



Original Research Article

doi: <http://dx.doi.org/10.20546/ijcrbp.2017.401.006>

## Agro-morphological and Molecular Characterization of Sorghum (*Sorghum vulgare* L.) for Water Stress Tolerance

Ismael A. Khatab<sup>1</sup>, A. A. El-Mouhamady<sup>2\*</sup>, H.M. Abdel-Rahman<sup>2</sup>, Mona A. Farid<sup>1</sup> and I. S. El-Demardash<sup>2</sup>

<sup>1</sup>Department of Genetics, Faculty of Agriculture, Kafrelsheikh University, 33516, Egypt

<sup>2</sup>Genetics and Cytology Department, Genetic Engineering and Biotechnology Division, National Research Centre, 33 El Buhouth ST., 12622, Dokki, Giza, Egypt

\*Corresponding author.

### Abstract

The present investigation was designed to study the genetic component in 23 entries of sorghum (eight parents and 15 their cross) using line × tester design under water stress. Moreover, to assess genetic diversity and find marker(s) that could be related to drought tolerance. Genotypes (PI534175), (CD550190), (CPI456765 × PI534175), (CP1987656 × PI534175), (Dorado × PI534175) (CPI456765 × CD550190), (CP1987656 × CD550190) and (Hybrid Shadwell 2 × CD550190) were the best under water deficit conditions compared with the control for most evaluated genetic parameters for important traits. Genetic diversity among selected 11 sorghum entries (8 parents and the best three crosses) were evaluated using eleven primers (six for RAPD and six for SRAP). Fifty and thirty two total bands were detected for SRAP and RAPD whereas, 27 and 29 were polymorphic respectively. Unfortunately, from RAPD primers the banding patterns could not be able to generate any marker linked to water stress among the parents and their hybrids. Moreover, SRAP primers generated polymorphic bands, ranged between 20.60% (primer me1+em3), with the lowest band number (five bands only) to 80.0% for (primer me2+em3), generated the highest band number (11 bands), which generate specific band with size 470 bp in parental genotypes (CPI456765) and (CD550190) which could be transmuted to the hybrids (CPI456765 × CD550190) and (Hybrid Shadwell2 × CD550190). This band could be considered as linked to hybrid vigor and drought stress tolerance. Phylogenetic tree using SRAP divided the tolerant parents and their hybrid in closed clusters.

### Article Info

Accepted: 28 December 2016

Available Online: 06 January 2017

### Keywords

Heterosis  
*Sorghum vulgare*  
Water stress

### Introduction

Sorghum is considering one of the most important crops for production cereal grains and fodder for humans and animals, and is the most famous Egyptian summer crop after rice and maize, vegetative leaves used as feed for

animals and birds in the summer season and contributes to solving the problem of fodder in summer. Also grain yield used to bridge the deficit in wheat flour to produce bread municipal. A biotic stress such as water stress and salinity was the incumbent in the first resistor work to improve the resistance for environmental stresses,

especially the problem of water shortage. Sorghum is predictable to play an increasingly significant function in cultivation and gathering world food desire in the countenance of climate modification, ground degradation and mounting water reduction (Amelework et al., 2015).

Water stress is a collection of stress effects caused by high temperatures (Prasad et al., 2008) and water shortage problem (Campos et al., 2004). Evapotranspiration is the most leadership power that affects the soil, plant, and atmospheric continuum of the hydrologic cycle. In previously papers, foretelling of water deficit were mainly based on countervail and apportionment of downpour (Blum, 2011). Generation and selecting for novel incorporations of genes to manufacture genotypes with eminent character performances than those of presenting genotypes, through the goal climate, is the main thematic of plant breeding (Chapman et al., 2003). Thus, the nominal aim is to be an attempt to improve the tolerance of sorghum for water shortage conditions through hybridization among some exotic genotypes with high tolerance with the Egyptian entries of sorghum which could be transfer a large number of quantitative traits. Boyer and Westgate (2004) assessed that drought stress is one of the most significant causes of crop yield loss. Drought stress has been often labelled as “complex trait” by genetics (Blum, 2011). Morphological variations are positively associated with genetic diversity but are also dependent on environmental factors, as well as, on the interaction between genotypes and environment (Moose and Mumm, 2008). Thus, determining genetic diversity through variation between genotypes, genotype groups, or populations is essential to plant genetic breeding programs.

Sorghum breeders interesting on the development of high yield sorghum hybrids resistance and/ tolerance biotic or a biotic stress such as drought tolerance and disease resistance (Klein et al., 2008; Kumar et al., 2011). In Egypt sorghum breeding programs focused on increase yielding cultivars and hybrids. Heterosis is vital component of hybrid production and it has been shown to be in wide genotypes for various agronomic traits and high yield (Quinby, 1962) reported that heterosis in sorghum for yield ranged from 39 to 80%. Moreover, information about the genetic diversity is a very important part in crop improvement, to identify diverse parental combination to create segregating progenies with maximum genetic variability for further selection

and introgression desirable gene(s) from diverse genotypes into the available genetic pool. Levels of genetic diversity among genotypes have been suggested as a predictor of heterotic potential and hybrid performance. Development of hybrids involves labors, time consuming. Thus, if possible or efficient method to evaluate heterotic potential of hybrids prior to field assessment is established, much of the field work could be eliminated (Xiao et al., 1996). Several sorghum linkage maps were built using different type of DNA markers (Mace et al., 2009). The advent of the polymerase chain reaction (PCR) favored the development of different molecular techniques such as random amplified of polymorphic DNA (RAPD) (Hausmann et al., 2002) in sorghum. Sequence related amplified polymorphism (SRAP) described by Li and Quiros (2001), it is a simple and efficient marker system that can be adapted for a variety of purposes in different crops. It is simple, has reasonable throughput rate, discloses numerous co-dominant markers, targets open reading frames (ORFs), and allows easy isolation of bands for sequencing (Li and Quiros, 2001). To date, SRAP markers have been used to determine genetic diversity in some crops.

This work aims to evaluate the genetic components of sorghum vulgare in field trials under drought and well-watered conditions to assess the suitability of newly developed genotypes to be cultivated and diversity existing marker that could be related or linked to drought tolerance, then identify potentially marker for marker assisted selection.

## Materials and methods

Erect Eight genotypes of sorghum (*Sorghum vulgare*) with different reaction to water stress tolerance were used in this study (Table 1), in three planting dates with ten days interval in order to overcome the differences in flowering time between parents in July 2015 (Lug Nile), while all entries (parents and their F<sub>1</sub> crosses) were grown under (normal irrigation, irrigate after 21 day from the first one , the subsequent irrigation was conducted every 15 day and prevented it before harvesting with 20 day) , while drought stress (no irrigation after the second irrigation until harvest) in a randomized complete block design through three replicates for each level of irrigate in the farm of (Nubaria in Behira Governorate, Egypt) in March 2016 (Lug summer). GYP: mean yield under normal conditions, GYD: mean yield under drought conditions,

YSI: Yield stability index, YI: Yield index, GMP – geometrical mean productivity, YI: yield index, DTI: drought tolerance index, MP: mean productivity, Yr: yield reduction ratio, DSI: drought susceptibility index, P.H: plant height, D.OF.M :Duration of maturity, CH.CO: Chlorophyll content, F.L.A: Flag leaf area,

P.L: Panicle length, P.W: Panicle weight, 1000-G.W: 1000-Grain weight, G.Y/P: Grain yield/plant, M.R.L: Maximum root length, R.V: Root volume, No. of. R/P: Number of roots/plant, R.X.V.No: Root xylem vessel number and R.D.W: Root dry weight were the most important measurements calculated under all conditions.

**Table 1.** The name, reaction to water stress and origin of the studied genotypes.

Genotypes	Name	Reaction to Water stress *	Origin
Line 1	CPI456765	Moderate	Sudan
Line 2	CP1987656	Susceptible	Sudan
Line 3	Dorado	Susceptible	Egypt
Line 4	Hybrid Shadwell 1	Moderate	Egypt
Line 5	Hybrid Shadwell 2	Susceptible	Egypt
Tester 1	PI534175	Tolerance	USA
Tester 2	MT789	Moderate	Sudan
Tester 3	CD550190	Tolerance	USA

\*Three Egyptian lines (line 3, 4, 5) were performed from (Barley research Department, Field Crops Research Institute, Agricultural Research Center, Ministry of Agriculture, Egypt), beside the two treatments of irrigation were isolated and isolation distance was ten meters between each of them to prevent nominated water from normal irrigation to drought treatment.

## Statistical analysis

**Analysis of variance:** The analysis of variance and expected mean squares of the studied characters for parents and their F<sub>1</sub> hybrids were computed using IRRISTAT V. 6 (IRRI, 2005) for line × tester design and according to Wyman et al. (1970) and Virmani et al. (1997).

**Tolerance indices and simple phenotypic correlation (r) coefficients:** These parameters were estimated according to Hossain et al. (1990), Fernandez (1992), Gavuzzi et al. (1997), Lin et al. (1986), Bouslama and

Schapaugh (1984), Golestani and Assad (1998), Fischer and Maurer (1978) and Kearsy and Pooni (1996).

## Molecular markers

**DNA isolation and PCR amplification:** Genomic DNA was isolated from 0.5g of leaves of the used sorghum genotypes using Cetyl trimethyl ammonium bromide (CTAB) based on the method of Doyle and Doyle (1990). The concentration of DNA obtained (ng/μl) was determined on NanoDrop spectrophotometer. Twelve primers (six for RAPD and six for SRAP) were used in this study as shown in (Table 2).

**Table 2.** RAPD and SRAP primers and their sequences.

RAPD 5'--3'			
OPA-04	AATCGGGCTG	OPA-12	TCGGCGATAG
OPA-06	GGTCCCTGAC	OPA-13	CAGCACCCAC
OPA-11	CAATCGCCGT	OPA-14	TCTGTGCTGG
SRAP 5'--3'			
me1+em1	TGAGTCCAAACCGGATA	GACTGCGTACGAATTAAT	
me1+em2	TGAGTCCAAACCGGATA	GACTGCGTACGAATTTGC	
me1+em3	TGAGTCCAAACCGGATA	GACTGCGTACGAATTGAC	
me2+em1	TGAGTCCAAACCGGAGC	GACTGCGTACGAATTAAT	
me2+em2	TGAGTCCAAACCGGAGC	GACTGCGTACGAATTTGC	
me2+em3	TGAGTCCAAACCGGAGC	GACTGCGTACGAATTGAC	

Polymerase chain reaction (PCR) amplification was done in a volume of 20μl using 40ng genomic DNA, 0.2 mM dNTP, 1.5 mM MgCl<sub>2</sub>, 10 pmol of primer and 0.5U Taq polymerase. PCR conditions were as follows: 96°C for 1 min, 35 cycles of 96°C for 30s, 30°C for 30 sec,

72°C for 1.30 min. then 72°C for 7 min. For SRAP the initial denaturation at 94°C for 4 min., followed by five cycles comprising 1 min., denaturation at 94°C, 1 min., annealing at 35°C, and 30 sec. of elongation at 72°C. In the following 30 cycles, denaturation at 94°C for 1 min.,

annealing at 50°C for 1 min., and elongation at 72°C for 30 sec. were carried out, ending with an elongation step for 10 min., at 72°C. The RAPD and SRAP products were separated by 1.5% agarose gels electrophoresis, which run with 1× TAE buffer. The 100bp DNA ladder was also run on each gel as a molecular weight standard. Photo documentation was performed under UV light using Gel Documentation System. Amplification of RAPD and SRAP profiles for tested 11 sorghum entries were compared with each other and DNA bands were scored as a binary data. Each band was scored as present (1) or absent (0), and pairwise comparisons between individuals were made to calculate the Jaccard (1908) coefficient using PAST program (Paleontological Statistics Version 1.94b) adapted by Hammer et al. (2001). Cluster analysis was performed to produce a dendrogram using unweighted pair-group method with arithmetical average (UPGMA).

