RESEARCH PAPER

Estimation of gene effects and combining ability study in sunflower (*Helianthus annuus* L.) for yield and yield attributing traits

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Abstract : The present study was aimed to study the combining ability in sunflower, study the gene action *GCA* and *SCA effect* and GCA and SCA variance in sunflower by evaluating the sunflower hybrids to identify the superior cross combination/ sunflower hybrids in respect to yield and yield components. The crossing was affected in the line x tester fashion and the resultant hybrids were subjected to combining ability studies. The results of this study may be used for the development of new high yielding and stable sunflower hybrids based on the hybridization between the best combiner. The estimates of SCA and GCA variances were highly influenced by highly significant mean square due lines x environments, tester x environments and lines x testers x environments variances in seed filling percentage, while for head diameter, significant interaction between lines x environments and lines x testers x environments variances revealed that testers and hybrids were influenced by environments. The magnitude of estimated component of GCA and SCA variances revealed greater importance of GCA for head diameter, while of SCA for seed filling percentage. Six parents, CMS-853A and CMS-852A and EC-623027(M), EC-601751, EC-623023 and EC-601725 had significant positive GCA effect for seed yield and some other yield components like head diameter, 100 seed weight and volume weight (g/100cc) depicted that these genotypes appeared to possess high concentration of additive genes for seed yield and component traits. Seed yield, the final expression of above component traits, was found to record high significant mean square for lines, testers and line x tester interaction indicating significant contribution of lines and testers towards general combining ability variance component for the trait. Whereas significant mean square for line x tester indicates the significant contribution of crosses for specific combining ability variance component. Significant L x T proved that variation among hybrid combination was considerably higher. Significant interaction between lines x environments and lines x testers x environments suggested that lines and hybrids were highly influenced by environments. On the basis of pooled analysis, SCA: GCA ratio variances indicated that the most of the total genetic variation for seed yield was resulted in by the non-additive gene effects.The studies revealed that the best cross combination for semi-dwarf plant height coupled with good seed yield per plant and high oil content are CMS-10A X EC-601725, P-89-1A X EC-601751 and P-2-7-1A X EC-601725, respectively. Among the hybrids, CMS-853 A X EC-623027, CMS-853 A X EC-623023, CMS-852 A X EC-623016 possessed superior SCA effects for seed yield as well as high 100 seed weight and high volume weight. These crosses involved at least one parent with high GCA effects and had high seed yield at *per se* performance.

Key Words : Sunflower, Combining ability, Gene action, Seed yield, Yield components

INTRODUCTION

Sunflower (*Helianthus annuus* L.; 2n=2x=34) is the fourth important source of vegetable oil in the world due to its low to moderate production requirements, high oil quality, protein content and utilization of all plant parts and it is considered as good quality oil due to high concentration of poly unsaturated fatty acids. The importance of sunflower as an oilseed crop in India is of very recent origin and date backs to three decades. But its contribution towards attaining self-sufficiency in edible oil as well as to "yellow revolution" in the country is note worthy. National sunflower hybrid (development) breeding programme is continuous programme which started in our country in early 1980s. In India, first ever sunflower hybrid developed in 1980s, gave a fillip and renewed the interest in crop because of well defined CMS system. Hybrids are preferred over varietal populations because of their high productivity in terms of seed and oil yield.

With the increase in demand for edible oils, there is a need to develop new sunflower hybrids with considerable magnitude of heterosis for economic traits and also suited to different agro-climatic zones of India. The selection of parent is one of the important aspects in developing the potential hybrid which is practiced after testing of parents for their combining ability effects. It is also useful in understanding the type of gene action controlling various traits. Line × Tester analysis (Kmpthorne, 1957) has been widely used for genetic analysis as it is an efficient technique for evaluating large number of inbreds.

Modern Sunflower breeding began with and became an oilseed crop around the world during the end of the 19th century, when 'popular selection' was practiced in several parts of Russia to improve sunflower populations grown at that time. Development of hybrids is the primary objective of most sunflower breeding programmes in the world.

In India, the sunflower is grown on about 0.7 million ha (Padmaiah *et al.,* 2015) and mostly grown in the states of Karnataka, Maharastra, A.P. and Tamil Nadu with potential scope of growing in the non-traditional areas like West Bengal (Dutta, 2011). In West Bengal, Sunflower is second important oilseed crop after rapeseed-mustard during *Rabi* summer season and it was grown on about 21,000 ha in last *Rabi* season (2014-15). Sunflower hybrid breeding was started economically in discovering CMS by Leclercq in 1960 (Miller and Fick,

1997). First sunflower hybrids were produced in US in 1972 and reached 80 per cent of production in five years. Single-cross hybrids quickly became dominantly in sunflower cultivars in the world. Hybrids were preferred by farmers due to its high yield and quality potential, homogeneity, same time maturing and easy possibility of cultural applications both in India and the world. Use of hybrids was reached over 95 per cent in India sunflower production in last 10 years.

