Journal of Plant Physiology and Breeding

2012, 2(2): 35-44 ISSN: 2008-5168

Combining Ability and Gene Action in Sunflower Using Line*Tester Method

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Received: July 27, 2012 Accepted: Dec 10, 2012
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Abstract
In order to analyze general and specific combining abilities and gene effects in sunflower for some agronomic traits, five CMS lines and four restorer lines (tester) were crossed in a line × tester scheme. Hybrids were evaluated in a randomized complete block design with three replications in the Agriculture Research Station, University of Tabriz, in 2009 and 2010 growing seasons. Plant height, head diameter, empty seeds per head, days to beginning of flowering, days to maturity, stem diameter and 1000 seed weight were found to be controlled mainly by additive gene effects and over-dominance effect was important for days to end of flowering. Oil yield, oil percent, head dry weight, seed weight per head, seed yield and hulled seed yield were under the control of both additive and non-additive effects. CMS lines 52, 148 and testers R_{50}, R_{25} were best general combiners for seed and oil yield. The hybrid combination of R_{50} × 222 showed high specific combining ability for seed and oil yield.

Keywords: Combining ability; Genotype × environment interaction; Line × tester; Sunflower

Introduction

Sunflower 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 quality and resistance to disease. 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 F_1 mean values (Mijic *et al.* 2008). Combining ability of inbred lines could be estimated with various methods such as top cross. Line × tester analysis is an extension of this method in which several testers are used (Kempthorne 1957).

Ashok *et al.* (2000) analyzed four male sterile lines and 10 testers and found additive gene effects for seed yield. However, Mohanasondaram (2010), Tan (2010) and Asish (2009) analyzed gene effects of inbred lines using line × tester method and reported that non-additive effects were more important for seed yield. Putt (1996) also observed that non-additive component was more important than the additive component in governing seed yield in sunflower. In addition, Gangappa *et al.* (1997) 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 in this crop is justified due to the existence of non-additive type of gene action for seed yield.

Additive gene action was reported for plant height, days to 50% flowering (Bhat *et al.* 2000) and head diameter (Gvozdenovic *et al.* 2005), however, non-additive gene effects have also been reported for plant height (Gvozdenovic *et al.* 2005, Gouri Shankar *et al.* 2007) and days to 50% flowering (Gouri Shankar *et al.* 2007). Karasu *et al.* (2010) showed significant general combining ability for plant height, seed number per head, 1000 seed weight and seed yield. Hity (1992) indicated the importance of both additive and non-additive gene action in controlling 1000 seed weight and oil percentage, while for oil percentage, Ortis *et al.* (2005) and Skoric *et al.* (2007) stressed the preponderance of additive type of gene effects and non-additive gene effects, respectively.

Though sunflower hybrids are high yielders, the G × E interaction influence their performance (Balu *et al.* 2007). Sharma *et al.* (2003) analyzed 60 hybrids in two environments and reported a significant line × tester × environment effects for head diameter, seed yield, days to beginning of flowering, plant height and 1000 seed weight. In a study of 80 hybrids, Ortis *et al.* (2005) reported significant line × environment and tester × environment for all traits and, also, significant line× tester × environment effects for all traits except plant height.

The aim of this study was to determine the combining ability, gene actions and G × E interactions in sunflower using a line × tester method with five lines and four testers.

Material and Methods

Plant materials used in this study consisted of five CMS lines (344, 330, 222, 148, 52) and four male restorer lines (R_{50}, R_{26}, $R_{25,}$ R_{23}), developed in the Khoy field station, West Azarbaijan province, Iran. The CMS lines were crossed with testers in a line × tester method. The progenies were evaluated in 2009 and 2010 growing seasons using randomized complete block design with three replications in each year. The plots consisted of two rows of 5 m long. The row to row spacing was 65 cm and the plants spaced at 25 cm within the rows. The following traits were measured during growing season: plant height, stem and head diameter, dry weight, empty seeds per head, seed weight per head, seed number per head, hulled seed yield, oil content, days to beginning and end of flowering, days to maturity, seed yield and 1000 seed weight.

