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## Identification of inbred lines with good combining ability and hybrids surpassing the best checks in sunflower (*Helianthus annuus L.*)

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### Abstract

The present study was carried out, in order to identify the combining ability of 47 new inbred lines on three Cytoplasmic Male Sterile (CMS) lines and also to identify the hybrids surpassing the best checks in sunflower by crossing them in a line × tester mating design. The resultant 141 hybrids along with their parents and two checks *viz.*, KBSH-44 and KBSH-53 were evaluated in simple lattice design. The analysis of variance for line × tester indicated the presence of substantial variability among the crosses and significance of mean sum of squares due to parents *v/s* crosses indicated the presence of heterosis in general. Highly significant variance due to line × tester interaction component indicated the involvement of non-additive gene action in the inheritance of these traits. The line CMS 234A was identified as a line with high overall general combining ability (*gca*) status. Whereas five of the 10 testers *viz.*, GMU-456, GMU-746, GMU-759, GP6-952 and GP6-990 had high overall *gca* status across traits. The hybrid CMS 234A × GMU-716 was identified as the best specific combination for some of the important economic traits in sunflower. The promising hybrids surpassing the best checks were identified *viz.*, CMS 234A × GMU-456, NDCMS 2A × GMU-746 and CMS 911A × GMU-456 for high seed yield plant-land its attributing traits. The resultant hybrids could be tested in large scale yield trials over locations and seasons to confirm their potentiality for commercial cultivation.

**Keywords:** Identification, inbred, combining, surpassing, *Helianthus annuus L.*

### Introduction

The efficiency of developing high frequency of heterotic CMS-based hybrids for commercial exploitation depends on the availability of large numbers of fertility restorer lines (R-lines). The R-lines should possess effective restorer genes for complete restoration of fertility in the hybrids developed from CMS lines. From among the identified R-lines, it is desirable to use only those R-lines with significant general combining ability (*gca*) effects. General combining ability is the average performance of a genotype in the cross combination with a set of other genotypes. The breeding value expressed as the deviation from the population mean is nothing but *gca* effects, which takes in to account the additive effects of the genes and also expressed in terms of *gca* variance. The specific combining ability (*sca*) effects and variances take into account the relative performance of a specific cross combination. The *sca* variance denotes non-additive or dominance portion of variance and generally non fixable on selfing but can be exploited in hybrid combination. The ratio of these variances indicates the nature of gene actions governing the traits, which is important to decide upon the breeding methods to be adopted, parents and crosses to be selected for exploiting the type of gene actions in a crop for selection of superior genotypes and for eventual success. (Jocković *et al.*, 2018)<sup>[6]</sup>.

The *gca* effect is being used as a dependable criteria for selection of parents for use in developing and identifying heterotic hybrids. The *gca* effect of a genotype also provide useful clues about the mode of action of genes controlling target traits. It is also useful in predicting the performance of untested hybrids in the absence of *sca* effects. The support for the use of *gca* as one of the criteria for choosing parents comes from theoretical results that indicate higher heterosis in the hybrids derived from the parents differing in their gene frequency. Parents differ in their *gca* due to differences in frequency of genes with additive effects. (Cvejić *et al.*, 2017)<sup>[4]</sup>.

In heterosis breeding of sunflower, the estimation of *gca* and *sca* helps in identifying the potential parents in the production of superior hybrids for seed yield and oil content.

It is useful in knowing the type of gene action controlling various characters and development of suitable breeding strategies. The line  $\times$  tester analysis (Kempthorne, 1957) [7] is one of the simplest and efficient method of evaluating large number of inbreds for combining ability and *per se* performance. The evaluation of genetic material involved in breeding process is of great importance in order to choose the most valuable genotypes with ability to efficiently combine desirable genes in progeny. The objective of this study was to identify inbred lines with good *gca* and their desirable specific combinations and also to identify hybrids surpassing the best checks.