After the discovery of the cytoplasamic male sterility (CMS) lines (Leclercq, 1969) and fertility restorer genes by Kinman (1970) which shifted the interest from population breeding to heterosis breeding. The study of combining ability is useful in testing of hybrid combinations and in choice of the desirable parents for use in the heterosis breeding. One of the techniques, which was widely used to extract the Information about the potentiality of the parental lines and the gene action governing the inheritance of traits is line x tester (L x T) analysis.

The present study was aimed to study the combining ability in sunflower, study the gene action *GCA* and *SCA effect* and GCA and SCA variance in sunflower by evaluating the sunflower hybrids to identify the superior cross combination/sunflower hybrids in respect to yield and yield components suitable for growing *Rabi* season in West Bengal agro-climatic condition.

MATERIAL AND METHODS

With a view to identify the lines (female and male) with good combining ability and to identify the good specific cross combination for further exploitation, the present investigation was undertaken in the 2014-15 and 2015-16 at AICRP on sunflower (ICAR-IIOR, Hyderabad-500030) Research Farm, Nimpith Centre, Ramkrishna Ashram Krishi Vigyan Kendra, Nimpith, South 24 Parganas, West Bengal to study the gene action, combining ability and heterosis for seed yield and certain yield attributing components in sunflower (*Helianthus annuuas* L.) involving 6 restorer and 8 CMS lines. The crossing was affected in the line x tester fashion and the resultant hybrids were subjected to combining ability studies. The genotypes were raised in Randomized Block Design with two replications where in each replications were represented by three rows of three meter length.

The soil texture was clay loam in "On station" plots. Three irrigations were provided during the cropping period. One foliar spray was given with Boron (@ 2g/lit.

of water in ray floret stage. The row per plot were five in number with a row spacing of 60 cm and plant to plant spacing was 30 cm. Uniform dose of fertilizer @80 kg N, 40 kg P_2O_5 and 40 kg K_2O per ha was applied. The germinated seed of sunflower used as the planting materials and one per hill were maintained throughout the cropping period. The data was recorded in ten randomly selected plants from each plot of all replications on the following characters *viz.,* days to 50 per cent flowering, days to maturity, plant height at harvest (cm), head diameter per plant (cm), seed weight per head (g), 100-seed weight (g), husk/hull content (%), No. of filled grain and unfilled grain per head, volume weight (g/100cc) and the seed yield/ plant. The seed yield (kg/ha), oil percentage and oil yield (kg/ha) were estimated on plot basis. The mean values were subjected to statistical analysis.

The analysis of variance shows significant differences among the genotypes for all the above said characters studied. The gene action governing different traits were inferred from combining ability. The variance due to specific combining ability was higher for all the traits studied. The σ2D values were also found to be higher than σ2A for all the traits study. Predominance of dominance genetic variance of all the traits except plant height indicated the influence of non-additive gene action as reported by Gaurishankar *et al.,* 2007 and Mohanasundaram *et al.,* 2010. The general combing ability effects quantitatively measure the comparative performance of the parents in relation to others. Out of 14 parents, for seed yield per plant, the positive the GCA effects were observed among the lines 8 CMS lines (Line) *viz.,* CMS-10A,CMS-103A, CMS-207A CMS-850A, CMS-852A, CMS-853A, PET-2-7-1A and PET-89-1A and 6 male parents (Tester) *viz.*, EC-623027

(mono), EC-601751, EC-601725, EC-623016, EC-623023 and EC-623021. The data pertaining to seed yield and other yield attributing traits for these test hybrids along with the checks are presented in Table 3.

RESULTS AND DISCUSSION

Highly significant means square due to parents x environments and hybrids x environments were observed for all the agronomic traits indicated appreciable influence of environment for expression of this traits in parents and F_1s. Whereas, parents *vs* hybrids x environments was highly significant for all the agronomic traits which revealed greater effect of environment on hybrids compared to parents in expression of these traits and existence of overall heterosis for these characters.

