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Heterosis and Inheritance of Some Physiological Criteria Imparting Drought Tolerance of Grain Sorghum in The Irrigated and Water-limited Environments

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THIS EXPERIMENT aimed to estimate heterosis, combining ability effect and some genetic components of relative water content (RWC), excised leaf water loss (ELWL), chlorophyll content (CC), stay green (Stg) and flag leaf area (FLA) under well-watered and drought stress conditions in grain sorghum. The plant materials consisted of 43 sorghum entries including 30 F_1 hybrids, five restorer lines, six B-lines and two check cultivars for comparison. The lines were crossed to testers in line × tester mating design in season 2013. The entries were evaluated in 2014 and 2015 seasons under well-watered and drought stress conditions at two locations represent clay and new reclaimed soils with three replications (eight environments). Surface and drip irrigation systems were applied in the clay and reclaimed soil, respectively in order to carry out the well-watered and drought stress conditions. The results of the combined analysis of combing ability revealed that, the lines, testers and line × testers were highly significant for most studied traits suggesting that the plant materials possessed considerable variability that both general (GCA) and specific (SCA) combining ability effects were involved in the genetic expression of these traits. However, the parental lines ICSA11, ICSA536 and ICSR102 were the best parents that showed GCA effects for one or two traits and involved in one or two cross combinations that showed highly desirable SCA effects or showed remarkable heterosis. The cross combination ICSA536 × ICSR628 had high positive and significant SCA effects for RWC and CC, while the cross combination ICSA11 × ICSR102 had high positive and significant SCA effects for stay green and flag leaf area. For heterosis, the cross combination ICSA598 × ICSR89034 exhibited desirable magnitude of mid-parent-heterosis for the physiological criteria. The degree of dominance of the RWC, CC and FLA were higher than unity, that means non-additive effect was found to be predominant and desirable in the inheritance of these traits and indicating that heterosis breeding would be more appropriate method for the improvement of this traits. While additive effect was the favorable direction in ELWL and Stg traits and can be easily select these traits in early generation. Chlorophyll content gave maximum narrow-sense heritability followed by stay green, indicating the role of additive gene action in the inheritance of these traits. Broad-sense heritability estimates appeared to be high for all physiological traits under study, indicating the role of non-additive gene action effects on the phenotypic expression of these traits.

Keywords: Heterosis, Sorghum, Combining ability, Drought tolerance, Physiological traits.

Sorghum bicolor is an important C4 crop of the semi-arid tropics as a main food source in many developing countries and consider the fifth most important cereal grown worldwide. In these regions, sorghum is influenced by water stress at any stages especially at terminal growth stages like flowering and in the grain filling which renders the most adverse effect on yield in sorghum. Sorghum displays large genetic diversity that offers an opportunity to investigate the genetic basis of adaptation to drought conditions (Doggett, 1988; Mullet *et al*., 2002 and Prasad *et al*., 2008).

Plants react and adapt to survive under several constraints conditions such as drought stress by the induction of various morphological, biochemical and physiological responses. Drought tolerance is defined as the ability to grow, flower and display economic yield under suboptimal water supply (Farooq *et al*., 2009). Several morphological and physiological traits related the water status of plants have been suggested to indicate the drought tolerance performance of plants in many published researches. Among these traits, excised-leaf water loss (Wang & Clarke, 1993 and Ahmad *et al*., 2009); relative water content (Rad *et al*., 2013 and Ahmad *et al*., 2009); stay green (Subudhi *et al*., 2000 and Borrell *et al*., 2014 a,b); chlorophyll content (Brito *et al*., 2011 and Asadi *et al*., 2015); flag leaf area (Karamanos & Papatheohari, 1999 and Asadi *et al*., 2015).

Relative water content (RWC) is a key indicator of the degree of plant cell and tissue hydration, which is crucial for optimum physiological functioning and growth processes (Ali *et al*., 2009). Plants that showed maintenance of a relatively high RWC during mild drought is an indicative of drought tolerance (Altinkut *et al*., 2001 and Colom & Vazzana, 2003). In the same context, evaluation of excised leaf water loss (ELWL) has shown a good promise for illustrating water stress tolerance (Clarke, 1987 and Bhutta, 2007). Stay-green is an integrated drought-adaptation trait in sorghum. Since, delayed leaf senescence during grain filling will improve the balance between the supply and demand of water, as well as the efficiency with which the crop converts water to biomass and grain yield (Borrell *et al*., 2009 and Jordan *et al*., 2012). Mohan *et al*. (2000) stated that the chlorophyll content is an indication of stress tolerance capacity of plants and its high value means that the stress did not have much effect on chlorophyll content of tolerant plants. Plants with stay-green characteristics and more photosynthetic tissue may produce more assimilates along with extracting more water from the soil and that may increase yield potential (Izanloo *et al*., 2008 and Hirasawa *et al*., 2010).

Understanding the physiological and genetic basis of the morphological and physiological criteria will assist breeding programmes seeking to improve drought tolerance in crop plants. Hybrids play an important role in enhancing yield production by heterosis breeding in sorghum and other crops. Developing sorghum hybrids for water-limited environments such in arid and semi-arid regions as in Egypt is extremely essential to maintain the yields of sorghum for the present and the near future to keep the sorghum production sustainable for the growing population with the available depleting water resources. Combining ability analysis offers a powerful tool for estimating the value of a parent to produce superior hybrid. Information of combining ability is useful to assess nicking ability among genotypes and at the same time elucidate the nature and magnitude of gene actions involved. Line × tester (Kempthorne, 1957) matting designs provides reliable information about the general and specific combining abilities (GCA and SCA) of parents and their cross combinations and is helpful in estimating various types of gene actions. It is also vital to estimate the genetic potential of parents in hybrid combination through systematic studies in relation to both general and specific combining abilities, which could be attributed to additive and non-additive components of gene action, respectively (Veeresha *et al*., 2015). Present study was initiated to 1) Estimate the general combining ability effect of parents and specific combining ability effect of hybrids for drought stress tolerance, 2) Determine the mid- and better parent heterosis existing among the physiological traits, and 3) Study the inheritance of the physiological traits related to drought tolerance in grain sorghum. The information generated by this study would be helpful for sorghum breeder to tailor high drought tolerant genotypes and to present some knowledge about the nature of inheritance of the physiological traits.

Materials and Methods

Plant materials and F_1 hybrids development

Plant material of the experiment comprised of 43 genotypes that included 30 F_1 grain sorghum crosses formed by crossing six inbred lines (cytoplasmic male sterility lines) to five testers in a line × tester mating design in the summer season of 2013 to generate the plant materials and two standard checks (Hybrid 305 and Dorado) for comparison. The female lines ICSA.11 (F1), ICSA.329 (F2), ICSA536 (F3), ICSA598 (F4), ICSA625 (F5) and ATXA629 (F6) and male lines ICSR 102 (T1), ICSR 59 (T2), ICSR628 (T3), ICSR 89013 (T4) and ICSR 89034 (T5) were obtained from India (International Crop Research Institute for Semi-Arid Tropics, ICRISAT) except one female line (ATXA629) was obtained from Texas A&M University, College Station, TX, U.S.A.

Experimental sites

The 30 F_1 hybrids, their parents and the check cultivars were grown in two locations in Assiut Governorate, Egypt. The first location was at Faculty of Agricultural Research Farm, Assiut University (AS location), while the second location was at the newly reclaimed area at the Experimental Station of the

Faculty of Agriculture, Al-Wadi Al-Assyouti Farm (WAD location), Assiut University (25 km South East of Assiut). The two locations (AS and WAD locations) represent two different soil types and conditions, the physical and chemical properties of representative soil samples in the two experimental sites were determined according to the methods described by Jackson (1967) are shown in Table 1.

TABLE 1. Some physical and chemical properties of representative soil samples in the experimental sites before sowing (0-30 cm depth).

Soil property	Al-Wadi Al-Assyouti Farm	Fac. Agric. Res. Farm
Particle - size distribution		
Sand (%)	84.4	27.4
Silt (%)	8.7	24.3
Clay (%)	6.9	48.3
Texture grade	Sandy	Clay
EC (1:1 extract) dSm^{-1}	1.66	0.74
pH (1:1 suspension)	8.34	8.2
Total $CaCO_3$ (%)	20.26	3.4
Organic matter (%)	0.097	1.75
$NaHCO_3$-extractable P (mg kg^{-1})	5.54	4.36
NH_4OAC-extractable K (mg kg^{-1})	52.45	49.24
Total nitrogen (%)	0.018	0.72
KCl-extractable N (mg kg^{-1})	28.26	41.23

* Each value represents the mean of three replications.

