

Diallel Analysis of Yield and It's related Traits in Sunflower (*Helianthus annuus* L.) under Well-watered and Water-stressed Conditions

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Summary

Drought stress is one of the factors which influence sunflower production. Hence, breeding for tolerance to drought stress has become a major focus. In this paper, combining ability, gene action and genetic analysis of several characteristics were studied for five sunflower inbred lines and their ten hybrids (fifteen genotypes). The materials were evaluated in two separate experiments using a Randomized Complete Block Design (RCBD) with three replications in well-watered and water-stressed states and in field condition. Data were analyzed by Griffing's diallel analysis model 1 (fixed effects) and method 2 (parents and crosses). Combined analysis of experiments revealed significant differences among genotypes for all studied traits. Combining ability analysis revealed that in well-watered conditions, general and specific combining abilities (GCA and SCA) effects were significant for all studied traits except for the leaf number. In water-stressed condition, GCA and SCA effects were significant for all studied traits except for the head and stem diameter. The Griffing diallel analysis showed that the genotype LR4 could be considered as the best combiner with the highest GCA effect for seed yield per plant, number of filled seed, stem diameter and head diameter in the sunflower breeding programs. In both water treatment conditions the cross 'RHA266×LR4' showed the highest positive SCA effects and the highest mean value for seed yield per plant.

Key words

sunflower, Griffing diallel analysis, general combining ability, specific combining ability

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Introduction

Abiotic stresses such as cold, salinity, heat and water stress are the principal cause of crop failure worldwide that are dipping average yields by more than 50% (Jaleel et al., 2007). Among the abiotic stresses, drought is the main abiotic factor affecting approximately 26% of the arable area (Singh, 2000). Plants that manage to survive under drought stress show a decrease in fertility, seed yield and quality of end product. Sunflower (*Helianthus annuus* L.) is one of the 67 species in the genus *Helianthus*. It is considered as a source of oil for domestic consumption and cooking worldwide (Hu et al., 2010). Fick and Miller (1997) reported that sunflower is moderately resistant to drought stress and can often grow in hot and semi-arid climatic regions. However, decrease in plant height, 100- achene weight, head diameter and seed yield per plant under water-stressed conditions had been observed (Human et al., 1990; Andria et al., 1995; Nezami et al., 2008). At any stage of sunflower development, water stress have a negative impact on plant yield, but the greatest yield reductions occurs when drought stress occur at flowering to seed maturation stages. Many researchers have exerted water stress on sunflower at flower bud formation stage (R₁) in order to evaluate its effect on physiological traits such as plant water status and photosynthesis rate (Maury et al., 2000; Poormohammad Kiani et al., 2007a, 2007b, 2008, 2009). Physiological changes that occur in plants in response to water stress are loss of cell turgor, closing of stomata and reduction in cell enlargement as well as leaf surface area. These abnormalities ultimately decrease photosynthesis and respiration rate (Human et al., 1990; Hall et al., 1990) and as a result overall production of crop trend to decrease.

So, breeding for drought tolerance is becoming an important challenge in crop plants, notably in sunflower. If drought tolerant cultivars are developed, sunflower can be grown successfully in areas where water is a limiting factor. Knowledge about genetic composition of the breeding stocks and gene action of the target traits is the prerequisite for achieving this aim. Diallel analysis is an efficient tool in studying combining abilities and the genetic structure of traits. Utility of diallel analysis in sunflower were reported by Bajaj et al. (1997), Skoric et al. (2000), Manivannan et al. (2005) and Rauf et al. (2009). According to literature, there were significant general and specific combining abilities for sunflower seed yield (Skoric et al., 2000; Manivannan et al., 2005), branching (Sandu et al., 1999) and relative water content (Rauf et al., 2009). Therefore, both additive and non-additive gene effects could be involved in control of sunflower traits.

The objectives of the present investigation were to study (i) specific and general combining ability as well as (ii) the genetic properties of several agronomic and one physiological traits in sunflower under well-watered and water-stress conditions.