Two testers *viz.,* EC-601725 and EC-601751 exhibited higher GCA effects for most of the traits studied (head diameter, No. of filled seeds/head, oil %), therefore, these parents can be considered as the good combiners. For hull content, CMS 103A and CMS-850A among testers and among lines EC-6018787 and Ec-623016 exhibited significant negative GCA effects, therefore, these parents can be considered as the good combiners (Table 3). Hybridization helps to augment the desirable genes of various parents in one combination. Specific combining ability (SCA) is defined as the deviation from mean performance predicted on the basis of general combining ability (GCA) and *specific combining ability* is due to non-additive gene action. Irrespective of general combining ability of the parents, certain combination of parents can give superior hybrids (Table 3). Higher seed volume weight in sunflower is often associated with higher seed yield as well as oil content. CMS 852A and CMS-853A testers recorded significant and positive GCA

Table 1 : Analysis of variance (Mean squares)											
Source of variation	d.f.	Days. to 50% flowering	Plant height	Head Diameter	Autogamy %	100 seed weight	No. of Filled seeds/head	Seed yield /plant	Hull content %	Oil content %	Oil yield (kg/ha)
Replication	1	0.96	7.25	0.58	4.77	0.28	10.85	9.57	1.45	2.35	1.45
Genotypes	70	25.68**	38.68**	45.25**	25.26**	16.48**	28.42**	1062.5**	24.62**	32.62**	48.11**
Parents	14	14.26**	19.41**	24.82**	26.72**	9.81*	25.2**	488.62**	11.78*	9.95*	9.25*
Line	7	9.52**	14.72**	20.56**	21.58**	9.42*	46.5**	362.28**	11.45*	9.28*	9.12*
Tester	6	8.26**	12.41**	16.82**	18.72**	7.81*	20.58**	245.62**	8.78*	7.95*	7.06*
P vs C	1	0.48	3.28	1.66	2.32	0.25	2.36	2.75	1.62	1.24	1.45
Hybrids(L xT)	42	15.82**	23.61**	25.87**	45.62**	11.52*	47.66**	952.51**	19.82**	18.6*	17.48**
Error	55	0.45	5.75	0.66	11.08	0.25	28.25	1.25	1.28	0.95	1.16

* and ** indicate significance of values at P=0.05 and 0.01, respectively

effects for the same trait. With regards to SCA effects, very few crosses displayed significant positive SCA effects for volume weight among them CMS-103 A x EC-601878, PET-89-1A x EC-601878, CMS-850A x EC-623016, PET-2-7-1A x EC-601878, PET-89-1A x EC-601751 and CMS-10A x EC-601725 are found promising. For 100 seed weight CMS 852A and CMS-853A and EC-623023 and Ec-623027 showed positive and significant GCA effects. Thus, these parents could be adjudged good general combiners for 100-seed weight.

Six parents, CMS-853A and CMS-852A and EC-623027(M), EC-601751, EC-623023 and EC-601725 had significant positive *GCA effect* for seed yield and some other yield components like head diameter, 100 seed weight and volume weight (g/100cc). On the basis of analysis these parents recorded significant and positive GCA effects for seed yield. Thus, these genotypes appeared to possess high concentration of additive genes for seed yield and component traits. Most of these parents also possessed high *per se* performance for seed yield as well as its important component traits. The studies revealed that the best cross combination for semi-dwarf plant height coupled with good seed yield per plant and high oil content are CMS-10A x EC-601725(100 days maturity and seed yield 2240kg /ha and oil yield 842 kg/

ha), P-89-1A x EC-601751(100 days maturity and seed yield 2245 kg /ha, oil yield 835 kg /ha) and P-2-7-1A x EC-601725 (100 days maturity and seed yield 2192 kg /ha, oil yield 824 kg /ha), respectively. Among the 48 hybrids, CMS-853 Ax EC-623027 (2462 kg/ha, 107 days maturity and oil yield 881 kg/ ha, 100 seed weight 6.2g), CMS-853 AXEC-623023 (seed yield 2428 kg/ha,105 days maturity, 861 kg oil/ha,100 seed weight 6.2g), CMS-852 Ax EC-623016 (2306 kg/ha, 105 days maturity, 840 kg oil/ha and 100 seed weight 5.9g) possessed superior SCA effects for seed yield as well as high 100 seed weight and high volume weight in comparison to the national check hybrids, *i.e.* KBSH-53 (seed yield 2212 kg/ha and 114 days maturity) and DRSH-1 (seed yield 2126 kg/ha and 108 days maturity), respectively. These crosses involved at least one parent with high *GCA effect* for yield attributing traits and had high seed yield at *per se* performance.

From the field experiments it was observed that the difference were significant among lines, testers and lines tester interaction for head diameter and seed filling percentage. Testers exhibited the highest proportional contributions for above characters. The estimates of SCA and GCA variances were highly influenced by highly significant mean square due lines x environments, tester

Table 2 : General combining ability effects of parents for yield and yield contributing characters