Experimental design and field management

At each location, two separate field treatments (well-watered and drought stress treatments) were performed. The field design was a strip plot design in a randomized complete block arrangement with three replications. Water regimes were allocated to the main plots and entries to subplots. Each entry (genotype) was placed in a one row plot of 3 m long and 0.6 m apart with 0.2 m between plants. Trial was hand planted with 3-4 seeds per hill, which was later thinned to two plants per hill. Planting was done in the two summer successive seasons at the 17^{th} and 18^{th} of June, 2014 and in 16^{th} and 17^{th} of June, 2015, in the first and second locations, respectively. Standard cultural practices for optimum sorghum production were carried out at each location. In the first location, to obtain well-watered conditions (WW), entries were watered using surface irrigation each 14 days and as recommended for optimum sorghum production, while to obtain drought stress conditions (DS), the third and the fifth irrigations were skipped. In the second location, in both treatments drip irrigation was used and plants were watered each 3 days. In WW treatments, plants were irrigated for 2 h while in

DS treatment, plants were irrigated for 1 (drought stress conditions started after 30 days from sowing and continued until fully ripening).

Data collected

The entries of current study were evaluated for five physiological traits related to drought tolerance in sorghum.

Relative water content (RWC)

Relative water content was determined according to Barrs (1968). At 50% flowering time, two fully developed and expanded flag leaves were collected from each genotype and each replication at early morning and before sunrise, then put in plastic bags in ice box and transferred to the laboratory to measure fresh weight (FW). Leaf blades were then sliced into 2 cm sections and floated on distilled water for 4 hr. The turgid leaf discs were then rapidly blotted to remove surface water and weighed to obtain turgid weight (TW). The leaf discs were dried in the oven at 72 °C for 24 h and then dry weight (DW) obtained. The RWC was calculated using the following equation the (Barrs, 1968):

RWC % = [(Fresh weight – Dry weight)/ (Turgid weight- Dry weight)] × 100.

Excised-leaf water loss (ELWL)

At 50% flowering time, the samples for ELWL were also weighed immediately as fresh weight (FW), then the leaves were dried at room temperature (37±2 °C) for 6 h, and weighted to obtain weight after 6 hr, after that the leaves were dried in the oven at 72 °C for 24 h and then dry weight (DW) as proposed by Clarke (1987). ELWL was then calculated from the following formula:

ELWL% $=[(\text{Fresh weight} - \text{weight after 6 h})/(\text{Fresh weight} - \text{Dry weight})] \times 100$

Chlorophyll content (CC)

At 50% flowering time, chlorophyll content (CC) of five flag leaves from each genotype and replication was measured using a self-calibrating SPAD chlorophyll meter (Model 502, Spectrum Technologies, Plainfield, IL), then the average of the five readings was calculated and recorded in SPAD unit. This measurement directly estimated the chlorophyll content of the flag leaf (Xu *et al*., 2000).

Stay green (Stg)

The visible green leaves of five randomly tagged plants from each genotype and each replication were counted at harvest time, then the average number of the green leaves was recorded (Wanous *et al*., 1991).

Flag leaf area (FLA)

From two fully developed and expanded flag leaves of each genotype, the average of maximum length and width of the two leaves was measured in centimeter (at 50% flowering time). FLA in cm^2 was calculated using the following function according to Montgomery (1911):

FLA; cm^2 = Flag leaf length × Flag leaf width × 0.75

Statistical analysis and procedures

Combined analyses of variance were performed as outlined by Gomez & Gomez (1984) after carrying out the homogeneity of variances using Bartlett test. Combined line × tester analysis of combining ability was performed according to Kempthorne (1957), Beil & Atkins (1967) and Singh & Chaudhary (1985) to estimate general (GCA) and specific combining ability (SCA) effects, their interaction with environments, additive and dominance variances and heritability. General and specific combining ability was estimated as follows:

1. Estimation (G.C.A) general combining ability effect for the parent L (lines)

$$\hat{g}i = \overline{Y}\, i.. - \overline{y}\, ..$$

2. Estimation (G.C.A.) general combining ability effect for the parent T (testers)

$$\hat{g}j = \overline{Y}\, .j. - \overline{y}\, ..$$

3. Estimation (S.C.A.) specific combining ability effect for the hybrids

$$\hat{S}ij = \overline{y}\, i.. - \overline{y}\, i.. - \overline{y}\, .j. - \overline{y}\, ...$$

The phenotype variance was estimated, which involved both genotypic and environment variance by using expected variance mean E.M.S according to the following formulas:

Environment variance $\sigma^2 e = MSe$

$$\sigma_L^2 = \left[Ms\,(L) - Mse \right] / rtysw = \tfrac{1}{2}\sigma_A^2 \;\therefore \sigma_A^2 = 2\sigma_L^2$$

$$\sigma_T^2 = \left[Ms\,(T) - Mse \right] / rlysw = \tfrac{1}{2}\sigma_A^2 \;\therefore \sigma_A^2 = 2\sigma_T^2$$

where, r number of replicates, t number of testers, l number of lines, y number of years, s number of sites, and w number of treatments.

Additive variance

$$\sigma_A^2 = \left[2\sigma_L^2 + 2\sigma_T^2 \right] / 2 \quad = \sigma_L^2 + \sigma_T^2$$

Dominance variance

$$\sigma_{LT}^2 = \left[Ms\,(L \times T) - Mse \right] / rysw = \sigma_D^2$$

Phenotypic variance

$$\sigma_P^2 = \sigma_L^2 + \sigma_T^2 + \sigma_{(L \times T)}^2 + \sigma_e^2 \quad = \sigma_A^2 + \sigma_D^2 + \sigma_E^2 = \sigma_G^2 + \sigma_E^2$$

Broad (H^2 b.s) and narrow (H^2 n.s.) sense heritability estimates were calculated depending on variance of general and specific abilities as follows:

$$H^2 b.s. = \sigma^2_G / \sigma^2_P \qquad H^2 n.s. = \sigma^2_A / \sigma^2_P$$

where: σ^2_G =genetic variance only $\sigma^2_A + \sigma^2_D$; σ^2_A =additive variance and σ^2_P =phenotypic variance

Average degree of dominance (ā) was calculated according to the following equation:

$$\bar{a} = \sqrt{2\sigma^2_D / \sigma^2_A}$$

Mid (MP) and better (BP) parent heterosis

Mid-parent (MP) and better-parent (BP) heterosis percentages were computed using the following formulas:

$$MP_{ij} = \frac{F_{1ij} - Mp_{(F1ij)}}{Mp_{(F1ij)}} \qquad BP_{ij} = \frac{F_{1ij} - BP_{(F1ij)}}{BP_{(F1ij)}}$$

where MP_{ij} is the heterosis of the *ij*th cross; BP_{ij} is the better parent of the *ij*th cross; F_{1ij} is the mean of the *ij*th F_1 cross; MP (F_{1ij}) is the mid-parent [(Parent1 + Parent2) / 2] for the $_{ij}$th cross; and BP (F_{1ij}) is the better parent values for the $_{ij}$th cross. Significance was tested by the appropriate LSD test.

Results and Discussion

Analysis of variance

The combined analysis of variance over all environments (Table 2) showed significant differences among environments for physiological traits related to drought tolerance reflecting the sensitivity of genotypes to fluctuation environmental conditions. In addition, high significant differences were observed among genotypes for all studied traits indicating the existence of the genetic variability. Moreover, the analysis of variance of the combining ability (Table 3) revealed significant variation for all the traits under study. Variance due to parents was highly significant for all the traits, indicating good amount of genetic variability present among the parents. Likewise, variance due to crosses was also highly significant for all the studied traits. Moreover, parents *vs* crosses was highly significant for all studied traits except RWC, indicating good amount of heterosis. In addition, the majority of the interactions obtained differed significantly for all studied traits reflecting the differential response of the genotypes to environments. The lines, testers and line × testers were highly significant for all the traits except stay green in testers suggesting that the plant materials possessed considerable variability that both general and specific combining ability were involved in the genetic expression of these traits. The interaction of parents, crosses, parents vs crosses, lines, testers and line × testers with environments were significant for all studied traits, reflecting that expression of these traits are controlled mostly by the non-additive effects of genes that are not stable overall environments. The significance variation of the physiological traits related to drought tolerance among genotypes in sorghum and the other cereal crops have been noted in many studies such Mourad & Anton (2007), Izanloo *et al*. (2008), Hasheminasab *et al*. (2012), Rad *et al*. (2013), Golparvar (2013), Abdo *et al*. (2014), Borrell *et al*. (2014a and b) and Saddam *et al*. (2014).