Material and methods

Plant materials and experimental design

Sunflower F₉ recombinant inbred lines (RILs) were developed through single seed descent (SSD) from F₂ plants of 'PAC2 × RHA266'. This public RILs population has been widely used for genetic analysis of complex traits in sunflower (Abou Al Fadil et al., 2007; Darvishzadeh et al., 2007; Poormohammad Kiani et al., 2007a, 2007b, 2008, 2009). Four RILs out of 126 including 'C104',

'LR25', 'LR4', 'LR55' and their paternal line 'RHA266' were selected on the basis of their contrasting responses to water stress (Poormohammad Kiani et al., 2007a; 2007b; 2008; 2009). 'C104' has good water status and osmotic adjustment as well as biomass and yield under water-stressed condition. 'LR25' has good water status and osmotic adjustment as well as biomass under water-stressed condition. 'LR4' has average water status and osmotic adjustment as well as biomass and yield under water-stressed condition. 'LR55' has the lowest water status and osmotic adjustment as well as biomass and yield under water-stressed condition. 'RHA266' was obtained from a cross between *Helianthus annuus* and *H. peredovik* by USDA and 'PAC2' (developed by INRA-France) is an inbred line from a cross between *H. petiolaris* and 'HA61' (Gentzbittel et al., 1995).

The five selected genotypes ('C104', 'LR25', 'LR4', 'LR55' and 'RHA266') were grown and crossed in a diallel mating system without reciprocals to produce 10 F₁ hybrid combinations. The parental genotypes and their F₁ hybrids were evaluated using a randomized complete block design with three replications in both well-watered and water-stressed states under field condition. The latitude and longitude of region are 37°32'N and 45°5'E and its elevation is 1313 m above sea level. Climate of the region is cold and semidry and the average rainfall and the area temperature according to 16 years statistics are 184 mm and 12°C, respectively. Experimental units comprised of one line of four meters long. Row to row and plant to plant spacing was 0.75 and 0.25 m, respectively. The sunflower seeds were sown and the plants were thinned (15 days after sowing) to one plant per hill. After eight-leaf stage of sunflower plants (V8) (Pourtaghi et al., 2011), the plots were irrigated according to their prescribed treatments. In well-watered condition, irrigations were carried out when an amount of evaporated water (from Class 'A pan' evaporation) reached to 60 mm. In water-stressed condition, irrigations were carried out when an amount of evaporated water (from Class 'A pan' evaporation) reached to 180 mm (Pourtaghi et al., 2011). Traits including days to 50% flowering (DF, days), plant height (PH, cm), stem diameter (SD, cm), head diameter (HD, cm), leaf number per plant (LN), relative water content (RWC), yield per plant (YP, g), 100-achene weight (100AW), number of filled seed per plant (NS), percentage of unfilled seed per plant (PU), and plant dry weight (PDW, g) were measured on five random plants per plot in each water treatment conditions. Relative water content (RWC) was determined on upper most fully expanded leaves as $RWC = (FW - DW) / (TW - DW)$, where: FW is the fresh weight and TW is the turgid weight after 24h rehydration at 4°C in dark room by placing the leaves in a container with distilled water. DW is dry weight after oven drying for 24h at 80°C.

Statistical analysis

Analysis of variance was performed using the general linear model (GLM) procedure in the SAS version 9.1 software (SAS Institute Inc, NC, USA). Diallel analyses were conducted according to Griffing's method 2 and model 1 (Griffing, 1956) using the SAS programme for Griffing's diallel analysis (Zhang et al., 2005). The statistical model is as following:

$$Y_{ij} = \mu + \lambda_i + \lambda_j + S_{ij} + e_{ij}$$

where: μ = general mean effect; λ_i (λ_j) = general combining ability (GCA) of the i^{th} (j^{th}) parent; S_{ij} = specific combining

Table 1. Mean squares of morphological traits in five lines and 10 F1 hybrids under two water treatment conditions

Source of variation	df	DF	PH	NL	SD	HD	PDW	YP	RWC	NS	PU	100AW
Environment	1	22.5**	1507.41**	52.9**	1.07**	64.94**	8175.02**	1127.7**	2141.63**	227205.3**	1351.09**	8.118**
Replication (Environment)	4	8.83**	967.38**	25.38**	0.81**	28.37**	4884.89**	53.93**	11.70 ns	13833.47*	6.3 ns	0.2 ns
Genotype	14	34.97**	1148.96**	17.52**	0.46**	56.31**	9870.34**	369.25**	39.95**	99129.25**	272.9**	7.04**
Genotype × Environment	14	1.38ns	121.62ns	5.06 ns	0.12 ns	13.18**	995.85 ns	28.187**	27.88**	16203.49**	120.91**	0.827**
Residual	56	1.66	144.94	4.74	0.066	4.83	713.25	8.55	9.27	4339.09	15.7	0.285
GE effect sliced by E for G												
Well-watered	14	-	-	-	-	35.63**	-	215.83**	31.25**	67008**	167.15**	4.39**
Water-stressed	14	-	-	-	-	33.87**	-	181.59**	36.58**	48325**	226.66**	3.47**
CV%		2.13	11.10	9.43	13.44	14.96	23.87	12.50	5.34	13.31	23.54	11.41