General combining ability (GCA) of lines and testers and specific combining ability (SCA) effects for each character were calculated using means of F1 hybrids over two years as follows:

$$\text{GCA (Line)} = \bar{Y}i. - \bar{Y}..$$

$$\text{GCA (Tester)} = \bar{Y}.j - \bar{Y}..$$

$$\text{SCAij} = \bar{Y}ij - \bar{Y}i. - \bar{Y}.j + \bar{Y}..$$

Where, $\bar{Y}ij$, $\bar{Y}i.$, $\bar{Y}.j$ and $\bar{Y}..$ are mean of F1 hybrid of the i^{th} line with j^{th} tester, mean of all F1 hybrids related to the i^{th} line, mean of all F1 hybrids related to the j^{th} tester and mean of all hybrids, respectively.

Estimates of GCA and SCA variances were obtained by expected values of mean squares, assuming lines and testers as fixed and years as random factors. Additive genetic variances were calculated by the pooled estimates of GCA variances for lines and testers as below:

$$\sigma^2_A = 2\sigma^2_{GCA}$$

where, σ^2_A and σ^2_{GCA} are additive genetic variance and pooled GCA variance of lines and testers, respectively, assuming that the coefficient of inbreeding is unity.

Dominance variance (σ^2_D), narrow sense heritability (h^2_N) and broad sense heritability (h^2_B) were obtained using the following formulae:

$$\sigma^2_D = \sigma^2_{SCA}$$
$$h^2_N = \sigma^2_A / \sigma^2_{Ph}$$
$$h^2_B = \sigma^2_A + \sigma^2_D / \sigma^2_{Ph}$$
$$\sigma^2_{Ph} = \sigma^2_A + \sigma^2_D + \sigma^2_{E/ry}$$

where, σ^2_{Ph}, σ^2_E, r and y are phenotypic variance on the entry mean basis, error variance, number of replications and number of years, respectively.

Results and Discussion

Combined analysis of variance over years showed significant differences among lines for all traits except plant height, head diameter, 1000 seed weight, empty seeds per head and days to end of flowering (Table 1). Variance among testers was also significant for all traits except empty seeds per head and days to beginning of flowering. Line × tester interaction was significant for all traits except plant height, head diameter and empty seeds per head. Line × year interactions were significant for 1000 seed weight, empty seed per head, seed number per head, days to beginning of flowering and days to end of flowering. Tester × year effect was significant for empty seed per head and line × tester × year interaction were significant for empty seed per head and days to end of flowering Table 1). This indicates that the differences among GCA of testers and lines were not similar in different years for these traits.

As it was indicated, dominance effects (line × tester interaction) were not significant for plant height, head diameter, head dry weight, days to end of flowering and oil yield. Therefore, these characters were controlled mainly by additive gene action. Additive type of gene action for head diameter was also observed by Gvozdenovic *et al.* (2005). For stem diameter, 1000 seed weight, seed weight per head, seed yield, seed number per head, days to beginning of flowering, days to maturity and oil percent both additive and dominance effects were involved in governing these traits. Hity (1992) also reported the role of both additive and dominance gene action in the inheritance of 1000 seed weight. However, for stem diameter, days to beginning of flowering, 1000 seed weight and days to maturity the GCA/SCA ratios were larger than unity showing the importance of additive gene effects (data not shown). Bhat *et al.* (2000) also observed additive type of gene action for plant height and days to 50% of flowering in sunflower. Furthermore, Karasu *et al.* (2010) reported significant general combining ability for plant height, 1000 seed weight and seed number per head. On the other hand, Putt (1996), Gvozdenovic *et al.* (2005) and Gouri Shankar *et al.* (2007) indicated non-additive gene effects for plant height and days to 50% flowering in sunflower. Similar to our finding, Hity (1992) reported the importance of both additive and non-additive gene effects in controlling the oil percentage while other workers has indicated the role of either additive gene action (Ortis *et al.* 2005) or non-additive gene action (Skoric *et al.* 2007) in relation to this character. Putt (1996) also stated that seed yield is controlled by both types of gene action, but according to his results, non-additive component was more important than the additive component. Gangappa *et al.* (1997) 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 under study.

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 2). Average degree of dominance for days to end of flowering was 1.93 indicating the presence of over-dominance effects in governing this trait (Table 2). Sanchez *et al.* (1999) also reported the preponderance of dominance effects for this trait.

As shown in Table 2, broad sense heritability ranged from 0.62 (head dry weight) to 0.96 (days to beginning of flowering). Most of the traits under investigation showed medium narrow sense heritability. Medium to high narrow sense heritability estimates over two years indicate the efficiency of selection for these traits. Khan *et al.* (2008) also reported high heritability estimates for 1000 seed weight, seed number per head, oil percent and seed yield in sunflower using line*tester analysis. Senevirathne *et al.* (2004) found similar results for other plant material in sunflower.

