COMBINING ABILITY STUDIES FOR SEED YIELD TRAITS IN SUNFLOWER

Syeda Nasreen*, Muhammad Ayub Khan*, Muhammad Arshad*, Maryam Kamal**, Doulat Baig *, M. Tariq*, Talat Gilani* and Musarrat Gilani*

ABSTRACT:- Six cytoplasmic male sterile inbred lines and six restorers/testers were selected on the basis of variability for yield related characters. The lines and tester restorers were crossed in a line x tester mating design resulting in 36 F_1 hybrids. The potential parents with high general combining ability (GCA) effects were identified for yield related traits. Among females, CMS-H55-2-2-1 expressed the highest significant GCA effects for 1000-seed weight whereas female, CMS-303 represented the highest and significant GCA estimates for head diameter, yield and harvest index. Among male parents, RHA-295 expressed the highest significant magnitude for head diameter while SF-187R possessed the highest significant GCA effects for 1000-seed weight, harvest index and moisture contents. Among male parents, the highest significant value for yield was observed in RHA-854. The potential parent lines with highest GCA estimates can be utilized in different desirable combinations for varietal improvement through breeding programme. The cross of CMS-303 x RHA-271 expressed the highest specific combining ability (SCA) value for yield while CMS 303 x RHA-854 hybrid exhibited the highest SCA estimates for harvest index. CMS-53 x RHA-854 and CMS-64 x SF-187 crosses exhibited the highest SCA estimates for head diameter and 1000-seed weight, respectively. The SCA variances were higher than GCA for seed yield and related traits revealing the involvement of non-additive type of gene action controlling the characters. Estimates of proportional contribution of inbred lines, testers and their inter-action to total variances for seed yield and related traits indicated the highest contribution of lines x testers in inheritance of all characters except harvest index where the contribution of lines was higher than testers and line x testers. Non-additive type of gene action can be utilized in a hybrid improvement programme through heterosis breeding in sunflower.

Key Words: Helianthus annuus; Parental Line; Combining Ability; Yield; Heterosis; Yield Components; Agronomic Characters; Pakistan.

INTRODUCTION

Sunflower (*Helianthus annuus* L.) is the third major contributor of edible oil in the world after soybean and groundnut (Meric et al., 2003). Recently, sunflower research has been expanded in Pakistan to produce more productive hybrids with high genetic potential for seed yield. Sunflower is a non-conventional oilseed crop and can play a vital role for edible oil production due to its high yield potential and adjustment in the present cropping pattern in the country. Moreover, it is a short duration crop not strictly seasons bound and

can be grown twice a year, as spring and autumn crop in major agro-ecological zones of irrigated and *barani* areas of Pakistan (Samiullah, 2000). Its seed contains 40-50% oil which can be used directly for cooking purposes and as salad oil. It has high percentage of unsaturated fatty acids (80%) including oleic and linoleic acids in oil. Unsaturated fatty acid facilitates improving health and oxidative stability for oil shelf life, flavor, durability and cold flow performance (Shannon, 2012; Anonymous, 2013). It also contains 20-25% proteins, 20% carbohydrates and 4% ash (Khalil and Jan, 2002). Its oil contains 20-25% essential vitamins such as A, D, E and K (Satyabrata et al., 1988). Moreover, it is a good source of calcium, phosphorus water soluble B-complex vitamins such as nicotinic acid, thiamine and riboflavin. Sunflower is also an economically important raw material used for industrial purposes (Fick and Miller, 1997).

Hybridization of inbred lines to produce high yielding hybrids or synthetics is the primary objective in a sunflower breeding programme, while breeding for hybrid vigor, emphasis has been placed on seed yield and seed oil content. Sunflower hybrids are more vigorous, self-fertile, high yielding and resistant to important foliar diseases (Seetharam et al., 1975; Ghaffari et al. (2011) and Waqas et al. (2012).

Genetic improvement depends on effective selection among individuals that differ in phenotypes. The ability of a parent to transmit desirable performance to its hybrid progeny is referred to as its combining ability. Combining ability studies provide useful information about potential parents with desirable characters that can be utilized in breeding programme for varietal improvement. Alone et al. (2003) conducted a combining ability analysis for 10 characters through line x tester involving 4 male sterile lines and 7 open pollinated sunflower genotypes in Rahuri, Maharashtra. A significant mean sum of square due to males and females for all the characters indicated enough variability between the studied males and females. For quantitative characters, effective selection becomes difficult due to environmental influence on the expression of genes controlling that trait. Sprague and Tatum (1942) split the term combining ability into general combining ability (GCA) and specific combining ability (SCA). GCA is used to describe the performance of the parent in general combinations and is determined by additive gene action. SCA is used to designate the hybrid performance in specific combinations and is determined by dominant genes. Genetic improvement in any quantitative trait depends on effective selection among individuals that differ in genotypic value that is determined by various types of gene actions such as additive, dominance and their interaction. In quantitative genetics, it is gene action that is associated with the breeding value of individuals (Falconer and Mackey, 1996). The breeding value of progeny by the average effects of genes is also referred to as additive effect of genes, dominance and their interaction. Dominant genetic effect, on the other hand is the result of interaction of genes within the locus and is important for hybrid development.

