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STUDY ON THE DETERMINATION OF COMBINING ABILITIES OF INBRED LINES FOR HYBRID BREEDING USING LINE × TESTER ANALYSIS IN SUNFLOWER (*Helianthus annuus* L.)

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SUMMARY

Combining ability studies in oilseed sunflower were undertaken with a set of 5 × 4 line × tester including parents for the characters seed yield, 1000-seed weight, days to flowering, days to physiological maturity, plant height, head diameter, stem diameter, oil content, fatty acid content (oleic, linoleic, palmitic, and stearic acids), protein content, seed length, seed width, and hull percentage. General (GCA) and specific combining abilities (SCA) and heterosis of inbred lines and their hybrids were estimated in a line × tester analysis during the first and second crop production seasons in Menemen, Izmir, Turkey. The variances due to GCA and SCA were highly significant for most of the characters in both environments. The ratio (H/D)1/2 and σ^2 GCA/ σ^2 SCA depicted the preponderance of non-additive type gene action for all the characters except plant height, head diameter, seed length, palmitic acid content, and stearic acid content. However, both types of gene action were observed for seed yield, hull percentage, 1000-seed weight, oil content, and stem diameter at stem curve point. In this study, GCA effects were found to be highly significant for all traits, while SCA effects were non-significant for most of the traits. Based on GCA effects in the first and second crop production seasons, the inbreds 0043 *cms*, 0046 *cms*, 0195 *cms*, 0583 *cms*, 0704 *cms*, 0708 *Rf*, 0845 *Rf*, 0951 *Rf*, and 1097 *Rf* exhibited desirable GCA effects and were found to be good general combiners for most of the traits. Thus, they can be exploited by further breeding for developing superior genotypes and hybrids in sunflower.

Key words: **sunflower, *Helianthus annuus* L., hybrid, breeding, genetics, general combining ability (GCA), specific combining ability (SCA), heterosis**

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INTRODUCTION

As the leading product in the production of oilseeds with great importance in human nutrition, sunflower has a significant place in the Turkish economy. Our vegetable oil deficit, which is increasing with the rapid population growth, will only be closed via increased production, which is possible, in turn, through the utilization of the existing potential area, the preference of sunflower specifically as a secondary product, and the application of new technologies. In hybrid breeding, grain and oil yields are increased by using the heterosis effect. The high performance of hybrid combinations depends on the combining abilities of parents and success in combination breeding is secured via the selection of the right parents (Tan, 1993; Tan, 2000; Tan, 2004; Tan, 2005; Tan, 2009). Therefore, parents must be examined in terms especially of economically significant properties to select the right ones to form hybrids. Properties addressed for heritability in plant breeding are also significant in terms of selection feasibility. As a general definition, heritability is defined as the ratio of total genotypic variance (encompassing additive, dominant and epistatic variances) to phenotypic variance (Kemptorne, 1957; Falconer, 1975). In the narrow sense, heritability is the ratio of additive variance (which is of great importance in terms of the properties to be transferred to the next generation) to the total variance (Falconer, 1975). Grain yield in sunflower depends on a number of factors, most notably the environment.

Plant breeders aim to reach the maximum level of heterosis during hybridization. Hallauer and Miranda (1981) divided heterosis-related studies into two categories:

a) physiological impulse, allelic interaction or over-dominance, and
b) correct dominance factor.

On the other hand, different views proposed to explain heterosis focus on three points, which are:

1. partial dominance,
2. super dominance and
3. varied epistasis.

However, the correct thesis has not yet been determined.

Studies on the properties under the influence of the combining ability are especially important for successful hybrid breeding. Combining ability is defined as the ability to transfer the desired properties of appropriated lines entered into hybrid combinations to hybrid offspring (Hayes and Immer, 1942). Sprague and Tatum (1942) define general combining ability as the average performance of a line in a hybrid combination and specific combining ability as the better or poorer performance than expected of a given hybrid combination. Properties under the influence of general combining ability are affected by additive gene action, while properties under the influence of specific combining ability are affected by non-additive gene action or dominant and/or epistatic gene action (Falconer, 1975). Falconer (1975)

established that the difference in general combining ability stems from additive variance and additive × additive interaction due to different environmental conditions, while the difference in specific combining ability is attributed to non-additive genetic variance. General/specific combining power can be estimated via various methods, the most common of which is diallel analysis (Griffling, 1956). Line × tester (multiple sequence) analysis is the modified version of the top-cross method proposed by Kemptorn (1957) and is used as a suitable method for hybrid variety breeding programs where especially cytoplasmic sterile and restorer lines are included as parents (Singh and Chaudary, 1977). The main objective of this study is to calculate general and specific combining ability and heterosis, heterobeltiosis values and heritability to identify hybrids that are suitable in terms of the addressed properties for parent breeding.

MATERIAL AND METHODS

In this study, five cytoplasmic male sterile (*cms*) lines (*cms* 0043, *cms* 0046, *cms* 0195, *cms* 0583 ve *cms* 0704) and four restorer (*Rf*) lines (0708 *Rf*, 0845 *Rf*, 0951 *Rf* ve 1097 *Rf*) were hybridized via the line × tester (multiple sequence) method. Five cytoplasmic male sterile (*cms*) and 4 restorer lines were crossed. The plant characters: seed yield (g), 1000-seed weight (g), days to flowering, days to physiological maturity, plant height (cm), head diameter (cm), stem diameter at the bottom internode (cm), stem diameter at stem curve point (cm), oil content %, oleic acid content %, linoleic acid content %, palmitic acid content %, stearic acid content %, protein content %, seed length (mm), seed width (mm), and hull percentage were studied.