Name of the parent	Plant height	Head diameter	Days to 50% flowering	Seed yield/plant	100 seed weight	No. of filled seeds/head	Autogamy % (Gr. Filling%)	Hull cont. (%)	Vol. Wt. (g/100cc)	Oil cont. %
CMS-850A	-6.25**	-0.22*	-1.82**	- 6.08*	-1.28*	3.25	0.35	-0.56*	-0.55*	-0.55*
CMS-852A	8.65**	0.66**	-0.61*	13.27**	1.22*	16.25**	0.32	0.45*	0.57*	-0.58*
CMS-10A	11.45**	0.45**	-0.55*	5.42	-1.08*	11.65**	0.41	0.45*	-0.48*	-0.65*
CMS-853A	14.45**	0.81**	0.41**	14.42**	1.62*	18.75**	0.32	0.41*	0.71*	-0.71*
P-89-1A	9.56**	0.52**	-0.35	10.55**	-1.16*	12.65**	0.71*	0.49*	0.35*	-0.55*
CMS-103A	-9.87**	-0.26*	-2.31**	-7.42*	-1.56*	3.45*	0.83*	-0.78*	-0.38*	-0.48*
P-2-7-1A	9.02**	0.46**	-0.29	10.51**	-1.02*	14.81**	0.65	0.41*	0.47	-0.56*
CMS-207A	7.12*	0.36**	-0.31	8.28*	-1.16*	12.58**	0.37	0.41*	-0.41*	-0.55*
S.E.±	2.62	0.14	0.12	3.48	0.05	4.67	0.25	0.27	0.31	0.31
EC-601878	3.41*	0.81 **	-0.72*	5.08*	-1.18*	11.51**	0.73*	-0.25*	-0.47*	0.39*
EC-623023	8.85**	0.89**	1.17**	10.08**	-1.18*	13.18**	-0.25	0.32*	0.55*	-0.37*
EC-623016	8.25**	0.49**	-1.14*	6.27**	-1.42**	7.68	0.65*	-0.35*	-1.06**	-1.25**
EC-623027	11.25**	1.58**	1.54**	14.27**	1.22**	17.44**	0.35	0.25*	1.21**	-0.38**
EC-601751	8.21**	1.17**	-0.72*	10.08**	0.75*	12.25*	-0.38	0.36*	-0.55*	-0.55*
EC-601725	6.28**	1.09**	-0.55*	14.55**	-1.28*	10.61**	-0.27	0.25*	0.57*	-1.26**
EC-623021	12.25**	1.60**	0.64*	11.23**	-1.02*	11.86**	-0.45	-0.40	-1.05**	-1.05**
S.E.±	4.28	0.21	0.38	1.28	0.07	3.28	0.36	0.56	0.41	0.36

* and ** indicate significance of values at P=0.05 and 0.01, respectively

x environments and lines x testers x environments variances in seed filling percentage, while for head diameter, significant interaction between lines x environments and lines x testers x environments variances revealed that testers and hybrids were influenced by environments. The magnitude of estimated component of GCA and SCA variances revealed greater importance of GCA for head diameter, while of SCA for seed filling percentage. Similar to present findings, head diameter was observed to be under the influence of additive effects by Makanda *et al.* (2012). Patil *et al.* (2012) and Jondhale *et al.* (2012) highlighted the importance and predominance of non-additive effects in for the same traits.

Volume weight, 100-seed weight and biological yield and hull content recorded significant mean squares due to lines, testers as well as line x tester on the basis of pooled analysis, with high magnitude of variance for lines and testers as compared to L x T. This indicated significant

contribution of lines, testers towards GCA and line x tester interaction towards SCA. The magnitude of estimated component of GCA and SCA variances revealed greater importance of SCA for all the characters. Among interactions, line x environments, testers x environments and line x tester x environments were highly significant for aforesaid traits except for lines x environments in hull content indicated that estimates of GCA and SCA variances were influenced by the environments. The SCA: GCA ratio is indicated that the most of the total genetic variation for aforesaid characters were resulted in by the non-additive gene effects.

Oil content recorded significant mean squares due to lines, testers as well as line x tester with high magnitude of variance for lines and testers as compared to L x T on the basis of analysis. This indicated significant contribution of lines, testers towards GCA and line x tester interaction towards SCA. Highly significant

Table 2A : Performance of the parents for yield and yield contributing characters

