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Genetic Analysis of Morpho-Physiological Characteristics of Sunflower Under Stress and Non-Stress Drought Conditions

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ABSTRACT

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*) Corresponding author: E-mail: farrokh_darvish@yahoo.com Five Cytoplasmic Male Sterility (CMS) lines and four restorer lines (tester) were crossed in a line x tester scheme in order to analyze general and specific combining abilities and gene effects on sunflower for some agronomic and physiologic traits. Hybrids were evaluated in a randomized complete block design, with three replications under optimum and limited water conditions. The results of combined analysis of variance for different traits in optimal conditions showed that the mean square, except for the % RWC traits in the limited conditions for plant height, head diameter, number of seeds per head, 1000-seeds weight, proline, catalase enzyme, superoxide dismutase enzyme, chlorophyll a, chlorophyll b, grain yield, and oil yield were significant. Results of data variance analysis indicated that the general combining ability for lines and tester was significant, as well as the specific combining ability (line x tester) for most traits. Based on the AGHK30 and AGHK44 combining ability, the RGHK25, RGHK50 and RGHK50 x AGHK56 and the RGHK56 x AGHK44 tester were identified as the most suitable line for the hybrid test in both conditions.

INTRODUCTION

Sunflower (*Helianthus annuus* L.) is an important oilseed crop with high quality of edible oil in the world. Sunflower hybrids are preferred by farmers because of their uniformity, high yield performance, better qualities, and resistance against diseases. Identification of superior parents for hybridization is an important step in plant breeding. Combining ability of parental lines should be estimated to find the best hybrid combinations. Furthermore, estimation of gene effects could be done by analyzing combining ability values based on F₄ mean values (Jocković et al., 2018).

Combining ability of inbred lines could be estimated with various methods, such as top cross; line x tester analysis, in which several testers are used (Ghaffari & Shariati, 2018). Jocić, Miladinović, & Kaya (2015) analyzed four male sterile lines and 10 testers and found additive gene effects for seed yield. However, Jocić, Miladinović, & Kaya (2015), Jocković et al. (2018), and Makanda et al. (2014) analyzed gene effects of inbred lines using line x tester method and they showed that non-additive gene effects were more important for seed yield. Larièpe et al. (2017) also observed the after that gene component was more important than the additive component in managing seed yield in sunflower. In addition, Saba, Khan, Sadaqat, & Rana (2016) reported the importance of dominant genes for seed yield in this crop. In general, most of the experiments carried out by breeders indicate the importance of non-additive gene effect for seed yield in sunflower. Therefore, production of hybrid varieties is justified due to the existence of nonadditive type of gene action for seed yield.

Not only additive gene action was reported to have significant impact on plant height (Razzaq, Nadeem Tahir, Ahmad Sadaqat, & Sadia, 2017) and head diameter (Rameeh & Andarkhor, 2017), but

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also non-additive gene effects have been reported to play crucial role in regard with plant height. Tan & Tan (2011) and Tyagi, Dhillon, & Kaushik (2018) showed significant general combining ability for plant height, seed number per head, 1000-seeds weight and seed yield. Abd El-Satar (2017) indicated the importance of both additive and non-additive gene action in controlling 1000-seeds weight and oil percentage, while Mohyaji, Moghaddam, Toorchi, & Valizadeh (2014) and Neelima & Parameshwarappa (2017) stressed the preponderance of additive type of gene effects and non-additive gene effects for oil percentage.

Though sunflower hybrids are high yielders, the G x E interaction influences their performance (Chigeza, Mashingaidze, & Shanahan, 2014). Biradar, Vijaykumar, Naidu, Vastrad, & Immadi (2019) analyzed 60 hybrids in two environments and reported a significant line x tester x environment effects for head diameter, seed yield, days of flowering, plant height and 1000-seeds weight. The main objective of the present study was to determine the combining ability in sunflower, using a line x tester method with five lines and four testers.

MATERIALS AND METHODS

Experimental Site

The Khoy experimental station (44°58' N 38°33 E, 1103 masl) has cold and dry climates. Minimum, average and maximum annual temperatures are 12.5, 30, and 42 °C, and the average annual rainfall in this region is 292.6 mm. The physical and chemical properties of the soil are presented at Table 1.

Value Character Standard Measured range values OC (%) 0.5-1 0.87 Total N (%) 0.1-0.007 0.008 Fe avalable (mg/kg) 4-5 4.9 300-400 K available (mg/kg) 361 P available (mg/kg) 10-15 9.4 Soil saturation (%) 42-46 46 pН 7-7.5 7.5 Clay (%) 26-28 27 Silt (%) 42-45 36 Sand (%) 25-27 18

Plant materials consisted of five CMS lines (AGHK2, AGHK30, AGHK44, AGHK110, AGHK260) and four male restorer lines (RGHK25, RGHK46, RGHK50, RGHK56) were used in this study. CMS lines were crossed with testers in a line x tester method. The progenies were evaluated during 2017 and 2018 growing seasons, using randomized complete block design with three replications in each year. Each plot consisted of two 5 m long rows. The distance between rows was arranged at 65 cm and between plants within the row was 25 cm. Samples of photos taken in conditions of stress and non- stress that three replications were non-stress and three replicates of stress on the field (Fig.1).