* and **: significant at 0.05 and 0.01 probability level, respectively; ns, not significant at 0.05 probability level.

ability (SCA) of the cross between the i^{th} and j^{th} parent; and e_{ij} = residual. The hypothesis that GCA estimates of the parents equaled zero was tested by a two-tailed t-test.

Results and discussion

Combined analysis of experiments revealed significant difference among genotypes for all studied traits (Table 1). Significant genotype × environment interaction was observed for head diameter (HD), yield per plant (YP), relative water content (RWC), number of filled seed per plant (NS), percentage of unfilled seed per plant (PU) and 100-achene weight (100AW) traits suggesting that response to water status by a given genotype in relation to other genotypes varies between two environments. Slicing of significant genotype × environment interactions for above-mentioned traits revealed that there are significant differences among studied genotypes in both well-watered and water-stressed conditions (Table 1).

Mean comparison between genotypes under studied conditions exhibited a decrease in average performance of sunflower genotypes for all of studied traits except for unfilled seed percentage (PU) and leaf number per plant (NL) (Table 2). Alza and Fernandez-Martinez (1997), Razi and Assad (1999) and Nezami et al. (2008) also reported a decrease in plant height, head diameter, 100-achene weight and yield per plant under water-stressed condition. In both conditions (Table 2), the crosses 'RHA266×LR4' and 'LR55×C104' showed a higher seed yield. These results are in agreement with Rosielle and Hamblin (1981) that indicated that selection under favorable conditions could produce genotypes with a good performance under both water states. However, Cercarelli (1987) reported that for improving yield in water-stressed condition, it is necessary to evaluate genotypes under water-stressed condition. In well-watered condition the cross 'LR4×R25' had the highest number of filled seed per plant, whereas in water-stressed condition the crosses 'LR4×R25', 'RHA266×LR4', 'RHA266×C104' and 'LR55×C104' showed the highest number of filled seed per plant (Table 2). In both conditions (Table 2), the cross 'LR4×C104' showed the highest relative water content. Decreasing in RWC could inhibit the photosynthesis capacity of sunflower (Tezara et al., 2002). Results showed that the cross 'LR4×C104' possessed the highest 100-achene weight in both states. Mean comparison revealed that the genotypes with a higher yield per plant usually have higher plant height, head diameter, stem diameter, and 100-achene weight (Table 2).

The combining ability analysis of variance (Table 3) showed that both general (GCA) and specific combining ability (SCA) variances were highly significant for majority of traits. The significant effects of general combining ability indicated the importance of additive genetic components in controlling traits. The additive variance is the main determinant of the observable genetic properties of the population and selection response (Falconer and Mackay, 1996). Higher genetic advances could be realized when working on traits with higher additive genetic variance. The significant effects of specific combining ability indicated the importance of non-additive genetic components in controlling traits. In this study, mean squares due to general combining ability (GCA) and specific combining ability (SCA) in each of water treatment conditions revealed that for days to 50% flowering (DF), plant height (PH), plant dry weight (PDW), yield per plant (YP), relative water content (RWC), number of filled seed per plant (NS), unfilled seed percentage (UP), and 100-achene weight (100AW), the general and specific combining abilities were significant (Table 3). For leaf number in water-stressed condition both variances due to general and specific combining abilities were significant, whereas in well-watered condition neither general and nor specific combining abilities were significant implying the existence of epistatic gene effects (Marinkovic et al., 2000; Skoric et al., 2000). For the stem diameter (SD) and head diameter (HD), in well-watered condition, both variances due to general and specific combining abilities were significant whereas in water-stressed condition only variance due to general combining ability was significant. Previous reports (Kaya, 2004; Kaya and Atakisi, 2004; Mijic et al., 2008) also indicated the importance of both additive and non-additive genetic effects in controlling seed yield and other traits in sunflower. In the case of traits, both variances due to general and specific combining abilities were significant; the magnitudes of GCA and SCA effects are indicative of the relative importance of genes in the inheritance of traits (Griffing, 1956; Kornegay and Temple, 1986).