Name of the parent	Pl. ht (cm)	Hd. dia. (cm)	50% flow.	Seed yield (kg/ha)	100 seed wt.(g)	Hull. cont. (g)	No. of filled grains/ Hd.	Gr. filling %	Vol. wt (g/100cc)	Oil%	Oil yield (kg/ha)
CMS line (L)											
CMS-853A	118.6	11.5	67.9	1385	5.7	30.2	298	83.3	42.8	36.2	501
CMS-852A	123.5	11.8	65.6	1140	5.0	32.1	280	86.8	42.2	35.6	406
CMS-850A	116.0	12.8	66.0	1090	4.9	28.9	286	90.2	42.0	35.4	386
CMS-103A	129.3	12.3	65.0	1035	5.3	26.5	321	87.8	45.4	36.2	375
PET-2-7-1A	131.8	13.2	70.4	1150	5.5	33.1	364	86.9	43.7	35.2	405
CMS-207A	136.0	12.6	68.8	1210	4.6	31.8	478	88.0	40.4	35.4	428
PET-89-1A	107.8	10.5	71.0	1100	4.9	29.3	408	84.0	45.4	35.2	387
CMS-10A	141.9	12.4	69.4	1225	5.3	31.4	340	87.1	42.1	34.0	417
S.E. ±	2.2	0.3	1.1	36	0.17	0.9	18	1.6	0.8	-	12.6
C.D. (P=0. 05)	6.2	0.8	3.2	108	0.52	2.8	54	4.8	2.4	NS	36
C.V.(%)	8.4	6.8	7.7	9.4	6.2	7.1	9.2	6.1	5.4	-	8.8
R line (T)											
EC-623027 (M)	104.8	9.9	71.5	1020	5.6	26.0	393	77.5	45.3	38.9	397
EC-623023	95.8	7.5	71.3	825	5.3	29.1	283	85.2	43.0	38.2	315
EC-623021	87.4	8.6	64.0	780	5.0	29.5	262	87.5	42.0	42.5	342
EC-601878	87.4	11.6	66.3	770	4.9	29.6	286	87.9	42.9	42.5	327
EC-601751	91.2	9.0	62.0	720	5.4	30.0	256	85.5	43.0	42.0	318
EC-601725	84.2	9.8	70.5	880	5.2	32.7	308	83.0	44.6	41.8	368
EC-623016	86.2	6.4	69.8	690	5.1	29.0	235	86.3	41.5	41.5	286
S.E. ±	2.8	0.4	1.4	41.5	0.14	1.1	16.2	1.58	0.82	0.94	14.2
C.D.(P=0.05)	8.6	1.1	4.2	120	0.42	3.4	48	4.6	2.4	2.8	41.6
C.V.(%)	7.2	6.1	5.8	8.8	5.5	6.4	8.2	6.6	5.8	8.5	8.6

NS= Non-significant

Table 3 : Performance of specific cross combination(Sunflower hybrids) for yield and yield attributing characters