TABLE 2. Combined analysis of variance for morphological and physiological traits under study across all environments.

S.V.	d. f.	Mean Squares				
		RWC %	ELWL %	CC	Stg	FLA; cm^2
Environments (E)	7	8175.1**	11406**	2528.7**	56.4**	7206.4**
Reps/E	16	75.5**	106.55	14.1	8.2**	68213.8**
Entries	42	137.0**	576.4**	109.4**	5.5**	12664.0**
Entries*E	294	59.8**	206.5**	25.7**	1.6**	2976.0
Error	672	34.5	65.8	12.9	1.1	2943.8

* and **: significant at P values of 0.05 and 0.01, respectively.

TABLE 3. Analysis of variance of combining ability for some of morphological and physiological traits in a line × tester of sorghum pooled across locations and years.

S.V.	d. f.	Mean Squares				
		RWC %	ELWL %	CC	Stg	FLA; cm^2
Environments (E)	7	7978.4**	11841.0**	2559.2**	52.4**	66158.3**
Reps/E	16	80.00	119.8*	12.19	7.41	7352.50
Genotypes (G)	40	132.39**	511.8**	74.72**	5.18**	13001.4**
Parents (P)	10	130.3**	953.4**	45.30**	6.49**	16073.3**
P vs C	1	4.00	48.5	377.1**	5.36*	24501.0**
Crosses (C)	29	137.5**	375.5**	74.4**	4.73**	11545.6**
Lines (L)	5	169.3**	649.5**	117.2**	16.47**	9737.6**
Testers (T)	4	209.8**	320.2**	231.22**	1.58	9873.0**
L*T	20	115.14**	318.1**	32.38**	2.42**	12332.1**
G*E	280	58.43**	196.8**	23.58**	1.63**	3078.53
P*E	70	31.08	130.4**	29.75**	1.67**	2344.31
P vs C*E	1	146.00*	2652.0**	211.13**	61.51**	34087.0**
C*E	203	69.15**	213.5**	21.23**	1.37**	3269.95
L*E	35	87.07**	223.2**	24.43**	2.23**	5000.2**
T*E	28	76.57**	338.0**	39.37**	2.34**	4561.4*
L*T*E	140	63.18**	186.1**	16.80*	0.97	2579.1
Error	640	33.41	65.9	12.80	1.01	2883.21

* and **: significant at P values of 0.05 and 0.01, respectively.

Performance, heterosis and combining ability of the physiological traits

Relative water content (RWC)

Relative water content (RWC) is a key indicator of the degree of cell and tissue hydration, which is crucial for optimum physiological functioning and growth processes (Ali *et al*., 2009). Also, RWC is closely associated to cell size and it may closely reflect the balance between water supply to the leaf and transpiration rate (Fischer & Wood, 1979). Based on genotypes average, RWC was higher at AS location under both treatments than at WAD site, that may due to the nature of the soil type and weather conditions of both locations (Tables 4 and 5; Fig.1 A). In addition, RWC decreased under DS conditions by percentages 6.1 and 5.8% at AS and WAD, respectively. However, at AS location, RWC ranged from (71 to 89.1%) and from (71.5 to 86.2%) under WW and DS conditions, respectively. While at WAD location, it ranged from (60.1 to 76.2%) and from (61.4 to 70.9%) under WW and DS conditions, respectively. Similar results were obtained by Abdo *et al.* (2014) who found that decreasing water applied treatments up to dry one significantly decreased RWC in grain sorghum genotypes. Asadi *et al*. (2015) found that water deficit conditions reduced relative water content. The data on estimates of mid-parent (MP) and better-parent (BP) heterosis are shown in Table 6, hence mid-parent heterosis for RWC ranged between -9.0 and 6.2% and for better-parent heterosis, RWC ranged from -11.5 to 4.4%. In this range, five crosses showed positive and highly significant mid-parent heterosis for RWC, while only one cross exhibited better-parent heterosis for RWC. The cross combination ICSA598 × ICSR89034 had the highest positive heterosis over both mid- and better-parent for RWC. Estimates of the combining ability effects of individual parental lines and crosses for physiological traits are given in Table 7. Among the parental lines, three lines showed positive and highly significant general combining ability (GCA). The female line ICSA625 had the highest positive GCA effects (1.89**) among females and involved in the two best crosses in RWC that showed positive heterotic effect, indicating that this line harboring the genes that underlay the water maintain in plant cells, whereas in testers, ICSR102 gave maximum GCA effect (1.31**). The crosses (ICSA11 × ICSR89013) and (ICSA536 × ICSR628) exhibited positive and highly significant SCA effects and may be considered to be good specific combiners for RWC overall environments. Rad *et al.* (2013) found that both GCA and SCA were highly significant for relative water content.

TABLE 4. Mean performance of parents and their crosses for physiological traits at Assiut (AS) location under well-watered (WW) and drought-stressed (DS) conditions across two seasons.

Genotype	RWC %		ELWL %		CC		Stg		FLA; cm^2	
	WW	DS	WW	DS	WW	DS	WW	DS	WW	DS
Female Lines										
ICSA11	86.5	73.6	54.5	54.0	48.3	46.5	7.2	5.5	172.0	158.5
ICSA329	86.4	75.7	77.2	77.6	52.6	46.5	5.7	5.4	236.5	225.2
ICSA536	82.0	80.7	63.5	79.9	49.5	47.8	3.5	4.9	211.5	160.9
ICSA598	79.3	77.8	74.3	73.1	48.6	45.1	5.1	4.8	152.5	135.9
ICSA625	85.3	79.2	69.9	64.7	52.9	45.2	5.5	4.9	160.9	177.5
ATXA629	83.6	82.6	69.1	58.3	52.4	43.0	5.9	6.1	206.9	169.4
Females Mean	83.9	78.3	68.1	68.0	50.7	45.7	5.5	5.3	190.1	171.2
Male Lines										
ICSR102	89.1	79.9	55.2	75.5	48.7	46.0	5.2	6.3	211.4	192.5
ICSR59	78.3	77.5	59.6	71.2	50.7	46.1	4.5	5.7	218.2	181.9
ICSR628	87.4	80.1	51.3	65.7	51.1	52.6	5.7	6.7	249.1	221.9
ICSR89013	81.4	71.5	57.9	70.2	49.3	46.5	6.9	6.8	200.7	184.6
ICSR89034	80.8	73.4	60.4	67.3	51.8	47.7	4.9	5.3	208.1	183.8
Males Mean	83.4	76.48	56.9	70.0	50.32	47.78	5.44	6.16	217.5	192.94
Crosses										
ICSA11 × ICSR102	88.4	86.2	59.8	74.0	53.3	50.5	6.1	5.9	216.8	180.3
ICSA11 × ICSR59	84.6	75.1	73.5	76.2	51.3	49.7	7.0	5.2	206.7	197.9
ICSA11 × ICSR628	88.4	80.2	54.1	65.7	47.5	50.7	6.5	5.2	188.6	210.0
ICSA11 × ICSR89013	77.6	79.9	67.6	74.0	53.6	48.2	6.1	6.0	286.7	236.5
ICSA11 × ICSR89034	80.8	75.2	48.1	76.7	53.7	51.2	6.4	5.5	229.2	168.7
ICSA329 × ICSR102	85.3	76.7	66.5	69.5	53.4	50.0	7.0	5.5	220.9	196.5
ICSA329 × ICSR59	85.7	77.8	75.2	85.6	52.4	47.5	6.3	5.4	186.6	203.4
ICSA329 × ICSR628	85.0	74.3	62.8	79.8	52.5	48.0	6.9	6.5	229.6	211.6
ICSA329 × ICSR89013	77.6	76.8	70.9	77.5	49.8	44.9	7.4	6.8	200.8	173.3
ICSA329 × ICSR89034	85.2	74.4	71.1	78.7	53.1	49.8	7.1	6.1	214.4	215.5
ICSA536 × ICSR102	81.4	77.5	55.5	77.4	54.7	52.5	5.2	4.4	238.8	162.1
ICSA536 × ICSR59	83.4	78.0	63.3	77.5	49.6	49.9	5.7	4.3	222.7	208.9
ICSA536 × ICSR628	82.1	85.3	62.5	75.2	57.1	55.2	6.1	5.4	233.3	249.9
ICSA536 × ICSR89013	88.7	76.2	59.5	71.3	53.9	50.2	4.3	4.9	191.5	186.7
ICSA536 × ICSR89034	82.5	71.9	44.2	77.0	54.9	51.8	4.8	4.7	303.5	184.7
ICSA598 × ICSR102	80.1	77.2	56.9	59.3	51.9	51.2	5.7	5.8	235.3	210.3
ICSA598 × ICSR59	77.2	81.1	65.1	78.3	52.4	47.1	5.4	5.1	188.4	191.0

TABLE 4 Cont.