Table 1. Summary of combined analysis of variance for sunflower characters in the line*tester cross

SV	df	Plant height	Stem diameter	Head diameter	Head dry weight	1000 seed weight	Seed weight per head	Seed yield
Year	1	5661.292*	137.645*	32.085**	9908.537**	5826.781**	12000.180**	7893.138**
R/Y	4	339.313**	6.650**	0.538**	146.649^{ns}	97.554*	70.677^{ns}	46.489^{ns}
Line	4	125.901^{ns}	20.931*	1.124^{ns}	524.809*	500.906^{ns}	913.462*	304.406*
Tester	3	1070.601*	18.732*	5.156*	315.531^{ns}	333.164*	271.4420*	178.515*
L × T	12	100.655^{ns}	3.017*	1.639^{ns}	209.446^{ns}	71.827*	131.853*	86.737*
L× Y	4	160.774^{ns}	0.355^{ns}	1.616^{ns}	139.084^{ns}	172.406*	104.888^{ns}	69.008^{ns}
T × Y	3	15.138^{ns}	0.147^{ns}	1.484^{ns}	131.890^{ns}	13.677^{ns}	87.462^{ns}	57.566^{ns}
L×T×Y	12	110.277^{ns}	1.779^{ns}	0.868^{ns}	140.005^{ns}	22.562^{ns}	58.956^{ns}	38.785^{ns}
Error	76	78.895	1.596	1.021	123.383	31.793	64.545	42.456

$^{*, **}$ and ^{ns} Significant at 5% and 1% probability levels and not significant, respectively

Table 1 Continued

SV	df	Seed number per head	Days to beginning of flowering	Days to end of flowering	Days to maturity	Oil percent	Oil yield
Year	1	2058612.666**	118.008**	46.875*	86.700^{ns}	198.044**	13.224**
R/Y	4	8373.355**	4.642^{ns}	4.300^{ns}	22.400**	3.347**	0.111^{ns}
Line	4	379130.802^{ns}	179.863*	43.242^{ns}	105.583*	27.351*	0.452*
Tester	3	130559.288*	4.697^{ns}	10.386*	60.989*	48.687*	0.354*
L × T	12	36466.707*	9.135*	4.331^{ns}	17.239*	10.923*	0.166^{ns}
L × Y	4	89424.287*	6.613*	25.708*	9.533^{ns}	3.958^{ns}	0.082^{ns}
T × Y	3	19909.145^{ns}	4.564^{ns}	3.519^{ns}	13.611^{ns}	5.408^{ns}	0.043^{ns}
L×T×Y	12	10476.622^{ns}	3.085^{ns}	4.297*	8.111^{ns}	5.131^{ns}	0.118^{ns}
Error	76	13230.710	2.150	1.879	5.575	4.215	0.087

$^{*, **}$ and ^{ns} Significant at 5% and 1% probability levels and not significant, respectively

Table 2. Broad and narrow sense heritability estimates on an entry mean basis and degree of dominance of sunflower characters in the line × tester analysis

	Broad sense heritability	Narrow sense heritability	Degree of dominance
Seed yield	0.74	0.57	0.96
Oil percent	0.83	0.57	0.94
Oil yield	0.71	0.46	1.05
1000 seed weight	0.84	0.63	0.83
Head dry weight	0.62	0.38	1.10
Stem diameter	0.86	0.73	0.60
Days to beginning of flowering	0.96	0.90	0.39
Days to end of flowering	0.67	0.23	1.93
Seed number per head	0.84	0.64	0.69
Seed weight per head	0.74	0.50	0.97
Days to maturity	0.87	0.65	0.87

Earliness is one of the desired characters in the sunflower breeding, therefore, negative GCA values are preferred for days to maturity, days to beginning of flowering and days to end of flowering. CMS lines 344 and 148 had significant and negative GCA for these traits (Table 3). All lines had non-significant general combining ability for plant height except CMS line 330, however, it was positive. CMS lines 52 and 330 had positive and significant GCA for stem diameter. CMS line 52 had the highest GCA for seed number per head. This line had also significant and positive GCA for oil percent. In general, it seems that CMS lines 344, 52 and 148 are suitable general combiners for most of the traits under study and could be utilized in sunflower breeding programs.