## Results and discussion

### Mean performance

The mean values of all traits studied from the genotypes of sorghum under normal irrigation and water stress treatment revealed in Table 3. The following genotypes; (PI534175), (CD550190), (CPI456765 × PI534175), (CPI1987656 × PI534175), (Dorado × PI534175) (CPI456765 × CD550190), (CPI1987656 × CD550190) and (Hybrid Shadwell 2 × CD550190) recorded the best and the most desirable mean values for all studied traits under normal and water stress conditions, which indicated that these genotypes were highly tolerance for drought stress and were able to short of their life cycle when the beginning of drought season beside keeping of highly yielding under this conditions through development of root system by increasing maximum root length, number of roots/plant, root volume and root xylem vessel number for water stress tolerance in addition, increasing adventitious roots for access to water in the deep layers of the soil and storage the largest amount of it during these conditions, respectively (Tuinstra et al., 1997; Bavei et al., 2010; Ahmed et al., 2015; Mostafa et al., 2016). Moreover, in other crops the effect of water deficit conditions was detected in wheat (El-Mouhamady et al., 2016), in barley (Mansour et al., 2016) and in maize (Esmail et al., 2016).

From the previous results it notes that these genotypes are the most superior and achieve the objectives of the breeding program for drought tolerance in the cultivars

of sorghum crop because it has proved a great resistance to water stress under the difficult conditions of water shortages and maintained at the moderately level of photosynthesis through increasing number of stomata in the cells of leaves, reduce the rate of transpiration at noon with a low degree of leaf temperature, as well as deepening on the root system through increase the number of adventitious roots for reaching to the water in the deep layers of the soil and all that achieved thanks from hybridization Egyptian varieties with imported lines of sorghum performed from abroad for improving the additive gene action of these lines. Therefore the continued of cultivation these genotypes will be feasible to get genetic stability of maintaining the status of water stress resistance and after all these results we can say that the choice of the promising parents before the hybridization process is one of the most basic requirements for a successful breeding program because these parents will cover the intended purpose through the recipe resistance and tolerance for water deficit conditions.

### Analysis of variance

The analysis of variance in all traits studied was detected in Table 4, significant and highly significant variations were observed between the two treatments in all studied traits. These significant variations ensured the effect of different water stress conditions on these traits in sorghum entries beside revealed highly significant variations between all entries for all traits, except plant height under drought stress, flag leaf area and panicle length traits under all conditions, for (parent VS crosses), respectively. These results mean that additive and additive × additive types of gene action played a fruitful role in the genetic control of these traits for water deficit tolerance (Tuinstra et al., 1997; Bavei et al., 2010; Ghorade et al., 2014; Mostafa et al., 2016).

Line × tester analysis give a good test and accurate see to examine the parents involved in the breeding program in sorghum for water stress tolerance, determine dimension and proximity between parents in this test and evaluation the largest number of species lines measured with vegetative, physiological and yielding traits under water deficit conditions. So, the interaction between lines and testers will be fruitfully to indicate the importance of additive, additive × additive types of gene action and its impact on the degree of inheritance for quantitative traits through generations' isolationism such as resistance to water stress, salinity tolerance, disease

resistance, high yield under stresses. It seems to be that these genotypes realized highest values of additive gene action, their interactions and considered the supreme entries for avoiding, escaping and tolerance for water stress under these conditions.

### Heterosis over better-parent

The data presented in Table 5 showed that six and two crosses out of the fifteen hybrids under normal and drought conditions for plant height trait in addition to three crosses out of the rest hybrids under water stress conditions for duration of maturity trait were revealed significant and highly significant negatively percentages of heterosis over better-parent and the most desirable crosses were (CPI456765 × PI534175) and (CP1987656 × CD550190) under normal irrigation only for plant height trait and (Dorado × MT789) under water stress conditions only for duration of maturity trait, respectively.

On the other hand, seven crosses for chlorophyll content trait, one cross for flag leaf area, panicle length, maximum root length and root volume traits, two crosses for 1000-grain weight trait, three crosses for grain yield/plant trait, four crosses for number of roots/plant, six crosses for root xylem vessel number trait and two crosses for root dry weight trait out of fifteen hybrids were exhibited significant and highly significant positively values of heterosis over better-parent under two levels of irrigation (normal and water deficit conditions) and the best crosses for yield traits were (CPI456765 × CD550190, Dorado × PI534175 and Hybrid Shadwell 2 × CD550190), while panicle weight trait no detected any significant and highly significant positively crosses under all conditions, respectively, which indicated that these crosses were very important for SCA effects and showed the role of (Dominance and Dominance × Dominance) types of gene action for controlling and inheritance of these traits for water stress tolerance.

It is noteworthy to indicate, herein, that the mean performances of the favored entries studied which would may played a big role in presenting and improved hybrid vigor and also to clarify the genetic strength resulting of transgressive segregation especially grain yield/plant and the extent of its stability and low wastage of it under water stress conditions. These findings indicate that the intrinsic performance of the parents involving in these crosses gave a good index of their SCA effects.

Therefore, selection for improving all traits studied could be practiced either on mean performance on SCA effects basis (Asifa et al., 2015; El-Mouhamady et al., 2016; Mansour et al., 2016).

### Combining ability effects

**General combining ability effects:** Five and two lines for plant height trait and three and four entries for duration of maturity trait out of eight parents exhibited significant and highly significant negatively values of GCA effects under normal and drought conditions, while, (four parents for chlorophyll content, flag leaf area, panicle length, grain yield/plant and number of roots/plant traits), (two and three lines for panicle weight trait, (three and four parents for 1000-grain weight and maximum root length traits) , (five and four parents for root volume and root xylem vessel number traits) and (three lines for root dry weight trait) out of eight entries were detected significant and highly significant positively values of GCA effects under normal and water stress conditions. The most parents revealed highly significantly positively values under the two conditions and recorded highly tolerance to drought stress for the most traits were CPI456765, CP1987656, PI534175 and CD550190 in Table 6, respectively.

These results presented in Table 6 showed that additive and additive × additive types of gene action played an important role in the inheritance of these traits for development the ability of water stress tolerance in sorghum vulgare under Egyptian conditions in addition , the possible by simultaneous exploitation of additive and additive × additive gene action will achieve by adopting through parental mating in the second generation among selection both general and specific combining ability effects which were found to be highly significant and positively for all traits under normal and water deficit conditions (Ghorade et al., 2014; El-Mouhamady et al., 2016; Mansour et al., 2016).

Esmail et al. (2016) studied GCA effects in 7 promising maize lines imported from (CIMMYT) through determining ear length, ear diameter, number of rows/ear, number of kernels/ row, 100 kernel weight, and grain yield/plant traits and revealed that the most desirable and combiner parents which detected significant and highly significant positively values of GCA effects for the most traits under two regimes of irrigation (normal and water stress conditions) were (P1, P2, P7), respectively.

**Table 3.** Mean performance of the genotypes of sorghum for all studied traits under all conditions.

Crosses	P.H		D.OF.M		CH.CO		F.L.A		P.L		P.W		1000-G.W	
	Normal	Stress	Normal	Stress	Normal	Stress	Normal	Stress	Normal	Stress	Normal	Stress	Normal	Stress
L1	211.00	153.33	114.67	117.67	26.67	19.33	32.67	26.67	27.37	22.33	25.93	23.90	19.90	16.50
L2	196.67	133.00	117.67	113.67	31.67	20.00	53.67	50.00	26.40	23.17	25.67	23.90	20.67	18.00
L3	213.33	150.67	121.67	124.67	32.33	25.00	29.33	24.00	27.53	23.00	34.00	32.17	22.80	20.67
L4	210.00	153.00	119.00	121.33	26.00	19.00	33.67	27.67	25.77	23.00	27.67	26.37	22.33	19.57
L5	201.67	115.67	116.67	118.33	33.00	25.67	30.00	26.00	25.67	22.00	30.00	27.73	23.80	19.67
T1	183.00	177.33	105.00	103.67	59.67	56.67	54.33	51.00	32.33	30.00	38.67	36.83	27.20	25.67
T2	201.00	132.67	120.00	124.00	33.00	20.00	27.00	21.00	26.07	21.33	32.17	27.00	20.00	17.17
T3	177.00	173.00	107.00	102.00	64.00	61.00	58.67	56.00	31.57	29.00	38.93	37.73	26.93	25.33
L1 × T1	174.67	160.00	104.33	101.00	69.00	67.00	58.33	55.67	33.70	31.57	40.50	39.87	30.00	27.00
L1 × T2	216.00	170.33	105.80	108.33	23.33	21.00	28.33	26.00	22.67	19.33	26.67	23.33	19.33	19.00
L1 × T3	166.33	163.00	110.67	105.33	67.33	65.33	63.33	59.33	34.27	36.67	40.50	39.20	29.67	28.67
L2 × T1	176.00	163.00	107.00	103.00	67.00	61.33	60.33	54.67	33.77	31.67	39.43	38.73	33.00	29.67
L2 × T2	224.33	193.33	115.67	119.33	36.33	31.33	24.33	21.00	23.17	19.33	25.00	24.00	23.00	19.33
L2 × T3	152.33	148.67	106.00	104.33	75.33	69.00	68.33	66.00	34.60	32.00	40.73	38.67	31.33	28.67
L3 × T1	171.00	158.00	103.67	100.00	71.00	67.33	51.00	47.33	31.77	30.33	40.10	39.37	29.00	27.00
L3 × T2	217.33	113.67	116.67	108.67	41.00	31.33	26.00	22.00	23.00	19.67	33.50	30.00	22.00	19.33
L3 × T3	223.67	162.67	119.00	113.33	25.67	22.33	26.67	21.67	25.00	21.00	34.33	31.00	19.67	17.67
L4 × T1	216.00	116.00	123.00	126.00	22.00	18.00	25.67	21.00	23.00	20.67	33.33	30.00	23.50	19.00
L4 × T2	226.67	138.67	117.00	104.00	34.67	30.67	27.33	22.33	22.43	18.00	31.00	27.33	25.67	20.67
L4 × T3	193.00	148.33	125.33	127.00	25.00	21.00	27.00	22.67	25.90	22.67	35.00	30.33	23.67	21.33
L5 × T1	221.00	127.67	119.67	120.00	24.33	19.67	29.00	23.00	22.50	19.00	33.67	29.67	22.33	19.67
L5 × T2	206.67	130.67	115.33	119.67	42.67	34.67	21.67	18.00	22.33	19.00	29.67	27.00	23.57	19.69
L5 × T3	144.3	140.7	104.3	102.3	66.3	62.7	66.0	62.3	32.3	30.0	40.8	40.0	31.5	29.2
LSD 0.05	6.50	14.52	9.62	9.93	7.25	6.53	7.20	6.68	2.11	3.24	2.93	3.42	3.67	3.53
0.01	8.70	19.42	12.87	13.29	9.71	8.74	9.64	8.93	2.82	4.33	3.92	4.58	4.91	4.72

Table3.Continued...