Parental lines (*cms* and *Rf*) in the study were as follows:

Parents	*cms* / *Rf*	Habitus	Type
0043	*cms**	Non-branched, Single headed	Oilseed
0046	cms	Non-branched, Single headed	Oilseed
0195	cms	Non-branched, Single headed	Oilseed
0583	cms	Non-branched, Single headed	Oilseed
0704	cms	Non-branched, Single headed	Oilseed
0708	RfRf	Non-branched, Single headed	Oilseed
0845	RfRf	Non-branched, Single headed	Oilseed
0951	RfRf	Non-branched, Single headed	Oilseed
1097	RfRf	Non-branched, Single headed	Oilseed

* *cms* : Cytoplasmic male sterile line; *Rf*: Restorer line

Parents and their hybrids were planted in three rows per plot. The rows were 0.70 m apart and 7.70 m in length. At the harvest, the 1st and 3rd rows and first and last plants of the middle row were removed as the edge effect and 20 plants in the middle were harvested for evaluation.

All values were first evaluated via variance analysis (VA) (Steel ve Torrie, 1980), after which line × tester analysis was applied (Singh ve Chaudary, 1977).

A two-sided table was created for lines (*cms*) and testers (*Rf*) in the line × tester analysis to degrade hybrid squares into the mother, father, and mother × father interaction components (Singh and Chaudary, 1977).

Hybrid values were created on the basis of average values (Arunachalam, 1974).

GCA effects of lines and testers, SCA effects of lines × testers, and the variances of these values were calculated (Griffling, 1956; Kempthorn, 1957; Rao *et al*., 1968; Singh and Chaudary, 1977).

The KOV(HS) average value was equivalent to the GCA variance and the KOV(FS) value was equivalent to the SCA variance. These values and additive variance (σ^2D) and dominance variance (σ^2H) components were used to identify proportional relations.

General (GCA) and specific combining ability (SCA) and heterosis of inbred lines and their hybrids were estimated in a line × tester analysis during the first and second crop production seasons in Menemen, Izmir - Turkey.

Heterosis, heterobeltiosis (Hallauer and Eberhard, 1966; Hallauer and Miranda, 1981):

$$\% \text{ Heterosis (Hs)} = \frac{F_1 - MP}{MP} \times 100$$

Significance check of heterosis (Cochran and Cox, 1957; Steel and Torrie, 1980):

$$\% \text{ Heterobeltiosis (Hb)} = \frac{F_1 - HP}{HP} \times 100$$

Significance check of heterobeltiosis was performed via LSD test (Fonseca ve Patterson, 1968).

Broad sense heritability (H) values were calculated according to Kempthorn (1957).

$H = (G / F)$ and $h^2 = (A / F)$

Narrow sense heritability (h^2) values were calculated according to Falconer (1975).

Floral receptacles of all *cms* and *Rf* lines were isolated before flowering for the purpose of preventing allogamy. Twenty hybrid (F_1) and nine parent seeds were cultivated according to a randomized block design with four replications under main (primary) and secondary product conditions and evaluated in terms of the addressed properties. The cultivation was in three rows per plot with a length of 7.70 cm and an interval of 70 cm. During the harvest, one plant each from the 1^{st} and 3^{rd} rows and the middle row of each plot were removed as the edge effect and 20 plants in the middle were harvested for evaluation. The properties addressed in

the main and secondary product in the trial plots and harvested seeds were plot yield, 1000-kernel weight, days to flowering, days to physiological maturity, plant weight, receptacle diameter, grain size, grain width, hull ratio, oil ratio, protein ratio, oleic acid ratio, linoleic acid ratio, palmitic acid ratio, stearic acid ratio, stem diameter and head diameter. The findings were processed through pre-variance analysis (Steel and Torrie, 1980) and in case of the presence of inter-genotypic variance; line × tester (multiple sequence) analysis was implemented (Singh and Chaudary, 1977).

Effects of general and specific combining abilities and general and specific combination variances were calculated according to the method proposed by Kempthorn (1957), Rao *et al*. (1968), and Singh and Chaudary (1977). First, a two-sided table (Singh and Chaudary, 1977) was created for lines (*cms*) and testers (*Rf*) in the line × tester analysis and the values thus obtained were used to calculate total repetition values of combinations via degrading hybrid squares into the mother, father, and mother × father interaction components. Hybrid values were created on the basis of average values (Arunachalam, 1974). Two-sided table values, general combining ability effects of lines and testers, and specific combining ability effects of lines × testers – via the method proposed by Griffling (1956) – and the standard deviations of these values were calculated. The KOV(HS) average value was equivalent to the general combining ability variance and the KOV(FS) value to the specific combining ability; these values and additive (D), dominance (H) variance components were used to identify proportional relations. Heterosis (%) and heterobeltiosis (%) values for the properties addressed in the study were calculated according to Hallauer and Eberhard (1966) and Hallauer and Miranda (1981). Significance check of heterosis was calculated according to Cochran and Cox (1957) and Steel and Torrie (1980), while the significance check of heterobeltiosis was performed via LSD test (Fonseca and Patterson, 1968). Narrow (h^2) and broad (H) sense heritability values were calculated according to Kempthorn (1957) and Falconer (1975).

In this study, the statistical significance of the mean square values of the addressed properties confirmed the presence of variance in the research material in terms of these properties.

RESULTS AND DISCUSSION

Variance estimates for GCA and SCA, dominance and additive variance components, and their proportional relations were determined.

All characters were evaluated via variance analysis and highly significant differences were found among the genotypes (Steel and Torrie, 1980) (Tables 1, 2, 3, 4, 5, and 6).

Line × tester analysis (Singh and Chaudary, 1977) indicated that there were significant variations present among the parents and their hybrids for all the traits studied (Tables 7, 8, 9, and 10).

Table 1: First crop mean values of the characters plot seed yield, days to flowering, days to physiological maturity, plant height (cm), head diameter (cm), and 1000-seed weight.