Line x tester design is widely used in predicting combining ability of parents and the type of gene actions involved in the expression of a trait. The combining ability of parents having desirable traits which deter-mine their potential to make a successful cross that may result

in a fertile hybrid with desirable characteristics. Present study is an effort to develop more productive sunflower hybrids using parental lines with high combining ability for yield and yield related traits.

MATERIALS AND METHOD

The inbred lines including six cytoplasmic male sterile (CMS) (CMS-H55-2-2-1, CMS-NDMTC, CMS-64, CMS-303, CMS-HAR-1 and CMS-53) and six fertility restorers (Rf) and testers (C-206R, PAC-8712, RHA-295, SF-187R, RHA-271 and RHA-854) obtained from the Oilseeds Programme, Crop Sciences Institute, National Agricultural Research Centre (NARC) Islamabad. The research was conducted at NARC field. Each parental line was evaluated before crossing for head diameter, 1000-seed weight, harvest index, seed moisture factor and seed yield per hectare. The 36 F_1 hybrids were obtained by crossing inbred lines in a line x tester design during spring 2004. The parental lines and their F_1 hybrids developed were grown in a randomized complete block design (RCBD) replicated thrice. Each parental line and hybrid was planted in 5 m long rows with plant to plant and row to row spacing of 0.3m and 0.5m, respectively. A basal fertilizer dose of 120:60 NP kg^{-1} was applied to the experimental field. The crop was irrigated four times at appropriate times. All other agronomical practices were followed for better crop stand and performance. At physiological maturity, the heads were cut, sun dried and threshed. Field data was recorded on head diameter (cm), 1000-seed weight (g), harvest index (%), moisture factor and yield (kg ha^{-1}). All the data were subjected to analysis of variance (Steel and Torrie, 1996) to evaluate the significance of variance among hybrids and parents for yield related traits. Combining ability studies were conducted by using line x tester analysis as outlined by Kempthorne (1957).

RESULTS AND DISCUSSION

Head Diameter

Among all the F_1 hybrids, the mean value for head diameter ranged from 10.33 to 23.00 cm. Maximum head diameter among parents was recorded in CMS-HAR-1 (23.00) while the minimum in RHA-295 (10.33 cm). Among F_1 hybrids, maximum head diameter was recorded in F_1 hybrid CMS-H55-2-2-1 x C-206R (18.66 cm) while the minimum in cross CMS-H55-2-2-1 x SF-187R (12.33 cm) representing a net difference of 6.33 cm among hybrids. Hybrids and parents exhibited moderate genetic variability for head diameter, with 12.13% coefficient of variation (Table 1). The average head diameter was 15.25 cm for parents vs 15.55 cm for F_1 hybrids representing a net difference of 0.30 cm as indicated by analysis of variance for lines x testers (Table 2).

Three lines (CMS-H55-2-2-1, CMS-64 and CMS-303) had significant GCA while the remaining three (CMS-NDMTC, CMS-HAR-1 and CMS-53) were non-significant. All the testers exhibited significant GCA effects except RHA-271. For head diameter, maximum positive significant GCA magnitude was observed in CMS-303 (5.555) among lines, followed by CMS55-2-2-1 (0.727). For testers, RHA-295 exhibited positive and significant GCA (1.505) followed by C-206R (1.061) (Table 3). For head diameter, significant SCA effects were observed for two hybrids while 34 hybrids remained non-

Table 1. **Mean squares and coefficient of variation (C.V) for seed yield, and yield related traits in 48 sunflower lines**

Source	df	Head diameter	1000 seed weight	Yield ha^{-1}	Harvest index	Moisture factor
Replication	02.0	10.333	10.194	3214.900	0.340	0.005
Genotypes	47.0	17.573**	517.686**	502048.663**	20.278**	0.057**
Error	94.00	3.525	15.079	26655.537	1.581	0.002
C.V%		12.13	8.78	18.47	18.09	6.27

*** Significant at 1% probability level*

significant. Maximum positive SCA estimates were observed for CMS-NDMTC x PAC-8712 (2.063) followed by CMS-I NDMTC x RHA-271 (2.056). The minimum SCA magnitude was indicated by CMS-NDMTC x RHA-295 (-3.606) followed by CMS H55-2-2-1x SF-187R (-2.716) (Table 4). These results were in accordance with the findings of Burli et al. (2001) who reported significant GCA effects for achieving medium head diameter in sunflower. Moreover, Kumar et al. (1999) also reported that CMS-852 is a good general combiner for head diameter in sunflower.