Crosses	G.Y/P		M.R.L		R.V		No.of.R/P		R.X.V.No		R.D.W	
	Normal	Stress	Normal	Stress	Normal	Stress	Normal	Stress	Normal	Stress	Normal	Stress
L1	26.00	18.00	35.87	28.33	44.67	30.67	230.00	116.67	12.67	10.67	5.67	4.67
L2	26.67	19.00	30.33	25.33	30.33	26.00	223.00	137.67	13.50	9.33	6.83	5.47
L3	23.33	17.67	32.00	26.67	49.00	33.33	239.33	148.67	10.67	8.67	8.67	7.97
L4	23.67	18.00	34.67	26.00	39.00	30.33	273.33	153.33	14.50	13.00	5.90	5.07
L5	24.67	16.67	37.33	33.00	44.33	32.67	320.67	153.00	10.83	9.33	4.33	3.43
T1	47.33	44.33	64.00	51.00	114.00	98.00	581.33	499.67	21.83	20.00	12.50	10.00
T2	32.00	28.33	37.67	31.33	40.00	26.33	134.00	117.00	10.33	9.00	5.00	4.10
T3	42.67	39.00	52.67	43.67	104.00	93.00	604.67	532.33	27.67	22.33	13.00	11.00
L1 × T1	51.00	46.00	70.00	61.33	119.00	113.00	640.00	620.00	32.33	28.67	15.53	14.73
L1 × T2	24.33	18.67	42.67	37.33	34.33	28.00	117.33	92.00	9.67	8.00	7.27	4.68
L1 × T3	55.67	51.33	60.00	53.33	116.33	106.33	687.33	600.33	50.00	46.00	13.77	12.00
L2 × T1	45.67	41.67	72.00	59.67	123.00	118.00	743.33	656.67	40.00	30.33	16.57	15.53
L2 × T2	34.00	27.67	36.33	29.00	40.67	32.00	378.33	236.00	13.70	11.33	7.87	6.33
L2 × T3	51.67	42.00	72.00	59.33	130.00	118.67	652.33	610.67	43.67	40.00	14.30	13.47
L3 × T1	56.00	50.00	69.67	53.00	127.67	117.67	700.00	679.67	39.67	35.67	13.80	13.07
L3 × T2	20.00	16.00	41.67	27.00	58.00	47.33	139.33	121.00	13.17	11.33	8.00	5.67
L3 × T3	23.33	15.67	29.33	23.67	77.00	39.67	236.67	156.00	15.30	12.60	5.80	4.50
L4 × T1	26.33	20.33	41.00	35.00	25.33	21.33	207.33	173.33	16.67	13.33	8.33	6.50
L4 × T2	25.33	15.67	44.00	28.33	28.00	22.67	167.67	116.67	7.90	6.33	7.77	4.93
L4 × T3	28.33	22.33	32.00	23.00	35.67	25.33	156.00	107.00	11.27	10.13	6.17	3.73
L5 × T1	25.67	18.00	30.00	23.00	40.33	33.00	136.67	114.33	11.00	8.33	6.43	4.00
L5 × T2	34.00	21.33	28.33	23.33	39.00	27.33	166.00	120.00	16.00	10.33	3.53	3.37
L5 × T3	53.3	47.3	62.0	47.7	115.0	106.3	785.3	665.3	60.3	49.7	4.2	3.4
LSD 0.05	6.34	5.61	8.58	6.70	16.29	13.06	102.81	68.92	6.89	5.32	2.33	1.83
0.01	8.49	7.51	11.48	8.96	21.80	17.47	137.55	92.21	9.21	7.12	3.11	2.44

**Table 4.** Mean squares from ordinary analysis of variance for the studied traits of genotypes of sorghum under all conditions.

S.O.V	df	P.H		D.OF.M		CH.CO		F.L.A		P.L		P.W		1000-G.W	
		Normal	Stress	Normal	Stress	Normal	Stress	Normal	Stress	Normal	Stress	Normal	Stress	Normal	Stress
Rep.	2	10.61	449.58**	77.52	58.28	32.19	26.54	107.15**	83.32**	1.81	3.59	4.34	0.38	2.17	1.51
Genotypes	22	1738.26**	1303.15**	624.36**	1011.02**	1092.21**	1198.51**	798.84**	853.20**	59.07**	89.64**	88.21**	106.53**	52.82**	57.43**
Parents	7	525.71**	1306.64**	338.95**	551.85**	826.90**	1071.05**	521.69**	618.23**	20.84**	33.07**	83.63**	90.24**	24.97**	36.32**
Crosses	14	2451.52**	1394.31**	797.08**	1286.61**	1284.77**	1305.18**	994.37**	1030.71**	82.15**	124.05**	84.46**	111.44**	61.36**	63.70**
P vs. C	1	240.45**	2.44	204.11**	366.91**	253.58**	597.36**	1.46	12.91	3.60	3.87	172.73**	151.63**	128.15**	117.44**
Lines	4	1322.70**	2477.80**	401.83**	813.97**	1329.59**	1321.98**	966.17**	1073.86**	77.04**	117.58**	12.11**	36.16**	41.85**	49.06**
Testers	2	6841.49**	225.69**	1165.09**	2251.80**	1238.47**	1550.29**	2536.69**	2449.27**	249.97**	372.82**	379.28**	437.48**	108.87**	136.25**
L x T	8	1918.43**	1144.72**	902.70**	1281.63**	1273.94**	1235.51**	622.88**	654.49**	42.74**	65.09**	46.94**	67.58**	59.24**	52.87**
Error	44	15.52	77.38	34.01	36.23	19.33	15.67	19.05	16.36	1.63	3.85	3.15	4.30	4.94	4.57

S.O.V	df	G.Y/P		M.R.L		R.V		No. of R/P		R.X.V.No		R.D.W	
		Normal	Stress	Normal	Stress	Normal	Stress	Normal	Stress	Normal	Stress	Normal	Stress
Rep.	2	29.35	72.04	13.79	61.28	15.01	24.83	754.96	954.10	2.80	4.78	2.28	1.04
Genotypes	22	459.51**	515.27**	725.41**	541.15**	4555.24**	4586.69**	169598.92**	163791.96**	674.86**	525.55**	47.54**	48.75**
Parents (P)	7	257.14**	359.14**	406.89**	261.43**	3003.62**	2854.09**	89936.66**	92847.57**	116.79**	86.95**	33.77**	24.12**
Crosses(C)	14	550.74**	600.58**	861.91**	682.49**	5395.09**	5418.94**	216305.50**	198486.39**	887.73**	698.16**	55.12**	62.76**
P vs. C	1	598.98**	413.79**	1043.91**	520.50**	3658.70**	5063.48**	73342.69**	174680.79**	1601.25**	1179.12**	37.78**	24.93**
Lines (L)	4	478.63**	552.81**	854.48**	958.26**	6879.09**	6196.67**	215832.02**	181374.48**	626.92**	466.87**	103.00**	108.60**
Testers (T)	2	1012.29**	1217.87**	1267.27**	1203.80**	13195.29**	11751.76**	453526.96**	455250.47**	2246.26**	1886.64**	105.38**	126.08**
L x T	8	471.40**	470.14**	764.29**	414.27**	2703.04**	3446.87**	157236.87**	142851.33**	678.50**	516.69**	18.62**	24.01**
Error	44	14.77	11.57	27.02	16.47	97.51	62.60	3881.61	1744.48	17.42	10.40	1.99	1.22

**Table 5.** Heterosis percentage over better parent in 15 cross of sorghum for all studied traits under all conditions.

Crosses	P.H		D.OF.M		CH.CO		F.L.A		P.L		P.W		1000-G.W	
	Normal	Stress	Normal	Stress	Normal	Stress	Normal	Stress	Normal	Stress	Normal	Stress	Normal	Stress
L1 x T1	-4.55**	4.35	-0.63	-1.94	15.63*	18.22**	7.36	9.15	4.23	5.23	4.74	8.24	10.29	5.19
L1 x T2	7.46**	28.39**	0.76	-7.93**	-29.30*	5.00	-13.28	-2.51	-17.17**	-13.43	-17.10**	-13.58*	-3.33	10.68
L1 x T3	-6.03**	6.30	3.42	3.26	5.20	7.09*	7.94	5.94	8.55*	26.44**	4.02	3.89	10.15	13.16
L2 x T1	-3.83*	22.56**	1.90	-0.64	12.28**	8.22*	11.04	7.19	4.45	5.56	1.98	5.16	21.32**	15.58*
L2 x T2	14.07**	45.73**	-1.69	4.97	10.09**	56.65**	-9.88	-58.00**	-12.23**	-16.57*	-22.28**	-11.11	11.29	7.41
L2 x T3	-13.94**	11.78**	-0.93	2.28	17.70**	13.11*	16.46**	17.85**	9.59**	10.34	4.62	2.47	16.34*	13.16
L3 x T1	-6.56**	4.87	-1.26	-3.54	18.98**	18.81**	-6.12	-7.19	-1.73	1.10	3.71	6.88	6.62	5.19
L3 x T2	8.13**	-14.32*	-2.77	-12.36**	24.24*	25.23**	-11.35	-8.33	-16.45**	-14.47*	-1.47	-6.74	-3.51	-6.45
L3 x T3	26.37**	7.96	11.21*	11.10*	-59.89**	-63.39**	-54.54**	-61.30**	-20.81**	-27.58**	-11.82**	-17.84**	-26.98**	-30.26**
L4 x T1	18.03**	-24.2**	17.14**	21.53**	-63.13**	-68.23**	-52.75**	-58.82**	-28.85**	-31.10**	-13.79**	-18.55**	-13.60*	-25.97**
L4 x T2	12.77**	4.52	-1.68	-14.28**	5.06	53.35**	-18.82	-19.29	-13.96**	-21.73**	-3.63	1.23	14.93	5.62
L4 x T3	9.04**	-3.05	17.13**	24.50**	-60.93**	-65.57**	-53.97**	-59.51**	-17.96**	-21.82**	-10.10**	-19.61**	-12.13	-15.79*
L5 x T1	20.77**	10.37	13.97**	16.50**	-59.22**	-65.29**	-46.62**	-54.90**	-30.40**	-36.66**	-12.93**	-19.46**	-17.89*	-23.38**
L5 x T2	2.82	12.97*	-1.14	1.13	29.30*	35.06**	-27.70*	-30.76*	-14.34**	-13.63	-7.77	-2.64	-0.98	0.10
L5 x T3	-18.46**	21.61**	-2.52	0.29	3.59	2.78	12.49*	11.25	2.31	3.44	4.88	6.01	16.96*	15.39*
LSD 0.05	6.50	14.52	9.62	9.93	7.25	6.53	7.20	6.68	2.11	3.24	2.93	3.42	3.67	3.53
0.01	8.70	19.42	12.87	13.29	9.71	8.74	9.64	8.93	2.82	4.33	3.92	4.58	4.91	4.72