Genotypes	No.	Seed yield	Days to flowering	Days to physiological maturity	Plant height	Head diameter	1000-seed weight
		(g plot^{-1})	(day)	(day)	(cm)	(cm)	(g)
0043 *cms*	1	1243	64.00	101.00	160.00	18.33	54.28
0046 *cms*	2	1041	62.75	103.50	134.40	18.38	48.17
0195 *cms*	3	969	65.25	106.50	129.10	17.15	80.22
0583 *cms*	4	1038	64.25	104.00	114.90	16.05	48.26
0704 *cms*	5	1155	66.00	108.30	146.70	16.63	56.55
0708 *Rf*	6	259	60.75	88.50	107.10	8.23	16.91
0845 *Rf*	7	396	67.25	101.00	116.30	9.35	24.12
0951 *Rf*	8	766	63.25	103.50	111.70	15.20	47.12
1097 *Rf*	9	293	57.00	96.25	112.00	7.90	25.32
0043 × 0708	10	1480	59.50	101.30	174.30	19.20	56.45
0043 × 0708	11	1544	63.75	104.00	178.20	19.23	54.74
0043 × 0951	12	1385	61.75	101.00	146.80	16.27	45.58
0043 × 1097	13	1399	60.50	101.00	168.90	18.63	57.95
0046 × 0708	14	1501	61.75	101.80	169.20	19.33	53.90
0046 × 0845	15	1433	64.00	104.00	164.00	18.55	59.47
0046 × 0951	16	1436	62.25	105.80	150.80	17.60	51.92
0046 × 1097	17	1329	61.00	104.00	165.60	17.33	53.48
0195 × 0708	18	1345	60.00	100.00	147.50	16.77	57.22
0195 × 0845	19	1328	61.75	102.80	139.30	17.55	59.81
0195 × 0951	20	1225	61.00	99.50	122.00	15.32	51.82
0195 × 1097	21	1350	60.00	103.50	149.60	16.60	62.33
0583 × 0708	22	1423	58.50	105.30	137.70	17.77	52.16
0583 × 0845	23	1358	61.75	102.00	140.90	17.95	51.08
0583 × 0951	24	1273	60.50	104.00	134.20	16.45	53.89
0583 × 1097	25	1366	56.50	101.30	135.10	17.95	56.86
0704 × 0708	26	1621	62.00	103.30	150.50	17.73	47.92
0704 × 0845	27	1388	63.75	106.00	153.30	17.75	52.03
0704 × 0951	28	1343	66.25	107.30	163.50	17.65	52.79
0704 × 1097	29	1420	60.50	106.00	164.60	18.85	62.74
LSD (α=0.05):		224.300	1.510	1.282	21.560	2.002	9.210
LSD (α=0.01):		297.300	2.001	1.699	28.570	2.654	12.210

* Significant α=0.01

Table 2: First crop mean values of the characters hull percentage (%), seed length (mm), seed width (mm), and stem lower part and curve diameters (mm).

Genotypes	No.	Hull percentage	Seed length	Seed width	Stem lower part diameter	Stem curve part diameter
		(%)	(mm)	(mm)	(cm)	(cm)
0043 *cms*	1	27.90	11.58	5.71	2.61	1.52
0046 *cms*	2	25.90	10.76	5.50	2.58	1.41
0195 *cms*	3	23.93	12.64	5.83	2.49	1.83
0583 *cms*	4	15.60	12.23	4.32	2.41	1.50
0704 *cms*	5	20.19	11.06	5.44	2.75	1.49
0708 *Rf*	6	28.66	9.28	3.36	2.12	0.92
0845 *Rf*	7	20.30	9.25	4.58	2.22	1.00
0951 *Rf*	8	25.58	12.39	5.09	2.35	1.42
1097 *Rf*	9	20.17	8.50	4.30	1.69	1.09
0043 × 0708	10	24.56	10.82	5.46	2.77	1.48
0043 × 0708	11	24.85	11.41	5.86	2.79	1.49
0043 × 0951	12	24.60	11.48	5.21	2.45	1.30
0043 × 1097	13	25.85	10.74	5.59	2.72	1.50
0046 × 0708	14	24.16	10.35	5.33	2.93	1.52
0046 × 0845	15	23.22	11.26	6.07	2.80	1.52
0046 × 0951	16	22.65	11.29	5.17	2.50	1.34
0046 × 1097	17	22.81	10.19	5.60	2.70	1.40
0195 × 0708	18	23.94	11.46	4.98	2.60	1.75
0195 × 0845	19	21.76	12.28	5.76	2.37	1.51
0195 × 0951	20	24.41	12.24	5.30	2.33	1.33
0195 × 1097	21	22.80	11.54	5.63	2.40	1.52
0583 × 0708	22	21.91	11.43	4.77	2.69	1.59
0583 × 0845	23	17.84	11.74	5.25	2.60	1.52
0583 × 0951	24	19.30	12.18	5.02	2.69	1.54
0583 × 1097	25	20.11	11.03	5.27	2.43	1.54
0704 × 0708	26	25.64	10.66	4.97	2.61	1.42
0704 × 0845	27	21.95	11.11	5.58	2.64	1.45
0704 × 0951	28	22.63	11.43	4.97	2.86	1.39
0704 × 1097	29	23.13	10.65	5.61	2.63	1.54
LSD (α=0.05):		2.583	0.380	0.305	0.393	0.235
LSD (α=0.01):		3.424	0.504	0.404	0.521	0.312

* Significant α=0.01

Table 3: First crop mean values of the characters oil content (%), oleic acid content (%), linoleic acid content (%), palmitic acid content (%), stearic acid content (%), and protein content (%).