Fig. 1. Plant performance under (A) non stress and (B) stress conditions

Table 1. Physical and chemical properties related to the soil of the site

The following traits were measured: plant height (cm), head diameter (cm), seed weight per head (g), seed number per head, Leaf Area Index, RWC (%), % proline content (%), CAT (unit per mg protein), SOD (unit per mg protein), chlorophyll a (mg/g), chlorophyll b (mg/g), oil content (kg/h), seed yield (kg/h) and 1000-seeds weight (g).

Data for hybrids were subjected to "Line x Tester" analysis (Singh & Chaudhary, 1977) to estimate general combining ability (GCA), specific combining ability (SCA), and their respective variance components. The estimation of general combining ability and specific combining ability effects of parents and hybrids were obtained through the following equations: Estimation of GCA effects:

Lines: GCA = (Xi../fr) - (X.../fmr)......1) Testers: GCA= (X.j./mr) - (X.../fmr)......2)

Where:

- f = number of CMS lines (female parent)
- m = number of testers (male parent)
- r = number of replications
- X_i = total number of the F₁ resulting from crossing ith lines with all the testers
- X._j = total number of all crosses of jth tester with all the lines
- X = total number of all crosses

Estimation of SCA effects was calculated through the following formula:

where X_{ij} is total number of F_1 resulting from crossing ith lines with jth testers.

Estimation of GCA and SCA variances were obtained by expected values of mean squares, assuming lines and testers as fixed and years as random factors. The additive genetic variances for lines and testers was calculated through the following formula:

$$\sigma_{GCA}^2 = \frac{1+F}{4}\sigma_A^2$$
.....4)

where, assuming that the coefficient of inbreeding is unity, σ_{A}^{2} and σ_{GCA}^{2} are additive genetic variance of lines and testers (Singh & Chaudhary, 1977).

Dominance variance (σ_{D}^{2}), narrow sense heritability (h_{N}^{2}) and broad sense heritability (h_{B}^{2})

were obtained using the following formula:

$$h_B^2 = \frac{\sigma_A^2 + \sigma_D^2}{\sigma_A^2 + \sigma_D^2 + \sigma_e^2}$$
.....6)

where σ_A^2 represents additive variance, σ_D^2 dominance variance and σ_e^2 represents error variance.

The MSTATC and SPSS22 software was used to analyze the data.

RESULTS AND DISCUSSION

The results of variance analysis of different traits in stress and non-stress conditions indicated that mean square for all traits was significant. Mean squares of lines were significant for plant height, head diameter, number of seeds per head, 1000-seeds weight, proline content, catalase, superoxide dismutase, chlorophyll a, chlorophyll b, grain yield and oil yield (Table 2). Significance of the mentioned traits indicates that there is a significant difference in the general combining ability of lines for these traits. The general combining ability of the lines indicates the additive effects of genes. Chahal et al. (2019) also indicated the importance of dominant genes in controlling the seed yield in sunflower.

According to the table of analysis of variance (Table 2), The mean squares of the line x tester for plant height, head diameter, number of seeds per head, 1000 grain weight, proline content, catalase, superoxide dismutase, chlorophyll a, chlorophyll b, grain yield and oil yield were significant in both normal and stress conditions. Significance of these traits indicates the hybrid specific combining ability for these traits. As a result, it shows the dominant effects of genes. Also, some traits (Table 3) were controlled by over-dominance effects. Tan & Kaya (2019) achieved similar results. But Bonnafous et al. (2018) indicated the importance of both additive and nonadditive gene action in controlling 1000 seed weight and oil percentage.