Crosses	G.Y/P		M.R.L		R.V		No. o f. R/P		R .X .V. No		R.D.W	
	Normal	Stress	Normal	Stress	Normal	Stress	Normal	Stress	Normal	Stress	Normal	Stress
L1 x T1	7.75	3.76	9.38	20.26**	4.39	15.31*	10.09	24.08**	48.09**	43.33**	24.27*	47.33**
L1 x T2	-23.96*	-34.12**	13.27	19.15	-23.13	-8.70	-48.99*	-21.37	-23.68	-25.00	28.24	0.21**
L1 x T3	30.47**	31.62**	13.92	22.14**	11.86	14.34*	13.67	12.77	80.72**	105.97**	5.90	9.09
L2 x T1	-3.52	-6.02	12.50	16.99*	7.89	20.41**	27.87**	31.42**	83.21**	51.67**	32.53**	55.33**
L2 x T2	6.25	-2.35	-3.54	-7.45	1.67	21.52	69.66**	71.43**	1.48**	21.43	15.12	15.85
L2 x T3	21.09**	7.69	36.71**	35.88**	25.00**	27.60**	7.88	14.72*	57.83**	79.10**	10.00	22.42**
L3 x T1	18.31**	12.78*	8.85	3.92	11.99	20.07**	20.41*	36.02**	81.68**	78.33**	10.40	30.67**
L3 x T2	-37.50**	-43.53**	10.62	-13.83	18.37	42.00*	-41.78	-18.61	23.44	25.93	-7.69	-28.87*
L3 x T3	-45.31**	-59.83**	-44.30**	-45.80**	-25.96**	-57.35**	-60.86**	-70.70**	-44.70**	-43.58**	-55.38**	-59.09**
L4 x T1	-44.37**	-54.14**	-35.94**	-31.37**	-77.78**	-78.23**	-64.33**	-65.31**	-23.66	-33.33*	-33.33**	-35.00**
L4 x T2	-20.83**	-44.71**	16.81	-9.57	-30.00	-25.27	-38.66*	-23.91	-45.52	-51.28*	31.64	-2.63
L4 x T3	-33.59**	-42.74**	-39.24**	-47.33**	-65.71**	-72.76**	-74.20**	-79.90**	-59.28**	-54.63**	-52.56**	-66.06**
L5 x T1	-45.77**	-59.40**	-53.13**	-54.90**	-64.62**	-66.33**	-76.49**	-77.12**	-49.62**	-58.33**	-48.53**	-60.00**
L5 x T2	6.25	-24.71*	-24.78*	-29.29**	-12.03	-16.33	-48.23**	-21.57	47.69	10.71	-29.33	-17.89
L5 x T3	25.00**	21.37**	17.72*	9.16	10.58	14.34*	29.88**	24.98**	118.07**	122.39**	-67.44**	-69.39**
LSD 0.05	6.34	5.61	8.58	6.70	16.29	13.06	102.81	68.92	6.89	5.32	2.33	1.83
0.01	8.49	7.51	11.48	8.96	21.80	17.47	137.55	92.21	9.21	7.12	3.11	2.44

**Table 6.** Estimates of general combining ability effects for the 8 parents of sorghum for all studied traits under all treatments of irrigation.

Parents	P.H		D.OF.M		CH.CO		F.L.A		P.L		P.W		1000-G.W	
	Normal	Stress	Normal	Stress	Normal	Stress	Normal	Stress	Normal	Stress	Normal	Stress	Normal	Stress
<b>Lines</b>														
L <sub>1</sub>	-9.62**	15.47**	-7.33**	-9.98**	7.16**	9.60**	9.78**	10.80**	2.85**	4.46**	0.94	1.57*	0.52	1.83*
L <sub>2</sub>	-11.07**	19.36**	-5.33**	-8.31**	13.49**	12.38**	10.78**	11.02**	3.15**	2.94**	0.10	1.23	3.30**	2.83**
L <sub>3</sub>	8.71**	-4.20	1.22	2.13	-0.18	-1.18	-5.67**	-5.87**	-0.77	-1.06	1.03	0.89	-2.26**	-1.73*
L <sub>4</sub>	16.60**	-14.64**	9.56**	13.47**	-18.84**	-18.29**	-13.56**	-14.20**	-3.58**	-4.28**	-1.84**	-3.34**	-1.54*	-2.73**
L <sub>5</sub>	-4.62**	-15.98**	1.89	2.69	-1.62	-2.51	-1.33	-1.76	-1.66**	-2.06**	-0.23	-0.34	-0.02	-0.20
LSD 0.05	<b>2.65</b>	<b>5.93</b>	<b>3.93</b>	<b>4.05</b>	<b>2.96</b>	<b>2.67</b>	<b>2.94</b>	<b>2.73</b>	<b>0.86</b>	<b>1.32</b>	<b>1.20</b>	<b>1.40</b>	<b>1.50</b>	<b>1.44</b>
0.01	<b>3.55</b>	<b>7.93</b>	<b>5.26</b>	<b>5.43</b>	<b>3.96</b>	<b>3.57</b>	<b>3.93</b>	<b>3.65</b>	<b>1.15</b>	<b>1.77</b>	<b>1.60</b>	<b>1.87</b>	<b>2.00</b>	<b>1.93</b>
<b>Testers</b>														
T <sub>1</sub>	-3.56**	-4.04	-2.69	-4.20**	4.60**	5.16**	4.64**	4.13**	1.59**	1.92**	2.46**	2.96**	1.75**	1.41*
T <sub>2</sub>	22.91**	0.36	9.84**	13.80**	-10.47**	-11.71**	-14.69**	-14.33**	-4.64**	-5.66**	-5.78**	-6.23**	-3.10**	-3.46**
T <sub>3</sub>	-19.36**	3.69	-7.16**	-9.60**	5.87**	6.56**	10.04**	10.20**	3.05**	3.74**	3.33**	3.27**	1.35*	2.05**
LSD 0.05	<b>2.06</b>	<b>4.59</b>	<b>3.04</b>	<b>3.14</b>	<b>2.29</b>	<b>2.07</b>	<b>2.28</b>	<b>2.11</b>	<b>0.67</b>	<b>1.02</b>	<b>0.93</b>	<b>1.08</b>	<b>1.16</b>	<b>1.12</b>
0.01	<b>2.75</b>	<b>6.14</b>	<b>4.07</b>	<b>4.20</b>	<b>3.07</b>	<b>2.76</b>	<b>3.05</b>	<b>2.82</b>	<b>0.89</b>	<b>1.37</b>	<b>1.24</b>	<b>1.45</b>	<b>1.55</b>	<b>1.49</b>

Parents	G.Y/P		M.R.L		R.V		No.of.R/P		R.X.V.No		R.D.W	
	Normal	Stress	Normal	Stress	Normal	Stress	Normal	Stress	Normal	Stress	Normal	Stress
<b>Lines</b>												
L <sub>1</sub>	6.69**	8.40**	8.82**	11.73**	15.93**	18.67**	87.31**	99.51**	5.30**	6.08**	2.90**	2.74**
L <sub>2</sub>	6.80**	6.84**	11.38**	10.40**	23.93**	25.78**	197.09**	163.18**	7.02**	5.75**	3.62**	4.05**
L <sub>3</sub>	-3.87**	-3.04*	-1.84	-4.38**	13.60**	4.44	-35.58	-19.04	-2.65	-1.60	-0.09	0.02
L <sub>4</sub>	-10.31**	-10.82**	-9.73**	-10.16**	-44.29**	-40.67**	-217.2**	-205.6**	-13.42**	-11.54**	-1.87**	-2.67**
L <sub>5</sub>	0.69	-1.38	-8.62**	-7.60**	-9.18**	-8.22**	-31.58	-38.04**	3.75*	1.31	-4.56**	-4.15**
LSD 0.05	<b>2.59</b>	<b>2.29</b>	<b>3.50</b>	<b>2.73</b>	<b>6.65</b>	<b>5.33</b>	<b>41.97</b>	<b>28.14</b>	<b>2.81</b>	<b>2.17</b>	<b>0.95</b>	<b>0.75</b>
0.01	<b>3.46</b>	<b>3.07</b>	<b>4.69</b>	<b>3.66</b>	<b>8.90</b>	<b>7.13</b>	<b>56.16</b>	<b>37.65</b>	<b>3.76</b>	<b>2.91</b>	<b>1.27</b>	<b>1.00</b>
<b>Testers</b>												
T <sub>1</sub>	3.96**	4.93**	7.80**	7.47**	13.11**	16.82**	91.22**	110.87**	2.57*	1.80*	2.84**	3.04**
T <sub>2</sub>	-9.44**	-10.40**	-10.13**	-9.93**	-33.96**	-32.31**	-200.5**	-200.8**	-13.32**	-12.00**	-2.40**	-2.73**
T <sub>3</sub>	5.49**	5.47**	2.33	2.47*	20.84**	15.49**	109.29**	89.93**	10.75**	10.21**	-0.44	-0.31
LSD 0.05	<b>2.01</b>	<b>1.78</b>	<b>2.71</b>	<b>2.12</b>	<b>5.15</b>	<b>4.13</b>	<b>32.51</b>	<b>21.79</b>	<b>2.18</b>	<b>1.68</b>	<b>0.74</b>	<b>0.58</b>
0.01	<b>2.68</b>	<b>2.38</b>	<b>3.63</b>	<b>2.83</b>	<b>6.89</b>	<b>5.52</b>	<b>43.50</b>	<b>29.16</b>	<b>2.91</b>	<b>2.25</b>	<b>0.98</b>	<b>0.77</b>

**Table 7.** Estimates of specific combining ability effects for 15 crosses of the studied traits of sorghum under all conditions.

