheat hybrids were confirmed very effective and fruitful for SCA effects and revealed the biggest role of non-additive types of gene action (Dominance and Dominance × Dominance) for controlling and inheritance of these traits for water deficit tolerance under Egyptian conditions (Table 4). These results were in agreement with those reported by other experiments of Khatab *et al.*[5], Ramadan *et al.*[8], El-Mouhamady *et al.*[23-24], El-Seidy *et al.*[28] and El-Mouhamady[34,35]. The great goal of improving plant breeding programs is the attempt to mix and collect a large number of genes during hybridization process between parents chosen with great care that are superior in a large number of traits, especially high yielding and disease resistance as well as withstand difficult environmental conditions such as salinity, water stress and high toxicity of heavy metals in the soil beside quality traits required for the consumer. This will only be achieved with a successful hybridization program including important genes for resistance the previous environmental stresses. Results related to GCA effects and viewed in Table 5 confirmed that the two types of gene action (additive and additive × additive) could be played fruitful and effective role in the inheritance and controlling of these traits especially grain yield/plant and its components beside increasing the ability of drought resistance in wheat genotypes under Egyptian conditions. The best five hybrids viewed in Table 6 were recorded excellent and positive results for SCA effects under both conditions confirmed importance of the two types of gene action (Dominance and Dominance × Dominance) for controlling and increasing water stress tolerance in wheat. These results were in agreement with those reported by Khatab *et al.*[5], El-Mouhamady *et al.*[7], Ramadan *et al.*[8], Eldessouky *et al.*[9], Esmail *et al.*[33], El-Mouhamady[34,35] and El-Keredy *et al.*[36]. Results in Table 7 indicated that the first superior group of promising genotypes observed for (YSI, MP, GMP, YI and DTI) and the second excellent group found for (YR and DSI) were highly tolerance and resistance for water stress conditions, because they recorded the highest level of grain yield under stress treatment compared with normal conditions. In addition, these genotypes had reduced proportion of yield losses under drought treatment compared with the control. There is no doubt that modern scientific trends have helped to screened, selected and genetically improved local lines of wheat crop that are rich in important traits for breeders such as high yielding, resistance to various diseases, tolerance for salinity, water stress and high toxicity of heavy metals. There is a striking example of this genetic improvement at the molecular level in wheat cultivar (Giza 168) which tolerance for water stress conditions after transferring (HAVA1) gene from local barley cultivars to it. This gene responsible for manufacturing type of proteins called (LEA) or (Late Embryogenesis Abundant). This protein helps to fill the grain volume of wheat in late maturity stages especially during water deficit conditions. However, the old methods of plant breeding are indispensable because it helps to preserve the

history and pedigree of local varieties and maintain their important characteristics during hybridization and simple selection programs after each segregation generation for producing rich lines of these traits, especially high yielding and resistance for water stress conditions under Egyptian conditions, so tolerance indices tests on all genotypes under investigation helped to light the way to observe the best genotypes for water stress tolerance which considering the real nucleus for development and improving the mechanism of drought tolerance in wheat crop and using also in breeding program to improve the rest of wheat cultivars which sensitive for environments stresses by transferring resistance traits from these. Lines to other sensitive local varieties for the previous stresses through hybridization. Also, to a thorough survey process, selection and choice the best parents involved in this study before starting in it and before doing the hybridization process (Table 7)[5,7,8,33,37]. Molecular genetics markers study succeeded in identification and comparing among the five wheat parents and the best five crosses for drought tolerance through using five RAPD-PCR primers (Table 8) and helped to progress in the recent investigation through screening some specific markers (bands) responsible for water deficit tolerance in wheat accessions under agriculture local conditions in addition, assessment number of total bands contributed for comparing among the previous entries (Table 9), similar results were in agreement with those reported by Khatab *et al.*[5], El-Mouhamady *et al.*[7], Ramadan *et al.*[8], Eldessouky *et al.*[9], Esmail *et al.*[33] and El-Mouhamady *et al.*[38,39]. Molecular genetics has also succeeded in drawing a clear picture that helps researchers to choose and select the promising wheat genotypes resistance for water deficit conditions and this was done by using the previous five RAPD-PCR markers especially OPA-10, OPC-4 and OPC-6 primers which were recorded highly polymorphism (%). These markers were the best way to detect the superior resistance-wheat genotypes for drought stress which included resistance genes. Thus, conventional and molecular genetics cannot be separated in improving plants for resistance any unfavorable environmental conditions, where these scientific trends have become a continuum that complement each other in this context. Result in Table 10 may be used as an indicator for determining positive and negative specific markers which were used as a taxonomic basis at the molecular level for drought tolerance in the ten previous genotypes and a compelling evidence that is not likely to be suspected for water stress tolerance, similar results were in agreement with those reported by Khatab *et al.*[5], El-Mouhamady *et al.*[7], Ramadan *et al.*[8], Eldessouky *et al.*[9], Esmail *et al.*[33] and El-Mouhamady *et al.*[38,39]. Genetic similarity analysis was the big evidence for highly genetic compatibility obtained among the ten wheat entries in this investigation, which will be the basis of the future program of breeding ideal use for the five superior crosses after reached it to highly genetic stability and then, to transfer water stress tolerance genes to sensitive wheat varieties (Table 11). This result of course could only be achieved by drawing the phylogenetic tree that determines the degree of convergence and spacing between the improved varieties and their promising five F1 crosses (Fig. 2). Similar results were in agreement with those reported by Khatab *et al.*[5], El-Mouhamady *et al.*[7], Ramadan *et al.*[8], Eldessouky *et al.*[9], Esmail *et al.*[33] and El-Mouhamady *et al.*[38,39]. After all that has been described in this context can be summarized in the future recommendation to continue to cultivate the five promising and superior hybrids (H1, H3, H6, H8 and H10) which were recorded highly resistance to water stress beside high yielding for several segregation generations to reach high genetic stability to product resistant wheat varieties for drought stress under Egyptian conditions.

CONCLUSION

The present investigation was carried out to study water deficit resistance in some wheat accessions with different response for drought tolerance under normal and drought conditions through studying some agro-morphological traits. The final results reported that the genotypes (P1, P2, P4 and P5) in addition, the crosses (H1, H3, H6, H8 and H10) exhibited the highest limit of water deficit tolerance based on physiological measurements and also at the molecular level where the five RAPD-PCR primers generated 66 fragments (19 of them were monomorphic and 47 polymorphic including 17 unique bands) divided into 13 positive and 4 negative markers, respectively.

SIGNIFICANCE STATEMENT

This study discovered some superior wheat genotypes with highly resistance for drought stress besides high yielding under this conditions compared with the control treatment that can be beneficial for breeding wheat genotypes to water deficit resistance under Egyptian conditions. This study also will help the researchers to uncover the critical areas of water stress tolerance indices and determined specific markers responsible for water deficit resistance in various wheat entries that many researchers were not able to explore. Thus a new theory on high drought resistance related with highly yielding may be arrived at.

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