The relative importance of general and specific combining ability in determining progeny performance was assessed according to the ratio presented by Baker (1978). The ratio closes to 1:1 for a given trait shows that additive gene effects are more important than non-additive ones. In well-watered condition the baker's ratio was near to one for all studied traits except for stem diameter (SD), number of filled seed per plant (NS) and seed yield per plant (YP). For stem diameter, number of filled

Table 2. Mean comparisons for 11 characters evaluated in five lines and 10 F1 hybrids of sunflower (*Helianthus annuus* L.) under well-watered (WW) and water-stress (WS) conditions

Genotype	DF		PH		NL		SD		HD		PDW											
	WW	WS	WW	WS	WW	WS	WW	WS	WW	WS	WW	WS										
RHA266	56	g	74.72	d	75.33	e	19	b	23	bc	1.98	bcde	1.67	bcd	9.7	f	15.08	ab	75.93	ef	58.64	fg
LR55	65	a	105.4	bc	84.06	de	19	b	19	d	1.45	f	1.29	d	9.71	f	6.86	e	46.58	f	45.26	g
LR4	64	ab	99.09	c	93.33	cde	21	ab	23	bc	1.86	def	2.03	abc	14.11	cde	16.93	ab	75.95	ef	113.3	cd
C104	62	bcde	61	abc	113.7	bc	23	ab	25	abc	1.89	cdef	1.73	abcd	15.8	bcd	12.81	bcd	109.4	cdef	92.65	cde
LR25	63	abc	61	ab	106.1	bc	23	ab	24	abc	1.59	ef	1.35	d	13.08	de	9.24	cde	97.12	def	52.77	fg
LR4 × R25	62	bcd	61	abc	124.6	ab	23	ab	25	abc	2.39	b	2.17	ab	20.61	a	16.72	ab	172.6	abc	150.9	b
RHA266 × LR25	61	bcde	61	abc	127.8	ab	23	ab	27	a	2.34	bc	2.02	abc	15.59	bcd	12.89	bcd	124.7	bcde	106	cde
LR55 × LR4	61	cde	59	cd	104.3	bc	21	ab	25	abc	1.98	bcde	1.65	bcd	18.33	ab	12.7	bcd	128.1	bcde	94.5	cde
RHA266 × LR55	59	ef	56	e	105	bc	21	bc	22	c	2.04	bcde	1.75	abcd	16.53	bcd	13.69	bcd	91.16	def	84.43	def
C104 × LR25	62	bcde	61	abc	124.8	ab	25	a	26	ab	2.15	bcd	2	abc	17.64	abc	15.52	ab	174	ab	111.5	cd
LR55 × LR25	62	bcd	61	abc	125.2	ab	22	ab	23	bc	2.09	bcd	1.58	cd	11.09	ef	9.14	de	126.4	bcde	75.15	efg
LR55 × C104	60	de	60	bc	134.9	a	24	ab	23	bc	1.96	bcde	1.69	bcd	16.74	bc	13.85	abc	142.5	bcd	104.7	cde
RHA266 × C104	58	fg	58	de	116.4	abc	26	a	24	abc	1.73	def	2.09	abc	16.06	bcd	18.5	a	98.91	def	117.8	cd
RHA266 × LR4	57	fg	56	e	109.8	bc	24	ab	24	abc	2.15	bcd	2.24	a	17.72	abc	16.72	ab	134.4	bcde	123.2	bc
LR4 × C104	61	bcde	61	bc	117.9	abc	22	ab	24	abc	2.83	a	1.95	abc	20.53	a	17.08	ab	223	a	204	a