Crosses		P.H		D.OF.M		CH.CO		F.L.A		P.L		P.W		1000-G.W	
		Normal	Stress	Normal	Stress	Normal	Stress	Normal	Stress	Normal	Stress	Normal	Stress	Normal	Stress
Line-1	T-1	-7.44**	-0.40	-9.87**	-10.02**	11.18**	10.73**	3.69	4.53	1.90*	0.46	2.16*	2.77*	1.92	0.70
	T-2	7.42**	5.53	12.93**	16.31**	-19.42**	-18.40**	-6.98**	-6.67**	-2.91**	-4.20**	-3.44**	-4.57**	-3.90**	-2.43
	T-3	0.02	-5.13	-3.07	-6.29	8.24**	7.67**	3.29	2.13	1.01	3.74**	1.28	1.79	1.98	1.72
Line-2	T-1	-4.67*	-1.29	-14.20**	-14.69**	2.84	2.29	4.69	3.31	1.67*	2.08	1.92	1.97	2.14	2.37
	T-2	17.20**	24.64**	11.93**	15.64**	-12.76**	-10.84**	-11.98**	-11.89**	-2.71**	-2.67*	-4.27**	-3.57**	-3.01*	-3.10*
	T-3	-12.53**	-23.36**	2.27	-0.96	9.91**	8.56**	7.29**	8.58**	1.04	0.59	2.35*	1.59	0.87	0.72
Line-3	T-1	-29.44**	17.27**	-14.09**	-17.13**	20.51**	21.84**	11.80**	12.87**	3.59**	4.75**	1.67	2.95*	3.69**	4.26**
	T-2	-9.58**	-31.47**	-3.62	-5.47	5.58*	2.71	6.13*	6.00*	1.05	1.66	3.31**	2.78*	1.55	1.46
	T-3	39.02**	14.20**	17.71**	22.60**	-26.09**	-24.56**	-17.93**	-18.87**	-4.64**	-6.41**	-4.97**	-5.73**	-5.24**	-5.72**
Line-4	T-1	7.67**	-14.29**	16.91**	18.53**	-9.82**	-10.38**	-5.64*	-5.13*	-2.37**	-1.70	-2.23*	-2.18	-2.53	-2.74*
	T-2	-8.13**	3.98	-15.62**	-21.47**	17.91**	19.16**	15.36**	14.67**	3.29**	3.22**	3.67**	4.34**	4.49**	3.79**
	T-3	0.47	10.31*	-1.29	2.93	-8.09**	-8.78**	-9.71**	-9.53**	-0.93	-1.52	-1.44	-2.16	-1.96	-1.05
Line-5	T-1	33.89**	-1.29	21.24**	23.31**	-24.71**	-24.49**	-14.53**	-15.58**	-4.79**	-5.59**	-3.51**	-5.52**	-5.22**	-4.60**
	T-2	-6.91**	-2.69	-5.62	-5.02	8.69**	7.38**	-2.53	-2.11	1.27	1.99	0.73	1.01	0.87	0.27
	T-3	-26.98**	3.98	-15.62**	-18.29**	16.02**	17.11**	17.07**	17.69**	3.52**	3.59**	2.78**	4.50**	4.35**	4.32**
<b>LSD 0.05</b>		<b>4.60</b>	<b>10.26</b>	<b>6.80</b>	<b>7.02</b>	<b>5.13</b>	<b>4.62</b>	<b>5.09</b>	<b>4.72</b>	<b>1.49</b>	<b>2.29</b>	<b>2.07</b>	<b>2.42</b>	<b>2.59</b>	<b>2.50</b>
	<b>0.01</b>	<b>6.15</b>	<b>13.73</b>	<b>9.10</b>	<b>9.40</b>	<b>6.86</b>	<b>6.18</b>	<b>6.81</b>	<b>6.32</b>	<b>2.00</b>	<b>3.06</b>	<b>2.77</b>	<b>3.24</b>	<b>3.47</b>	<b>3.34</b>

Crosses		G.Y/P		M.R.L		R.V		No. of. R/P		R. X. V. No		R.D.W	
		Normal	Stress	Normal	Stress	Normal	Stress	Normal	Stress	Normal	Stress	Normal	Stress
Line-1	T-1	3.38	2.40	4.64	3.20	16.00**	13.73**	67.22	71.69**	-0.90	-0.68	0.50	1.22
	T-2	-9.89**	-9.60**	-4.76	-3.40	-21.60**	-22.13**	-163.71**	-144.64**	-7.68**	-7.55**	-2.52**	-3.07**
	T-3	6.51**	7.20**	0.11	0.20	5.60	8.40	96.49*	72.96**	8.58**	8.24**	2.02*	1.84**
Line-2	T-1	-2.07	-0.38	4.09	2.87	12.00*	11.62*	60.78	44.69	5.04*	1.32	0.81	0.71
	T-2	-0.33	0.96	-13.64**	-10.40**	-23.27**	-25.24**	-12.49	-64.31*	-5.57*	-3.88*	-2.64**	-2.71**
	T-3	2.40	-0.58	9.56**	7.53**	11.27	13.62**	-48.29	19.62	0.53	2.57	1.83*	2.00**
Line-3	T-1	18.93**	17.84**	14.98**	10.98**	27.00**	32.62**	250.11**	249.91**	14.39**	14.00**	1.76*	2.28**
	T-2	-3.67	-0.82	4.91	2.38	4.40	11.42*	-18.82	2.91	3.77	3.47	1.20	0.65
	T-3	-15.27**	-17.02**	-19.89**	-13.36**	-31.40**	-44.04**	-231.29**	-252.82**	-18.16**	-17.48**	-2.96**	-2.93**
Line-4	T-1	-4.29	-4.04*	-5.80	-1.24	-17.44**	-18.60**	-60.89	-69.87**	2.15	1.60	-1.93*	-1.60*
	T-2	8.11**	6.62**	15.13**	9.49**	32.29**	31.87**	191.18**	185.13**	9.27**	8.40**	2.75**	2.61**
	T-3	-3.82	-2.58	-9.33**	-8.24**	-14.84*	-13.27**	-130.29**	-115.27**	-11.43**	-10.01**	-0.82	-1.01
Line-5	T-1	-15.96**	-15.82**	-17.91**	-15.80**	-37.56**	-39.38**	-317.22**	-296.42**	-20.68**	-16.24**	-1.14	-2.62**
	T-2	5.78*	2.84	-1.64	1.93	8.18	4.09	3.84	20.91	0.21	-0.44	1.20	2.52**
	T-3	10.18**	12.98**	19.56**	13.87**	29.38**	35.29**	313.38**	275.51**	20.47**	16.68**	-0.06	0.10
<b>LSD 0.05</b>		<b>4.48</b>	<b>3.97</b>	<b>6.07</b>	<b>4.74</b>	<b>11.52</b>	<b>9.23</b>	<b>72.70</b>	<b>48.73</b>	<b>4.87</b>	<b>3.76</b>	<b>1.64</b>	<b>1.29</b>
	<b>0.01</b>	<b>6.00</b>	<b>5.31</b>	<b>8.12</b>	<b>6.34</b>	<b>15.42</b>	<b>12.35</b>	<b>97.26</b>	<b>65.20</b>	<b>6.52</b>	<b>5.03</b>	<b>2.20</b>	<b>1.73</b>

GCA effects is considering the most acceptable genetic evidence to find out the nature of the parents about the convergence and integration of each other and which often give the genetic basis in all practicability of hybridizations, so the parents (CPI456765, CP1987656, PI534175, CD550190) proved to be a high potential for general combining ability effects among themselves and that the hybridization between them will be successful and will contribute to maximize the values of additive gene action and its interactions in each of the traits, especially grain yield. As well as it is the only strategic way in expanding the genetic base to enter several hundreds or even thousands of parents that cover all the qualities, quantity traits and descriptive to set up a high genetic and nutritional value, high-yielding and resistant class for diseases, tolerant to salinity, water deficit conditions and this will only be achieved if the high coalition of those parents among them.

If we take into account the genetic background of the parents involved in the hybridization, we find that parents were imported from abroad, except three Egyptian lines. we have thus keen to use eight promising entries which fruitful of hereditary excellent brings us to the super border of the transgressive segregation in these traits, such as high yielding and water stress resistance in sorghum, in addition considering the GCA effects of different characters was suggested that population involving these parents could be considered in making multiple crossing because they might possess desirable genes for earliness and/or short stature as well as high grain yielding ability under normal and water stress conditions. Accordingly, these parents would be the best choice as base populations. Finally, we can say that GCA effects was the main entrance in the hybridization program using promising lines in the finder to determine the appropriate parents and the most appropriate in this program. The parents that demonstrate superior noticeable will be the most appropriate in the hybrid program and continue to hybridization with promising crosses to get some excellent lines and high genetic stability, while lines which were recorded the low-efficiency values in all traits studied of this test, based on the results of hybridized with testers could be excluded from the national program of sorghum breeding for water stress tolerance.

### Specific combining ability effects

Significant and highly significant negatively values of SCA effects were detected in Table 7 from (eight and

three crosses) for plant height trait and (five and five crosses) for duration of maturity trait out of fifteen crosses under normal and drought conditions and the best crosses under all conditions were (CP1987656 × CD550190) and (Dorado × MT789) for plant height trait and (CPI456765 × PI534175) and (CP1987656 × PI534175) for duration of maturity trait, respectively. On the other hand (eight and seven crosses) for chlorophyll content trait, (Five and four crosses) for panicle length, grain yield/plant and root xylem vessel number traits, (five and five crosses) for panicle weight and flag leaf area traits, (three and three crosses) for 1000-grain weight trait, (four and four crosses) for maximum root length trait, (five and seven crosses) for root volume trait, (four and five crosses) for number of roots/plant and root dry weight traits out of fifteen crosses were detected significant and highly significant positively values of SCA effects under normal and water deficit conditions, respectively. The most desirable crosses revealed highly degree of water stress tolerance in several traits and detected significant and highly significant positively values of SCA effects under all conditions were (CPI456765 × CD550190), (Dorado × PI534175), (Hybrid Shadwell 1 × MT789) and (Hybrid Shadwell 2 × CD550190), which indicated that these crosses revealed the importance of (Dominance and Dominance × Dominance) types of gene action for controlling these traits for water stress tolerance in sorghum vulgare under Egyptian conditions, these results agreement with those reported by Ghorade et al. (2014) and El-Mouhamady et al. (2016).

Estimates of SCA effects of the 15 sorghum hybridizations under both treatments (normal irrigation and water deficit conditions) were calculated for all studied traits and revealed in Table 7. Several crosses exhibited desirable positively SCA effects for the studied traits while the same superior crosses, showing desirable SCA effects for earliness and short stature (negatively values) and were detected from (CP1987656 × CD550190), (Dorado × MT789) for plant height trait, beside the crosses ((Hybrid Shadwell 1 × MT789) and (Hybrid Shadwell 2 × CD550190) under all conditions of irrigation recorded the same trend of results for duration of maturity trait. These crosses could be used in breeding programmers as early and short stature donors either under stress or non-stress conditions, depending on their non-additive gene effects. On the other hand significant and highly significant positively of SCA effects were observed in the crosses (Dorado × PI534175), (Hybrid Shadwell 1 × PI534175) and [(Hybrid Shadwell 2

(Susceptible) × CD550190] for grain yield/plant, maximum root length, number of roots/plant, root volume, root xylem vessel number and root dry weight under all treatments, respectively, which indicated that most of the crosses, revealed high SCA effects, included diverse parents. The superior F<sub>1</sub>'s having SCA effects are expected to produce desirable transgressive segregates, provided the desirable complementary genes and epistatic effects which are coupled in the same direction to maximize the trait in view. In view of the present findings, it can be stated that these crosses might be bespoken to be utilized in hybrid sorghum breeding, the population would possess desirable genetic for all traits also and this different origin of these parents would widen the genetic base for selection tolerance plants of sorghum under normal and water deficit conditions.