Sr. No.	Hybrid combination	Pl. ht (cm)	Hd. dia. (cm)	50% flow.	Seed yield (kg/ha)	100 seed wt.(g)	Hull cont (%)	No. of filled grain/Hd	Gr. fill. %	Vol. wt (g/100 cc)	Oil%	Oil yield. (kg/ha)
1.	CMS-853 A X EC623027	194.5	16.4	73.0	2462	6.2	32.3	766	87.0	42.8	35.8	881
2.	CMS -853 A X EC623023	192.5	16.0	75.5	2428	6.0	30.0	812	87.5	43.0	35.6	864
3.	CMS-853 AX EC 623021	144.0	15.7	74.5	2292	5.0	28.0	922	87.0	43.7	36.4	834
4.	CMS-853A X EC-601878	145.0	15.5	71.5	2075	5.6	25.0	674	86.5	45.3	37.4	776
5.	CMS-853A X EC-601725	192.5	17.4	75.5	2278	4.8	33.3	916	87.0	40.0	35.2	802
6.	CMS853A X EC-623016	160.5	15.0	72.0	2072	5.6	32.1	813	87.5	43.8	37.2	770
7.	CMS-852A X EC-623027	185.0	15.1	76.0	2270	4.9	30.0	916	92.0	40.0	35.8	814
8.	CMS-852A X EC-623023	180.0	15.4	76.0	2328	4.6	34.8	1021	88.5	43.2	36.1	840
9.	CMS 852 AX EC-623021	184.0	15.4	77.5	2272	5.0	30.0	888	91.0	40.0	35.8	813
10.	CMS-852AX EC-601878	170.0	15.4	74.5	2284	4.8	31.3	930	90.0	41.6	36.4	831
11.	CMS-852 A X EC-601725	155.0	16.7	70.5	2072	5.6	32.1	813	87.5	43.8	37.2	771
12.	CMS-852A X EC-623016	175.5	15.3	73.0	2306	5.9	25.4	741	88.5	42.7	35.8	826
13.	CMS-850A X EC-601751	133.0	15.4	69.0	1861	5.1	27.5	663	91.5	42.6	36.8	685
14.	CMS-850 A X EC-601878	92.5	9.6	65.0	1500	5.0	28.0	565	94.0	39.7	39.2	588
15.	CMS-850A X EC-623016	122.5	13.3	64.0	1472	4.5	31.1	595	91.0	43.6	38.4	565
16.	CMS-103A X EC-623023	124.0	12.7	64.0	1340	4.8	29.2	507	90.0	42.2	37.2	498
17.	CMS-103 A X EC-601878	134.5	11.8	66.0	1733	5.8	23.8	536	90.5	48.5	38.4	665
18.	CMS-103A X EC-601751	137.5	10.5	64.5	1232	4.7	30.0	532	91.0	43.4	38.9	486
19.	P-2-7-1A X EC-623027(M)	190.0	16.4	73.0	2094	5.2	34.6	767	89.0	43.2	37.0	775
20.	PET-2-7-1A X EC601878	137.5	11.5	64.5	1340	4.5	31.1	582	90.0	45.6	38.7	518
21.	P-2-7-1A X EC-601751	177.5	15.8	76.0	2340	5.6	32.1	818	87.5	42.6	35.2	824
22.	PET-2-7-1A X EC601725	145.5	15.7	68.0	2192	5.5	32.7	758	88.5	43.5	37.6	824
23.	PET-2-7-1A X EC623016	155.5	14.9	70.0	1878	6.9	33.8	495	90.0	42.4	37.8	710
24.	CMS-207AX EC-623027	142.5	14.0	63.5	1567	4.7	32.8	606	92.0	39.6	39.0	611
25.	CMS -207A X EC623023	142.5	14.7	73.0	2194	4.4	29.5	907	88.0	39.9	36.4	799
26.	CMS207AX EC-623021	169.0	14.4	70.5	1886	5.0	34.0	715	90.0	38.0	37.5	707
27.	CMS-207A X EC-601878	115.0	13.5	67.0	1431	5.3	32.1	491	90.5	39.2	38.5	551
28.	CMS207AX EC-601725	172.5	14.8	71.5	2017	4.8	33.3	764	86.0	40.0	36.8	742
29.	CMS-207AX EC-623016	123.0	14.0	66.5	1447	4.3	32.6	612	92.0	40.2	38.5	557
30.	PET-89-1A X EC-623027	185.0	15.0	73.5	2218	4.5	31.1	982	88.0	45.1	35.6	790
31.	PET-89-1A X EC-601878	123.0	12.0	68.5	1444	5.0	26.0	525	91.5	45.2	38.8	560
32.	PET-89-1A X EC-601751	154.0	15.1	71.0	2244	5.2	30.8	844	85.5	45.9	37.2	835
33.	PET-89-1A X EC-601725	148.5	15.0	73.0	1960	4.6	31.8	762	89.0	39.7	36.8	711
34.	PET-89-1A X EC-623016	136.5	13.9	67.0	1611	5.1	33.3	767	90.0	41.0	37.5	604
35.	CMS-10 AX EC-623023	154.0	14.6	64.0	1380	4.8	29.2	523	92.0	42.2	38.6	533
36.	CMS -10A X EC-623021	162.5	15.2	71.5	1722	5.5	30.9	569	88.0	40.8	36.5	629
37.	CMS-10A X EC-601751	142.5	14.7	73.5	1967	4.4	31.8	813	87.0	39.6	36.4	716
38.	CMS-10 AX EC-601878	119.0	12.8	64.5	1306	5.0	30.0	612	92.0	40.3	38.2	499
39.	CMS-10A X EC-601725	156.5	15.4	70.5	2240	5.2	32.7	818	86.0	44.6	37.6	842
40.	CMS-10 AX EC-623016	145.5	15.0	68.0	1792	5.5	32.7	625	87.5	41.5	38.2	685
	KBSH-44	185.0	15.6	80	2224	5.1	36.5	793	86.5	36.0	28.6	636
	DRSH-1	175.0	15.1	78	1916	5.5	32.0	633	90.0	40.5	39.2	736
	LSFH-171	181.0	15.7	80	2260	5.1	35.0	806	87.5	36.5	31.0	701
	G. Mean	152.2	15.1	69.9	1864	5.1	32.0	710.2	88.1	41.2	36.5	711
	S.E.±	2.3	0.6	1.1	21.4	0.2	0.5	20.3	0.6	0.4	0.22	28.2
	C.D. (P=0.05)	6.8	1.7	3.4	61.8	0.6	1.4	60.4	1.8	1.1	0.68	84.5
	C.V. (%)	9.2	5.1	6.8	9.6	5.8	8.2	9.2	7.5	7.1	8.2	9.4

Table 4 : Specific combining ability effects of hybrids for yield and yield attributing characters