The value for variance of dominance for all the characters was higher than that of variance of additive indicating the pre-dominance of non-additive type of gene action controlling the character (Table 5). The proportional contribution of lines, testers and lines x testers were 6.9076, 27.8751 and 65.2138, respectively, showing lines x testers as the major contributors in inheritance of characters (Table 6). Non-additive type of gene action revealed most of the genetic variability due to SCA effects. This type of genetic variability can be exploited in hybrid development. The results corroborates by Goksoy et al. (2000, 2002),

Table 2. **Analysis of variance for lines x testers including parents for seed yield and yield related traits in 48 sunflower genotypes**

Source	df	Head diameter	1000 seed weight	Yield h^{-1}	Harvest index	Moisture factor
Replication	2	10.333ns	10.194ns	3214.900ns	0.340ns	0.005ns
Genotypes	47	17.573**	517.686**	502048.663**	20.278**	0.057ns
Parents	11	329.219**	534.793**	92913.287**	9.285**	0.031ns
Crosses	35	7.676**	232.853**	425538.918**	17.806**	0.061ns
Parents vs Crosses	1	2.520ns	10167.506**	7681490.797**	228.958**	0.230ns
Lines	5	3.711ns	210.568**	996974.451**	63.723**	0.014ns
Testers	5	14.978**	231.648**	77248.751**	2.069ns	0.224ns
Lines x Testers	25	7.008**	237.550**	280905.84**	11.770**	0.037ns
Error	94	3.525	15.079	26655.537**	1.581	0.002
Total	143					

** Significant at 1% probability level, ns = Non-significant*

Table 3. **Estimates of GCA effects for seed yield and yield related traits in 12 sunflower genotypes (parents)**

Source	Head diameter	1000 seed weight	Yield ha^{-1}	Harvest index	Moisture factor
Females					
CMS-H55-2-2-1	0.727*	-2.557*	-134.166	0.313*	0.047*
CMS-NDMTC	-0.105	0.853	-265.220	-1.892*	-0.027*
CMS-64	-0.550*	6.700*	-133.444	-1.675*	-0.015*
CMS-303	5.555*	0.653	385.211	2.652*	-0.022*
CMS-HAR-1	-0.327	-3.207*	149.797	1.735*	0.018*
CMS-53	0.283	-2.402*	-0.510	-1.081*	-0.001*
Males					
C-206-R	1.061*	-5.548*	-33.244	-0.170	0.014*
PAC-8712	-0.161*	-3.147*	-74.492	-0.264*	-0.111*
RHA-295	1.505*	1.292	16.828	-0.147	0.019*
SF-187R	-1.216*	0.731	-55.612	0.396*	0.169*
RHA-271	0.172	5.258*	60.747	-0.247*	-0.125*
RHA-854	-0.772*	1.370	87.582	0.485*	0.073*
Standard Error	0.195833	0.837722	1480.8631	0.087833	0.000111

Significant at 5% probability level if the respective value is greater than twice the Standard Error

Sassikumar et al. (1999) and Shekar et al. (1998) reported the major contribution of line x tester in inheritance of head diameter and pre-dominance of non-additive gene action in determination of head diameter in sunflower.

1000- Seed Weight

The average value for 1000-seed weight among F_1 hybrids ranged from 33.47-77.33 g representing a net difference of 43.86g. Among parents, the maximum 1000-seed weight was recorded in SF-187R (52.50 g) and was significantly higher than the other parents. While the minimum 1000-seed weight was observed in CMS-NDMTC (12.03 g) representing a net difference of 40.18 g. Among F_1 hybrids, the maximum 1000-seed weight was observed in CMS-64 x SF-187R (77.33 g) and minimum in CMS-H55-2-2-1x SF-187R (33.47g). The genotypes exhibited a low level of genetic variability as revealed by analysis of variance, 8.78% coefficient of variation (Table 1). The average 1000-seed weight was 29.76 g for parents vs. 49.04 g for F_1 hybrids representing a net difference of 19.28 g. The values of head diameter remained highly significant for parents and hybrids as indicated by analysis of variance for lines x testers (Table 2).

For 1000-seed weight, maximum positive and significant GCA estimates among lines were observed in SMS-64(6.700) followed by CMS-NDMTC having a GCA effects of 0.853. Among testers, RHA-271 showed maximum positive GCA effects of 5.258 followed by RHA-854 (1,370) (Table 3). Twenty crosses exhibited significant

Table 4. **Estimates of specific combining ability effects for seed yield and yield related traits in 36 sunflower crosses**