Genotypes	No.	Oil content	Oleic acid content	Linoleic acid content	Palmitic acid content	Stearic acid content	Protein content
		(%)	(%)	(%)	(%)	(%)	(%)
0043 *cms*	1	40.60	43.38	42.57	7.68	5.53	20.76
0046 *cms*	2	41.42	48.08	38.75	6.69	5.74	21.47
0195 *cms*	3	43.16	44.49	43.24	6.43	5.13	20.39
0583 *cms*	4	49.06	34.39	52.16	6.91	5.52	22.77
0704 *cms*	5	52.34	40.14	48.37	6.88	3.88	18.99
0708 *Rf*	6	37.91	40.92	45.95	7.39	4.49	20.12
0845 *Rf*	7	50.67	35.69	48.64	7.62	6.63	21.32
0951 *Rf*	8	39.56	40.53	46.02	7.04	5.17	21.49
1097 *Rf*	9	45.22	38.50	47.54	8.24	4.75	23.49
0043 × 0708	10	50.16	45.17	42.44	6.48	4.60	18.56
0043 × 0845	11	49.92	42.62	44.71	6.85	4.86	17.55
0043 × 0951	12	43.60	38.85	47.63	7.00	5.11	18.76
0043 × 1097	13	48.15	44.17	43.51	6.72	4.55	19.44
0046 × 0708	14	49.60	46.40	41.87	6.27	4.48	19.55
0046 × 0845	15	50.69	42.47	44.97	6.80	4.98	18.58
0046 × 0951	16	50.53	39.84	48.02	6.84	4.55	18.44
0046 × 1097	17	50.36	44.32	43.50	6.79	4.53	19.05
0195 × 0708	18	47.76	40.22	47.63	6.63	4.42	17.29
0195 × 0845	19	52.41	38.58	48.79	6.88	4.88	16.47
0195 × 0951	20	42.65	38.24	48.17	7.35	5.32	19.44
0195 × 1097	21	49.46	43.57	44.14	6.54	4.91	18.91
0583 × 0708	22	52.03	41.50	46.58	6.19	4.61	17.67
0583 × 0845	23	54.83	38.11	48.32	6.56	5.72	18.74
0583 × 0951	24	47.04	40.30	46.83	6.43	5.65	22.58
0583 × 0197	25	51.58	43.52	43.35	7.06	5.44	20.37
0704 × 0708	26	48.64	40.87	47.86	7.02	3.91	17.34
0704 × 0845	27	51.88	37.22	50.60	7.33	4.26	16.24
0704 × 0951	28	51.13	37.77	50.19	6.96	3.90	17.58
0704 × 1097	29	49.71	42.24	46.01	7.04	4.42	19.40
LSD (α=0.05):		4.818	2.957	3.035	0.716	0.716	2.433
LSD (α=0.01):		6.386	3.919	4.022	0.943	0.949	3.224

* Significant α=0.01

Table 4: Second crop mean values of the characters plot seed yield, days to flowering, days to physiological maturity, plant height (cm), head diameter (cm), and 1000-seed weight.

Genotypes	No	Seed yield	Days to flowering	Days to physio-logical maturity	Plant height	Head diameter	1000- seed weight
		(g plot^{-1})	(day)	(day)	(cm)	(cm)	(g)
0043 *cms*	1	1040	47.25	90.25	160.90	17.60	59.04
0046 *cms*	2	839	46.25	91.75	162.00	19.88	56.93
0195 *cms*	3	718	46.00	88.50	128.20	16.45	80.86
0583 *cms*	4	829	47.00	90.50	142.40	16.68	68.51
0704 *cms*	5	878	49.25	91.00	155.90	17.05	53.74
0708 *Rf*	6	301	43.25	78.00	107.60	9.14	14.90
0845 *Rf*	7	301	47.00	88.25	114.10	9.10	18.95
0951 *Rf*	8	684	47.50	89.75	132.20	15.25	47.97
1097 *Rf*	9	344	43.75	88.50	128.90	7.71	21.07
0043 × 0708	10	1134	42.00	88.00	164.70	18.24	55.22
0043 × 0708	11	1074	44.25	90.00	176.90	17.30	53.95
0043 × 0951	12	1356	44.75	89.00	177.40	17.34	52.80
0043 × 1097	13	1463	43.75	90.25	180.50	19.09	64.89
0046 × 0708	14	1269	42.75	91.00	169.60	18.80	55.10
0046 × 0845	15	1179	45.25	90.50	175.90	18.36	58.23
0046 × 0951	16	1345	45.25	90.50	167.90	18.46	52.26
0046 × 1097	17	1366	44.50	90.50	183.10	19.09	61.28
0195 × 0708	18	1171	42.00	86.25	147.10	17.24	51.20
0195 × 0845	19	1221	42.50	88.75	157.40	17.65	68.79
0195 × 0951	20	1180	43.25	86.50	147.60	16.71	60.62
0195 × 1097	21	1288	42.75	90.50	165.20	17.55	72.83
0583 × 0708	22	1230	42.00	88.75	150.50	18.54	47.32
0583 × 0845	23	1176	43.25	89.00	157.10	17.43	55.25
0583 × 0951	24	1291	44.25	89.25	157.40	17.45	52.37
0583 × 1097	25	1270	41.25	89.00	156.40	18.50	65.88
0704 × 0708	26	1205	43.25	89.25	160.80	18.56	42.89
0704 × 0845	27	1114	46.25	91.00	167.90	18.03	52.14
0704 × 0951	28	1126	47.75	93.00	173.10	17.96	47.98
0704 × 1097	29	1378	44.25	93.25	165.80	18.39	61.87
LSD (α=0.05):		186.100	1.001	0.780	18.920	1.537	7.905
LSD (α=0.01):		246.600	1.327	1.034	25.080	2.036	10.480

* Significant α=0.01

Table 5: Second crop mean values of the characters hull percentage (%), seed length (mm), seed width (mm), and stem lower part and curve diameter (mm).