Genotype	RWC %		ELWL %		CC		Stg		FLA; cm^2	
	WW	DS	WW	DS	WW	DS	WW	DS	WW	DS
ICSA598 × ICSR628	84.5	72.7	67.4	75.3	48.7	47.7	6.4	5.6	160.2	184.9
ICSA598 × ICSR89013	83.7	77.8	74.3	76.6	53.0	44.1	5.5	5.0	195.9	156.8
ICSA598 × ICSR89034	85.9	75.7	61.0	74.8	50.6	49.0	7.0	5.4	185.1	233.0
ICSA625 × ICSR102	86.1	81.7	54.1	67.2	50.7	46.3	8.0	5.5	255.2	228.5
ICSA625 × ICSR59	81.5	73.0	76.9	71.5	52.0	48.5	6.6	5.2	184.6	186.6
ICSA625 × ICSR628	87.2	80.4	56.0	77.2	51.7	48.9	6.1	5.7	180.3	196.4
ICSA625 × ICSR89013	83.1	84.8	76.9	74.7	50.8	45.6	6.6	5.4	216.2	163.8
ICSA625 × ICSR89034	87.8	80.4	51.5	77.7	56.0	49.6	7.2	5.0	232.1	187.6
ATXA629 × ICSR102	83.1	79.5	64.4	68.7	52.2	46.4	7.3	5.8	222.0	187.3
ATXA629 × ICSR59	76.7	82.7	51.1	77.4	50.9	46.2	6.4	5.5	189.2	145.5
ATXA629 × ICSR628	84.6	79.0	59.3	80.6	54.4	45.9	7.0	6.0	258.2	224.0
ATXA629 × ICSR89013	81.2	78.0	63.1	73.0	50.9	47.4	5.5	7.5	247.0	197.3
ATXA629 × ICSR89034	71.0	74.9	72.6	72.1	52.6	50.4	7.8	5.7	184.0	156.0
Crosses Mean	83.0	78.1	62.8	73.4	52.3	48.8	6.4	5.5	216.8	194.5
Checks Cultivar										
H305	84.3	84.4	61.8	55.6	57.9	61	7.7	5.6	199.5	193.8
Dorado	83.7	77.9	61.3	58.3	49.1	50.9	6.3	6.9	237.4	230.7
General Mean	83.2	78.0	62.8	72.3	51.8	48.2	6.1	5.6	213.0	190.9
LSD5%	6.6	7.5	8.2	11.6	4.3	4.1	1.2	1.2	65.4	72.5

Table 5. Mean performance of parents and their crosses for physiological traits at Al-Wadi Al-Assiouti (WAD) location under well-watered (WW) and drought-stressed (DS) conditions across two seasons.

Genotype	RWC %		ELWL %		CC		Stg		FLA; cm^2	
	WW	DS	WW	DS	WW	DS	WW	DS	WW	DS
Female Lines										
ICSA11	70.6	65.5	66.6	70.5	47.8	44.2	6.4	5.0	129.0	131.9
ICSA329	71.7	65.3	82.6	91.9	45.4	40.7	5.6	5.1	172.3	148.9
ICSA536	68.8	69.6	70.4	87.9	45.9	41.2	4.1	5.0	169.9	178.9
ICSA598	67.2	66.2	79.6	86.4	44.4	40.7	5.0	5.0	126.9	111.4
ICSA625	71.5	66.4	68.2	83.0	48.9	42.7	6.2	6.0	161.8	126.0
ATXA629	69.8	69.6	68.4	72.4	45.3	39.7	6.2	5.2	148.2	150.0
Females Mean	69.9	67.1	72.6	82.0	46.3	41.5	5.6	5.2	151.4	141.2
Male Lines										
ICSR102	76.2	66.2	64.5	78.6	42.5	41.3	4.3	4.9	172.0	159.8
ICSR59	66.1	64.9	62.6	76.9	42.4	40.3	5.1	4.8	167.8	162.3

TABLE 5.Cont.

Genotype	RWC %		ELWL %		CC		Stg		FLA; cm^2	
	WW	DS	WW	DS	WW	DS	WW	DS	WW	DS
ICSR628	73.1	67.8	58.6	77.2	45.8	46.3	5.0	5.0	215.8	206.7
ICSR89013	68.0	62.2	70.4	74.9	47.9	42.9	5.8	5.2	161.4	155.0
ICSR89034	69.2	65.1	66.7	77.2	46.5	43.8	5.7	4.8	190.3	162.1
Males Mean	70.52	65.24	64.6	76.9	45.02	42.92	5.18	4.94	181.46	169.18
Crosses										
ICSA11 × ICSR102	72.9	70.8	74.6	77.7	44.0	43.6	5.7	4.8	158.0	160.3
ICSA11 × ICSR59	68.8	61.4	74.4	62.9	47.2	45.3	5.9	4.9	187.6	151.2
ICSA11 × ICSR628	73.8	65.2	69.3	82.5	42.3	46.3	5.1	4.9	189.8	150.6
ICSA11 × ICSR89013	67.9	67.2	60.8	78.2	46.6	44.3	5.2	5.6	217.6	184.5
ICSA11 × ICSR89034	70.1	63.0	59.7	79.1	48.3	44.6	5.6	5.0	149.7	169.8
ICSA329 × ICSR102	70.9	64.7	68.4	79.9	47.3	42.2	5.8	4.8	181.0	129.9
ICSA329 × ICSR59	74.0	64.3	68.9	85.1	48.4	42.1	6.1	4.5	180.9	126.8
ICSA329 × ICSR628	70.2	63.0	72.6	79.4	44.5	42.0	5.6	4.6	196.8	163.7
ICSA329× ICSR89013	67.0	64.4	73.2	76.6	42.3	39.4	6.1	6.0	158.5	136.3
ICSA329 × ICSR89034	72.7	62.7	64.8	79.7	49.5	46.6	5.4	4.7	185.8	146.4
ICSA536 × ICSR102	71.8	64.1	59.3	83.9	45.6	46.1	5.4	4.3	169.4	181.4
ICSA536 × ICSR59	69.7	67.0	63.8	83.7	48.0	43.9	5.4	4.7	185.8	165.5
ICSA536 × ICSR628	71.0	70.9	63.1	88.0	46.4	46.7	6.3	4.9	235.7	192.2
ICSA536 × ICSR89013	72.8	64.7	59.5	76.2	45.5	42.5	4.1	4.5	155.5	138.4
ICSA536 × ICSR89034	71.5	63.0	53.8	85.8	48.6	45.9	4.2	4.2	190.4	221.9
ICSA598 × ICSR102	71.1	67.8	65.2	76.0	47.5	42.5	5.5	5.0	185.7	174.1
ICSA598 × ICSR59	66.2	69.4	63.2	80.7	45.7	40.5	5.8	5.4	172.2	142.3
ICSA598 × ICSR628	70.6	62.1	65.1	85.3	44.2	42.3	6.2	5.1	168.7	138.6
ICSA598 × ICSR89013	70.8	65.7	66.7	82.4	44.8	39.2	4.4	4.7	135.3	128.9
ICSA598 × ICSR89034	71.3	64.1	70.3	84.1	48.3	43.7	6.3	5.0	205.5	144.1
ICSA625 × ICSR102	76.0	67.3	53.7	76.4	48.1	40.5	6.0	4.8	200.4	185.8
ICSA625 × ICSR59	71.0	61.4	67.7	76.3	49.8	40.9	5.3	4.6	157.1	127.7
ICSA625 × ICSR628	74.5	66.8	67.5	83.9	46.4	44.0	5.8	4.8	187.0	150.0
ICSA625 × ICSR89013	69.9	70.8	67.2	85.4	42.1	37.1	5.4	5.2	154.9	143.5
ICSA625 × ICSR89034	72.7	68.0	62.0	88.8	49.2	44.2	6.2	5.2	156.7	171.6
ATXA629 × ICSR102	69.8	65.2	64.8	83.9	47.3	43.5	5.0	4.7	169.8	142.5
ATXA629 × ICSR59	63.8	68.4	62.7	83.6	44.2	41.6	5.3	5.8	149.9	148.0
ATXA629 × ICSR628	70.7	67.1	60.5	88.3	46.3	41.6	6.0	5.0	196.0	173.4
ATXA629 × ICSR89013	70.1	66.8	55.6	84.4	45.0	42.2	4.1	5.5	181.4	173.9
ATXA629 × ICSR89034	60.1	64.4	68.4	86.4	49.5	46.5	6.0	5.2	154.7	152.8
Crosses Mean	70.5	65.7	64.9	81.5	46.4	43.1	5.5	4.9	177.3	157.2
Checks Cultivar										
H305	68.6	77.4	70.0	72.7	49.6	53.7	6	4.8	164	170.8
Dorado	70.4	69.9	67.4	59.0	43.1	46	5.7	5.8	189.5	192
General Mean	70.4	65.9	66.2	80.3	46.2	42.8	5.5	5.0	174.0	156.3
LSD5%	5.7	6.7	6.8	9.5	3.9	3.8	1.1	1.1	52.8	54.3