Genotypes (Crosses)	Head diameter	1000 seed weight	Yield ha^{-1}	Harvest index	Moisture factor
CMS-H55-2-2-1 x C-206R	1.336	0.166	360.140*	3.523*	0.142*
CMS-H55-2-2-1 x PAC-8712	-0.100	5.716*	-5.730	-0.043	-0.027
CMS-H55-2-2-1 x RHA-295	0.563	5.376*	-246.860*	-1.530*	0.129*
CMS-H55-2-2-1 x SF-187R	-2.716*	-13.763*	-253.920*	-2.803*	-0.087*
CMS-H55-2-2-1 x RHA-271	0.433	-6.050*	43.050	-2.263	-0.153*
CMS-H55-2-2-1 x RHA-854	1.176	8.396*	101.543	1.106	0.002
CMS NDMTC x C-206R	-0.166	-4.310	55.646	1.166	-1.453*
CMS NDMTC x PAC-8712	2.063	-0.260	19.583	0.066	0.101*
CMS NDMTC x RHA-295	-3.606*	-8.033*	-52.620	-0.386	-0.249*
CMS NDMTC x SF-187R	-0.553	-1.406	-152.193	0.940	0.061*
CMS NDMTC x RHA-271	2.056	5.870*	-31.213	-0.353	-0.115*
CMS NDMTC x RHA-854	-0.326	8.020*	159.280	-1.416	0.124*
CMS 64 x C-206R	-1.393	1.763	152.740	-0.186	-0.090*
CMS 64 x PAC-8712	-1.496	-5.916*	54.003	1.113	0.141*
CMS 64 x RHA-295	0.833	-1.716	128.020	-0.340	0.099*
CMS 64 x SF-187R	1.886	20.176*	200.416*	-0.313	0.001
CMS 64 x RHA-271	1.163	3.323	-277.740*	0.593	-0.079*
CMS 64 x RHA-854	-1.553	-17.463*	-259.206*	-0.870	-0.070*
CMS 303 x C-206R	1.056	-2.523	-542.310*	-4.280*	-0.009
CMS 303 x PAC-8712	-1.380	-9.740*	-60.606	-0.550	-0.092*
CMS 303 x RHA-295	-0.050	7.986*	-217.216*	0.330	-0.010
CMS 303 x SF-187R	0.003	-10.086*	-524.376*	-1.976*	0.028
CMS 303 x RHA-271	-0.720	8.526*	976.800*	2.263*	0.168*
CMS 303 x RHA-854	0.563	5.940*	367.980*	4.200*	-0.083*
CMS HAR-1 x C-206R	-0.613	-0.233	-155.776	0.303	-0.003
CMS HAR-1 x PAC-8712	0.616	10.416*	-59.796	-1.130	-0.059*
CMS HAR-1 x RHA-295	-2.053	-5.256*	167.920	0.583	0.007
CMS HAR-1 x SF-187R	1.333	2.770	310.566*	1.876*	-0.086*
CMS HAR-1 x RHA-271	-0.723	-6.650*	-433.756*	-0.883	0.142*
CMS HAR-1 x RHA-854	0.893	-0.903	127.846	-0.746	0.003
CMS 53 x C-206R	-0.223	-4.716*	127.823	-0.543	-0.024
CMS 53 x PAC-8712	0.340	-0.333	9.550	0.556	-0.080*
CMS 53 x RHA-295	1.003	2.193	219.096*	1.336	0.009
CMS 53 x SF-187R	0.056	7.520*	417.790*	2.296*	0.067*
CMS 53 x RHA-271	-1.000	-4.100	-276.853*	-1.363	0.021
CMS 53 x RHA-854	-0.716	-4.120	-499.186*	-2.260*	0.009
Standard Error	1.083974	2.241948	94.260000	0.725947	0.025819

Significant at 5% probability level if the respective value is greater than twice the Standard Error

SCA effects and 15 non-significant effects for the 1000-seed weight. CMS 64xSF-187R(20.176) exhibited positive and significant SCA estimate while significantly lowest SCA estimates were observed for the cross

Table 5. Estimates of genetic components for seed yield and yield related traits in sunflower genotypes

Genetic components	Variance of dominance	Variance of additive
Head diameter	1.161	0.024
1000 seed weight	70.200	0.278
Yield ha^{-1}	118083.434	1735.618
Harvest index	3.396	0.234
Moisture content	0.012	0.001

Table 6. Estimates of proportional contribution of lines, testers and their interactions to total variances for seed yield and yield related traits in sunflower genotypes

Genetic components	Lines	Testers	Lines x Testers
Head diameter	6.9076	27.8751	65.2138
1000 seed weight	12.9185	14.2118	72.8696
Yield ha^{-1}	33.4693	2.5933	63.9367
Harvest index	51.1240	1.6600	47.2158
Moisture content	3.3490	52.7264	43.7264

CMS-64 x RHA-854 (-17.463) (Table 4). These findings are in accordance with the results reported by Burli et al. (2001) and Kumar et al. (1998) while doing combining ability studies for yield related traits in sunflower.

The estimates of SCA variance (70.200) were higher than GCA variance (0.278) for 1000-seed weight showing the pre-dominance of non-additive gene action in determination of the character (Table 5).The proportional contribu-tion was 12.92 for lines, 14.21 for testers and 72.87 for lines x testers which revealed that lines x testers were the major contributors in inheritance of this character. According to Kovacik and Skaloud (1972), the non-additive component of genetic variance was nine times larger than the additive component. However, Putt (1966) and Marinkovic and Skoric (1985) found that both gene effects were important in the inheritance of 1000-seed mass. Rao and Singh (1977) and Kesteloot et al. (1985) also reported similar results. Fick et al. (1978) found that in non-oilseed sunflower type, both additive and non-additive gene actions are important. Non-additive type of gene action in the inheritance of 1000-seed mass was also reported by Goksoy et al. (2000, 2002), Jayant-Bhat et al. (2001), Radhika et al. (2001) and Sassikumar et al. (1999).