Combining ability estimates serve as a useful guide during selection of parents for hybridization programs (Shukla and Pandey, 2008). The selection is based on the performance of hybrids and are related to the general (GCA) and specific (SCA) combining abilities of the inbred lines involved in the cross. Breeders aim to produce *Sorghum vulgare* lines superior high grain yielding, tolerant to water deficit conditions and contain highly quality traits. So, the problem of bread wheat and reduce the gap between production and consumption by adding sorghum flour to wheat flour when bread flour industry could be

solved. Hybridization of Egyptian cultivars of sorghum vulgare with imported lines to get highly breeding positive values (Additive and Additive × Additive gene action) in their F<sub>1</sub> hybrids and tested it in several seasons for the ability of water stress resistance. Then, proceeding with the extraction of its flour and mixed it with wheat and rice flours will be the second stage (Yano and Fukui, 2015). In choosing parents, hybrids and to estimate the combining abilities of parental genotypes in early generations, breeders use the line × tester analysis to provide an efficient approach for identification of suitable parents and crosses showing good performance in character under investigation (Ahuja and Dhayal, 2007).

### Tolerance indices

The results in Table 8 exhibited that the entries, (PI534175), (MT789), (CP1987656), (CPI456765 × PI534175), (CPI456765 × CP1987656), (CP1987656 × PI534175) and (Dorado × PI534175) recorded mean values less than the unity of (DSI) and low values also of (YR), while these genotypes were showed highly values of (MP, YSI, DTI, GMP and YI), respectively, indicating that these genotypes were more tolerance for water deficit conditions, because they exhibited the highest grain yield under stress conditions compared with normal conditions and reduced the proportion of yield losses under water deficit conditions compared with the control.

**Table 8.** Estimates of tolerance indices in the genotypes of sorghum for grain yield trait under normal and water deficit conditions.

Genotypes	GYP	GYD	YSI	YI	MP	DTI	GMP	YR	DSI
L1	26.00	18.00	0.69	0.74	22	0.38	21.63	0.30	1.72
L2	26.67	19.00	0.71	0.78	22.83	0.42	22.51	0.28	1.61
L3	23.33	17.67	0.75	0.73	20.5	0.34	20.30	0.24	1.36
L4	23.67	18.00	0.76	0.74	20.83	0.35	20.64	0.24	1.34
L5	24.67	16.67	0.67	0.69	20.67	0.34	20.27	0.32	1.82
T1	47.33	44.33	0.93	1.83	45.83	1.73	45.80	0.06	0.36
T2	32.00	28.33	0.88	1.17	30.16	0.74	30.11	0.11	0.64
T3	42.67	39.00	0.91	1.61	40.83	1.37	40.79	0.08	0.48
L1 × T1	51.00	46.00	0.90	1.90	48.5	1.93	48.43	0.09	0.55
L1 × T2	24.33	18.67	0.76	0.77	21.5	0.37	21.31	0.23	1.30
L1 × T3	55.67	51.33	0.92	2.12	53.5	2.35	53.45	0.07	0.44
L2 × T1	45.67	41.67	0.91	1.72	43.67	1.56	43.62	0.08	0.49
L2 × T2	34.00	27.67	0.81	1.14	30.83	0.77	30.67	0.18	1.04
L2 × T3	51.67	42.00	0.81	1.74	46.83	1.78	46.58	0.18	1.05
L3 × T1	56.00	50.00	0.89	2.07	53	2.31	52.91	0.11	0.6
L3 × T2	20.00	16.00	0.80	0.66	18	0.26	17.88	0.20	1.12
L3 × T3	23.33	15.67	0.67	0.65	19.5	0.30	19.12	0.33	1.84
L4 × T1	26.33	20.33	0.77	0.84	23.33	0.44	23.13	0.22	1.28
L4 × T2	25.33	15.67	0.62	0.65	20.5	0.32	19.92	0.38	2.14
L4 × T3	28.33	22.33	0.78	0.92	25.33	0.52	25.15	0.21	1.19
L5 × T1	25.67	18.00	0.70	0.74	21.83	0.38	21.49	0.29	1.67
L5 × T2	34.00	21.33	0.63	0.88	27.66	0.59	26.92	0.37	3.47
L5 × T3	53.3	47.3	0.88	1.96	50.3	2.08	50.21	0.11	1.05

Genotypes with low DSI values (less than the unity) can be considered to be water stress tolerance (Bruckner and Froberg, 1987), because they recorded the lowest yield reductions under drought conditions compared with the control than the mean of all genotypes. Low DSI values of a genotype could be due to lack of yield production under normal treatments of irrigation rather than an indication of its ability to tolerate water deficit conditions. Kumar et al. (2015) found highly yield of maize hybrids under normal as well as drought environments. Esmail et al. (2016) confirmed that DSI was less than the unity in most wheat lines which were highly tolerance for water stress conditions. Esmail et al. (2016) studied tolerance indices in 21 maize inbred lines through normal and drought stress experiments and revealed that the most entries highly tolerance for water deficit conditions were recorded the lowest values of YR and showed values less than the unity for DSI, while these genotypes revealed the highest values of MP, GMP, DTI, YSI and YI, found to be highly tolerance for drought stress. DSI will be a low value in all entries which were the most tolerant for water stress and *vice versa*, while the highest values of MP, GMP, YI and DTI give a direct reflection of the high degree of water stress tolerance in the genotypes which including these high values because it has maintained the highest value of the yield and reduced the damage of it under the drought stress. After reviewing the results of the indications for stress-related with genetic compositions of sorghum vulgare we can say that water deficit tolerance is considering the most important trait of this relationship with knives and a change in the yield, according to the degree of sensitivity, endurance obtained from those directories and bear in mind that some varieties of sorghum imported from outside Egypt and characterized by short-life span, so the response to water stress tolerance will be great and helpful in transferring this genetic structures trait among other genotypes through hybridization using line  $\times$  tester design. Drought susceptibility index will record the lowest values less than one in the parents and crosses which were the most tolerant for water stress and vice versa, so the decline in the value of low yield will be accompanied by a high degree of drought tolerance. The highest values of MP, GMP, YI and DTI give a direct reflection of the high degree of water stress tolerance in the genotypes which including these high values because it has maintained the highest value of the yield and reduced the damage of it under the drought stress.

From the previous results it can be concluded that the

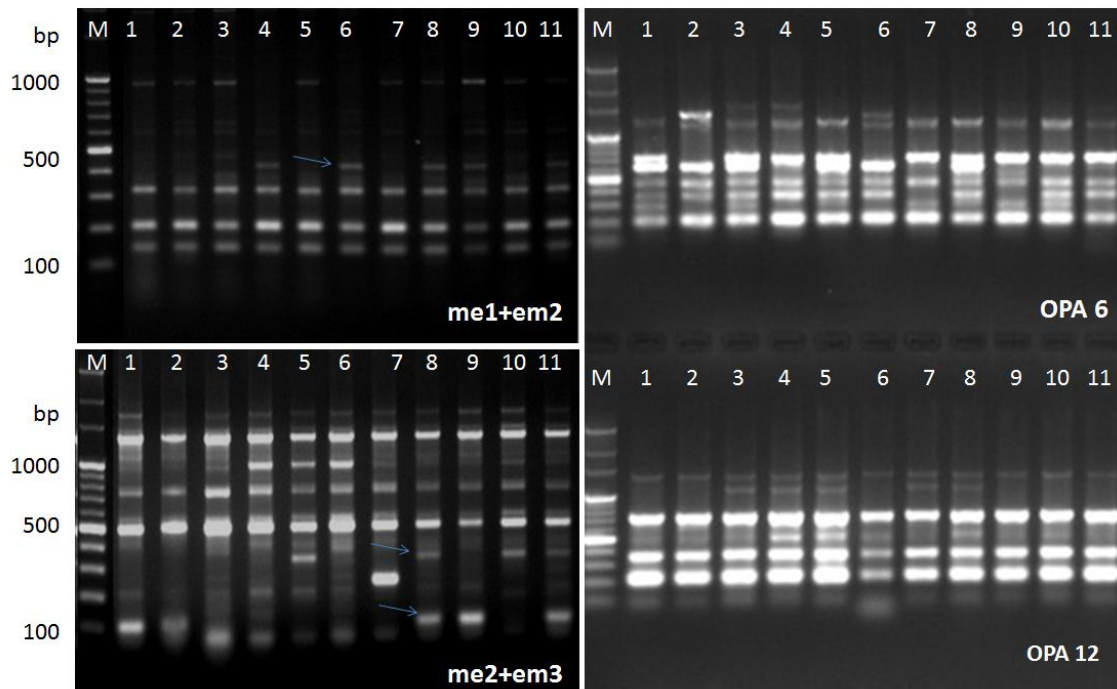
genotypes (PI534175), (CD550190), (CPI456765  $\times$  PI534175), (CP1987656  $\times$  PI534175), (Dorado  $\times$  PI534175), (CPI456765  $\times$  CD550190), (CP1987656  $\times$  CD550190) and (Hybrid Shadwell 2  $\times$  CD550190) were the most resistance for water deficit conditions for all traits studied under both treatments of irrigation measured by mean performance and all genetic parameters estimated in addition, tolerance indices.

### Molecular markers

#### SRAP and RAPD analysis

Twelve preselected primers (six for SRAP and six for RAPD) were used in the present study to identify 11 entries of sorghum as shown in (Fig. 1, Table 9). Eight parental genotypes and selected three crosses, mainly CPI456765, CP1987656, Dorado, Hybrid Shadwell 1, Hybrid Shadwell 2, PI534175, MT789, CD550190, (CPI456765  $\times$  CD550190), (Dorado  $\times$  PI534175) and (Hybrid Shadwell2  $\times$  CD550190) as a best in grain yield and other traits. Fifty and thirty two total bands were detected for SRAP and RAPD whereas, 27 and 29 were polymorphic respectively. Among the tested RAPD primers, only four generated polymorphic bands, resulting polymorphic rate with values between 60.60% in case of OPA 11 and 83.3% for oligonucleotides OPA12. Primer OPA 6 generated the highest No., of bands (nine bands). Unfortunately, from RAPD primers the banding patterns could not be able to generate any marker linked to water stress among the parents and their hybrids. Moreover, all six tested SRAP primers generated polymorphic bands, resulting a polymorphic rate with values between 20.60% in case of primer combination me1+em3, which generated the lowest band number, (five bands only) to 80.0% for primer combination me2+em3, generated the highest band number, (11 bands) as shown in Table 9.

There was band using SRAP primer combination (me1+em2) with size approximately 470 bp found in parental genotypes (CPI456765) and (CD550190) which could be transmuted to the hybrids (CPI456765  $\times$  CD550190) and (Hybrid Shadwell 2  $\times$  CD550190) but not found in other hybrid (Dorado  $\times$  PI534175). This band could be considered as linked to hybrid vigor and drought stress. Similarly, using primer me2+em3 in the parent CD550190 there were two bands with size approximately 130 and 390 bp which found in hybrid (Hybrid Shadwell 2  $\times$  CD550190) which considered as linked marker with water stress tolerance.