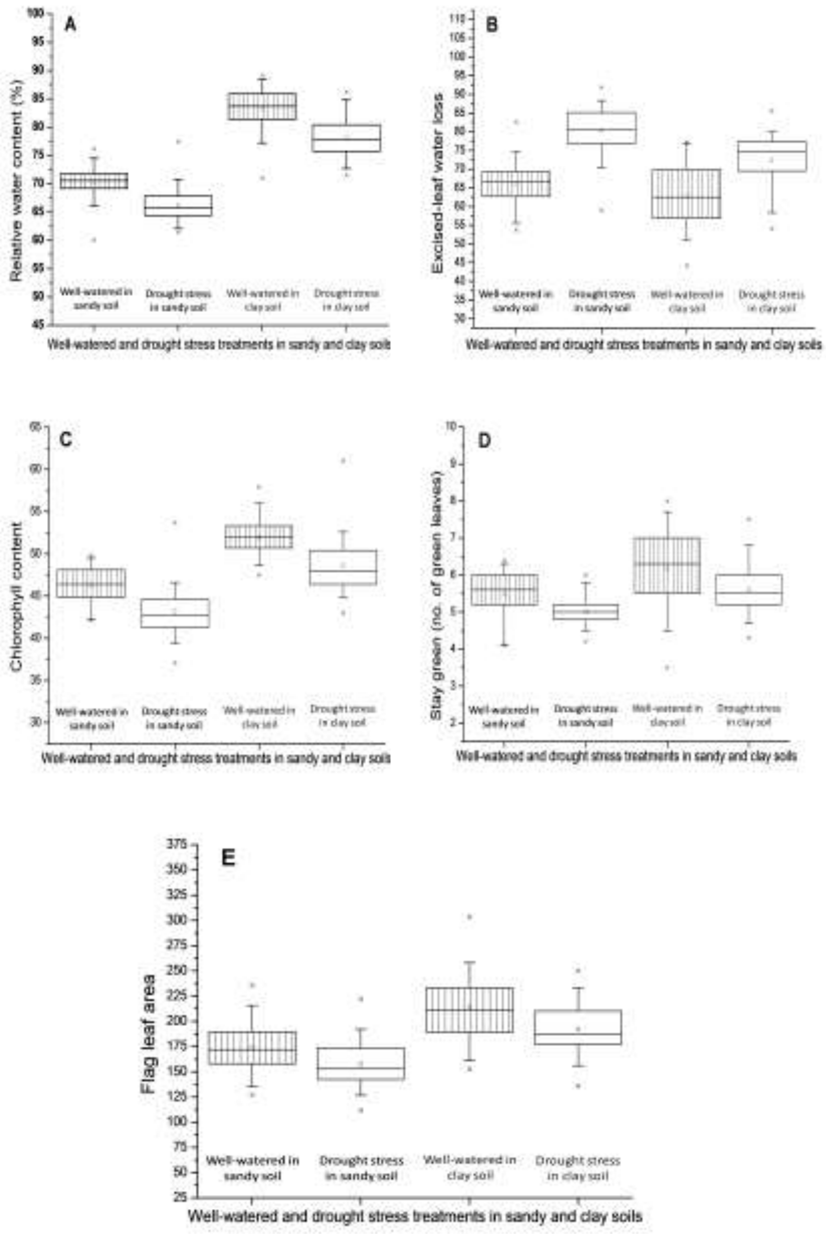

Fig. 1. Average of the five physiological studied traits under well-watered (WW) and drought stress (DS) conditions at AS (clay soil) and WAD (sandy soil) locations. A) Relative water content, B) Excised leaf water loss, C) Chlorophyll content, D) Stay green, and E) Flag leaf area.

TABLE 6 Estimation of percentage mid-parent (MP%) and best-parent (BP%) heterosis for the physiological traits related to drought tolerance across all environments.

Crosses	RWC %		ELWL %		CC		Stg		FLA; cm^2	
	BP	MP	BP	MP	BP	MP	BP	MP	BP	MP
ICSA11 × ICSR102	4.8*	2.2	10.1	16.5	4.9*	2.5	0.0	-6.9	7.7	-2.8
ICSA11 × ICSR59	-0.5	-2.1	-4.2	0.6	5.6*	3.6	3.7	-4.8	12.4	1.8
ICSA11 × ICSR628	1.8	-0.3	9.0	10.6	-2.4	-4.6*	-6.6	-9.9*	-0.4	-17.2**
ICSA11 × ICSR89013	1.0	-1.2	8.1	14.2	3.2	3.2	-6.0	-7.3	42.6**	31.5**
ICSA11 × ICSR89034	-1.1	-2.3	1.9	7.3	5.1*	4.2	1.1	-6.4	7.4	-3.5
ICSA329 × ICSR102	-1.9	-3.8	-5.7	3.8	5.6*	4.2	8.5	8.2	23.9**	17.3*
ICSA329 × ICSR59	6.2**	3.9	5.0	16.5	4.6*	3.6	3.5	2.1	6.0	0.7
ICSA329 × ICSR628	-2.2	-3.7	1.2	16.5	-3.1	-6.2**	3.1	-0.8	6.3	-7.8
ICSA329 × ICSR89013	-0.6	-3.3	-1.1	9.0	-7.6**	-8.4**	3.4	-5.1	2.7	-0.6
ICSA329 × ICSR89034	-1.7	-3.5	-2.1	8.4	6.1**	4.3	8.9	8.6	11.9	5.4
ICSA536 × ICSR102	-3.7	-5.3*	-4.1	0.8	9.7**	7.9**	0.5	-7.2	3.0	1.9
ICSA536 × ICSR59	1.4	-1.0	0.8	6.7	5.2*	3.9	6.6	-0.1	8.0	7.3
ICSA536 × ICSR628	1.5	0.3	4.1	14.2	8.1**	4.9*	13.1*	1.0	13.0	2.0
ICSA536 × ICSR89013	3.5	0.4	-7.3	-2.5	3.5	2.9	-15.3**	-27.5**	-5.5	-6.7
ICSA536 × ICSR89034	-2.0	-4.1	-9.0	-3.9	7.6**	6.0**	-6.0	-12.7*	22.7**	20.8**
ICSA598 × ICSR102	-2.2	-5.5*	-12.3	-6.0	8.6**	7.9**	8.3	7.6	-3.7	-9.2
ICSA598 × ICSR59	-1.4	-2.0	-1.6	6.2	3.4	3.1	11.5*	9.1	-4.9	-10.0
ICSA598 × ICSR628	-4.7*	-7.5**	3.5	15.9	-1.1	-4.9*	12.9*	9.5	-18.5*	-29.5**
ICSA598 × ICSR89013	2.6	1.4	2.2	9.7	1.5	-0.1	-1.7	-9.0	-13.5	-16.6*
ICSA598 × ICSR89034	4.7*	4.4*	-0.8	6.9	3.9	1.5	17.4**	16.0**	7.1	0.6
ICSA625 × ICSR102	1.4	-0.1	-10.1	-8.2	0.8	-2.2	12.0*	7.4	27.7**	18.2*
ICSA625 × ICSR59	-2.6	-5.1*	5.1	8.2	3.5	0.8	1.1	-4.4	-3.3	-10.1
ICSA625 × ICSR628	1.1	0.1	5.7	12.6	-0.9	-2.4	0.1	-0.4	-6.0	-20.1**
ICSA625 × ICSR89013	5.4*	2.0	8.8	11.2	-6.7**	-7.5**	-4.7	-8.8	1.8	-3.6
ICSA625 × ICSR89034	4.6*	2.2	0.5	3.1	4.9*	4.9*	9.6	4.6	9.2	0.7
ATXA629 × ICSR102	-3.5	-4.4*	3.9	5.0	5.6*	5.0*	3.6	-2.1	2.1	-2.1
ATXA629 × ICSR59	-1.5	-4.6*	2.1	2.4	1.6	1.3	5.8	-1.4	-10.0	-13.4
ATXA629 × ICSR628	-1.8	-2.3	10.8	14.2	0.0	-3.9	4.4	2.3	8.5	-4.8
ATXA629 × ICSR89013	0.6	-3.1	2.0	2.9	1.0	-0.7	-6.1	-8.8	16.0	13.7
ATXA629 × ICSR89034	-9.0**	-11.5	11.0	11.7	7.5**	4.8*	12.4*	5.8	-8.6	-12.9