Genotypes	No	Hull percentage	Seed length	Seed width	Stem lower part diameter	Stem curve part diameter
		(%)	(mm)	(mm)	(cm)	(cm)
0043 *cms*	1	29.39	12.15	6.04	2.38	1.32
0046 *cms*	2	24.08	11.25	5.85	2.91	1.50
0195 *cms*	3	23.72	13.19	5.96	2.30	1.70
0583 *cms*	4	16.30	12.98	5.18	2.37	1.46
0704 *cms*	5	22.24	11.34	5.04	2.62	1.42
0708 *Rf*	6	27.04	9.20	3.17	1.85	1.00
0845 *Rf*	7	16.05	8.62	4.06	2.00	0.95
0951 *Rf*	8	28.80	12.88	5.47	2.29	1.52
1097 *Rf*	9	17.91	8.36	3.82	1.82	1.00
0043 × 0708	10	28.13	11.25	6.05	2.42	1.35
0043 × 0708	11	29.54	11.99	6.19	2.65	1.34
0043 × 0951	12	27.12	12.13	5.71	2.78	1.29
0043 × 1097	13	26.48	11.44	6.20	2.77	1.47
0046 × 0708	14	24.75	10.74	5.76	2.67	1.43
0046 × 0845	15	25.99	11.31	6.35	2.84	1.33
0046 × 0951	16	24.88	11.62	5.55	2.71	1.34
0046 × 1097	17	23.07	10.79	5.89	2.87	1.35
0195 × 0708	18	26.12	12.02	5.48	2.27	1.37
0195 × 0845	19	22.21	12.66	6.28	2.46	1.66
0195 × 0951	20	24.43	13.08	5.85	2.40	1.60
0195 × 1097	21	23.68	11.97	5.86	2.44	1.54
0583 × 0708	22	24.91	11.61	5.01	2.26	1.45
0583 × 0845	23	19.74	11.99	5.53	2.52	1.54
0583 × 0951	24	21.81	12.53	5.30	2.47	1.63
0583 × 1097	25	18.75	11.24	5.36	2.42	1.57
0704 × 0708	26	27.71	10.93	5.12	2.56	1.52
0704 × 0845	27	23.68	11.21	5.92	2.60	1.40
0704 × 0951	28	24.94	11.66	5.23	2.81	1.55
0704 × 1097	29	23.24	11.01	5.82	2.60	1.60
LSD (α=0.05):		2.351	0.388	0.375	0.333	0.196
LSD (α=0.01):		3.116	0.514	0.497	0.441	0.257

* Significant α=0.01

Table 6: Second crop mean values of the characters oil content (%), oleic acid content (%), linoleic acid content (%), palmitic acid content (%), and stearic acid content (%), and protein content (%).

Genotypes	No	Oil content	Oleic acid content	Linoleic acid content	Palmitic acid content	Stearic acid content	Protein content
		(%)	(%)	(%)	(%)	(%)	(%)
0043 *cms*	1	37.56	22.02	61.94	7.83	6.85	22.62
0046 *cms*	2	39.11	21.28	62.27	7.27	7.31	24.05
0195 *cms*	3	38.06	24.01	58.57	7.09	7.63	24.69
0583 *cms*	4	42.25	20.28	62.13	6.89	7.57	27.65
0704 *cms*	5	38.56	19.80	66.53	7.37	5.73	22.97
0708 *Rf*	6	32.35	18.40	65.58	9.26	5.80	23.38
0845 *Rf*	7	42.31	17.62	67.13	8.25	6.49	26.07
0951 *Rf*	8	31.60	19.39	65.04	7.88	5.80	25.84
1097 *Rf*	9	42.88	18.78	64.08	9.37	6.81	25.60
0043 × 0708	10	38.06	23.46	60.88	7.31	6.32	21.89
0043 × 0845	11	37.45	21.42	62.32	7.71	7.43	23.07
0043 × 0951	12	35.72	21.68	63.24	7.18	6.93	22.17
0043 × 1097	13	40.97	23.42	61.65	7.06	6.68	22.59
0046 × 0708	14	38.33	22.73	63.21	6.78	6.45	23.19
0046 × 0845	15	40.04	20.85	64.79	7.13	6.65	22.46
0046 × 0951	16	38.19	21.12	64.24	6.77	6.55	23.58
0046 × 1097	17	41.90	22.36	63.03	6.80	6.57	22.27
0195 × 0708	18	38.95	20.52	64.54	7.36	6.46	21.43
0195 × 0845	19	42.83	23.17	62.19	6.76	7.01	22.82
0195 × 0951	20	37.36	21.77	62.96	6.79	6.98	22.93
0195 × 1097	21	43.30	24.45	60.64	6.42	7.10	22.98
0583 × 0708	22	41.56	21.72	64.13	6.43	6.36	20.85
0583 × 0845	23	41.99	21.36	63.62	6.65	7.51	23.23
0583 × 0951	24	39.05	19.35	65.70	6.80	7.13	24.67
0583 × 0197	25	44.81	24.12	61.09	6.34	7.02	23.46
0704 × 0708	26	38.06	20.74	64.91	7.39	5.94	20.77
0704 × 0845	27	41.08	19.46	66.48	7.47	6.01	21.46
0704 × 0951	28	37.96	18.59	67.41	7.46	5.70	22.15
0704 × 1097	29	43.35	22.27	64.00	7.19	5.91	23.16
LSD (α=0.05):		4.592	1.635	2.366	0.816	0.702	2.230
LSD (α=0.01):		6.086	2.955	3.135	1.080	0.930	2.955

* Significant α=0.01

Table 7: Line × tester variance analysis for the characters plot seed yield, 1000-seed weight, days to flowering, and days to physiological maturity.

Source of variance	Crop production time	Df	Plot seed yield	1000- seed weight	Days to flowering	Days to physiological maturity
					(day)	(day)
Block	M-1	3	28471.55	81.01	3.23*	0.57
	M-2	3	420839.00**	750.17**	0.47	0.79
Genotype	M-1	28	512262.60**	587.75**	25.55**	55.99**
	M-2	28	417303.00**	868.10**	16.95**	26.06**
Crosses	M-1	19	33422.32	80.39*	18.01**	19.03**
	M-2	19	42329.69**	230.98**	10.28**	12.32**
Line	M-1	4	59262.00*	51.88	34.20**	45.50**
	M-2	4	18152.00	306.54**	22.04**	32.36**
Tester	M-1	3	72474.66*	201.21**	49.63**	8.04**
	M-2	3	147773.30**	855.71**	26.78**	14.17**
Line x tester	M-1	12	14916.00	59.68	4.71**	12.96**
	M-2	12	24028.00	49.62	2.23**	5.18**
Error	M-1	84	25442.38	42.90	1.15	0.83
	M-2	84	17510.65	31.60	0.51	0.31

* Significant α=0.05; ** Significant α=0.01; M1: first crop, M2: second crop

Table 8: Line × tester variance analysis for the characters plant height (cm), head diameter (cm), and stem lower part and curve diameters (mm).