Year 1 1 R/Y 4 2 Line 4 2 L×Y 4 1 Tester 3	ر	m)		diameter cm)	Numbe	er of seed head	ds per	1000-s	eeds weight (g)	H %	RWC	%	Proline
Year 1 1 R/Y 4 2 Line 4 2 L×Y 4 1 Tester 3	S	NS	S	NS	s		NS	S	NS	S	NS	S	NS
R/Y 4 Line 4 2 L×Y 4 1 1 Tester 3	147.40 ^{ns}	19.20 ^{ns}	1.50 ^{ns}	45.53**	11623.00) ^{ns} 276	94.40 ^{ns}	50.83 ⁿ	^s 151.65 ^{ns}	0.43 ^{ns}	290.87 ^{ns}	20.83 ^{ns}	0.033
Line 4 2 L×Y 4 1 Tester 3	447.28	1005.11	4.11	14.12	5851.79	9 118	889.13	23.53	67.41	34.10	103.43	89.63	23.98
L×Y 4 1 Tester 3	378.02**	321.90*	11.06**	5.42"	54145.74	4" 432	882.33**	3.19**	31.05**	11.87 ^{ns}	49.16**	935.24**	219.63**
Tecter 3 5	125.22 ^{ns}	103.42 ^{ns}	2.85**	0.40^{ns}	663.88 ⁿ	° 29)5.24 ^{ns}	0.70 ^{ns}	0.79 ^{ns}	8.30 ^{ns}	5.76 ^{ns}	15.66 ^{ns}	4.72 ^{ns}
	350.49 ^{ns}	742.96**	8.57**	2.14 ^{ns}	6257.80	110	909.47**	2.05 ^{ns}	11.24**	17.09 ^{ns}	80.62**	297.83**	9.93*
Т×Ү 3	21.23 ^{ns}	93.55 ^{ns}	2.06**	0.90 ^{ns}	193.98 ⁿ	° 16	s0.69 ^{ns}	1.58 ^{ns}	0.62 ^{ns}	20.33 ^{ns}	7.09 ^{ns}	4.23 ^{ns}	2.90 ^{ns}
L×T 12 (967.37**	149.76**	3.95**	12.77"	25796.53	3" 143	861.35**	2.99"	10.12**	10.64 ^{ns}	42.58**	437.31**	113.48**
L×T×Y 12	45.96 ^{ns}	16.81 ^{ns}	0.76 ^{ns}	0.48 ^{ns}	1062.63	^{ns} 46	31.28 ^{ns}	1.08 ^{ns}	0.48 ^{ns}	13.35 ^{ns}	12.59**	18.06 ^{ns}	11.64 ^{ns}
Error 76	133.23	68.66	0.42	0.79	7923.11	4	48.73	1.77	1.45	12.16	11.85	12.44	7.39
CV %	6.71	6.34	4.48	7.67	19.44		3.86	4.07	2.82	5.41	4.35	6.06	8.84
	neu)												
SV df	CA (Unit pe prote	r r mg in)	SC (Unit p prot)D er mg ein)	Chlorop (mg/	hyll a (g)	Chlorol (mg	phyll b J/g)	ы Х	yield g/h)		Seed y (kg/ł	ield (r
	s	NS	S	NS	s	NS	s	NS	S	NS		s	NS
Year 1 3.3	35 ^{ns} 1	14.58 ^{ns} 1	141.41*	7.96 ^{ns}	3.76 ^{ns} 1	2.66 ^{ns}	7.25**	0.07 ^{ns}	54502.88 ^{ns}	177356.78	8 ^{ns} 1833(00.83 ^{ns} 5	545940.30 ^{ns}
R/Y 4 117	7.92 1	132.61 3	34.78	87.06	3.29 9	.41	0.22	1.65	22602.84	71202.17	84758	3.93 2	242684.40
Line 4 92.	.61** 3	386.26" 8	324.87"	228.72**	0.92" 5	.64"	8.35**	6.89**	3069.07*	32650.45	* 11535	.90	111801.45**
L×Y 4 9.8	33 ^{ns} E	5.19 ^{ns} C).04 ^{ns}	1.68 ^{ns}	0.15 ^{ns} 0	.47*	0.02 ^{ns}	0.25 ^{ns}	929.18 ^{ns}	6295.66 ^{ns}	2525.	25 ^{ns} 2	2858.55 ^{ns}
Tester 3 58	8.75** 1	109.76** 2	207.78**	64.07**	0.47** 4	85**	2.23**	3.69*	2050.69 ^{ns}	15960.13	. 7352.	47 ^{ns} 2	10494.70**
Т×Ү 3 0.7	20 ^{ns} 2	2.34 ^{ns} C	.59 ^{ns}	0.31 ^{ns}	0.06 ^{ns} C	.78**	0.24 ^{ns}	0.64 ^{ns}	1344.69 ^{ns}	3367.11 ^{ns}	5702.	87 ^{ns} 2	2258.70 ^{ns}
L×T 12 59	0.35** 6	303.15" 1	1189.34**	349.34**	1.28 ^{ns} 2	00	1.21**	1.89**	3347.31**	9831.77**	10802	2.83**	36461.45**
L×T×Y 12 4.7	73 ^{ns} 6	3.77 ^{ns} C).34 ^{ns}	2.34*	0.09 ^{ns} 0	.58**	0.08 ^{ns}	0.37 ^{ns}	1116.21 ^{ns}	1463.52 ^{ns}	3917.	73 ^{ns}	1742.95 ^{ns}
Error 76 8.6	37 1	15.05 2	2.72	1.09	0.17 0	.16	0.09	0.24	2094.63	3156.10	6393.	60 5	5234.71
CV % 3.8	33 E	3.65 3	3.10	3.63	7.8 3	.42	9.75	7.81	4.54	3.97	4.07		2.82

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Character	Br h	oad sense eritability	Nar ł	rrow sense neritabili	De don	gree of ninance
	S	NS	S	NS	S	NS
Plant height	0.30	0.553	0.077	0.039	2.41	5.13
Seed number head	0.35	0.98	0.013	0.117	6.99	3.83
1000-seeds weight	0.14	0.562	-	0.08	-	3.46
% Proline	0.85	0.7	0.05	0.014	5.37	96.98
Chlorophyll a	0.18	0.65	-	0.148	-	2.60
Chlorophyll b	0.74	0.578	0.25	0.136	1.97	2.54
Oil yield	0.14	0.354	-	0.068	-	2.87
Seed yield	0.14	0.56	-	0.08	-	3.46