Table 3. General combining ability for CMS lines of sunflower in the line × tester analysis

CMS	Plant height	Stem diameter	Head diameter	Head dry weight	1000 seed weight	Seed weight per head	Seed yield
52	1.294^{ns}	1.026^{**}	0.133^{ns}	1.536^{ns}	-3.774^{*}	2.0286^{ns}	1.654^{ns}
148	-1.295^{ns}	0.260^{ns}	-0.165^{ns}	2.743^{ns}	-1.269^{ns}	2.997^{ns}	2.430^{ns}
222	-1.922^{ns}	$-1/033^{**}$	0.041^{ns}	1.072^{ns}	-3.768^{*}	0.705^{ns}	0.580^{ns}
330	3.816^{*}	0.670^{*}	0.261^{ns}	2.898^{ns}	1.700^{ns}	1.9892^{ns}	1.622^{ns}
344	0.356^{ns}	-0.919^{*}	-0.270^{ns}	-8.247^{*}	7.110^{**}	-7.720^{**}	-6.252^{**}
SE (GCA)	1.765	0.252	0.204	2.252	1.089	1.651	1.330
SE(g_i-g_j)	2.497	0.357	0.288	3.185	1.541	2.335	1.890

*, ** and ^{ns} Significant at 5% and 1% probability levels and not significant, respectively

Table 3. Continued

CMS	Seed number per head	Days to beginning of flowering	Days to end of flowering	Days to maturity	Oil percent	Oil yield
52	99.171^{**}	3.717^{**}	1.192^{**}	2.625^{**}	1.191^{*}	0.080^{ns}
148	51.683^{ns}	-2.283^{**}	-1.225^{**}	-1.042^{*}	0.539^{ns}	0.112^{ns}
222	48.030^{ns}	-1.158^{**}	-0.308^{ns}	-0.958^{ns}	0.454^{ns}	0.057^{ns}
330	20.137^{ns}	2.050^{**}	1.608^{**}	1.750^{**}	-0.739^{ns}	-1.019^{ns}
344	-219.020^{**}	-2.325^{**}	-1.267^{**}	-2.375^{**}	-1.448^{*}	-0.230^{*}
SE (GCA)	25.971	0.278	0.264	0.466	0.391	0.068
SE(g_i-g_j)	36.720	0.394	0.373	0.660	0.553	0.0957

$^{*, **}$ and ^{ns} Significant at 5% and 1% probability levels and not significant, respectively

The highest negative GCA effect for days to maturity, days to beginning of flowering and days to end of flowering were achieved for R_{25} and R_{26}, however, only days to maturity was significant for R_{25} (Table 4). R_{23} had genes for short stature. R_{23} also had the highest positive GCA for oil yield and 1000 seed weight. R_{50} restorer line, had significant GCA for stem diameter, seed weight per head and seed yield. On the other hand, R_{25} showed high and significant GCA for oil percent. It looks like R_{50} and R_{25} restorer lines were good testers for additive genes for most of the traits under study.

Table 4. General combining ability for restorer lines of sunflower in the line × tester analysis (average of two years)

Restorer	Plant height	Stem diameter	Head diameter	Head dry weight	1000 seed weight	Seed weight per head	Seed yield
R_{50}	7.904^{**}	1.167^{**}	0.315^{ns}	4.397^{ns}	-0.238^{ns}	4.224^{*}	3.430^{*}
R_{26}	-2.450^{ns}	-0.197^{ns}	0.216^{ns}	0.471^{ns}	-1.061^{ns}	0.048^{ns}	0.047^{ns}
R_{23}	-6.171^{*}	-0.494^{ns}	0.068^{ns}	-2.178^{ns}	4.605^{**}	-2.426^{ns}	-1.958^{ns}
R_{25}	0.717^{ns}	-0.476^{ns}	-0.603^{*}	-2.692^{ns}	-3.640^{*}	-1.847^{ns}	-1.488^{ns}
SE (GCA)	1.579	0.226	0.1825	2.014	0.974	1.477	1.19
SE(g_i-g_j)	2.233	0.319	0.258	2.849	1.378	2.089	1.69

$^{*, **}$ and ^{ns} Significant at 5% and 1% probability levels and not significant, respectively