Source of variance	Crop production time	Df	Plant height	Head diameter	Stem lower part diameter	Stem curve diameter
			(cm)	(cm)	(mm)	(mm)
Block	M-1	3	249.52	10.93**	0.26*	0.08*
	M-2	3	4822.78**	91.04**	1.92**	0.35**
Genotype	M-1	28	1653.74**	36.29**	0.26**	0.14**
	M-2	28	1466.79**	36.01**	0.31**	0.14**
Crosses	M-1	19	929.77**	4.57**	0.11	0.05*
	M-2	19	460.55**	1.78	0.14**	0.05**
Line	M-1	4	2983.22**	8.22**	0.23*	0.04
	M-2	4	1565.38**	4.03*	0.43**	0.15**
Tester	M-1	3	784.33*	10.50**	0.10	0.17 **
	M-2	3	486.33*	3.74*	0.18 *	0.03
Line x tester	M-1	12	281.65	1.87	0.08	0.02
	M-2	12	85.83	0.54	0.03	0.03
Error	M-1	84	234.98	2.03	0.09	0.03
	M-2	84	181.04	1.19	0.06	0.02

* Significant α=0.05; ** Significant α=0.01; M1: first crop, M2: second crop

Table 9: Line × tester variance analysis for the characters seed length (mm), seed width (mm), hull percentage (%), and protein content (%).

Source of variance	Crop production time	Df	Seed length	Seed width	Hull percentage	Protein content
			(mm)	(mm)	(%)	(%)
Block	M-1	3	0.14	0.27**	11.24*	3.02*
	M-2	3	0.44**	0.24*	89.78**	5.37
Genotype	M-1	28	3.67**	1.28**	34.04**	13.54**
	M-2	28	5.61**	2.17**	52.67**	10.03**
Crosses	M-1	19	1.29**	0.47**	18.60**	8.06**
	M-2	19	1.64**	0.61**	28.92**	3.70
line	M-1	4	3.09**	0.60**	59.38**	11.55**
	M-2	4	4.31**	1.46**	86.80**	3.22
Tester	M-1	3	3.75**	1.79**	22.10**	17.50**
	M-2	3	4.27**	1.44**	36.24**	8.54
linextester	M-1	12	0.08	0.09	4.13	4.54
	M-2	12	0.09	0.13	7.80**	2.65
Error	M-1	84	0.07	0.05	3.38	2.99
	M-2	84	0.08	0.08	2.80	2.51

* Significant α=0.05; ** Significant α=0.01; M1: first crop, M2: second crop

Table 10: Line × tester variance analysis for the characters; oil percentage (%), oleic acid (%), linoleic acid (%), palmitic acid (%), and stearic acid (%).

Source of Variance	Crop Production time	Df	Oil	Oleic acid	Linoleic acid	Palmitic acid	Stearic acid
			(%)	(%)	(%	(%)	(%)
Block	M-1	3	11.21	10.93	21.53**	0.30	0.30
	M-2	3	89.93**	5.27**	4.51	5.80**	1.82**
Genotype	M-1	28	76.86**	41.07**	35.85**	0.80**	1.60**
	M-2	28	38.59**	13.41**	17.53**	2.09**	1.36**
Crosses	M-1	19	32.18**	29.25**	26.38**	0.40	1.04**
	M-2	19	24.61**	9.93**	13.25**	0.60	1.03**
Line	M-1	4	36.73*	41.91**	49.50**	0.64*	3.18**
	M-2	4	30.96*	13.23**	31.91**	1.89**	3.22**
Tester	M-1	3	82.60**	100.03**	71.94**	0.66	1.20**
	M-2	3	101.26**	28.56**	24.00**	0.54	1.28**
linextester	M-1	12	18.06	7.34	7.28	0.25	0.29
	M-2	12	3.32	4.18**	4.33	0.18	0.24
Error	M-1	84	11.74	4.43	4.66	0.26	0.26
	M-2	84	10.66	1.35	2.83	0.34	0.25

* Significant α=0.05; ** Significant α=0.01; M1: first crop, M2: second crop.

The variances due to GCA and SCA were highly significant for most of the characters in both environments (Table 11 and 12). The ratio (H/D)1/2 and GCA/ SCA suggested that additive gene action was significant for plant height, head diameter, seed length, palmitic acid ratio, stearic acid ratio, stem diameter bottom, and bottom 2. – 3. node point.

Table 11: GCA and SCA variances, additive and dominance variance components, and their relations for hybrids.

Character	Location	GCA	SCA	GCA/SCA	D	H	(H/D)1/2
Seed yield (g plot^{-1})	M - 1	16.877	-109.582	_	33.755	-109.582	_
	M - 2	16.686	67.819	0.246	33.373	67.819	1.426
1000-seed (g)	M - 1	0.453	4.196	0.108	0.906	4.196	2.152
	M - 2	3.970	4.504	0.881	7.940	4.504	0.753
Flowering (day)	M - 1	0.291	0.889	0.327	0.582	0.889	1.236
	M - 2	0.176	0.430	0.409	0.352	0.430	1.105
Physiological maturity (day)	M - 1	0.133	3.032	0.044	0.266	3.032	3.376
	M - 2	0.305	1.219	0.250	0.610	1.219	1.414
Plant height (cm)	M - 1	14.187	11.667	1.216	28.374	11.667	0.641
	M - 2	8.202	-23.802	_	16.405	-23.802	_
Head diameter (cm)	M - 1	0.059	-0.040	_	0.118	-0.040	_
	M - 2	0.027	-0.163	_	0.054	-0.163	_
Stem lower part diameter (mm)	M - 1	0.001	0.000	_	0.002	0.000	_
	M - 2	0.002	-0.007	_	0.005	-0.007	_
Stem curve diameter (mm)	M - 1	0.001	-0.002	_	0.001	-0.002	_
	M - 2	0.001	0.003	0.182	0.001	0.003	1.634

M1: first crop, M2: second crop

Table 12: GCA and SCA variances, additive and dominance variance components, and their relations for hybrids.