Table 3. Broad and narrow sense heritability estimates on an entry mean basis and degree of dominance of sunflower morpho-physiological characteristics under stress (S) and non-stress (NS)

In the study of general combining ability of lines (Table 4), the best lines for AGHK2 and AGHK30 plant height were the highest and most suitable for general and negative traits in normal and stress conditions. A negative and significant combining ability for plant height is a desirable breeding trait. Also, the AGHK44 line had the most positive and significant GCA under normal conditions. In examining other AGHK30 lines traits, the number of seeds per head, 1000 grain weight, grain yield and oil yield had the highest positive and significant GCA under stress condition. In normal conditions AGHK2 had the most positive and significant combining ability with a thousand seed weight attribute, which could be selected from the hybrid under normal conditions as the preferred line. Also, AGHK44 line for relative water content and superoxide dismutase has the most positive and significant general combining ability. For proline content, chlorophyll a, chlorophyll b assessments, AGHK110 had the most positive and significant general combining ability under stress and normal conditions which indicates the additive effects of genes and the top line can be chosen. But According to the results Smith et al.(2018) non-additive component was more important than the additive component.

In examining the testers for plant height, the RGKH50 and RGKH25 testers had the most negative and significant general combining ability in normal conditions, which could be corrected for the trait. Also, the RGHK25 for head diameter had the highest positive and significant under stress and normal conditions. The RGHK56 tester had the most positive and significant combining ability under optimum and limited conditions. For proline traits, the RGHK46 tester had the most positive and significant combining ability under stress conditions. RGHK50 and RGHK56 testers have positive highest combining ability catalase and superoxide dismutase and significant genotypes in stress condition. Also, RGHK56 tester had the most positive and significant general combining ability in chlorophyll a under stress conditions. RGHK56 and RGHK25 had the highest positive and significant combining ability with chlorophyll b in stress conditions and RGHK56 testers under normal conditions. RGHK50 and RGHK25 testers also had the highest positive and significant general combining ability in grain yield and oil yield under normal and stress conditions (Table 5). Ghaffari & Shariati (2018) also achieved similar results.

In the study of hybrids, the RGHK46 x AGHK260 and RGHK46 x AGHK30 had the most negative and significant specific combining ability for plant height, which can be identified as superior hybrids. RGHK25 x AGHK260 had the most positive and significant combining ability for head diameter in stress conditions, which is a good hybrid for selection. RGHK50 x AGHK30 had the most positive and significant combining ability for normal head diameter and for the number of seeds per head.

Table 4. Ge	neral con	nbining abil	ity for mo	orpho-physi	iological ch	aracteristics	CMS lin€	es of sunfl	ower unde	r stress an	d non-stre	SS
CMS	Plant	reight (cm)	Head)	diameter cm)	Number o	of seeds per ead	1000-see	ds weight g)	% F	RWC	Ч %	roline
	S	NS	S	NS	S	NS	S	NS	S	NS	s	NS
AGHK2	-4.48**	-8.48**	1.96**	0.48 ^{ns}	-132.12**	408.58**	-0.66**	2.70**	-0.65 ^{ns}	-4.65**	-18.78**	-9.20**
AGHK30	-9.73**	-26.07**	1.76**	0.07 ^{ns}	135.47**	-0.92 ^{ns}	1.18**	-0.92**	1.05*	1.88**	14.13**	6.63**
AGHK44	9.35**	-1.73 ^{ns}	0.21*	0.68 ^{ns}	10.05 ^{ns}	-110.08**	-0.53*	1.49**	2.32**	-0.88 ^{ns}	4.38**	2.55**
AGHK110	1.93 ^{ns}	8.85 ^{ns}	-0.44**	0.43 ^{ns}	0.38 ^{ns}	31.83 ^{ns}	-0.1 ^{ns}	-3.22**	0.95 ^{ns}	2.14**	4.95**	-2.37**
AGHK260	2.93*	27.43**	0.44**	-1.65 ^{ns}	-13.78 ^{ns}	-329.42**	0.11 ^{ns}	-0.05 ^{ns}	0.32 ^{ns}	1.50**	5.52"	2.38**
SE (GCA)	2.39	3.33	0.18	0.48	25.69	6.11	0.38	0.34	~	0.99	1.01	0.78
SE (gi-gj)	3.38	4.71	0.26	0.68	36.33	8.64	0.54	0.49	1.42	1.40	1.44	1.11
Table 4. (C	ontinued)											
CMS	CAT (L pi	Jnit per mg rotein)	sod (U	Init per mg otein)	Chlor (n	ophyll a ng/g)	Chlorc (m	phyll b g/g)	Oil (kg	yield g/h)	See (k	d yield g/h)
	တ	NS	S	NS	S	NS	S	NS	S	NS	S	NS
AGHK2	-6.12**	-12.71**	-7.60**	0.42 ^{ns}	-0.36**	-0.85**	-0.76**	-0.93**	-23.25**	73.24**	39.37**	161.80**
AGHK30	1.64**	3.54"	0.41 ^{ns}	-1.05**	0.04 ^{ns}	-0.25 ^{ns}	-0.66**	-0.21**	34.78**	-47.01**	70.80**	-55.20**
AGHK44	-015 ^{ns}	3.46**	20.12**	10.22**	-0.33**	-0.91	-0.64**	-0.71**	-12.91 ^{ns}	68.88	-32.37*	89.30**
AGHK110	4.65**	8.10**	-7.76**	-4.56**	0.61**	1.27**	2.04**	1.79**	-5.82 ^{ns}	-97.73**	-5.87 ^{ns}	-193.20**
AGHK260	-0.02 ^{ns}	-2.40**	-5.18**	-5.04**	0.03 ^{ns}	0.74**	0.03**	0.06 ^{ns}	7.89 ^{ns}	2.61 ^{ns}	6.80 ^{ns}	-2.70 ^{ns}
SE (GCA)	0.85	1.11	0.47	0.3	0.12	0.11	0.089 ^{ns}	0.14	13.21	16.21	23.08	20.88
SE (gi-gj)	1.20	1.58	0.67	0.42	0.17	0.16	0.12	0.2	18.68	22.93	32.64	29.53
Remarks: *, * sterility; RWC	* and ns =) = Relativ	significant a e Water cont	it 5 % and tent; CAT	1 % probabi = catalase; {	ility levels ar SOD = supe	nd not signific; roxide dismut;	ant, respec [.] ase	tively; S = {	stress; NS =	non-stress;	CMS = cyto	plasmic male