* and **: significant at P values of 0.05 and 0.01, respectively

TABLE 7. Estimates of GCA and SCA for physiological traits in a line (6) × testers (5) mating design of grain sorghum across all environments.

Genotypes	RWC %	ELWL %	CC	Stg	FLA; cm^2
Female Lines	GCA estimates of female lines				
ICSA11	0.55	-4.33**	0.45	0.05	5.86
ICSA329	-0.71	4.95**	-0.37	0.32**	-3.82
ICSA536	0.34	-2.18*	1.79**	-0.68**	15.20**
ICSA598	-0.59	1.02	-0.93**	-0.12	-9.92*
ICSA625	1.89**	-0.01	-0.53	0.15	-3.23
ATXA629	-1.47**	0.55	-0.41	0.27**	-4.11
SE of Lines	0.53	0.74	0.33	0.09	4.90
Male Lines	GCA estimates of male lines				
ICSR102	1.31**	-3.60**	0.32	0.01	5.04
ICSR59	-0.92	0.56	-0.36	-0.08	-11.67**
ICSR628	1.07*	1.60	-0.09	0.15	8.74
ICSR89013	-0.03	1.85	-1.69**	-0.11	-5.14
ICSR89034	-1.44**	-0.41	1.82**	0.04	3.06
SE of Testers	0.48	0.68	0.30	0.08	4.47
Crosses	SCA estimates of crosses				
ICSA11 × ICSR102	-0.58	3.93**	-0.03	0.14**	3.36**
ICSA11 × ICSR59	0.62	-3.66**	0.19	-0.11**	-1.49
ICSA11 × ICSR628	-1.32	-0.38	-0.36	0.04	0.96
ICSA11 × ICSR89013	1.76*	0.87	0.21	0.01	-1.70
ICSA11 × ICSR89034	-0.48	-0.76	-0.02	-0.08*	-1.14
ICSA329 × ICSR102	0.61	-0.48	-0.12	-0.14	-0.53
ICSA329 × ICSR59	0.67	2.42**	-0.21	0.03	2.71*
ICSA329 × ICSR628	-0.44	-1.05	-0.16	-0.04	-1.56
ICSA329 × ICSR89013	-1.49*	-0.62	0.61**	0.08*	-2.15
ICSA329 × ICSR89034	0.65	-0.27	-0.12	0.07	1.55
ICSA536 × ICSR102	-0.04	1.45	-0.08	0.10**	-2.28
ICSA536 × ICSR59	-1.23	1.61	0.22	-0.01	0.77
ICSA536 × ICSR628	1.99**	1.26	0.61**	-0.02	1.58
ICSA536 × ICSR89013	0.25	-2.20*	-0.30	0.08*	0.94
ICSA536 × ICSR89034	-0.98	-2.13*	-0.44*	0.00	-1.01
ICSA598 × ICSR102	1.25	-2.78*	0.04	0.01	-1.03
ICSA598 × ICSR59	0.08	0.01	0.05	0.04	0.62
ICSA598 × ICSR628	-0.88	0.49	0.19	-0.04	-2.33*
ICSA598 × ICSR89013	0.22	1.41	-0.43*	-0.01	0.79
ICSA598 × ICSR89034	-0.67	0.88	0.15	0.00	1.95
ICSA625 × ICSR102	-1.04	-3.22**	0.33	-0.07	0.23
ICSA625 × ICSR59	1.04	1.25	-0.24	-0.01	-3.57**
ICSA625 × ICSR628	0.73	-0.34	-0.25	0.04	-0.07
ICSA625 × ICSR89013	-1.53*	2.51*	0.01	0.07	0.95
ICSA625 × ICSR89034	0.80	-0.21	0.15	-0.03	2.46*
ATXA629 × ICSR102	-0.20	1.09	-0.14	-0.03	0.25
ATXA629 × ICSR59	-1.18	-1.64	-0.01	0.06	0.96
ATXA629 × ICSR628	-0.09	0.02	-0.03	0.02	1.42
ATXA629 × ICSR89013	0.79	-1.97*	-0.10	-0.07*	1.19
ATXA629 × ICSR89034	0.68	2.50*	0.29	0.04	-3.82**
SE of Crosses	1.18	1.66	0.73	0.20	10.96

* and **: significant at P values of 0.05 and 0.01, respectively.

Excised-leaf water loss (ELWL)

Genetic variation in ELWL has been reported in crop species (Clarke *et al*., 1992) and evaluation of ELWL has shown a good promise for illustrating water stress tolerance (Clarke, 1987 and Bhutta, 2007). Therefore, data in Tables 4 and 5 showed that, the effects of drought stress were significant for ELWL at both locations, since the ELWL was increased from 62.8 (WW) to 72.3% (DS) and from 66.2 (WW) to 80.3% (DS) at AS and WAD locations, respectively (Fig.1 B). ELWL ranged from (44.2 to 77.2%) and from (54 to 85.6%) under WW and DS conditions, respectively. While at WAD location, it ranged from (53.7 to 82.6%) and from (59 to 91.9%) under WW and DS conditions, respectively. The comparison of mean values of the genotypes for ELWL at flowering stage of plant growth in AS location and under DS conditions indicated that only five genotypes, namely, the cross ICSA11 × ICSR59; Dorado; ICSB11; Hybrid 305; ATXB629 and the cross ICSA598 × ICSR102 were significantly lower in water loss than overall mean values over year. However, under DS at WAD the genotypes Dorado, (ICSA11 × ICSR59) and ICSB11 had the lowest ELWL values. These genotypes are less affected by evapo-transpiration losses. These findings are in agreement with those obtained in wheat by Dhanda *et al*. (1998). No evidence for significant heterosis for ELWL was observed, but negative heterosis values implies that these crosses had low values of ELWL than their respective parents. With regard to combining ability, the female line ICSA11 (-4.33**) and the male line ICSR102 (-3.60**) showed the highest negative and highly significant GCA effects for ELWL among parental lines. These two lines were involved in the best crosses and proved to be the best general combiners for ELWL, hence may be useful for hybridization and selection programms to improve leaf water maintaining ability in sorghum. Few crosses showed significant SCA effects. However, the top crosses that showed significant and negative SCA effects were ICSA11 × ICSR59 and ICSA625 × ICSR102. Both crosses are worth to be exploited for hybrid crop development to improve this trait. Dhanda *et al.* (1998) estimated GCA and SCA effects for ELWL in wheat.