Character	Location	GCA	SCA	GCA/SCA	D	H	(H/D)1/2
Seed length (mm)	M - 1	0.027	0.001	27.000	0.053	0.001	0.137
	M - 2	0.034	0.003	11.333	0.068	0.003	0.210
Seed width (mm)	M - 1	0.008	0.011	0.727	0.016	0.011	0.829
	M - 2	0.011	0.014	0.793	0.021	0.014	0.794
Hull (%)	M - 1	0.317	0.190	1.668	0.633	0.190	0.548
	M - 2	0.462	1.252	0.513	0.925	1.252	1.163
Protein (%)	M - 1	0.077	0.387	0.199	0.154	0.387	1.585
	M - 2	0.023	0.035	0.657	0.046	0.035	0.872
Oil (%)	M - 1	0.309	1.580	0.196	0.618	1.580	1.599
	M - 2	0.466	-1.835	_	0.932	-1.835	_
Oleic acid (%)	M - 1	0.480	0.727	0.660	0.960	0.727	0.870
	M - 2	0.126	0.706	0.178	0.252	0.706	1.674
Linoleic acid (%)	M - 1	0.418	0.657	0.636	0.836	0.657	0.885
	M - 2	0.195	0.376	0.519	0.390	0.376	0.982
Palmitic acid (%)	M - 1	0.003	-0.002	_	0.006	-0.002	_
	M - 2	0.009	-0.038	_	0.018	-0.038	_
Stearic acid (%)	M - 1	0.016	0.007	2.730	0.003	0.007	0.452
	M - 2	0.017	-0.004	_	0.035	-0.004	_

M1: first crop, M2: second crop

Dominance (non-additive) gene action was significant for days to flowering, days to physiological maturity, seed width, protein ratio, oleic acid, and linoleic acid ratio. Both types of gene action were significant at different cultivation times: GCA and SCA effects were variable in different seasons; therefore, both types of gene action were observed for seed yield, hull percentage, 1000-seed weight, oil content, and stem diameter at stem curve point. Properties under the dominant gene action demonstrated an (H/D)1/2 ratio of more than 1, which indicated the presence of super dominance for these properties.

As a result genetic analysis in different seasons will give better understanding of gene expression before embarking on selection.

In the first and second crop production seasons, the inbreds 0043 *cms*, 0046 *cms*, 0195 *cms*, 0583 *cms*, 0704 *cms*, 0708 *Rf*, 0845 *Rf*, 0951 *Rf*, and 1097 *Rf* exhibited desirable GCA effects and were found to be good general combiners for most of the traits; thus they can be exploited by further breeding for developing superior genotypes and hybrids in sunflower.

When the general combining ability (GCA) values of the parents are concerned, 0195 *cms*, 0583 *cms*, 0704 *cms*, 0708 *Rf* and 0845 *Rf* were identified as lines with high general combination ability. These lines can be recommended to be used as parents in different hybrid combinations.

When the specific combining ability of the hybrids is concerned, some combinations can be recommended as hybrids for the first and second crop production times with statistical significance in SCA in terms of the characters studied.

Table 13: Maximum and minimum heterosis and heterobeltiosis values under first crop production time.

Characters	First crop			
	Heterosis (%)		Heterobeltiosis (%)	
	min.	max.	min.	max.
Seed yield (g)	37.90	130.96	11.47	44.18
1000-seed weight (g)	-18.61	65.64	-35.40	17.82
Days to flowering (day)	-6.80	2.51	-12.06	0.38
Days to physiological maturity (day)	-5.24	9.35	-6.57	2.97
Plant height (cm)	1.38	40.14	-8.24	25.92
Head diameter (cm)	-5.22	53.69	-11.18	13.55
Oil content (%)	0.71	28.16	-7.05	23.61
Oleic acid (%)	-10.09	19.41	-17.14	13.04
Linoleic acid (%)	-13.04	13.29	-16.89	4.69
Palmitic acid (%)	-15.58	10.46	-20.63	10.81
Stearic acid (%)	-20.07	5.94	-35.75	2.90
Protein content (%)	-21.06	2.03	-23.83	-0.83
Hull percentage (%)	-13.15	14.62	-24.55	26.99
Seed length (mm)	-4.21	12.54	-9.81	4.65
Seed width (mm)	-5.60	24.22	-14.58	21.99
Stem diameter (at the bottom, cm)	-3.72	26.39	-6.43	13.79
Stem diameter (stem curve point, cm)	-18.19	31.43	-27.38	7.94

The highest level of heterosis (%) was identified as 142.64% for seed yield in the hybrid No.21 (195 *cms* × 1097 *Rf*), The lowest heterosis level was observed in the palmitic acid ratio with -22.02% in the hybrid No. 25 (0583 *cms* × 1097 *Rf*).

The highest heterobeltiosis value was observed in the plot yield with 79.44% (hybrid No.21). The lowest value was observed in 1000-kernel weight with -36.68% (hybrid No.18) in the second production time (Tables 13 and 14).

Table 14: Maximum and minimum heterosis and heterobeltiosis values under second crop production time.