Sr. No.	Hybrid combination	Pl. ht. (cm)	Hd. dia. (cm)	Days to 50% flow.	Seed yield (kg/ha)	100 seed wt (g)	Husk wt. (g)	Autogamy %	Vol. wt. (g/100cc)	Oil (%)	Oil yield (kg/ha)
1.	CMS-853 A X EC-623027(M)	10.62*	1.96**	1.52**	28.89**	1.33**	1.45*	-2.78	-1.24	-1.63*	9.28**
2.	CMS -853 A X EC623023	9.78**	1.82**	1.46**	25.59**	1.63**	-1.22	-3.64**	1.18	-2.48	8.36**
3.	CMS-853A X EC-623021	4.86**	1.71**	-2.18**	23.16**	1.14	1.17*	-3.97**	1.40*	-1.71	7.82**
4.	CMS-853 A EC-601718	5.62**	1.36**	-1.60**	20.62**	4.8	1.01	2.85	1.18	-1.56	7.24**
5.	CMS-853A XEC-601725	7.56**	1.77**	1.35*	17.81**	1.02	1.19*	-4.72**	-4.78**	-2.84**	6.61**
6.	CMS-853A X EC-623016	4.55**	1.76**	-1.60**	15.45**	1.18**	-1.58**	-4.40**	1.78**	-1.52	5.23**
7.	CMS-852A X EC-623027(M)	9.82**	1.91**	-1.87**	22.85**	0.85	-1.35**	-4.18*	1.68**	-1.68*	7.42**
8.	CMS 852 AX EC-623021	7.17**	1.65**	-1.98**	18.25**	1.11	1.17	-2.36*	-2.92**	-2.81**	6.12**
9.	CMS-852A X EC-601878	4.62**	1.36**	-1.60**	16.20**	-1.12	-2.36**	1.38	1.61	-1.56	6.82**
10.	CMS-852A X EC-601751	6.82**	2.08**	-1.61**	15.56**	-1.37**	1.63*	-1.26	-1.68	1.52	5.22*
11.	CMS-852 A X EC-601725	8.48**	1.67**	1.12	17.25**	1.27*	1.22*	1.25	2.68**	1.41	6.27**
12.	CMS-852A X EC-623016	6.17**	2.08**	-1.76**	19.85**	1.21**	-1.35**	-1.58*	1.88*	-2.68**	7.45**
13.	CMS-850 A X EC-601878	-2.56**	-5.67**	-2.05**	15.12**	1.06	1.08	-3.45**	1.02*	1.42	5.42**
14.	CMS-850A X EC-601751	4.18**	1.92**	-2.52**	19.08**	5.1	-1.21**	-1.29	1.76*	-1.86**	6.08
15.	CMS-850A X EC-623016	2.24	1.15	-1.72**	14.56**	-1.18*	-1.07	1.72	1.60*	-1.47	4.66*
16.	CMS-103A X EC-623023	7.25**	1.66**	-2.85**	20.51**	-1.74**	-1.02	-3.11**	-1.35	1.12	6.71**
17.	CMS-103 A X EC-601878	2.18	-1.25	-1.46*	17.26**	1.28	-2.42**	3.48**	2.08*	1.68*	5.68**
18.	CMS103A XEC -601751	6.22**	1.49**	-1.85**	14.25**	0.86	-1.02	-1.45	-1.52	1.22	4.85**
19.	P-2-7-1A X EC 623027	8.59**	1.68**	1.41**	22.58**	1.45**	1.56**	-2.58**	-1.25*.	-1.32	7.22**
20.	P-2-7-1A X EC-601878	4.68**	-1.18	-3.36*	20.52**	-1.58*	-1.37**	1.18	3.28**	-1.84**	7.26**
21.	P-2-7-1A X EC-601751	6.18**	1.52**	-1.68	17.75**	1.42**	0.70	-1.24	1.42	-2.36**	5.21**
22.	P-2-7-1A X EC-601725	6.12**	1.68**	-1.64**	17.12**	-1.18**	-1.08	-1.21	1.39**	-1.32	4.82*
23.	P-2-7-1A X EC-623016	5.45**	1.88**	-1.76**	18.21**	1.82**	1.12	1.18	1.35*	-1.38	6.32**
24.	CMS-207AX EC-623027	8.31**	1.62**	1.05	24.57**	-1.62**	1.12	-1.32	-3.37**	1.32	8.17**
25.	CMS207AX EC-623021	6.56**	1.35**	1.10	20.12**	1.07	-1.27*	-3.28**	-3.25**	-1.27	7.42**
26.	CMS -207A X EC-623023	7.18**	1.47**	1.21	17.25**	1.18**	-1.42**	-2.72**	-2.47**	1.22	5.45**
27.	CMS-207A X EC-601878	4.36*	1.21	-1.58**	16.88**	-1.51**	-1.38**	-2.81**	-3.62**	-1.41	5.18**
28.	CMS207AX EC-601725	7.76**	1.29**	-1.78**	18.18**	1.21**	1.07	-1.32	-3.11**	-1.25	6.78**
29.	CMS-207AX EC-623016	3.18	1.32**	-1.88**	15.25**	1.68**	1.18*	1.25	-1.12	-1.40	5.25**
30.	PET-89-1A XEC-623027	8.38**	1.42**	-1.08	18.65**	-1.16	-1.28**	-3.28**	-1.38**	-1.28	6.45**
31.	PET-89-1A X EC-601878	3.09	1.28	-1.61**	21.89**	1.49**	-1.33**	-1.22	3.42**	-2.17**	9.28**
32.	P-89--1A X EC-601725	4.52**	1.81**	-1.24*	20.06**	1.47**	-1.08	-1.23	1.35**	-1.32	4.06**
33.	PET-89-1A X EC-601751	4.58**	1.78**	1.02	22.85**	1.68**	1.12	-2.47*	-1.29**	-1.31	6.85**
34.	PET-89-1A X EC-623016	2.56	1.44**	-1.73**	17.25**	1.86**	-1.25	1.31	1.37**	-2.08**	9.11**
35.	CMS-10 AX EC-623023	3.81*	1.38**	1.16	22.62**	-1.52**	1.11	-1.35	-3.84**	-1.58**	8.24**
36.	CMS -10A X EC-623021	4.51**	1.33*	1.11	18.22**	1.53**	1.09	-3.28**	-1.36	2.32**	7.02**
37.	CMS-10 AX EC-601878	5.81**	1.60**	-1.61**	16.25**	1.31**	-1.07	1.15	-1.05	1.45	6.18**
38.	CMS-10A X EC 601751	1.78	1.16	1.28	5.31	1.21	1.46**	-2.43**	-1.32*	-1.45	6.47**
39.	CMS-10A X EC-601725	4.95**	1.68**	1.12	19.67**	2.20**	1.10	-2.35*	-1.45**	-1.31	10.92**
40.	CMS-10 AX EC-623016	4.54**	1.57**	-1.52**	16.28**	1.76**	-1.28**	1.22	-1.44	1.16	7.36**
	S.E.±	1.82	0.21	0.38	3.18	0.58	0.76	2.36	0.82	1.48	2.16