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Restorer	Plant h	eight (cm)	Head (diameter cm)	Number	of seeds per head	100 wei	0-seeds ght (g)	%	RWC	Ч %	roline
	S	NS	S	NS	S	NS	S	NS	S	NS	S	NS
RGHK25	10.43**	-2.25**	1.11**	0.73**	38.45**	145.18**	0.17 ^{ns}	-0.01 ^{ns}	-0.86 ^{ns}	-3.82**	-4.10**	-0.53 ^{ns}
RGHK46	6.43**	0.55**	-1.45**	-0.51*	-27.42*	50.78**	-0.45*	-0.32*	0.94*	-1.13*	9.37"	-0.20 ^{ns}
RGHK50	9.97**	-7.32**	0.03 ^{ns}	0.04 ^{ns}	-15.82 ^{ns}	-125.42*	0.66"	1.64"	-1.65**	3.92**	-3.23**	-0.93*
RGHK56	6.90**	9.02**	0.3**	-0.25 ^{ns}	4.78 ^{ns}	-70.55**	-0.39*	-1.31**	1.58"	1.03*	-2.03**	1.67**
SE (GCA)	2.13	2.98	0.16	0.43	22.98	5.46	0.34	0.31	0.9	0.88	0.91	0.7
SE (gi-gj)	3.02	4.21	0.23	0.61	32.50	7.73	0.48	0.44	1.27	1.25	1.28	0.99
Restorer) Unit pre	CAT per mg otein)	CUnit pro	SOD per mg otein)	Chlo Chlo	rrophyll a mg/g)	Chlo (r	rophyll b ng/g)	io –	yield ‹g/h)	See (k	d yield g/h)
	S	NS	S	NS	S	NS	S	NS	S	NS	S	NS
RGHK25	-4.63**	-0.37 ^{ns}	-4.44**	-2.29**	0.28**	0.03**	0.57**	0.3**	4.88 ^{ns}	-9.63 ^{ns}	10.43 ^{ns}	-0.5 ^{ns}
RGHK46	1.29**	-2.56**	-3.72**	-1.06**	-0.1 ^{ns}	-0.99	-0.74**	-1.05**	-6.23 ^{ns}	-24.90**	-27.03*	-19.30*
RGHK50	11.84**	5.52**	1.24**	-0.94**	-0.3**	-0.03 ^{ns}	0.05 ^{ns}	0.26**	20.13**	67.44**	39.63**	98.30**
RGHK56	-8.50**	-2.59**	6.93**	4.29**	0.12*	0.98**	0.13**	0.49**	-18.77**	-32.92**	-23.03*	-78.50**
SE (GCA)	0.76	-	0.42	0.27	0.1	0.1	0.08	0.12	11.81	14.50	20.64	18.68
SE (gi-gj)	1.07	1.41	0.6	0.38	0.15	0.14	0.11	0.17	16.71	20.51	29.19	26.41

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The RGHK50 x AGHK260 hybrid had the highest positive and significant combining ability, which is a good hybrid in stress conditions and also the RGHK25 x AGHK30 hybrid has the highest specific combining ability in normal conditions. For 1000-seeds weight, RGHK56 x AGHK44 hybrid had the highest positive and significant combining ability under stress and normal conditions. While, RGHK25 x AGHK44 had the highest positive and significant specific combining ability in normal conditions. For the relative water content of the hybrid RGHK50 x AGHK30 showed that it was superior in terms of hybrid combining ability in stress conditions and RGHK56 x AGHK2 hybrids had the highest combining ability in normal conditions (Table 6).