**Fig. 1:** Banding pattern for SRAP (me1+em2 and me2+em3) and RAPD (OPA6 and OPA12) M marker, 1-CPI456765, 2-CP1987656,3- Dorado, 4-Hybrid Shadwell 1, 5-Hybrid Shadwell 2, 6-PI534175, 7-MT789, 8-CD550190, 9-(CPI456765 × CD550190), 10- (Dorado × PI534175) and 11- (Hybrid Shadwell2 × CD550190).

**Table 9.** Polymorphism rate of 11 Sorghum genotypes through SRAP and RAPD primers.

No.	Primers	No. of bands		Polymorphism (%)
		Total No of bands	Polymorphic	
1	OPA 4	2	2	0.0
2	OPA 6	9	7	77.7
3	OPA 11	5	3	60.0
4	OPA 12	6	5	83.3
5	OPA 13	4	4	0.0
6	OPA 14	6	6	66.6
	<b>Total</b>	<b>32</b>	<b>27</b>	-
7	me1+em1	7	4	57.1
8	me1+em2	8	3	37.5
9	me1+em3	5	1	20.0
10	me2+em1	10	5	50.0
11	me2+em2	9	4	44.4
12	me2+em3	11	8	80.0
	<b>Total</b>	<b>50</b>	<b>29</b>	

### Phylogenetic tree

The diversity analysis among the eight sorghum entries and the best three F1 hybrids using twelve markers (six for SRAP and six for RAPD) associated with drought indicated that the drought tolerance parents and their hybrids were genetically less diverse than the sensitive and their hybrids. The dendrogram expressing the diversity among 11 entries (Figs. 2 and 3) allowed the identification of three parental and heterotic groups. The

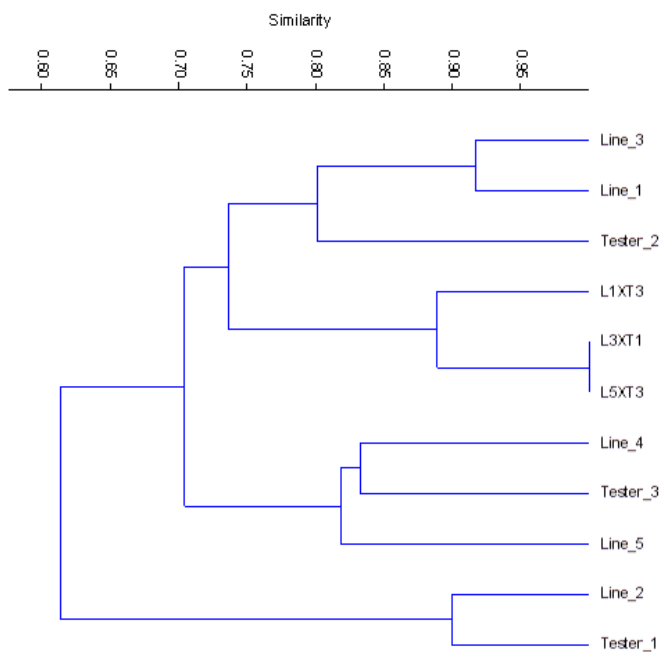
profile of eight sorghum parents and the selected three crosses hybrid showed that RAPD dendrogram (Fig. 2 and Table 10) did not cluster all studied 11 entries clearly. However, SRAP illustrated a clear picture about classification and genetic diversity for the 11 sorghum entries. The dendrogram as shown in Fig. 3 have mainly three clusters. First cluster includes (line 4, tester1, tester 3 and both hybrids (line 1×tester 3 and line 5 × tester 3), moreover this cluster was divided into two sub clusters one includes tester 3 and the hybrid (line 1×tester 3 and

Line 5 × Tester3) with high similarity percentage 92% among tester 3 and both hybrids (Line 1 × Tester 3 and Line 5 × Tester3) as shown in Table 11, which indicates that cluster for hybrids. However, second sub-cluster includes Line 4 and tester 1 with others in the main cluster considered as tolerant genotypes. Second cluster which still closely related to the aforementioned cluster,

the second cluster includes the parents which share in the hybrids. The third cluster comprised the remained genotypes which considered as sensitive genotypes. Similarly, as shown in (Table 11) the lowest similarity 50% was observed between line 2 and each of tester 1 and line 5 which are located in different and was located in highly diverged group.

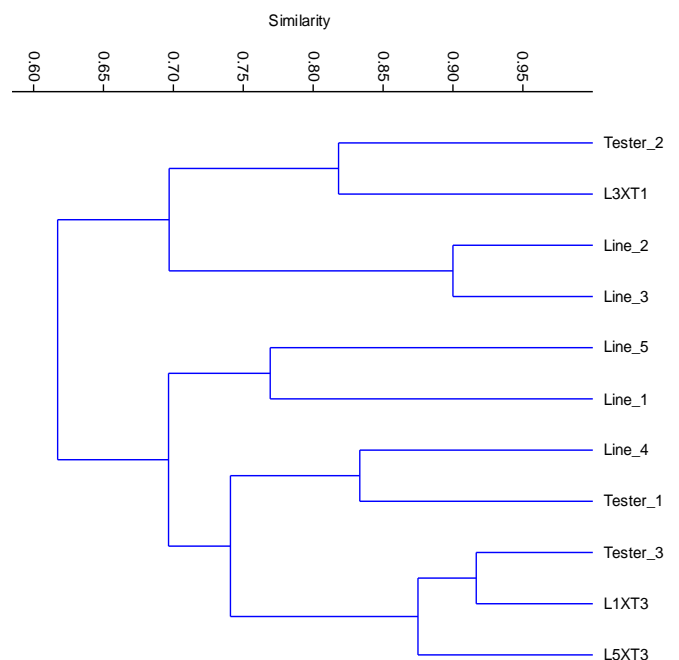
**Table 10.** Similarity matrix of total analysis of RAPD markers for 11 sorghum entries based on Jaccard.

L5×T3	L3×T1	L1×T3	Tester_3	Tester_2	Tester_1	Line_5	Line_4	Line_3	Line_2	0.00
0.73	0.73	0.82	0.83	0.83	0.62	0.67	0.69	0.92	0.67	Line_1
0.70	0.70	0.64	0.67	0.54	0.90	0.50	0.54	0.62	1.00	Line_2
0.67	0.67	0.75	0.77	0.77	0.57	0.62	0.77	1.00		Line_3
0.73	0.73	0.67	0.83	0.69	0.62	0.82	1.00			Line_4
0.70	0.70	0.64	0.82	0.67	0.58	1.00				Line_5
0.64	0.64	0.58	0.75	0.50	1.00					Tester_1
0.73	0.73	0.82	0.69	1.00						Tester_2
0.73	0.73	0.67	1.00							Tester_3
0.89	0.89	1.00								L1×T3
1.00	1.00									L3×T1



**Fig. 2:** UPGMA clustering of 11 sorghum entries based on Jaccard using the RAPD.

Many DNA-based markers have been used for analysis of genetic differentiation and description of sorghum germplasm including RAPDs (Amrapaliet al., 2008; Mehmood et al., 2008), SRAP marker was studied in maize that revealed the genetic diversity and heterotic grouping germplasm (Jiang et al., 2007). Although SRAP markers were studied in maize, some researchers have studied it in other plants.



**Fig. 3:** UPGMA clustering of 11 sorghum entries based on Jaccard using the SRAP.

Seven SRAP markers closely linked to salt tolerance were found in zoysia grasses (Chen et al., 2009). This research could not only provide guidance for sorghum drought breeding, but also help the selection and cultivation of new genotypes of water stress tolerant sorghum. Greatly improving the potential application of marker-assisted selection (MAS) in sorghum improvement has been done (Wu and Haung, 2006;

Madhusudhana et al., 2012). Generally, molecular marker in cereal breeding have been varied and include identification and fingerprinting of parental genotypes, assessing genetic diversity, detection of quantitative trait

loci (QTL) and MAS with introgression of QTL into elite germplasm. Therefore these genotypes were found to be a good parental for hybrid seed production as well as cross pollinated varieties development programs.

**Table 11.** Similarity matrix of total analysis of SRAP markers for 11 sorghum entries based on Jaccard.

L5×T3	L3×T1	L1×T3	Tester_3	Tester_2	Tester_1	Line_5	Line_4	Line_3	Line_2	0.00
0.69	0.75	0.83	0.77	0.75	0.77	0.77	0.62	0.75	0.67	Line_1
0.54	0.73	0.67	0.62	0.73	0.50	0.50	0.58	0.90	1.00	Line_2
0.62	0.67	0.75	0.69	0.67	0.57	0.57	0.67	1.00		Line_3
0.75	0.54	0.75	0.69	0.54	0.83	0.57	1.00			Line_4
0.64	0.69	0.64	0.71	0.57	0.71	1.00				Line_5
0.77	0.57	0.77	0.71	0.57	1.00					Tester_1
0.50	0.82	0.62	0.57	1.00						Tester_2
0.92	0.69	0.92	1.00							Tester_3
0.83	0.62	1.00								L1×T3
0.62	1.00									L3×T1

## Conclusion

Twenty three sorghum entries with different reaction for water stress tolerance were evaluated under the control and water deficit conditions. DNA fingerprinting technique was done for 11 entries (8 parents and the best three crosses) using twelve primers (six for RAPD and six for SRAP), respectively. The obtained results proved that the genotypes; (PI534175), (CD550190), (CP1987656 × CD550190) and (Hybrid Shadwell 2 × CD550190) recorded the most important values for all traits studied under the two studied conditions. The highest polymorphism % were obtained from the primers (OPA 6, OPA 12) of RAPD markers where the values were (77.7 %, 83.3%), while the highest values of polymorphism % resulting from SRAP markers were revealed from the primers (me1+em1, me2+em3) where the values were (57.1%, 80.0%), respectively. SRAP primer (me2+em3), generate specific band with size 470 bp in parental genotypes (CPI456765) and (CD550190) which could be transmuted to the hybrids (CPI456765 × CD550190) and (Hybrid Shadwell2 × CD550190). This band could be considered as linked to hybrid vigor and drought stress tolerance.

## Conflict of interest statement

Authors declare that they have no conflict of interest.

## References

Ahmed, M.A., Shalaby, M. A. F., El-komy, M.B.A., 2015. Alleviation of water stress effects on corn by polyamine compounds under newly cultivated sandy

soil conditions. Int. J. ChemTech Res. 8(12), 497-508.

Ahuja, S.L., Dhayal, L.S., 2007. Combining ability estimates for yield and fibre quality traits in 4 × 13 line × tester crosses of *Gossypium hirsutum*. Euphytica. 153, 87-98.

Amelework, B., Shimelis, H., Tongoona, P., Laing, M., 2015. Physiological mechanisms of drought tolerance in sorghum, genetic basis and breeding methods: A review. Afr. J. Agric. Res. 10(31), 3029-3040.