### Material and Methods

The material used for the study consisted of three cytoplasmic male sterile lines *viz.*, CMS 234A, NDCMS 2A and CMS 911A, 47 new inbred lines as testers and two standard check hybrids KBSH 44 and KBSH 53. The CMS lines and the testers were collected from AICRP on sunflower, ZARS, UAS, GKVK, Bengaluru.

### Crossing programme

All the three CMS lines and 47 inbred lines were sown in the field to effect crossing in a Line  $\times$  Tester fashion in order to obtain F<sub>1</sub>'s. Staggered sowing of all CMS lines were carried out three times at an interval of two days to ensure synchronized flowering with inbred lines for crossing. A day prior to opening of first ray floret all the heads of CMS lines and testers were covered with cloth bags in order to prevent undesirable pollination. Pollen from the inbred lines was collected separately in petri dishes with the help of camel hair brush and applied to the flowers of female lines using brushes during morning hours. The pollination was repeated for five to six days in each of the combination to ensure sufficient seed set and simultaneously all inbreds were sib pollinated. The capitulum of all the resultant 141 hybrids were harvested, dried and threshed separately at physiological maturity. The well filled seeds from each cross were separated out for hybrid evaluation and sib mated seeds of 47 inbred lines were collected for future evaluation.

### Evaluation of hybrids

The resultant 141 experimental hybrids and two standard checks *viz.*, KBSH-44 and KBSH-53 were evaluated with two replications along with parents. Experiment was laid out in simple lattice design (14  $\times$  14 involving hybrids, parents and checks). Each genotype was sown in a single row of three-meter length with a row spacing of 60 cm and 30 cm between plants within a row. Observations were recorded in each entry on randomly selected five plants for ten characters *viz.*; days to 50 per cent flowering, plant height (cm), head diameter (cm), stem diameter (cm), volume weight (g/100 ml), seed yield per plant (g), 100 grain weight, hull content (%), oil content (%) and oil yield (kg/ha).

### Results and Discussion

#### Analysis of variance for seed yield and yield attributing traits

Analysis of variance for combining ability (Table 1) revealed that variance due to lines was significant for days to 50 per cent flowering, plant height, stem diameter, seed yield per plant and oil content. Testers exhibited significant differences for days to 50 per cent flowering, plant height, seed yield per plant and oil content. Line  $\times$  tester interaction variance was

highly significant for all the traits which indicated the significance of dominance variance. The significance due to line  $\times$  tester variance indicated the presence of heterosis for the respective traits. Similar results were also noticed by earlier workers (Pavani *et al.*, 2006; Shankar *et al.*, 2007 and Meena *et al.*, 2013) [12, 16, 9].

#### General combining ability effects of parents

The breeding value expressed as deviation from the population mean is nothing but the *gca* effect, has proved to be very useful tool in identifying the potential parents for hybrid cultivar development. The estimates of *gca* effects provide a relative measure of additive variance, which aids in the selection of superior genotypes for breeding programme. The results obtained on general combining ability for various traits are discussed here under.

The *gca* effects of parental lines (Table 2a) revealed the line CMS 234A exhibited significant *gca* effects for days to 50 per cent flowering, stem diameter, seed yield plant-1, oil content and oil yield in desirable direction. On the other hand, the CMS line NDCMS 2A showed significant *gca* effects for days to 50 per cent flowering, seed yield plant-1, volume weight, hull content, oil content and oil yield in desirable direction. The lines CMS 234A and NDCMS 2A were good general combiners for most of the characters. For simultaneous improvement of seed yield and oil content in the hybrids, either the male or female parent should possess good *gca* for these two traits together or the parents involved in the cross combinations should have good *gca* for one of the traits and able to nick well in the hybrids to produce superior heterosis and high *sca*. Hull content is one of the major yield components exhibiting a strong association with seed yield but associated negatively with oil content. As a consequence, seed yield plant-1 and oil content are negatively correlated and makes simultaneous improvement difficult. The scenario of *gca* of CMS lines has been almost similar to that of associations among these three traits.