Genotype	SY		RWC		NS		UP		100AW					
	WW	WS	WW	WS	WW	WS	WW	WS	WW	WS				
RHA266	12.26	f	7.19	g	365.7	g	204	c	31.74	a	3.37	d	3.51	d
LR55	11.04	f	9.08	fg	374.7	g	357	b	14.95	c	2.96	d	2.54	e
LR4	24.13	e	19.51	de	428	fg	397	b	33.07	a	5.68	bc	4.92	bc
C104	22.21	e	21.22	cde	417.7	fg	396.7	b	27.61	ab	5.3	c	5.44	ab
LR25	23.1	e	7.63	g	463.3	efg	311.3	bc	12.05	c	4.99	c	2.44	e
LR4 × LR25	30.63	cd	24.24	cd	886	a	677	a	16.7	c	3.46	d	3.58	d
RHA266 × LR25	25.33	cd	19.33	e	479	efg	402	b	19.16	bc	5.28	c	4.83	bc
LR55 × LR4	30.74	de	19.6	de	675.3	bc	424.3	b	19.79	bc	4.57	c	4.65	bc
RHA266 × LR55	24.17	e	21.86	cde	63	bc	430.7	b	2.22	d	5.3	c	5.07	bc
C104 × LR25	25.24	de	18.86	e	456	fg	423.3	b	15.6	c	5.23	c	4.46	c
LR55 × LR25	26.09	de	13.21	f	746.3	b	412.3	b	16.09	c	3.55	d	3.19	de
LR55 × C104	37.12	ab	30.08	a	566.3	a	621	a	20.18	bc	5.55	bc	5.33	abc
RHA266 × C104	33.08	bc	29.19	ab	578.3	cde	626.3	a	25.75	ab	5.72	bc	4.73	bc
RHA266 × LR4	41.07	a	31.27	a	628.7	cd	626.3	cd	21.1	bc	6.55	ab	5.03	bc
LR4 × C104	37.48	ab	25.23	bc	517	def	417.3	b	34.61	a	7.24	a	6	a

Table 3. Mean squares for GCA and SCA and baker's ratio (2Sgca/2Sgca+Ssca) for different sunflower characters studied in a diallel trial

Source of variation	df	DF		PH		NL		SD		HD		PDW	
		WW	WS	WW	WS	WW	WS	WW	WS	WW	WS	WW	WS
GCA	4	49.15**	43.46**	934.76**	679.9*	16.34ns	23.17**	0.25**	0.5**	45.68**	89.69**	6854.57**	8686.9**
SCA	10	6.88**	6.96**	526.77**	606.18**	8.75ns	7.05**	0.37**	0.14ns	31.61**	11.53 ns	5810.91**	3259.3**
2Sgca/2Sgca+Ssca		0.93	0.93	0.78	0.69	0.78	0.87	0.57	0.88	0.74	0.94	0.7	0.84

Source of variation	df	YP		RWC		NS		PU		100AW	
		WW	WS	WW	WS	WW	WS	WW	WS	WW	WS
GCA	4	177.64**	234.65**	36.59*	59.68**	36533.93**	17238.97*	477.67**	465.46**	6.6**	7.67**
SCA	10	231.11**	160.37**	29.12*	27.34**	79197.97**	60758.72**	43.84**	132.35**	3.51**	1.79**
2Sgca/2Sgca+Ssca		0.61	0.75	0.71	0.81	0.47	0.36	0.97	0.88	0.79	0.9

* and **: significant at 0.05 and 0.01 probability level, respectively; ns, not significant at 0.05 probability level.

Table 4. Estimates of general combining effects of parents for yield and its components in sunflower (*Helianthus annuus* L.)

Parents	DF		PH		NL		SD		HD		PDW	
	WW	WS	WW	WS	WW	WS	WW	WS	WW	WS	WW	WS
RHA266	-2.56**	-2.56**	-9.83**	-5.9	-0.4	0.22*	0.007	0.07	-1.14*	1.26*	-18.74*	-9.23*
LR55	0.96**	0.62*	0.75	-4.86	-1.02*	-1.81**	-0.17**	-0.23**	-1.59**	-2.85**	20.15**	-23.37**
LR4	0.53	0.67**	-2.88	0.67	-0.36	0.27	0.12*	0.17**	1.73**	1.99**	12.50*	26.61**
C104	-0.18	0.43	6.64**	1.91	1.16*	0.41	0.03	0.04	1.32**	1.06*	17.85*	15.17**
LR25	1.24**	0.81**	5.32*	8.8*	0.63	0.89	-0.004	-0.05	-0.31**	-1.47**	8.53	-9.18*

Parents	YP		RWC		NS		UP		100AW	
	WW	WS	WW	WS	WW	WS	WW	WS	WW	WS
RHA266	-1.89**	-0.42	0.008	2.72**	-56.6**	-25.52	0.12	1.1	-0.045	0.056
LR55	-3.03**	-2.29**	0.76	-1.05	4.34	-17	-4.23**	-5.19**	-0.71**	-0.42**
LR4	3.81**	2.9**	0.36	0.28	41.91**	38.9**	-2.5**	4.83**	0.47**	0.4**
C104	2.26**	3.82**	1.1	-0.33	-25.84*	22.09	8.04**	3.91**	0.63**	0.73**
LR25	-1.14	-4.01**	-2.24**	-1.62**	36.2**	-18.47	-1.42*	-4.66**	-0.34**	-0.76**