Amrapali, A. A., Sakhare, S.B., Kulwal, P. L., Dhumale, D. B., Kharkar, A., 2008. RAPD profile studies in sorghum for identification of hybrids and their parents. Int. J. Integr. Biol. 3, 18-24.

Asifa, K., Soomro, Z. A., Mari, S. N., Sial, M. A., Baloch, M., 2015. Assessing yielding ability of wheat genotypes under water deficient state. Int. J. Biol. Biotechnol. 12(2), 247-259.

Bavei, V., B. Shiran., M. Khodambashi., A. Ranjbar., 2010. Protein electrophoretic profiles and physiochemical indicators of salinity tolerance in sorghum (*Sorghum bicolor* L.). Afr. J. Biotech. 10(14), 2683-2697.

Blum, A., 2011. Drought resistance and its improvement. In: Plant Breeding for Water-Limited Environments (Ed.: Blum, A.). Springer Science and Business Media, NY. pp.53-137.

Bousslama, M., Schapaugh, W.T., 1984. Stress tolerance in soybean. Part 1: evaluation of three screening techniques for heat and drought tolerance. Crop Sci. (24), 933-937.

Boyer, J.S., Westgate, M.E., 2004. Grain yields with limited water. J. Exp. Bot. 55(407), 2385-2394.

- Bruckner, P.L., Froberg, R.C., 1987. Stress tolerance and adaptation in spring wheat. *Crop Sci.* 27, 31-36.
- Campos, H., Cooper, M., Habben, J.E., Edmeades, G.O., Schussler, J.R., 2004. Improving drought tolerance in maize: A view from industry. *Field Crops Res.* (90), 19-34.
- Chapman, S., Cooper, M., Podlich, D., Hammer, G., 2003. Evaluating plant breeding strategies by simulating gene action and dryland environment effects. *Agron. J.* (95), 99-113.
- Chen, X., Guo, H., Xue, D., 2009. Identification of SRAP molecular markers linked to salt tolerance in *Zoysia* grasses. *Acta Pratacult. Sinica.* 18(2), 66-75.
- Doyle, J.J., Doyle, J.L., 1990. A rapid DNA isolation procedure for small quantities of fresh leaf tissue. *Focus.* 12, 13-15.
- El-Mouhamady, A. A., El-Ashary, Z.M., Mohamed, F. I., Elewa, T.A., Aboud, K. A., 2016. Study the effect of water stress conditions on some genotypes of bread wheat (*Triticum aestivum* L.) based on morphological, physiological traits and DNA fingerprinting. *Res. J. PharmaBiol. ChemSci.* 7(4), 2065-2077.
- Esmail, R.M., Abdel Sattar, A.A., Abdel-samea, N.S., El-Mouhamady, A. A., Abdelgany, E. M., Fathallaha, F.B., 2016. Assessment of genetic parameters and drought tolerance indices in maize diallel crosses. *Res. J. Pharmaceut. Biol. Chem. Sci.* 7(6), 2409-2428.
- Esmail, R.M., Eldessouky, S. E. I., Mahfouze, S. A., EL-Demardash, I.S., 2016. Evaluation of new bread wheat lines (*Triticum aestivum* L.) under normal and water stress conditions. *Int. J. ChemTech Res.* 9(5), 89-99.
- Fernandez, G.C.J., 1992. Effective selection criteria for assessing plant stress tolerance. In: *Proceedings of the International Symposium on Adaptation of Vegetables and Other Food Crops in Temperature and Water Stress* (Ed.: Kuo, C.G.). AVRDC Publication, Tainan, 257-270.
- Fischer, R.A., Maurer, R., 1978. Drought resistance in spring wheat cultivars. I. Grain yield response. *Aust. J. Agric. Res.* 29, 897-907.
- Gavuzzi, P., Rizza, F., Palumbo, M., Campaline, R.G., Ricciardi, G.L., Borghi, B., 1997. Evaluation of field and laboratory predictors of drought and heat tolerance in winter cereals. *Can. J. Plant Sci.* 77, 523-531.
- Ghorade, R.B., Kalpande, V.V., Bhongle, S.A., Band, P.A., 2014. Combining ability analysis for drought tolerance and grain yield in Rabi sorghum. *Int. J. Agric. Sci.* 10(1), 344-347.
- Golestani, S. A., Assad, M.T., 1998. Evaluation of four screening techniques for drought resistance and their relationship to yield reduction ratio in wheat. *Euphytica.* 103, 293-299.
- Hammer, Q., Harper, D.A.T., Ryan, P.D., 2001. Paleontological statistics software package for education and data analysis. *Pala Electr.* 4, 1-9.
- Hausmann, B.I.G., Hess, D.E., Seetharama, N., Welz, H.G., Geiger, H.H., 2002. Construction of a combined sorghum linkage map from two recombinant inbred populations using AFLP, SSR, RFLP, and RAPD markers, and comparison with other sorghum maps. *Theor. Appl. Genet.* 105, 629-637.
- Hossain, A.B., Sears, A.G., Cox, T.S., Paulsen, G.M., 1990. Desiccation tolerance and its relationship to assimilate partitioning in winter wheat. *Crop Sci.* 30, 622-627.
- IRRI, 2005. IRRISTAT for Windows, V6. Manila, Philippines. International Rice Research Institute.
- Jaccard, P., 1908. *Nouvelles Recherches Sur La Distribution Lorale.* Bull. Soc. Vaud. Sci. Nat. 44, 223-270.
- Jiang, S., Ma, H., Liu, J., 2007. Genetic diversity in maize inbred lines revealed by SRAP marker. *Mol. Plant Breed.* 15(3), 412-416.
- Kearsey, M., Pooni, H., 1996. *The Genetical Analysis of Quantitative Traits.* Chapman and Hall, London, U.K.
- Klein, R.R., Mullet, J.E., Jordan, D.R., Miller, F.R., Rooney, W.L., Menz, M.A., Franks, C.D., Klein, P.E., 2008. The effect of tropical sorghum conversion and inbred development on genome diversity as revealed by high-resolution genotyping. *Plant Gen.* 1, 12-26.
- Kumar, R., Kaul, J., Dubey, R.B., Singode, A., Manivannan, A., Debnath, M. K., 2015. Assessment of drought tolerance in maize (*Zea mays* L.) based on different indices. *Sabrao J. Breed Genet.* 47(3), 291-298.
- Kumar, A.A., Reddy, B.V.S., Sharma, H.C., Hash, C.T., Srinivasa, Rao, P., Ramaiah, B., Sanjana, Reddy, P., 2011. Recent advances in sorghum genetic enhancement research at ICRISAT. *Am. J. Plant Sci.* (2), 589- 600.
- Li, G., Quiros, C.F., 2001. Sequence-related amplified polymorphism (SRAP) a new marker system based on a simple PCR reaction, its application to mapping and gene tagging in *Brassica*. *Theor. Appl. Genet.* 103, 455-461.

- Lin, C.S., Binns, M.R., Lefkovitch, L.P., 1986. Stability analysis: Where do we stand. *Crop Sci.* 26, 894-900.
- Mace, E.S., Rami, J.F., Bouchet, S., Klein, P.E., Klein, R.R., Kilian, A., Wenzl, P., Xia L., Halloran, K., Jordan, K., 2009. A consensus genetic map of sorghum that integrates multiple component maps and high-throughput Diversity Array Technology (DArT) markers. *BMC Plant Biol.* 9(13), 1-14.
- Madhusudhana, R., Balakrishna, D., Rajendrakumar, P., Seetharama, N., Patil, J.V., 2012. Molecular characterization and assessment of genetic diversity of sorghum inbred lines. *Afr. J. Biotechnol.* 11(90), 15626-15635.
- Mansour, M., E.E. El-Shawy., Sh. I. Abaas., 2016. Genetic improvement of water stress tolerance in some barley genotypes. *Egypt. J. Plant Breed.* 20(1), 119-134.
- Mehmood, S., Bashir, A., Amad, A., Akram, Z., 2008. Molecular characterization of regional *Sorghum bicolor* varieties from Pakistan. *Pak. J. Bot.* 40, 2015-2021.
- Moose, S.P., Mumm, R.H., 2008. Molecular plant breeding as the foundation for 21<sup>st</sup> century crop improvement. *Plant Physiol.* 147, 969-977.
- Mostafa, E. A. H., El-Atroush, H., El-Ashry, Z. M., Mohamed, F. I., El-Khodary, S. E., Osman, S. A., 2016. Genetic variation and agro-morphological criteria of ten Egyptian barley under salt stress. *Int. J. ChemTech Res.* 9(7), 119-130.
- Prasad, P.V.V., Pisipati, S.R., Mutava, R.N., Tuinstra, M.R., 2008. Sensitivity of grain sorghum to high temperature stress during reproductive development. *Crop Sci.* (48), 1911-1917.
- Quinby, J.R., 1962. Manifestation of hybrid vigor in sorghum. *Crop Sci.* 3, 288-291.
- Shukla, S.K., Pandey, M.P., 2008. Combining ability and heterosis over environments for yield and yield components in two-line hybrids involving thermosensitive genic male sterile lines in rice (*Oryza sativa* L.). *Plant Breed.* 127, 28-32.
- Tuinstra, M.R., Grote, E.M., Goldsbrough, P.B., Ejeta, G., 1997. Genetic analysis of post-flowering drought tolerance and components of grain development in *Sorghum bicolor* (L.) Moench. *Mol. Breed.* 3, 439-448.
- Virmani, S.S., Viraktamath, B.C., Cassal, C.L., Toledo, R.S., Lopez, M.T., Manalo, J.O., 1997. *Hybrid Rice Breeding Manual*. International Rice Research Institute, Manila.
- Wu, Y.Q., Haung, Y., 2006. An SSR genetic map of *Sorghum bicolor* (L.) Moench and its comparison to a published genetic map. *Genome.* 50, 84-89.
- Wyanne, J.C., Emery, D.A., Rice, P.W., 1970. Combining ability estimates in *Arachis hypogea* L. II- Field Performance of F1 hybrids. *Crop Sci.* 10, 713-715.
- Xiao, X., Li, J., Yuan, L., Mc Couch, S.R., Tanksley, S.D., 1996. Genetic diversity and its relationship to hybrid performance and heterosis in rice as revealed by PCR based markers. *Theor. Appl. Genet.* 92, 637-643.
- Yano, H., Fukui, A., 2015. Effect of sorghum flour on glutathione-rice bread. *Rep. Nat'l Food Res. Inst.* 79, 9-17.

**How to cite this article:**

Khatib, I. A., El-Mouhamady, A. A., Abdel-Rahman, H.M., Farid, M.A., El-Demardash, I. S., 2017. Agro-morphological and molecular characterization of sorghum (*Sorghum vulgare* L.) for water stress tolerance. *Int. J. Curr. Res. Biosci. Plant Biol.* 4(1), 37-55. doi: <http://dx.doi.org/10.20546/ijcrbp.2017.401.006>