Harvest Index (%)

Among parents, the maximum and significant harvest index (HI) was observed in CMS-H55-2-2-1 (5.83%) whereas, the minimum in SF-187R (0.20%). The average harvest index ranged from 0.20% to 5.83% among parents representing a net difference of 5.63%. For crosses, the maximum HI was recorded for CMS-303 x RHA-854(15%) and the minimum in CMS-53 x RHA-854 (4.80%). The average percentage for HI among F_1 hybrids ranged from 4.80% to 15.00%, representing a net difference of 10.20%. The co-efficient of variation for HI was 18.09 (Table 1) suggesting appropriate genetic variability among hybrids. The average percentage for HI was 4.76 for parent vs 7.76 for F_1 hybrids showing a net difference of 3.0% (Table 1). Analysis of variance for lines x testers indicated highly significant HI values for parents and hybrids (Table 2).

For harvest index, all lines were significant in GCA estimates while four testers were significant and remaining two were non-significant. Among parent lines, CMS-303 exhibited maxi-mum positive GCA estimates (2.652) followed by CMS-HAR-1(1.735). RHA-

854 had maximum and positive GCA estimate of 2.657 among the testers. For harvest index, 10 crosses were found significant in their SCA estimates and 26 remained non-significant. Maximum positive significant SCA estimates were observed for CMS-303 x RHA-854 (4.200) followed by CMS-H55-2-2-1 x C-206R (3.523) the lowest SCA estimates were observed in CMS-303 x C-206 (-4.280) followed by CMS-H 55-2-2-1 x SF-187R (-2.803) (Table 4). These results corroborates with findings of Singh and Singh (2000) and Ashok et al. (2000) who identified the parental lines as good general combiners on the basis of GCA and SCA for harvest index.

Among all F_1 hybrids variance of dominance (3.396) was higher than additive variance (0.234) revealing the pre-dominance of non-additive variance for the character (Table 5). For HI, the proportional contribution of lines, testers and lines x testers were 51.124, 1.660 and 47.216, respectively, showing lines as major contributor for inheritance of this character (Table 6). Present results are supported by those of Lande et al. (1997) who observed the pre-dominance of non-additive gene action for yield components.

Moisture Factor

Among parents, the maximum moisture factor was observed for RHA-854 (0.70) whereas, the minimum for RHA-295 (0.42). The value for moisture factor among parents ranged from 0.42 to 0.70 representing a net difference of 0.28. Among F_1 hybrids, the maximum moisture factor was observed for CMS-53 x SF-187R (0.95), while the minimum for CMS-NDMTC x RHA-295 (0.43) hybrid representing a net difference of 0.52. A low level of variability was observed among the genotypes, the co-efficient of variation being 6.27% for moisture factor. Analysis of variance for lines x testers were non-significant for moisture factor (Table 2).

High seed moisture is favorable for getting high seed yield (Robelin, 1967). Therefore, positive values of GCA and SCA are desirable for this character. In the present investigations, all lines and testers exhibited significant GCA estimates for moisture factor. Among lines maximum positive GCA estimates were observed for CMS-H55-2-2-1 (0.047) followed by CMS-HAR-1 (0.018) whereas among testers, GCA magnitude was significantly positive for SF-187R (0.169) followed by RHA-854 (0.073) (Table 3). Based on GCA, the parents CMS-H55-2-2-1 and SF-187R were the best general combiners for moisture content. Among hybrids, 23 exhibited significant SCA estimates while 13 hybrids remained non-significant. The CMS-303 x RHA-271 cross exhibited the highest significant SCA magnitude and the lowest were observed for CMS-NDMTC x C-206R (-1.453) hybrid (Table 4).

The value for variance of dominance for moisture factor was higher (0.012) than the additive variance (0.001) showing the pre-dominance of non-additive type of gene action controlling this character (Table 5). Non-additive type of gene action can be utilized for hybrid improvement through heterosis breeding. The proportional contribution for lines, testers and lines x testers were 3.349, 52.924 and 43.726, respectively revealing the highest contribution of testers followed by lines and lines x testers for this character (Table 6). Non-additive gene action for yield and related characters in sun-flower have also been reported by Shakthivel (2003).

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Seed Yield (kg ha^{-1})

Among parents, maximum yield was recorded for CMS-53 (829.20 kg) and minimum in CMS-64 (265.70 kg). The average yield among parents ranged from 265.70 to 563.50 kg ha^{-1}. Among hybrids, the maximum yield was recorded for CMS-303x RHA-271 (2437.80 kg ha^{-1}) whereas the minimum for CMS-NDMTC x SF-187R (543.99 kg ha^{-1}). A high level of variability was observed among hybrids for yield ha^{-1}, the coefficient of variation being 18.47% as revealed by analysis of variance (Table 1). A highly significant value for yield ha^{-1} was observed for parents and hybrids as indicated by analysis of variance for lines x testers (Table 2).