Among the testers (Table 2b), GMU-456 was found to be exhibit significant and positive *gca* effect for days to 50 per cent flowering, head diameter, seed yield plant-1, hundred seed weight, hull content and oil yield. Whereas the tester GMU-746 has shown positive *gca* effects for head diameter, seed yield plant-1, volume weight, oil content and appeared to be a desirable parent for developing hybrids as also a good combiner for most of useful traits.

Similar results have also been reported by Reddy and Madhavi Latha (2005) [14], Parameshwarappa *et al.* (2008). Hence, the testers GMU-456 and GMU-746 can be utilized in development of commercial hybrids after looking to their heterotic effects in cross combinations.

#### Specific combining ability effects of crosses

The term "specific combining ability" is used to designate those cases in which certain combinations do relatively better or worse than would be expected on the basis of the average performance of the lines involved. The hybrids from different combinations of the parents with high or low *gca* effects are referred to as H  $\times$  H (high  $\times$  high), H  $\times$  L (high  $\times$  low) and L  $\times$  L (low  $\times$  low) combinations.

The specific combining ability effects for different characters are presented in Table 3a. The analysis of 30 hybrids revealed that no single cross showed maximum *sca* effects for all the characters. Cross combination CMS 234A  $\times$  GMU-716 had high *sca* for stem diameter, seed yield plant-1, hundred seed

weight, hull content, oil content and oil yield. The hybrid CMS 911A x GMU-456 was found to be superior for seed yield plant-1, volume weight and hundred seed weight and oil yield. The cross CMS 911A x GMU- 1092 showed significant *sca* effects for plant height, head diameter, seed yield plant-1, hundred seed weight and oil yield. The hybrid CMS 234A × GMU-759 has been considered as the best specific combination for seed yield plant-1 and oil yield involved parents with high x high *gca* effects in cross combination, indicating the role of additive x additive effects. The highest *sca* effects for seed yield plant-1 was reported in the study occurred as a result of high x high and low x high combinations. These findings are in harmony with the findings of Goksoy *et al.* (2000) [5], Radhika *et al.* (2001) [13], Madrap *et al.* (1993) [8], Parameshwarappa *et al.* (2008) and Tavade *et al.* (2009) [18].

#### Overall specific combining ability effects of crosses

Out of 30 crosses, 16 had high overall specific combining ability status, indicating that 53.33 percent of hybrids were high overall specific combinations. Based on *sca* effects crosses were classified into H × H (both the parents with high overall *gca* status), H × L (one parent with high and other with low overall *gca* status) and L × L (both the parents with low overall *gca* status). Out of 30 crosses, 10, 5 and 15 were H × H, L × L and H × L type of crosses, respectively. Predominance of H × L type of crosses indicated the presence of non-additive gene action there by suggesting population improvement approach in the segregating generations of these crosses to isolate superior inbreds. It is evident that more than 50 percent of the hybrids (16 out of 30 hybrids) had high (H) overall *sca* status across traits. Hence, these crosses can be utilized for exploitation of heterosis. Mohan Rao (2001) [10] reported that nearly 50 percent of the hybrids exhibited high overall *sca* status across the traits.

#### Heterosis

Heterosis is the increase or decrease in vigour of F1 over its mid or better parental value. One of the objectives of present study was to estimate the extent of heterosis for various characters and to isolate promising hybrids over standard check hybrids for seed yield and oil content for commercial exploitation. The nature and magnitude of heterosis for seed yield and its component characters is helpful in heterosis breeding. The maximum utilization of heterosis is possible when the variance due to both additive and non-additive gene actions are fully exploited since they play a significant role in determining the magnitude of expression of yield and its component characters.