In the proline content, RGHK56 x AGHK2 hybrid had the highest positive and significant combining ability in stress conditions, which is a good hybrid in stress conditions. Also, RGHK46 x AGHK260 hybrids had the most positive and significant combining ability for catalase in stress and normal conditions. In the observation of superoxidase dismutase, RGHK50 x AGHK260 hybrids showed it has the highest potential for positive and significant combining ability under stress and normal conditions. While other tested accessions, the RGHK46 x AGHK30 hybrid had the highest positive and significant combining ability for chlorophyll a under stress conditions and RGHK46 x AGHK260 in normal conditions.

In examining the trait of chlorophyll b, RGHK50 x AGHK44 hybrid had the most positive and significant combining ability in stress conditions. While, RGHK46 x AGHK30 hybrids gave the highest combining ability in normal conditions. The RGHK56 x AGHK44 hybrids had the highest positive and significant combining ability for seed yield and oil yield under stress conditions. The hybrids of RGHK50 x AGHK30 and RGHK25 x AGHK44 showed similar patterns in seed yield and oil yield (Table 6), with the highest degree of combining ability in normal conditions that indicate the non-additive effects of genes, or those of dominant effects (Table 3). Andarkhor, Mastibege, & Rameeh (2012) achieved similar results.

As it was indicated, dominance effects (line x tester interaction) were significant for

plant height, head seed number, % proline and chlorophyll b under water stress. Therefore, these characters were controlled mainly by dominant gene action. Andarkhor, Mastibege, & Rameeh (2012) reported the role of both additive and dominant gene action in the inheritance of 1000-seeds weight. However, for stem diameter, days of flowering, 1000-seeds weight and days to maturity of GCA/SCA ratios were > 1 showing the importance of additive gene effects (not proved by obtained data). Azad et al. (2016) also observed that additive type of gene action was of paramount importance for plant height and days to 50 % of flowering in sunflower. Furthermore, Hladni et al. (2018) reported significant general combining ability for plant height, 1000-seeds weight and seed number per head. On the other hand, Gami, Patel, Patel, Chaudhary, & Soni (2018) indicated the significance of non-additive gene effects for plant height in sunflower. Dhillon & Tyagi (2016) and Panda, Wali, Kachapur, & Harlapur (2017) also reported the role of either additive or non-additive gene effects on oil pecentage. The study also confirmed that the non additive were more important than additive components in controlling seed yield, though Rajesh, Sudheer Kumar, Narsimha Reddy, & Siva Sankar (2018) concluded the balance strenght for both components. Riaz, Tahir, Rizwan, Nazir, & Riaz (2017) also indicated the importance of dominant genes in controlling the seed yield in sunflower. Non-additive type of gene action for seed yield justifies the production of hybrid varieties in this crop. However, different results obtained by different researchers may be attributed to different genetic material and the environmental conditions in these studies. Our results are also restricted to the lines and testers used in the study. The average degree of dominance for most of the traits ranged from incomplete dominance to over-dominance, suggesting the existence of non-additive gene action for these agronomic traits in sunflower (Table 3). Tan (2010) also reported high heritability estimates for 1000 seed weight, seed number per head, oil content and seed yield in sunflower using line x tester analysis. Kaya, Balalic, & Milic (2015) found similar results for other accessions in sunflower.