Estimates of variation due to GCA were partitioned for both male and female parents (Table 3). Among lines, the maximum positive GCA magnitude for yield was noticed for CMS-303 (385.211) followed by CMS-HAR-1 (149.797). While the maximum negative GCA estimates were recorded for CMS-NDMTC (-265.22). In testers, the maximum positive GCA estimates were recorded for RHA-854 (87.582) followed by RHA-271 (60.747) while the maximum negative GCA estimates by PAC-8712 (-74.492) followed by SF-187R (-55.612). Among the lines, CMS-303 while among testers, RHA-854 were the best general combiners for yield. Significant SCA estimates for yield were observed for 17 F$_1$ hybrids while 19 F$_1$ hybrids remained non-significant in their SCA magnitude. The maximum positive significant SCA effects were observed for CMS-303 x RHA-271 (974.800) followed by CMS-53 x SF-187R (417.79). The lowest SCA value was indicated by CMS-303 x C-206R (-542.310) (Table 4). For yield, good combining ability among parental lines has also been reported by Shekar et al. (1998), Bajaj et al. (1997) and Tan (2010). A female line CMS-852 was reported by Kumar et al.(1999) as a good general combiner for seed yield.

The variance value of dominance for yield was higher (118083.434kg ha^{-1}) than that of variance for additive (1735.618 kg ha^{-1}) revealing the non-additive type of gene action controlling this character (Table 5). The proportional contribution of lines, testers and lines x testers for yield were 33.47, 2.59 and 63.93, respectively, indicating lines x testers as the major contributor in inheritance of this character (Table 6). Similar results were also reported by Sassikumar et al. (1999) and Kandalkar (1997) who reported pre-dominance of non-additive gene action in determination of seed yield in sunflower.

In general, the combining ability of parents having desired traits determine their potential to make a successful cross, that may result in a fertile hybrid with desired characteristics. The line x tester analysis for GCA was conducted for yield and yield related characters to determine the potential of parental lines in a cross for the desirable characters.

For head diameter, maximum positive GCA estimates among female parents were observed for CMS-303 (5.555). Among males, RHA-295 exhibited the maximum positive GCA magnitude of 1.505. As positive GCA and SCA are desirable for head diameter, therefore, among female parents, CMS-303 while among males, RHA-295 are the potential parents which can be utilized in hybrid improvement programme. CMS-NDMTC x PAC-8712 and CMS-NDMTC x RHA-271 are the potential cross combinations with SCA magnitudes of 2.063 and 2.056, respectively. Higher values of 1000-

seed weight results in an increase in seed yield. CMS-64 while among males RHA-271 were the potential cross combiners with maximum positive GCA values for 1000- seed weight (Table 3). CMS-64 x SF-187R is a potential cross for 1000- seed weight with SCA magnitude of 20.176 (Table 4). Increased harvest index usually contributes for yield increase. Therefore, positive values of GCA and SCA are desirable for increasing seed yield.

In present study, among parental lines, a female CMS-303 while among males, RHA-854 are potential parents with maximum positive GCA values of 2.652 and 0.485, respectively. CMS-303 x RHA-854 is a potential combina-tion with SCA magnitude of 4.200. High seed moisture is an important character for getting higher seed yield. Therefore, positive values of GCA and SCA are desirable. According to the study the maximum positive GCA estimates among females and males were observed for CMS-H55-2-2-1 (0.047) and SF-187R (0.169), respectively indicating both as potential lines for this character. Among crosses, CMS- H55-2-2-1 x C-206R was the potential combination with SCA magnitude of 0.142. An important objective of sunflower breeding is always to increase seed yield. The co-efficient of variation for yield was 18.47% indicating high level of variability among genotypes for the character. The maximum positive GCA estimate among females was observed for CMS-303 (385.211) while among males, RHA-854 had maximum positive GCA estimates of 87.582. Therefore, these two are the potential parents which can be utilized in a crossing programme for yield increase. CMS-303x RHA-271, CMS-53x SF-187R and CMS-H55-2-2-1 x C-206R were the potential crosses with highest SCA of 974.800, 417.79 and 367.80, respectively.

Parental lines and hybrids with high GCA and SCA, respectively for seed yield and yield component in sunflower were reported by Rustan and Drevon (2005), Whetsell et al. (2003), Ortis et al.(2005), Shaktivel (2003), Dagastu et al. (2002a). Significant GCA effects for seed yield was also reported by Burli et al. (2001). Ashok et al. (2000) reported parental lines as a good general combiner on the basis of GCA and SCA for seed yield. In present study higher SCA variances for yield and related characters were observed than GCA variances. A non-additive type of gene action can be utilized for improvement of characters through heterosis breeding. These results are supported by the findings of Shankara (1981) Giriraj et al. (1987), Goksoy et al. (2000), Radhika et al. (2001), Shekar et al. (1998), Kumar et al. (1998), Lande et al. (1997), Gangappa et al. (1997) who reported non-additive type of gene action for seed yield.