Table 4. Continued

Restorer	Days to beginning of flowering	Days to end of flowering	Days to maturity	Oil percent	Oil yield	Seed number per head
R_{50}	0.292^{ns}	0.858^{*}	0.083^{ns}	-9.206^{**}	0.156^{*}	72.127^{*}
R_{26}	-0.175^{ns}	-0.442^{ns}	-0.683^{ns}	-1.229^{*}	-0.011^{ns}	6.984^{ns}
R_{23}	0.358^{ns}	-0.108^{ns}	1.950^{**}	-0.436^{ns}	0.933^{**}	-87.906^{*}
R_{25}	-0.475^{ns}	-0.308^{ns}	-1.350^{*}	1.777^{**}	-0.059^{ns}	8.794^{ns}
SE (GCA)	0.249	0.236	0.417	0.350	0.060	23.23
SE(g_i-g_j)	0.352	0.334	0.59	0.495	0.085	32.85

$^{*, **}$ and ^{ns} Significant at 5% and 1% probability levels and not significant, respectively

F_1 hybrid R_{50} × 222 showed positive and significant SCA for head dry weight, 1000 seed weight, seed yield, oil percent and oil yield (Table 5). Based on Table 6, Hybrid R_{25} × 148 had the highest oil percent (51.76%) while R_{50} × 222 had the highest oil yield (1.763). Hybrids R_{26} × 148, R_{50} × 52 and R_{23} × 222, R_{50} × 52 had negative and significant SCA for days to beginning of flowering and days to end of flowering. R_{50} × 344, R_{25} × 344, R_{23} × 344 and R_{26} × 344 had highest negative and significant SCA for days to maturity. In all of these hybrids, CMS line 344 which had high GCA for days to maturity was one of the parental lines. R_{50} × 344 had positive and significant SCA for stem diameter and seed number per head. Hybrids R_{50} × 222, R_{50} × 52, R_{50} × 330 and R_{50} × 344 had highest positive and significant SCA for oil percent. R_{50} was one of the parents in these hybrids. Based on Table 6, 1000 seed weight had the highest value (71.01 g) in R_{23} × 344 hybrid. Since 1000 seed weight is one of the important yield components, any breeding action for increasing this trait will be useful in improving the seed yield. Hybrid R_{50} × 222 had high and significant SCA for seed yield. In general, R_{50} × 222 and R_{50} × 344 were more promising hybrids for some important agronomic characters in this investigation. The presence of non-additive type of gene action for seed yield in this study justifies the production of hybrid varieties in sunflower.

Table 5. Specific combining ability for 20 hybrids of sunflower in the line × tester analysis ((average of two years)