		Plant	height	Head di	iameter	Number	of seeds	1000-	weight	1%	RWC	Ч Р 1 %	oline
CMS	Restorer		(m)	C	Ē	ber	neau	sec	(6) bi				
		S	NS	S	NS	S	NS	S	NS	S	NS	S	NS
AGHK2	RGHK25	9.15 ^{ns}	-1.58 ^{ns}	-1.81**	1.85**	0.05 ^{ns}	112.15**	1.97**	-2.75**	038 ^{ns}	-1.71 ^{ns}	-0.15 ^{ns}	-0.8 ^{ns}
A30		6.48*	5.62 ^{ns}	-0.26 ^{ns}	0.99**	-16.75 ^{ns}	324.55**	-0.56 ^{ns}	0.30 ^{ns}	1.44 ^{ns}	3.53"	-0.95 ^{ns}	0.87 ^{ns}
A44		-8.12**	-16.48**	2.43**	-2.05"	-22.68 ^{ns}	-339.25**	0.05 ^{ns}	3.97"	1.02 ^{ns}	-6.79**	-9.35**	-5.40**
A110		-7.52"	-20.52**	-0.36 ^{ns}	-1.79"	39.38 ^{ns}	-97.45**	-1.46**	-1.52**	-2.85**	4.98**	10.45**	5.33**
A260		4.40 ^{ns}	-25.67**	2.59"	0.64 ^{ns}	103.80**	253.65**	-0.99*	2.37**	0.25 ^{ns}	1.93 ^{ns}	-33.40**	-17.30**
AGHK2	RGHK46	5.07*	10.87**	-0.63**	0.62 ^{ns}	-86.33**	-340.95*	0.64 ^{ns}	-0.72*	-1.21 ^{ns}	-1.95 ^{ns}	18.47**	2.70**
A30		-11.87**	4.40 ^{ns}	-1.02**	-1.53"	-29.93 ^{ns}	-135.08*	-0.81*	-0.31 ^{ns}	-1.55 ^{ns}	4.40**	12.73**	8.77"
A44		2.40 ^{ns}	10.40**	-0.94**	0.27 ^{ns}	12.47 ^{ns}	222.38**	1.17**	-1.33**	2.51*	-4.37**	2.20*	5.83**
A110		0.98 ^{ns}	-24.67**	-1.12**	0.15 ^{ns}	-89.45**	203.48**	0.53 ^{ns}	0.66 ^{ns}	-2.37**	3**	7.68**	2.78**
A260		-18.02**	-10.47**	0.74**	-4.97**	-14.25 ^{ns}	-416.45*	-1.05*	-3.33**	-3.33**	5.48**	-2.78*	3.12**
AGHK2	RGHK50	6.05*	-2.60 ^{ns}	-1.26**	1.46**	-9.85 ^{ns}	160.75**	-0.23 ^{ns}	-0.99	0.62 ^{ns}	-1.14 ^{ns}	2.15*	0.52 ^{ns}
A30		10.98**	37.73**	1.64**	3.36**	113.55"	52.22**	-0.75 ^{ns}	3.66**	5.08**	-7.34"	-7.05**	-6.42**
A44		-9.60	21.08**	0.68"	0.2 ^{ns}	62.22*	-376.77*	-0.32 ^{ns}	1.73**	1.66 ^{ns}	-1.56 ^{ns}	10.02**	5.70**
A110		4.07 ^{ns}	-13.05**	0.28 ^{ns}	0.56 ^{ns}	123.58**	402.63**	-1.29**	1.38**	1.94 ^{ns}	-2.46*	-15.12**	-6.30**
A260		5.47*	-21.52**	-1.65**	-2.12"	201.82"	125.17**	1.76**	-2.55**	-0.41 ^{ns}	-2.38*	-11.85**	-5.90**
AGHK2	RGHK56	0.07 ^{ns}	-13.48**	0.69**	1.36*	-140.45*	-151.03*	-0.16 ^{ns}	-0.57 ^{ns}	-3.19**	6.40**	16.95**	6.50**
A30		-4.93*	30.83**	-0.33 ^{ns}	-2.85"	-76.62**	-192.52*	-1.19**	-2.01**	0.08 ^{ns}	-1.65 ^{ns}	15.85**	9.62**
A44		2.40 ^{ns}	7.03*	-0.13 ^{ns}	1.80**	240.92**	30.22**	2.27**	2.37**	1.15 ^{ns}	-4.456**	0.38 ^{ns}	-0.38 ^{ns}
A110		8.47**	3.23 ^{ns}	1.49**	4.23**	-139.35*	188.42**	-0.78*	-0.12 ^{ns}	0.31 ^{ns}	5.92**	6.32**	2.02*
A60		-5.93*	-41.10**	-1.03**	-3.19**	-24.95 ^{ns}	-26.12**	-0.3 ^{ns}	-0.24 ^{ns}	-1.54 ^{ns}	0.33 ^{ns}	-22.55**	-11.25**
SE (SCA)		4.78	6.66	0.37	0.96	51.39	12.23	0.76	0.69	2.01	1.98	2.03	1.57