Estimates of heterosis of 30 hybrids for seed yield over standard checks (Table 4). As far standard heterosis is concerned, five hybrids over KBSH-44 and ten hybrids over KBSH-53 showed significant heterosis. The hybrid CMS 234A × GMU-456 recorded high heterosis of 12.1 percent over KBSH-44 followed by CMS911A × GMU- 456 (28.65%). Although, the magnitude of standard heterosis is to an extent of around 10 percent with less number of hybrids revealing significant positive heterosis yet it is worthy to consider, as majority of crosses with parents belonging to CMS 911A base have shown negative heterosis. The extent of standard heterosis over KBSH-44 and KBSH-53 may be enhanced through parental improvement. The present task of developing hybrid is to maintain the yield level of KBSH-44 and oil content near or above that of KBSH-53. Prevalence of significant standard heterosis for seed yield has also been reported by Nehru *et al.* (2000) [11], Radhika *et al.* (2001) [13], Alone *et al.* (2003) [1] and Sawant *et al.* (2007) [15]. Attaining higher standard heterosis for seed yield in the experimental hybrids with the use of CMS lines / tester lines have also been made by Sujatha *et al.* (2009) [17] and Channamma (2009) [3].

#### Overall heterotic status of hybrids

As in the case of *gca* and *sca*, the magnitude and direction of heterosis also varied considerably among the characters. Therefore, it was difficult to decide the superiority of a hybrid over better parent. Hence, to decide whether a hybrid could be of overall heterotic or not, the method proposed by Arunachalam and Bandyopadhyay (1979) [2] with slight modification by Mohan Rao *et al.* (2001) [10] was used. The results revealed that, 13 hybrids showed high (H) overall heterotic status, while the remaining 17 hybrids had low (L) heterotic status. The hybrids, CMS 234A × GMU-456 (H × H) manifested highest heterotic status over final norm followed by CMS 911A × GMU-456 (L × H), NDCMS 2A × GMU- 746 (H × H), CMS 234A × GMU-759 (H × H), CMS 234A × GMU-716 (H × L), CMS 234A × GMU-746 (H × H), NDCMS 2A × GP6- 952 (H × H) and CMS 234A × GP6- 990 (H × H). The hybrids involving both parents (male and female parents) having high overall *gca* status (H × H) and hybrids involving high (female) and low (male) (H × L) overall *gca* status produced hybrids with overall high (H) heterotic status. On the other hand, hybrids involving (L × H) and (L × L) overall *gca* status had low (L) overall heterotic status. This clearly indicated the need for using parents having high overall *gca* status or at least using the parents having high *gca* status as female to produce hybrids with high overall heterotic status.

Table 1: Analysis of variance for combining ability

Source of variation	df	Days to 50% flowering	Plant height (cm)	Head diameter (cm)	Stem diameter (cm)	Seed yield plant-1 (g)
Replication	1	0.82	2.93	0.86	0.01	0.38
Crosses	29	24.37**	475.26**	1.13**	0.20**	121.87**
Line Effect	2	209.32**	2349.06**	0.66	0.95**	575.19**
Tester Effect	9	18.59*	648.54*	1.58	0.19	161.30*
Line × Tester Effect	18	6.71**	180.42**	0.96**	0.12**	51.79**
Error	29	2.51	54.27	0.15	0.02	2.81
Total	59	13.22	260.33	0.65	0.11	61.29
Source of variation	df	Volume weight (g/100ml)	100 seed weight (g)	Hull content (%)	Oil content (%)	Oil yield (kg/ha)
Replication	1	1.99	0.01	9.11	5.06	1174.96
Crosses	29	14.47**	0.58**	26.42**	3.85**	56922.64 **
Line Effect	2	39.68	0.75	33.44	11.71	201436.20**
Tester Effect	9	13.09	0.47	29.34	2.91	82662.41*
Line × Tester Effect	18	12.35**	0.62**	24.17**	3.44**	27995.70**