CMS	Restorer	Plant height	Stem diameter	Head diameter	Head dry weight	1000 seed weight	Seed weight per head	Seed yield
52	R_{50}	-8.461^{**}	-1.097^{*}	-0.465^{ns}	-4.550^{ns}	-3.032^{ns}	-4.969^{ns}	-4.033^{ns}
330	R_{50}	1.008^{ns}	-0.421^{ns}	-0.560^{ns}	-6.604^{ns}	2.456^{ns}	-4.070^{ns}	-3.304^{ns}
344	R_{50}	6.736^{*}	1.074^{*}	0.691^{ns}	4.130^{ns}	-0.483^{ns}	4.650^{ns}	3.781^{ns}
222	R_{50}	-1.326^{ns}	0.183^{ns}	0.563^{ns}	8.490^{*}	5.376^{*}	7.580^{ns}	6.074^{*}
148	R_{50}	-0.163^{ns}	0.308^{ns}	-0.183^{ns}	-1.450^{ns}	-1.770^{ns}	-3.116^{ns}	-2.519^{ns}
222	R_{26}	-1.135^{ns}	-0.112^{ns}	-0.361^{ns}	-4.376^{ns}	3.771^{*}	-3.450^{ns}	-2.870^{ns}
52	R_{26}	3.488^{ns}	0.873^{ns}	0.528^{ns}	6.060^{ns}	4.420^{*}	4.162^{ns}	3.370^{ns}
148	R_{26}	-1.738^{ns}	-0.138^{ns}	0.051^{ns}	2.330^{ns}	3.673^{ns}	1.884^{ns}	1.537^{ns}
330	R_{26}	2.916^{ns}	0.655^{*}	0.588^{ns}	2.768^{ns}	1.288^{ns}	2.092^{ns}	1.695^{ns}
344	R_{26}	-5.755^{ns}	-1.250^{*}	-0.741^{*}	-6.764^{ns}	-3.071^{ns}	-4.594^{ns}	-3.720^{ns}
148	R_{23}	0.581^{ns}	-0.209^{ns}	-0.128^{ns}	-5.766^{ns}	5.283^{*}	-3.746^{ns}	-5.033^{*}
222	R_{23}	3.351^{ns}	0.091^{ns}	-0.286^{ns}	-2.030^{ns}	-3.073^{ns}	-2.680^{ns}	-2.257^{ns}
52	R_{23}	5.761^{ns}	0.185^{ns}	-0.056^{ns}	-2.200^{ns}	-0.615^{ns}	1.548^{ns}	1.249^{ns}
344	R_{23}	0.856^{ns}	0.487^{ns}	0.483^{ns}	7.015^{ns}	2.223^{ns}	3.312^{ns}	2.680^{ns}
330	R_{23}	-3.780^{ns}	-0.223^{ns}	0.046^{ns}	2.975^{ns}	-1.260^{ns}	1.656^{ns}	1.337^{ns}
52	R_{25}	-0.756^{ns}	0.347^{ns}	-0.046^{ns}	0.693^{ns}	-0.430^{ns}	-0.743^{ns}	-0.609^{ns}
330	R_{25}	-0.145^{ns}	-0.002^{ns}	-0.125^{ns}	0.868^{ns}	-2.090^{ns}	0.321^{ns}	0.250^{ns}
344	R_{25}	-1.800^{ns}	-0.274^{ns}	-0.404^{ns}	-4.360^{ns}	1.694^{ns}	-3.373^{ns}	-2.735^{ns}
148	R_{25}	1.350^{ns}	0.087^{ns}	0.307^{ns}	4.872^{ns}	3.186^{ns}	4.960^{ns}	4.034^{ns}
222	R_{25}	-0.888^{ns}	-0.133^{ns}	0.116^{ns}	-2.059^{ns}	1.841^{ns}	-1.092^{ns}	-0.962^{ns}
SE(SCA)		3.531	0.505	0.408	4.505	2.179	3.303	2.670

$^{*, **}$ and ^{ns} Significant at 5% and 1% probability levels and not significant, respectively

Table 5. Continued

CMS	Restorer	Days to beginning of flowering	Days to end of flowering	Days to maturity	Oil percent	Oil yield	Seed number per head
52	R_{50}	-1.240**	-1.015*	-1.616*	9.390**	-0.116ns	-78.07ns
330	R_{50}	0.928ns	0.408ns	0.420ns	9.305**	-0.146ns	-90.62*
344	R_{50}	-0.701ns	-0.388ns	-7.616**	9.130**	0.127ns	92.06*
222	R_{50}	-0.528ns	-0.181ns	1.296ns	10.69**	0.284*	63.60ns
148	R_{50}	1.591**	1.228*	0.553ns	6.990**	-0.192ns	13.05ns
222	R_{26}	1.998**	1.285*	1.566ns	-0.717ns	-0.108ns	-9.16ns
52	R_{26}	0.950ns	-0.048ns	1.153ns	0.531ns	0.165ns	-160.98**
148	R_{26}	-2.215**	-0.638ns	-3.010**	-1.530*	-0.011ns	36.94ns
330	R_{26}	0.121ns	0.198ns	-0.143ns	1.020ns	0.0885ns	21.61ns
344	R_{26}	1.158*	-0.755ns	-6.513**	0.731ns	-0.123ns	-52.62ns
148	R_{23}	0.855ns	-0.301ns	2.683**	1.370*	0.072ns	-118.77*
222	R_{23}	-0.765ns	-1.045*	-2.240*	-0.784ns	-0.034ns	11.36ns
52	R_{23}	0.021ns	0.955*	-0.986ns	0.276ns	-0.006ns	27.33ns
344	R_{23}	0.228ns	0.581ns	-6.653**	-0.296ns	0.0320ns	56.26ns
330	R_{23}	-0.308ns	-0.131ns	0.216ns	-0.523ns	-0.0398ns	23.76ns
52	R_{25}	0.685ns	-0.045ns	1.480ns	-1.076ns	-0.039ns	47.45ns
330	R_{25}	-0.311ns	-0.431ns	-0.483ns	-0.680ns	0.117ns	45.25ns
344	R_{25}	-0.275ns	0.615ns	-7.186**	-0.438ns	-0.115ns	-95.70*
148	R_{25}	0.185ns	-0.268ns	-0.183ns	2.280**	0.154ns	68.79ns
222	R_{25}	-0.268ns	-0.0116ns	-0.606ns	-0.087ns	-0.097ns	-65.80ns
SE(SCA)		0.557	0.528	0.933	0.783	0.135	51.94