Table 6 . (C	ontinued)												
CMS	Restorer	C (Unit pro	AT per mg tein)	S (Unit pro	OD per mg otein)	Chlore (m	phyll a g/g)	Chlore (m	phyll b g/g)	(ků	yield g/h)	Seed (kg	yield (h)
		s	NS	s	NS	s	NS	S	NS	s	NS	s	NS
AGHK2	RGHK25	-3.96**	-13.78**	-29.71**	-16.84**	1.49**	0.36**	0.40**	0.04 ^{ns}	64.13**	-83.33*	118.57**	-165**
A30		-9.63**	-21.63**	13.54**	10.12**	-1.03**	-0.39**	0.11 ^{ns}	0.16 ^{ns}	-10.67 ^{ns}	21.35 ^{ns}	-33.97 ^{ns}	17.80 ^{ns}
A44		2.92**	6.08**	-22.43**	-13.11**	-0.59**	-0.77**	-0.42**	-0.70**	10.25 ^{ns}	103.89**	-3.37 ^{ns}	238.20**
A110		16.51**	29.33**	38.60**	19.83**	0.13 ^{ns}	0.80**	0.7**	0.49**	-63.71**	-41.91 ^{ns}	-87.97**	-91**
A260		22.21**	14.70**	37.51**	20.25**	-0.51**	0.34**	-1.02**	-0.37**	-30.93**	82.07**	-59.60*	142**
AGHK2	RGHK46	-10.69**	-13.60**	-18.40**	-13.40**	-0.42**	-1.25**	-0.12 ^{ns}	-1.73**	34.98**	-25.81 ^{ns}	37.87 ^{ns}	-43.20*
A30		12.68**	12.06**	-12.33**	-6.31**	0.91"	0.75**	0.51**	1.86**	-35.90**	-26.50 ^{ns}	-48.80*	-18.80 ^{ns}
A44		-24.20**	-13.16**	-6.78**	-0.53 ^{ns}	0.02 ^{ns}	0.16**	0.64**	0.23 ^{ns}	31.85**	-29.76 ^{ns}	70.53"	-80
A110		-7.37**	-12.75**	8.45**	2.83**	-0.37**	-0.88	-0.64**	-0.77	17.12 ^{ns}	10.07 ^{ns}	31.53 ^{ns}	39.50 ^{ns}
A260		26.13**	29.77**	-18.55**	-7.39**	*-	1.67**	0.74**	1.58**	-43.59**	-112.44**	-62.97*	-199.70**
AGHK2	RGHK50	su 🔽	9.48**	-2.52**	-2.21**	-1.1	-0.97	0.12 ^{ns}	-1.01**	6.37 ^{ns}	1.89 ^{ns}	-13.63 ^{ns}	-59.30**
A30		-17.76**	-26.50**	12.62**	6.77"	0.47**	0.18 ^{ns}	-0.22**	0.19 ^{ns}	-20.09 ^{ns}	100.48**	45.03 ^{ns}	291.50**
A44		-6.13**	-1.89 ^{ns}	-29.92**	-14.05**	-1.08**	-1.34**	1.60**	0.16 ^{ns}	-19.10 ^{ns}	69.88	-18.93 ^{ns}	104**
A110		17.90**	2.39*	8.90	3.45**	0.76**	-0.08 ^{ns}	-0.53**	-0.03 ^{ns}	-39.87**	13.98 ^{ns}	-77.47**	82.80**
A260		-21.80**	-9.22**	39.18**	20.43**	0.31*	1.50**	0.44**	0.81**	57.32**	-45.82**	105.87**	-152.80**
AGHK2	RGHK56	10.03**	8.72**	-18.16**	-9.82**	0.01 ^{ns}	-0.08 ^{ns}	-1.52**	-0.94	1.64 ^{ns}	-38.04 ^{ns}	-9.47 ^{ns}	-34 ^{ns}
A30		-4.75**	13.72**	13.66**	7.81**	0.47**	1.52**	0.46**	0.93**	-31.22**	-78.68**	-71.60**	-120.50**
A44		-23.71**	3.06*	14.51**	7.22**	-0.31*	0.05 ^{ns}	-0.20*	0.01 ^{ns}	59.15**	102.93**	136.53**	142.30**
A110		13.03**	-18.40**	-1.89**	1.21**	0.47**	-0.51**	-0.65**	-0.96	-38.05**	-33.47 ^{ns}	-46.80*	-7.30 ^{ns}
A260		15.42**	1.62 ^{ns}	-26.29**	-16.25**	-0.63**	-1.06**	0.40**	0.02 ^{ns}	10.12 ^{ns}	9.23 ^{ns}	-18.13 ^{ns}	-14.50 ^{ns}
SE (SCA)		1.7	2.23	0.95	0.6	0.24	0.23	0.17	0.28	26.42	43.32	46.16	41.77
Remarks: *, superoxide c	** and ns = 5 lismutase	significant e	at 5 % and ′	1 % probat	oility levels	and not sig	gnificant, r	espective	ely; S = str	ess; NS = r	ion-stress; (CAT = catala	lse; SOD =

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The average degree of dominance for most of the traits ranged from incomplete dominance to over-dominance, suggesting the existence of non-additive gene action for these agronomic traits in sunflower (Table 3). Rauf, Shahzad, Teixeira da Silva, & Noorka (2012) also reported the preponderance of dominance effects for this trait. As shown in Table 3, broad sense heritability ranged from 0.3 (plant height) to 6.99 (head seed number). Most of the traits under investigation showed average narrow sense heritability. Average to high narrow sense heritability estimates over two years indicates the efficiency of selection for these traits. Memon, Baloch, Baloch, & Jatoi (2015) also reported high heritability estimates for 1000-seeds weight, head seed number, oil content and seed yield in sunflower using line x tester analysis. Naghavi, Pour Aboughadareh, & Khalili (2013) and Tan & Kaya (2019) found similar results for other plant material in sunflower.

CONCLUSION

In terms of general combining ability under stress conditions, the AGHK30 line was the best line and RGHK50 was the best tester. Hybridization of RGHK56 x AGHK44 was considered the best hybrid in optimum and stress conditions. The hybrids were examined for the first time and their hybrids were resistant and had optimum performance under optimum and limited conditions. It is suggested that the best lines and the best parent pair should be tested for stability analysis in different areas.

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