Estimates of proportional contri-bution of lines, testers and lines x testers to total variances for seed yield and yield related characters revealed the highest contribution of lines x testers in the inheritance of all characters except harvest index and seed moisture content. The contri-bution of lines and testers was the highest for harvest index and seed moisture content. Present results are supported by those of Ortis et al. (2005) who observed major contri-bution of lines x testers in inheritance of quality characters in sunflower due to the presence of non-additive genes.

LITERATURE CITED

Alone, R.K., S.N. Mate, K.C. Garare and

M.R. Mangare. 2003. Heterosis in sunflower (*Helianthus annuus* L.). Indian J. Agric. Res. 37(1): 56-59.

Anonymous. 2013. Classic and higholeic canola oils: Zero trans, low saturated fat solutions to partially hydrogenated oils. (Available at: http://www.cano-lainfo.org/quadrant/media/health/pdfs/canola-higholeic.pdf Accessed on 21-02-2013).

Ashok, S., S.N. Mohamed and S.L. Narayanan. 2000. Combining ability studies in sunflower (*Helianthus annuus* L.). Crop Res. Hisar. 20(3): 457-446.

Bajaj, R.K., K.K. Aujla and G.S. Chahal. 1997. Combining ability studies in sunflower (*Helianthus annuus* L.). Crop Improv. 24(1): 50-54.

Burli, A.V., B.B. Pawar and M.G. Jadhav. 2001. Combining ability studies of some male sterile lines and restorers in sunflower. J. Maharashtra Agric. Univ. 26(2): 190-191.

Dagustu, N. and A.T. Goksoy. 2002. Combining ability and hybrid performances in Sunflower (*Helianthus annuus* L.). Tur. J. Field Crops, 7(1): 6-14.

Falconer, D.S. and T.F.C. Mackey. 1996. Introduction to quantitative genetics, 4th edn. Longman Group Limited, England. 464 p.

Fick, G.N. and J.F. Miller. 1997. Sunflower breeding.In: Schneiter, A.A. (ed.) sunflower techno-logy and production. No.35. ASA, CSSA, SSSA, Inc. publishers, Madison, Wisconsin, USA. p. 395-439.

Fick, G.N., E.D. Putt and D.L. Smith. 1978. Sunflower Science and Technology. In: Carter, J.F. (ed.) Morphology and anatomy. No. 19. ASA, CSSA, SSSA, Madison Wisconsin. USA. p. 55-85.

Gangappa, E., K.M. Channakrishnaiah, M.S. Harini and S. Ramesh. 1997. Studies on combining ability in sunflower (*Helianthus annuus* L.) restorer lines. Sementi-Elette. 48(3): 39-42.

Ghaffari, M., I. Farrokhi and M. Mirzapour. 2011. Combining ability and gene action for Agronomic traits and oil content in sunflower (*Helianthus annuus* L.) using F_1 hybrids. Crop Breed. J. 1(1): 73-84.

Giriraj, K., R.H. Shantha and K. Seenappa. 1987. Combining ability of converted male sterile lines of sunflower (*Helianthus annuus* L.). Indian J. Genetics and Plant Breed. 47(3): 315-317.

Goksoy, A.T., A. Turkee and Z.M. Turan. 2000. Heterosis and combining ability in sunflower (*Helianthus annuus* L.). Indian J. Agric. Sci. 70(8): 525-529.

Goksoy, A.T., A. Turkee and Z.M. Turan. 2002. Determination of some agronomic characteristics and hybrid vigor of new improved synthetic varieties in sunflower (*Helianthus annuus* L.). Helia, 25(37): 119-130.

Jayant, B., K.Giriraj, R.D. Singh and J. Bhat. 2001. Characterization of sunflower genotypes for yield and confectionery characteristics. New Botanist, 28(1-4): 97-101.

Kandalkar, B.S. 1997. Combining ability analysis in sunflower. Bhartiya Krishi Anusandhan Patrica. 12(2): 103-106.

Kempthorne, O. 1957. An introduction to genetics statistics. John Willey and Sons, Inc New York. p. 545.

Kesteloot, J.A., J. Heursel and F.M. Pauwels. 1985. Estimation of the heritability and genetic variation in sunflower. Helia, 8: 17-20.

Khalil, I.A. and A. Jan. 2002. Text Book of Agric. Cropping, Technology National Book Foundation, Islamabad, Pakistan.

Kovacik, A. and V. Skaloud. 1972.

Combining ability and prediction of heterosis in sunflower. Sci. Agr. Bohem. 4(21): 4.

Kumar, A.A., M. Ganesh, S.S. Kumar and A.V.V. Reddy. 1999. Heterosis in Sunflower (*Helianthus annuus* L.). Annals of Agric. Res. 20(4): 478-480.

Lande, S.S., M.C. Patel and D.G. Weginwar. 1997. Combining abi-lity study in sunflower (*Helian-thus annuus* L.) through line x tester analysis. PKV. Res. J. 21(2): 139-142.

Marinkovic, R. and D. Skoric. 1985. Inheritance of 1000 seed and hecto-liter mass in F_1 sunflower and components of genetic variability. Zbornik radova (IFVC) 14: 62-71.