Error	29	1.81	0.09	6.52	0.57	1142.09
Total	59	8.03	0.34	16.35	2.26	28560.21

Significant @ P=0.05 \*\*Significant @ P=0.01

**Table 2a:** Estimates of general combining ability effects of lines for seed yield and its attributes in sunflower

Sl. No.	Lines	Days to 50% flowering	Plant height (cm)	Head diameter (cm)	Stem diameter (cm)	Seed yield plant-1 (g)
1	CMS 234B	-2.82**	11.00**	0.21	0.08*	4.66**
2	NDCMS 2B	-0.72*	-0.33	-0.12	-0.10**	1.21**
3	CMS 911B	3.53**	-10.67**	-0.08	0.03	-5.86**
	S.Em±	0.34	1.44	0.11	0.03	0.33
	CD at P=0.05	0.71	2.94	0.24	0.06	0.69
	CD at P=0.01	0.95	3.97	0.32	0.08	0.93
Sl. No.	Lines	Volume weight (g/100 ml)	Hundred seed weight (g)	Hull content (%)	Oil content (%)	Oil yield (kg/ha)
1	CMS 234B	0.03	0.13	1.08	-0.87**	79.69**
2	NDCMS 2B	1.45**	0.09	-1.43*	0.65*	33.00**
3	CMS 911B	-1.42**	-0.22**	0.35	0.53*	-112.98**
	S.Em±	0.28	0.07	0.62	0.19	6.78
	CD at P=0.05	0.56	0.16	1.27	0.40	13.88
	CD at P=0.01	0.76	0.20	1.72	0.54	18.70

Significant @ P=0.05 \*\*Significant @ P=0.01

**Table 2b:** Estimates of general combining ability effects of testers for seed yield and its attributes in sunflower

Sl. No.	Testers	Days to 50% flowering	Plant height (cm)	Head diameter (cm)	Stem diameter (cm)	Seed yield plant-1 (g)
1	DOR-P-40	61.50	113.00	12.00	2.08	19.7
2	GMU-456	60.00	109.50	9.30	1.55	15.5
3	GMU-716	63.00	89.85	9.25	1.44	11.9
4	GMU-746	62.50	114.00	12.95	1.62	26.2
5	GMU-759	62.50	110.75	12.85	2.04	15.00
6	GMU-773	61.00	99.50	10.30	1.91	9.80
7	GMU-785	62.00	115.50	11.60	2.18	22.60
8	GMU-1092	63.00	130.50	13.00	1.95	10.50
9	GP6-952	63.00	144.50	13.20	1.99	22.70
10	GP6-990	60.00	145.50	14.00	1.99	23.90
	S.Em±	0.85	2.22	0.61	0.09	0.78
	CD at P=0.05	1.93	7.09	1.95	0.29	2.44
	CD at P=0.01	2.76	10.19	2.81	0.41	3.51
Sl. No.	Testers	Volume weight (g/100 ml)	Hundred seed weight (g)	Hull content (%)	Oil content (%)	Oil yield (kg/ha)
1	DOR-P-40	-0.26	0.08	-0.92	-1.012*	-68.34**
2	GMU-456	0.92	0.56**	-3.89*	0.63	219.39**
3	GMU-716	-0.19	0.19	2.08	-0.32	-98.12**
4	GMU-746	1.81**	-0.29*	-2.07	0.81*	137.20**
5	GMU-759	2.67**	-0.14	0.59	0.49	-34.51**
6	GMU-773	-1.16*	-0.45**	3.65**	0.18	76.49**
7	GMU-785	-0.16	-0.11	1.42	-1.28**	-69.36**
8	GMU-1092	-1.69**	0.01	-0.14	0.38	-129.97**
9	GP6-952	-2.01**	-0.02	-1.64	0.33	65.66**
10	GP6-990	2.10**	0.18	0.92	-0.19	-98.42**
	S.Em±	0.50	0.14	1.14	0.36	12.39
	CD at P=0.05	1.04	0.27	2.33	0.73	25.34
	CD at P=0.01	1.34	0.37	3.14	0.98	34.15