Chlorophyll content (CC)

Chlorophyll content is one of the major chloroplast components for photosynthesis and has a positive relationship with photosynthetic rate (Guo & Li, 1996). As an average of the genotypes, CC values were higher at AS location under both treatments than at WAD, that may due to the conditions of the soil type and climate of both locations (Tables 4 and 5; Fig. 1 C). Furthermore, CC values decreased due to DS conditions from 51.8 to 48.2 and from 46.2 to 42.8 at AS and WAD locations, respectively. At AS location, CC ranged from (47.5 to 57.9) and from (43 to 61) under WW and DS conditions, respectively. While at WAD location, it ranged from (42.1 to 49.8) and from (37.1 to 53.7%) under WW and DS conditions, respectively. Abdo *et al.* (2014) found that decreasing water applied up to dry treatment gradually deceased the values of photosystem II (PSII). Kumar *et al.* (2014) and Asadi *et al.* (2015) reported significant variation among tested genotypes and stated that water deficit conditions reduced chlorophyll content. For heterosis, ten crosses out of 30 showed positive and highly significant mid-parent heterosis for CC while seven crosses exhibited better-parent heterosis for CC. The cross combination ICSA536 × ICSR102 had the highest positive heterosis over mid- and better parent. El-Namaky *et al.* (2010) estimated significant positive heterosis relative to better parent values for chlorophyll content in rice. Regarding to combining ability effects, the female line ICSA536 and the male ICSR89034 had the highest positive and significant GCA effects for chlorophyll content among the parental lines. The female line ICSA536 was involved in the best cross combination (ICSA536 × ICSR628) in CC that showed positive and significant SCA effects and also involved in the best cross that showed positive heterotic effect. This result indicates that this line harboring the genes that underlay the chlorophyll content. Similar results that both GCA and SCA were highly significant for chlorophyll content were obtained in rice by El-Namaky *et al.* (2010), in wheat by Rad *et al.* (2013) and in sunflower by Pourmohammad *et al.* (2014).

Stay green (Stg)

Stay green has been found useful in sorghum and other cereal crops for heat stress tolerance and drought-adaptation. In sorghum and under water limited conditions, stay-green genotypes are reported to not only remain green but also contain significantly more carbohydrate in the stem at all maturity stages than go-brown types and have a higher grain weight (Rosenow, 1983; Mc Bee *et al.*, 1983 ; Benbella & Paulsen, 1998 and Borrell *et al.*, 2014b). On average of the genotypes, the number of green leaves (stay green) per plant was reduced at both locations due to drought stress conditions. However, stay green mean at AS was 6.1 and 5.6 leaf under WW and DS conditions, respectively, while at WAD location, stay green mean was 5.5 and 5 leaf under WW and DS conditions, respectively (Tables 4 and 5; Fig. 1 D). The best genotype that gave the maximum number of green leaves at harvest time was the cross ICSA625 × ICSR102 and recorded 8 green leaves, while the cross ICSA629 × ICSR89013 gave the maximum stay green and recorded 7.5 leaves under WW and DS conditions at AS, respectively. Few crosses showed significant mid- and better-parent heterosis, since the best cross combination was ICSA598 × ICSR89013 and gave the highest positive heterosis values (17.4%**). For combining ability. the female lines ICSA329 and ATXA629 gave positive and significant GCA effects for stay green trait, these lines can be considered as good general combiners for stay green. The cross combination ICSA11 × ICSR102 gave the highest positive and significant SCA effects (1.99**) for stay green. These findings suggesting that these genotypes are post flowering drought tolerant. Chen *et al.* (2013) found significant variation among maize genotypes for stay green components. Lee & Tollenaar (2007) concluded that the functional stay-green and the sink establishment dynamics still represent opportunities for yield improvements.

Flag leaf area (FLA)

Flag leaf area has positive correlation with grain yield in many cereal crops but more leaf area might cause more water losses due to more evapotranspiration from the surface. Therefore, optimum leaf area is required for carrying out enough photosynthesis to run the essential processes of plant (Khaliq *et al.*, 2008). As an average of the genotypes, FLA were bigger at AS location under both treatments than at WAD, that may due to the effect of soil and climate conditions in both locations (Tables 4 and 5; Fig. 1 E). In addition, FLA decreased due to DS conditions from 212.9 to 191.5 cm^2 and from 173.8 to 157.4 cm^2 at AS and WAD locations, respectively. At AS location, FLA ranged from (152.5 to 303.5 cm^2) and from (135.9 to 249.9 cm^2) under WW and DS conditions, respectively. While at WAD location, it ranged from (126.9 to 235.7 cm^2) and from (111.4 to 221.9 cm^2) under WW and DS conditions, respectively. Abdo et al. (2014) found significant differences in leaf area index (LAI) of hybrid-305 and Dorado cultivars between wet- and moist treatments. Asadi *et al.* (2015) found that water deficit conditions reduced flag leaf area. Similarly, Cabuslay *et al.* (2002) and Kumar *et al.* (2014) reported that the water deficit in rice caused a larger reduction in leaf area demonstrating the greater sensitivity of leaf enlargement to water stress. Regarding to hererosis, four crosses out of 30 showed positive and highly significant mid-parent and better parent heterosis for FLA. The cross combination ICSA11 × ICSR89013 had the highest positive heterosis over mid- and better parent. Among the parental lines, the female line ICSA536 had the highest positive and significant GCA effects for flag leaf area. The female line ICSA11 was involved in the best cross combination (ICSA11 × ICSR89013) that showed positive and significant heterosis over both mid- and better parent. The cross combination ICSA11 × ICSR102 gave the highest positive and significant SCA effects for flag leaf area. Dorado surpassed Hybrid-305 cultivar in FLA under both treatments and in both locations. Higher genotypes in FLA revealed that these genotypes were well adapted to the drought stress conditions providing a well-developed source and sink association between leaf and grain yield (Misra *et al.*, 2002; Izanloo *et al.* 2008 and Ali *et al.* 2009).

Genetic components of the physiological criteria

Data in Table 8 show the genetic components and contribution of the lines, testers and line × testers interaction of all studied traits overall environments. The line × tester analysis revealed that the contribution of the lines to the total sum of squares was higher than of testers in all physiological traits under study except in CC. Since the maximum contribution (60.08%) of the lines was noted for stay green while the lowest values was recorded for RWC (21.22%). Testers were contributed as maximum value (42.85%) in CC and the lowest one was observed for stay green (4.62%). For the line × tester interaction, the maximum contribution to the total some of squares was 73.66% for flag leaf area whereas the minimum contribution was 30.0% in case of chlorophyll content. It was observed that the variance due to lines was higher than those of testers in the most of physiological traits and that confirmed by the contribution of lines and testers in previous discussion. Rad *et al.* (2013) found that, the mean square of SCA was higher than the mean square of GCA for RWC and chlorophyll content, indicating the importance of both additive and non-additive gene effects. Small additive effect for polygenic traits is predictable (Mather & Jinks, 1982).

TABLE 8. Genetic components and contributions to the total variance of lines, testers and LxT obtained from combined analysis for drought tolerance related traits along with grain across all environments.