* and ** indicate significance of values at P=0.05 and 0.01, respectively

interaction between line x environments, testers x environments and line x testers x environments suggested that lines, testers and hybrids were influenced by environments. The values of SCA: GCA ratio indicated that the most of the total genetic variation for aforesaid characters were resulted in by the non-additive gene effects in all the environments and on the basis of pooled analysis. The similar type of findings also reported by Patil *et al*. (2012) and Jondhale *et al*. (2012).

Seed yield, the final expression of above component traits, was found to record high significant mean square for lines, testers and line x tester interaction. The significant mean squares indicated significant contribution of lines and testers towards general combining ability variance component for the trait. Whereas significant mean square for line x tester indicates the significant contribution of crosses for specific combining ability variance component. Significant LxT proved that variation among hybrid combination was considerably higher. Significant interaction between lines x environments and lines x testers x environments suggested that lines and hybrids were highly influenced by environments. On the basis of pooled analysis, SCA: GCA ratio variances indicated that the most of the total genetic variation for seed yield was resulted in by the non-additive gene effects. The importance and predominance of non-additive or dominance effects for seed yield in sunflower was also highlighted by many earlier workers like Parameshwarappa *et al.* (2008); Karasu *et al*. (2010); Patil *et al*. (2012) and Jondhale *et al*. (2012).

Conclusion:

The results of this study may be used for the development of new high yielding and stable sunflower hybrids based on the hybridization between the best combiner. The estimates of SCA and GCA variances were highly influenced by highly significant mean square due lines x environments, tester x environments and lines x testers x environments variances in seed filling percentage, while for head diameter, significant interaction between lines x environments and lines x testers x environments variances revealed that testers and hybrids were influenced by environments. The magnitude of estimated component of GCA and SCA variances revealed greater importance of GCA for head diameter, while of SCA for seed filling percentage.

Seed yield, the final expression of above component

traits, was found to record high significant mean square for lines, testers and line x tester interaction. The significant mean squares indicated significant contribution of lines and testers towards general combining ability variance component for the trait. Whereas significant mean square for line x tester indicates the significant contribution of crosses for specific combining ability variance component. Significant L x T proved that variation among hybrid combination was considerably higher.

Significant interaction between lines x environments and lines x testers x environments suggested that lines and hybrids were highly influenced by environments. On the basis of pooled analysis, SCA: GCA ratio variances indicated that the most of the total genetic variation for seed yield was resulted in by the non-additive gene effects.

The studies revealed that the best cross combination for semi-dwarf plant height coupled with good seed yield per plant and high oil content are CMS-10A x EC-601725, P-89-1A x EC-601751 and P-2-7-1A x EC-601725, respectively. Among the hybrids, CMS-853 Ax EC-623027, CMS-853 Ax EC-623023, CMS-852 Ax EC-623016 possessed superior SCA effects for seed yield as well as high 100 seed weight and high volume weight. These crosses involved at least one parent with high GCA effects and had high seed yield at *per se* performance.

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