Meric, C., F. Dane and G. Olgun. 2003. Histological aspects of anther wall in male fertile and cytoplasmic male sterile sunflower (*Helianthus annuus* L.) Helia, 26: 7-18.

Ortis, L., G.Nestures, E.Frutos and N.Machado. 2005. Combining ability analysis for agronomic traits in sunflower (*Helianthus annuus* L.) Helia, 28: 125-134.

Pouzet, A. and D. Delplancke. 2000. Evolution compare dela production etde la competitivite du tournesal dars differentes aires de production. Toulouse, France. Tomel. Proc. 15th Intl. Sunflower Conf. p. 1-9 .

Putt, E.D. 1966. Heterosis, combining ability and predicted synthetics from a diallel cross in sunflower (*Helian-thus annuus* L.). Can. J. Plant Sci. 46: 59-67.

Radhika, P., K. Jagadeshwar and K.A. Khan. 2001. Heterosis and com-bining ability through line x tester analysis in sunflower (*Helianthus annuus* L.). J. Res. ANGRAU 29(2-3): 35-43.

Radhika, P., K. Jagadeshwar and P.S. Sharma. 1999. Genetic analysis of seed yield and certain physiolo-gical parameters in sunflower. J. Res. ANGRAU. 27(1-2): 5-17.

Rao, N.M. and B. Singh. 1977. Inheritance of some quantitative characters in sunflower. Pantnagar J. Res. 2(2): 144-146.

Robelin, M. 1967. Effects and after-effects of drought on the growth and yield of sunflower. (In French). Ann. Agron. 18: 579-599.

Rustan, A.C. and C.A. Drevon. 2005. Fatty acids structure and proper-ties. Encyclopedia of Life Sciences. John Wiley & Sons, Ltd. www.els.net. Accessed on 21-02-2013.

Sakthivel, K. 2003. Line x tester analysis for combining ability in *kharif* sunflower (*Helianthus annuus* L.). J. Ecobiology. 15(4): 299-303.

Samiullah, K. 2000. Heat unit requirement of sunflower hybrids. MS Thesis. Deptt. of Agron. Faculty of Crop and Food Sci. Univ. of Arid Agric., Rawalpindi, Pakistan.

Sassikumar, D., A. Goplan and T. Thirumurugan. 1999. Combining ability analysis in sunflower (*Helianthus annuus* L.). Tropical Agric. Res. 11: 134-142.

Satyabrata, M., M.R. Hedge and S.B. Chattapadhyay. 1988. Hand Book of Annual Oilseed Crops. Oxford and IBH publishing Co. (Pvt.) Ltd. New Dehli. p 176.

Seetharam, A.P., K. Kumari and N.M. Patil. 1975. Performance of hybrid sunflower produced by means of cytoplasmic male sterility. Sabro J. TR. 9(1): 51-55.

Shankara, A.C. 1981. Evaluation of sunflower inbreds for their combin-ing ability for line x tester analysis. M.Sc. (Agri) Thesis, University of Agricultural Sciences, Bangalo. 323p.

Shannon, G. 2012. High oleic acid soybeans for wider use of oil in food,

fuel and other products. Proc.15th Annual National Con-servation on Systems Cotton & Rice. 43 p.

Shekar, G.C., H. Jayaramaiah, K. Virupakshappa and B.N. Jaga-deesh. 1998. Combining ability of high oleic acid in sunflower. Helia, 21(28): 7-14.

Singh, D.P. and S.B. Singh. 2000. Genetic analysis for quantitative traits in sunflower (*Helianthus annuus* L.). Crop Improv. 27(1): 87-88.

Sprague, G.F. and L.A. Tatum 1942. General versus specific combining ability in single cross of corn. J. Amer. Sci. Agron. 34: 923-932.

Steel, R.G.D. and J.H. Torrie. 1996. Principles and Procedures of Statis-tics. McGraw Hill Book Co., New York.

Tan, A.S. 2010. Studies on determin-ation of combining abilities of inbred lines for hybrid breeding using lines x tester analysis in sunflower (*Helianthus annuus* L.). Helia, 33(53): 131-148.

Waqas, A.M., M.S. Ahmad and H.N. Tahir. 2012. Combining ability analysis for achene yield and related traits in sunflower (*Helianthus annuus* L). Chilean. J. Agric. Res. 72(1): 21-26.

Whetsell, M.S., E.B. Rayburn and J.D.Lozier. 2003. Why saturated fatty acids are harmful. (Available at http://www.fitday.com /fitness-articles/nutrition /fats/why-saturated-fatty-acids-are-harmful).

AUTHORSHIP AND CONTRIBUTION DECLARATION

S. No	Author Name	Contribution to the paper
1.	Dr. Syeda Nasreen	Conceived the idea, Overall management of the article
2.	Mr. Muhammad Ayub Khan	Technical input
3.	Mr. Muhammad Arshad	Conclusion
4.	Maryam Kamal	Data collection
5.	Mr. Doulat Baig	Data collection
6.	Mr. M. Tariq	Results and Discussion
7.	Ms. Talat Gilani	Data collection
8.	Ms. Musarrat Gilani	Introduction