Genetic components	RWC %	ELWL %	CC	Stg	FLA; cm^2
Cov. H. S. Lines	0.45	2.76	0.71	0.12	-21.62
Cov. H. S. Tester	0.66	0.01	1.38	-0.006	-17.07
Cov F.S.	5.46	45.40	4.73	0.24	323.96
Additive Variance (σ^2 A)	2,36	6.63	2.39	0.13	105.66
Dominance Variance (σ^2 D)	3.41	10.51	0.82	0.06	393.70
σ^2 A/ σ^2 D	0,69	0.63	2.93	2.26	0.27
Degree of dominance	1.70	1.78	0.83	0.94	2.73
$h^2_{b.s.}$	80.54	86.19	85.72	81.99	80.61
$h^2_{n.s.}$	32.95	33.34	63.89	56.84	17.06
Contribution %					
Lines (L)	21.22	29.8	27.15	60.08	14.54
Testers (T)	21.03	11.8	42.85	4.62	11.79
L x T	57.73	58.4	30.00	35.3	73.66

The results revealed that, dominance variance (σ_D^2) was higher than additive variance in traits, RWC, CC and FLA while additive genetic variance (σ_A^2) was higher than dominance variance in cases ELWL and Stg. Estimation of additive effects for FLA was negative, while the other traits had positive additive genetic effects. The ratio of (σ_A^2/σ_D^2) ranged from 0.27 (flag leaf area) to 2,93 (CC). The observations on portioning of combining ability variance into additive variance (σ_A^2) and dominance variance (σ_D^2) indicated role of both additive and dominance gene action. If dominance deviation is equal to or near one will confirms that the magnitude and sign of dominance for all the genes monitoring the character is equal. Therefore, the degree of dominance is a good estimator of dominance. If dominance deviation is equal to zero or close to zero, the magnitude and sign of the genes controlling the character is not equal and hence degree of dominance explains average dominance (Asadi *et al*., 2015). Results revealed that, the degree of dominance was higher than unity in traits RWC, CC and FLA, that means the magnitude of non-additive variance was higher than the additive variance for these traits. It could be argued that non-additive effect was predominant and desirable in the inheritance of the relative water content, chlorophyll content and flag leaf area, reflecting that heterosis breeding would be more appropriate method for the improvement of this traits. On the other hand, additive effects were in favorable direction in ELWL and Stg traits and can be easily select these traits in early generation. This result was confirmed by the heritability estimates. Since, narrow-sense heritability ranged between 17.06 (FLA) and 63.89 (CC) while broad-sense heritability estimates were high for all physiological traits under study and ranged from 80.54 (RWC) to 86.19% (ELWL). High estimates of narrow sense heritability such as in chlorophyll content reflecting the role of additive effects in the inheritance of this trait. In contrast high estimates of broad sense heritability indicating the importance of non-additive effects in the control of the traits under study. Shahbazy *et al.* (2012) stated that dominance effect was higher than additive effect in chlorophyll fluorescence parameter in wheat and this trait is controlled with over dominance effects thus this trait had great broad sense heritability. Similar results were obtained by several studies on physiological traits (Chen *et al*., 2013; Farshadfar *et al.*, 2012; Rad *et al*., 2013; Farshadfar *et al.*, 2013a&b and Karande & Lad, 2015).

Conclusion

At any breeding program, presence of substantial amount of variability in the available germplasm is very important condition to success this program (Ali *et al.,* 2008). Measurements of different physiological processes for plants responses to drought are important information on the various strategies of the plant intended to remove or to reduce the harmful effects of water deficit in soil or plant tissues. In current report, the genotypes studied showed significant statistical and genetically differences for all the physiological traits under study which suggested that selection might be fruitful for drought tolerance contributing physiological traits. In addition, the majority of the interactions obtained differed significantly for all studied traits reflecting the differential response of the genotypes to environments. Moreover, the lines, testers and line × testers were highly significant for most studied traits suggesting that the plant materials possessed considerable variability that both general and specific combining ability were involved in the genetic expression of these traits. It was noted that there was no line showed favorable GCA effects for all physiological traits, indicating that these traits are inherited independently. Likewise, there was no hybrid showed desirable SCA effects for all physiological traits under study. However, the parental lines ICSA11. ICSA536 and ICSR102 were the best parents that showed GCA effects for one or two traits and involved in one or two cross combinations that showed highly desirable SCA effects or showed remarkable heterosis. The cross combination ICSA598 × ICSR89034 exhibited desirable magnitude of mid parent-heterosis for the physiological criteria. The cross combination ICSA536 × ICSR628 had high positive and significant SCA effects for RWC and CC, while the cross combination ICSA11 × ICSR102 had high positive and significant SCA effects for stay green and flag leaf area. It was observed that the variance due lines was higher than those of testers in the most of physiological traits and that confirmed by the contribution of lines and testers to the total sum of squares. Furthermore, the degree of dominance of the RWC, CC and FLA were higher than unity, that means non-additive effect was found to be predominant and desirable in the inheritance of these traits, indicating that heterosis breeding would be more appropriate method for the improvement of this traits. While additive effects were in favorable direction in ELWL and Stg traits and can be easily select these traits in early generation. Chlorophyll content gave maximum narrow-sense heritability (63.89%) followed by stay green (56.84%), indicating the role of additive gene action in the inheritance of these traits. Broad-sense heritability estimates appeared to be high for all physiological traits under study and ranged from 80.54 (RWC) to 86.19% (ELWL), indicating the role of non-additive gene action effects on the phenotypic expression of these traits.

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قوة الهجين ووراثة بعض المعايير الفسيولوجية ذات العلاقة بتحمل الذرة الرفيعة للجفاف في البيئات المروية ومحدودة المياه

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هدفت هذه الدراسة إلى تقدير قوة الهجين والقدرة الإئتلافية وبعض المكونات الوراثية لصفات المحتوي المائي النسبي (RWC) ، فقد الماء من الورقة المقطوعة (ELWL)، محتوى الكلوروفيل (CC)، عدد الأوراق الخضراء عند الحصاد (Stg)و مساحة ورقة العلم (FLA) تحت ظروف مروية وأخرى ذات اجهاد مائى في الذرة الرفيعة للحبوب. شملت المواد النباتية المستخدمة ٤٣ تركيب وراثي وهي ثلاثون هجيناً (F_1), خمس سلالات معيدة للخصوبة, ستة سلالات (خصبة ذكرياً) واثنين من الأصناف القياسية للمقارنة. تم تهجين السلالات (العقيمة ذكرياً) إلى السلالات المعيدة للخصوبة من خلال نظام تزاوج السلالة في الكشاف في موسم ٢٠١٣. تم تقييم كل التراكيب الوراثية خلال موسمي ٢٠١٤, ٢٠١٥ تحت ظروف الري والجفاف في كلا النوعين من التربة. كان نظام الري المتبع في الأرض الطينية والمستصلحة, الرى السطحى والرى بالتنقيط على التوالى وذلك من أجل تنفيذ معاملتى الرى العادي والجفاف. أظهر تحليل السلالة في الكشاف للقدرة على الائتلاف وجود اختلافات عالية المعنوية بين السلالات, والكشاف, والتفاعل بينهما لمعظم الصفات المدروسة مما يدل أن هذه السلالات تمتلك قدر من التباين الذي أدى إلى اشتراك كل من القدرة العامة والخاصة على الائتلاف في التعبير الوراثى لهذه الصفات. كما بين التحليل أن السلالات ICSA11, ICSA536 و CSR102 تعتبر أفضل الأباء التي أعطت تأثيراً مرغوباً من القدرة العامة على الائتلاف كما أنها شاركت في واحد أوأكثر من الهجن التى أعطت قدرة خاصة عالية على الائتلاف وقوة هجين مرتفعة. و كان الهجين ICSR89034 × ICSA598 أفضل الهجن فى قوة الهجين بالنسبة لمتوسط الأبوين وأفضلهما للصفات الفسيولوجية المدروسة. أمتلك الهجين ICSR628 × ICSA536 قدرة عالية موجبة ومعنوية خاصة علي الائتلاف لصفتي محتوى الماء النسبي ومحتوى الكلوروفيل بينما كان الهجين ICSR102 × ICSA11 هو الأفضل في صفتى عدد الأوراق الخضراء عند الحصاد ومساحة ورقة العلم. أظهر التحليل ايضاً أن درجة السيادة لصفات المحتوي المائي النسبي, محتوي الكلوروفيل و مساحة ورقة العلم زادت عن الوحدة مما يعني أن التأثير الغير مضيف هو المرغوب في وراثة هذه الصفات كما يمكن استغلال ظاهرة قوة الهجين في تحسينها. في المقابل أشار التحليل إلى أهمية الفعل الاضافي للجين في وراثة صفتي فقد الماء من الورقة المقطوعة وعدد الأوراق الخضراء عند الحصاد. أعطت صفة محتوى الكلوروفيل أعلى قيمة في درجة التوريث بمعناها الضيق تلتها صفة عدد الأوراق الخضراء مما يعني أهمية الفعل الجيني المضيف في وراثية هذه هاتين الصفتين بينما كانت درجة التوريث بمعناها الواسع عالية في كل الصفات المدروسة مما يدل على الدور الذي يلعبه الفعل الغير مضيف في وراثة هذه المعاييرالفسيولوجية.