*, ** and ns Significant at 5% and 1% probability levels and not significant, respectively

Table 6. Means of different traits for sunflower hybrids in a line*tester cross (average of two years)

Line	Tester	Plant height	Stem diameter	Head diameter	Head dry weight	1000 seed weight	Seed weight per head	Seed yield
52	R_{50}	131.9	18.54	14.09	67.65	50.04	44.17	35.47
330	R_{50}	143.9	18.86	14.12	66.97	61	45.03	36.17
344	R_{50}	146.2	18.76	14.84	66.55	63.46	44.05	35.37
222	R_{50}	135.8	17.76	15.03	80.23	58.45	55.31	44.50
148	R_{50}	137.6	19.17	14.07	71.97	51.30	46.99	37.76
222	R_{26}	125.7	16.10	14	63.44	48.48	40.10	32.17
52	R_{26}	133.5	19.15	14.98	74.34	56.68	49.12	39.49
148	R_{26}	125.7	17.36	14.20	71.83	55.92	47.81	38.43
330	R_{26}	135.5	18.58	15.17	72.41	58.98	47.01	37.78
344	R_{26}	123.3	15.07	13.31	51.73	60.06	30.62	24.48
148	R_{23}	124.3	16.99	13.88	61.08	63.19	39.71	31.85
222	R_{23}	126.4	16.01	13.93	63.14	54.84	38.39	30.79
52	R_{23}	123.1	17.87	14.25	63.44	57.29	44.04	35.36
344	R_{23}	126.2	16.51	14.39	62.87	71.01	36.05	28.88
330	R_{23}	125.1	17.40	14.48	69.97	62.12	44.11	35.42
52	R_{25}	132.4	18.34	13.68	65.82	49.24	42.33	33.97
330	R_{25}	135.6	17.64	13.73	67.35	53.05	43.35	34.80
344	R_{25}	130.4	15.77	12.84	50.97	62.25	29.94	23.93
148	R_{25}	131.9	17.31	13.65	71.2	52.86	49.01	39.39
222	R_{25}	129.1	15.80	13.67	62.59	51.51	40.56	32.55
LSD5%		10.256	1.459	1.167	12.826	6.511	9.277	7.524

Table 6. Continued

line	tester	Seed number per head	Days to beginning of flowering	Days to end of flowering	Days to maturity	Oil percent	Oil yield
52	R_{50}	883.9	68.83	77.50	115.3	48.52	1.393
330	R_{50}	792.3	69.33	79.33	116.5	46.51	1.263
344	R_{50}	735.8	63.33	75.67	111.3	45.2	1.420
222	R_{50}	974.4	64.67	76.83	114.7	49.10	1.763
148	R_{50}	927.5	65.67	77.33	113.8	45.48	1.347
222	R_{26}	836.5	66.33	77	114.2	45.66	1.210
52	R_{26}	900	70.17	77.17	117.3	47.64	1.513
148	R_{26}	886.3	61	74.17	109.5	44.93	1.367
330	R_{26}	839.4	67.67	77.83	115.2	46.2	1.337
344	R_{26}	526	64.33	74	111.7	45.2	0.920
148	R_{23}	635.7	65	74.83	117.8	48.62	1.373
222	R_{23}	762.1	64.50	75	113.0	46.39	1.203
52	R_{23}	829.3	70.17	78.5	117.8	48.18	1.277
344	R_{23}	540	64.33	75.67	114.2	44.97	0.9900
330	R_{23}	746.6	68.17	77.83	118.2	45.45	1.130
52	R_{25}	946.1	70	77.50	117.0	49.05	1.260
330	R_{25}	864.8	67.33	77.33	114.2	47.51	1.317
344	R_{25}	484.7	63	75.50	110.3	47.04	0.8733
148	R_{25}	919.9	63.5	74.67	111.7	51.76	1.483
222	R_{25}	781.7	64.17	75.83	111.3	49.30	1.173
LSD5%		132.819	1.693	1.583	2.726	2.371	0.341

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