* and **: significant at 0.05 and 0.01 probability level, respectively; ns, not significant at 0.05 probability level.

seed per plant and seed yield per plant (YP) the baker's ratio was near to 0.5 indicating that both additive and non-additive genetic effects are involved in controlling traits. In water-stressed condition baker's ratio was near to one for all studied traits except for plant height (PH) and number of filled seed per plant (NS). For number of filled seed per plant (NS) the baker's ratio was less than 0.5 supporting the preponderance of non-additive genetic effect in controlling this trait.

GCA effects can be considered as the numerical values assigned to the parents in relation to their mean performance in cross-combinations. Table 4 showed the relative values of GCA effects of all the parents for the studied characters in both states. In well-watered condition the highest GCA value for seed yield per plant (YP) was observed in line LR4 (3.81), followed by lines C104 (2.26) whereas the lowest one was observed in line LR55 (-3.03). In water-stressed condition the highest GCA value for seed yield per plant (YP) was observed in line C104 (3.82), followed by line LR4 (2.9). In well-watered condition LR55 had the highest GCA value for plant dry weight (PDW), whereas LR4 had the highest GCA value for it in water-stressed condition. In

both water treatment conditions, LR4 had significantly positive GCA value for number of filled seed per plant, stem diameter and head diameter whereas LR55 exhibited significantly negative GCA value for stem diameter and head diameter. RHA266 had significantly negative GCA value for number of filled seed per plant, plant height, and days to 50% flowering in well watered condition. C104 showed significantly positive GCA value for 100-achene weight. LR55 and LR25 exhibited significantly negative GCA value for 100-achene weight. LR55 had significantly negative GCA estimates for unfilled seed per plant. Therefore, LR4 and C104 were the best combiners for seed yield per plant. LR4 was the good combiner for number of filled seed per plant, stem diameter and head diameter. C104 was the best combiner for 100-achene weight.

Specific combining ability (SCA) effects of studied traits were shown in Table 5. In both water states, the highest SCA value for seed yield was observed in cross 'RHA266×LR4', followed by the cross 'LR55×C104' whereas the lowest SCA value for seed yield was observed in the cross 'C104×LR25'. In well-watered condition, the highest SCA for 100-achene weight was observed

Table 5. Estimates of specific combining effects for yield and its components in 10 F1 hybrids of sunflower (*Helianthus annuus* L.)

F1 hybrid	DF		PH		NL		SD		HD		PDW	
	WW	WS	WW	WS	WW	WS	WW	WS	WW	WS	WW	WS
RHA266 × LR55	-0.33	-1.33*	1.58	11.36	0.12	-0.25	0.17	0.09	3.72**	1.43	8.02	14.76
RHA266 × LR4	-1.9	-2.04**	9.97	4.37	2.12	-0.01	-0.01	0.17	1.58	-0.39	18.56	3.57
RHA266 × C104	-0.52	-0.14	7.14	-1.8	2.60*	-0.15	-0.34*	0.15	0.32	2.31	-22.22	9.56
RHA266 × LR25	1.71*	-0.19	17.48	21.21*	0.12	2.36*	0.31	0.18	1.49	-0.74	12.85	22.41*
LR55 × LR4	-1.76*	-1.9**	-6.02	-0.28	0.41	3.03**	-0.006	-0.1	2.65*	-0.29	23.49	-10.28
LR55 × C104	-1.38	-1	14.99*	11.77	1.55	0.22	0.06	0.07	1.46	1.79	22.8	10.58
LR55 × LR25	-0.8	-0.04	6.64	-1.8	0.41	0.07	0.23	0.05	-2.54*	-0.37	15.96	5.44
LR4 × C104	0.04	-0.04	1.65	2.11	-1.44	-0.53	0.63**	-0.07	1.92	0.16	29.53**	59.89**
LR4 × LR25	-0.38	-0.09	9.65	18.42*	0.74	0.31	0.23	0.24	3.64**	2.35	29.53	31.18**
C104 × LR25	0.71	0.71	-13.39	-8.1	0.36	1.03	-0.76**	0.1	-3.24	-1.26	-93.37**	-98.3**