Characters	Second crop			
	Heterosis (%)		Heterobeltiosis (%)	
	min.	max.	min.	max.
Seed yield (g)	44.28	142.64	3.25	79.44
1000-seed weight (g)	-10.08	65.41	-36.68	15.13
Days to flowering (day)	-9.09	-1.11	-12.23	-3.05
Days to physiological maturity (day)	-2.95	7.22	-3.62	2.47
Plant height (cm)	13.35	29.94	2.34	28.20
Head diameter (cm)	5.10	51.70	-7.65	11.15
Oil content (%)	-6.22	11.42	-11.49	13.79
Oleic acid (%)	-5.13	23.50	-14.49	18.93
Linoleic acid (%)	-4.60	3.89	-7.36	1.32
Palmitic acid (%)	-22.02	-2.16	-32.34	-5.33
Stearic acid (%)	-6.94	11.39	-15.98	8.47
Protein content (%)	-18.28	-2.21	-24.59	-3.58
Hull percentage (%)	-6.95	30.02	-24.27	21.10
Seed length (mm)	-11.02	16.19	-13.41	0.83
Seed width (mm)	-1.94	31.38	-8.05	17.46
Stem diameter (at the bottom, cm)	4.23	32.16	-8.25	16.71
Stem diameter (stem curve point, cm)	-11.26	32.23	-19.41	12.68

The highest and lowest narrow sense heritability (h^2) values in the main production time were 0.810 and 0.059 for seed size and 1000-seed weight, respectively. In the second production time, the highest and lowest values were 0.756 and 0.065 for seed size and protein ratio, respectively.

The highest and lowest broad sense heritability (H) values in the main production time were 0.990 and 0.239 for seed size and seed yield, respectively, while in the second production time they were 0.951 and 0.330 for days to flowering and head diameter, respectively.

As for variance estimates for general and specific combining ability, dominance and additive variance components, and their proportional relations, additive gene action was significant for plant height, receptacle diameter, grain size, palmitic acid ratio, stearic acid ratio and stem diameter, while non-additive gene action was significant for days to flowering, days to physiological maturity, grain width, protein ratio, oleic acid, and linoleic acid ratio. In addition, different gene actions were significant at different cultivation times for grain yield, 1000-kernel weight, oil ratio, and hull ratio, and head diameter. Accordingly, the non-additive gene effect was sig-

nificant for the main product and additive gene action for the secondary product for 1000-kernel weight and oil ratio. Additive gene action was significant in the main product and non-additive gene action for the secondary product for head diameter. Properties under the dominant gene action demonstrated an (H/D)1/2 ratio of more than 1, which indicated the presence of super dominance for these properties.

When general combining ability values of the parents are concerned, 0195 *cms*, 0583 *cms*, 0704 *cms*, 0708 *Rf* and 0845 *Rf* were identified as lines with high general combination ability in terms of the stearic acid ratio of products. These lines can be recommended to be used as parents in hybrid combinations.

When specific combining ability of hybrids is concerned, hybrid No. 18 (0195) × 0708) can be recommended as hybrids with statistical significance in specific combining ability in terms of the linoleic acid ratio of secondary products.

The highest level of heterosis (%) was identified as 142.64% for plot yield in the hybrid No. 21, whereas the lowest heterosis level was observed in the palmitic acid ratio with -22.02% in the hybrid No. 25.

As for heterobeltiosis, the highest value was observed for plot yield with 79.44% (hybrid No.21), while the lowest value was observed for 1000-kernel weight with -36.68% (hybrid No. 18) in the secondary product.

The highest and lowest values of heritability in the narrow sense were 0.810 (in grain size) and 0.059 (in 1000-kernel weight) in the main product, respectively, and 0.756 (in grain size) and 0.065 (in protein ratio) in the secondary product, respectively. The highest and lowest values of heritability in the broad sense were 0.990 (for grain size) and 0.239 (for plot yield) in the main product, respectively, and 0.951 (for days to flowering) and 0.330 (for receptacle diameter) in the secondary product, respectively (Table 15).

Table 15: Broad (H) and narrow (h^2) sense heritability values.

Characters	First crop		Second crop	
	H	h^2	H	h^2
Seed yield (g)	0.239	0.178	0.586	0.118
1000-seed weight (g)	0.466	0.059	0.863	0.390
Days to flowering (day)	0.936	0.331	0.951	0.387
Days to physiological maturity (day)	0.960	0.080	0.579	0.195
Plant height (cm)	0.747	0.287	0.607	0.433
Head diameter (cm)	0.556	0.202	0.330	0.284
Oil content (%)	0.635	0.120	0.567	0.529
Oleic acid (%)	0.849	0.346	0.864	0.194
Linoleic acid (%)	0.823	0.315	0.786	0.265
Palmitic acid (%)	0.354	0.094	0.440	0.281
Stearic acid (%)	0.751	0.316	0.758	0.374
Protein content (%)	0.629	0.119	0.654	0.065
Hull percentage (%)	0.820	0.380	0.903	0.322
Seed length (mm)	0.990	0.810	0.954	0.756
Seed width (mm)	0.900	0.410	0.884	0.406
Stem diameter (at the bottom) (cm)	0.310	0.080	0.596	0.415
Stem diameter (stem curve point) (cm)	0.417	0.183	0.648	0.121

CONCLUSION

In this study, cytoplasmic male sterile and restorer lines were used as parents and line × tester analysis was used as an appropriate method for the determination of general and specific combining abilities, various gene action types and heterosis (%) and heterobeltiosis (%) values of parents and hybrids in the development of suitable hybrid varieties in terms of high seed yield and oil content and other yield components in sunflower under both first and second crop production times. Significant differences were found among the hybrids and their parents. GCA effects were found to be highly significant for all traits. SCA effects, on the other hand, were non-significant for most of the traits. Based on GCA effects in the first and second crop production seasons, the inbreds 0043 *cms*, 0046 *cms*, 0195 *cms*, 0583 *cms*, 0704 *cms*, 0708 *Rf*, 0845 *Rf*, 0951 *Rf*, and 1097 *Rf* exhibited desirable GCA effects and were found to be good general combiners for most of the traits. These genotypes can be exploited by further breeding for developing superior genotypes and hybrids in sunflower.

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