F1 hybrid	YP		RWC		NS		PU		100AW	
	WW	WS	WW	WS	WW	WS	WW	WS	WW	WS
RHA266 × LR55	2.19	4.75**	0.4	1.01	-36.66	28.74	1.57	-14.41**	1.074**	1.055**
RHA266 × LR4	12.24**	8.94**	0.92	-2.75*	98.42**	168.5**	0.46	-5.48*	1.14**	0.19
RHA266 × C104	5.8**	5.95**	-1.16	-0.98	115.85**	179.98**	-4.87**	0.28	0.15*	-0.44
RHA266 × LR25	1.46	3.93**	-1.66	-2.44	-45.52	1.55	-1.98	2.03	0.68**	1.15**
LR55 × LR4	3.05	-0.84	-1.19	-2.19	84.14*	-42.01	3.24*	-0.77	-0.16	0.28
LR55 × C104	10.98**	8.71**	-2.98	-2.39	149.57**	116.79**	-5.54**	0.72	0.64*	0.64**
LR55 × LR25	3.35	-0.31	-2.12	6.05*	160.85**	3.36	3.45*	5.22*	-0.37**	-0.001*
LR4 × C104	4.48*	-1.33	6.26**	3.51**	-44	-88.11*	2.65	5.13*	1.15**	0.48
LR4 × LR25	1.04	5.51**	2.26	-0.31	262.95**	212.12**	-2.09	-4.29*	-1.65**	-0.44
C104 × LR25	-16.51**	-5.72*	-8.24**	-2.98	-101.85	-28.58	-0.17	-10.33*	-2.15**	-0.77

* and **: significant at 0.05 and 0.01 probability level, respectively; ns, not significant at 0.05 probability level.

in the cross 'LR4×C104', followed by the cross 'RHA266×LR4'. 'LR4×C104' had also the highest mean value for this trait. In water-stressed condition the highest SCA value for 100-achene weight was observed in the cross 'RHA266×LR25', while the best average performance for this trait was observed in the cross 'LR4×C104'. In water-stressed condition the highest SCA value for RWC was observed in the cross 'LR55×LR25', followed by the cross 'LR4×C104', while the best mean value for this trait was observed in the cross 'LR55×C104'. In this study, there was no any significant SCA effect for head and stem diameter in the water-stressed condition.

From breeder view, developing sunflower varieties with short growth period to use in crop rotation could be ideal. Hence, earliness together with low percentage of unfilled seed per plant and short plant height are consider as the most desired characters and negative SCA values would preferred for these trait. In both water treatment conditions the highest negative SCA value for plant height was observed in the cross 'C104×LR25'. In well-watered condition for percentage of unfilled seed per plant, the crosses 'LR55C104' and 'RHA266×C104' had the highest negative and significant SCA value. In water-stressed condition the highest negative and significant SCA value for percentage of unfilled seed per plant was observed in the cross 'RHA266×LR55', followed by the 'C104×LR25' and 'RHA266×LR4' crosses. In well-watered condition for days to 50% flowering, the cross 'RHA266×LR55' had the highest negative and significant SCA value. In water-stressed condition the highest negative and significant SCA value for days to 50% flowering was observed in the cross 'RHA266×LR4', followed by the 'LR55×LR4' and 'RHA266×LR55' crosses.

Conclusion

In conclusion water-stressed condition influenced the average performance of sunflower genotypes and decreased all studied traits except for unfilled seed percentage (PU) and leaf number per plant (NL). Mean squares due to GCA and SCA in each of water treatment conditions revealed that for most of studied traits, the general and specific combining abilities were significant. In both water states, high estimates of non-additive gene effects and low baker's ratio were observed for number of filled seed per plant supporting the preponderance of non-additive genetic effect in controlling trait. The diallel analysis showed that the genotype LR4 could be considered as the best combiner with the highest GCA value for seed yield per plant (SY), number of filled seed per plant (NS), stem (SD) and head diameter (HD) in the sunflower breeding programs as well as the genotype C104 with positive and significant GCA value has high potential to be considered as a good combiner for seed yield and 100-achene weight (100AW). In both conditions, the cross 'RHA266×LR4' showed the highest positive SCA effects and the highest mean value for seed yield per plant. In well-watered condition 'LR4×C104' showed the highest positive SCA effects and the highest mean value for 100-achene weight. In general, the genotypes LR4 and C104 revealed good potential to be used as superior parents in further improvement programs.

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