\* Significant @ P=0.05 \*\*Significant @ P=0.01

**Table 3a:** Estimates of specific combining ability effects of hybrids for seed yield and its attributes in sunflower

Sl. No.	Hybrids	Days to 50% flowering	Plant height (cm)	Head diameter (cm)	Stem diameter (cm)	Seed yield plant-1 (g)
1	CMS 234A× DOR-P-40	2.32*	-3.87	-0.01	0.36**	1.48
2	CMS 234A× GMU-456	-0.85	-15.83**	-0.03	0.18	-3.79**
3	CMS 234A× GMU-716	-0.68	7.27	0.69	0.44**	6.11**
4	CMS 234A× GMU-746	0.15	2.10	0.42	-0.18	1.98
5	CMS 234A× GMU-759	-1.02	0.42	0.47	-0.19	7.68**
6	CMS 234A× GMU-773	-1.35	-0.97	0.41	-0.01	-1.89
7	CMS 234A× GMU-785	-0.18	5.70	0.19	-0.11	1.01
8	CMS 234A× GMU-1092	0.98	-5.28	-1.62**	-0.20	-4.39**
9	CMS 234A× GP6-952	-0.52	6.30	-0.42	-0.11	-4.62**
10	CMS 234A× GP6-990	1.15	4.17	-0.11	-0.17	-3.56**
11	NDCMS 2A× DOR-P-40	-2.28*	-7.33	-0.12	-0.06	-4.47**
12	NDCMS 2A× GMU-456	1.05	19.75**	-0.64	-0.25*	-3.74**

13	NDCMS 2A × GMU-716	0.72	-1.95	-0.32	-0.20	-0.04
14	NDCMS 2A × GMU-746	0.55	-3.07	0.71	0.18	3.83**
15	NDCMS 2A × GMU-759	-0.62	0.12	-0.39	-0.04	-6.57**
16	NDCMS 2A × GMU-773	0.05	-4.43	-0.11	-0.06	4.26**
17	NDCMS 2A × GMU-785	0.72	-14.77**	-0.27	-0.16	0.86
18	NDCMS 2A × GMU-1092	2.38*	4.55	0.81*	0.12	1.56
19	NDCMS 2A × GP6-952	0.88	2.13	0.41	0.10	1.13
20	NDCMS 2A × GP6-990	-3.45**	4.49	-0.07	0.14	3.19**
21	CMS 911A × DOR-P-40	-0.03	11.20	0.13	-0.11	2.99**
22	CMS 911A × GMU-456	-0.20	-3.92	0.66	-0.34**	7.53**
23	CMS 911A × GMU-716	-0.03	-5.32	-0.37	-0.23*	-6.07**
24	CMS 911A × GMU-746	-0.70	0.97	-1.13**	-0.01	-5.80**
25	CMS 911A × GMU-759	1.63	-0.54	-0.08	0.23*	-1.10
26	CMS 911A × GMU-773	1.30	5.40	-0.30	0.07	-2.37*
27	CMS 911A × GMU-785	-0.53	9.07	0.08	0.27*	-1.87
28	CMS 911A × GMU-1092	-3.37**	0.73	0.81*	0.08	2.83*
29	CMS 911A × GP6-952	-0.37	-8.43	0.015	0.00	3.49**
30	CMS 911A × GP6-990	2.30*	-9.17	0.18	0.02	0.36
	CD at P=0.05	2.23	9.32	0.77	0.21	2.19
	CD at P=0.01	3.00	12.55	1.03	0.28	2.95

Sl. No	Hybrids	Volume weight (g/100 ml)	Hundred seed weight (g)	Hull content (%)	Oil content (%)	Oil yield (kg/ha)
1	CMS 234A× DOR-P-40	-0.75	0.39	1.10	-1.86**	-10.37
2	CMS 234A× GMU-456	2.58**	-0.18	1.05	1.88**	-36.38**
3	CMS 234A× GMU-716	-4.52**	0.82**	-5.74**	1.57*	158.22**
4	CMS 234A× GMU-746	2.01*	0.11	-0.26	0.26	44.44*
5	CMS 234A× GMU-759	0.25	0.26	-2.31	0.61	176.04**
6	CMS 234A× GMU-773	1.78	-0.04	-2.50	0.88	-23.94
7	CMS 234A× GMU-785	0.69	-0.33	0.31	-1.60*	-16.66
8	CMS 234A× GMU-1092	-1.18	-0.57*	-1.88	-0.37	-93.95**
9	CMS 234A× GP6-952	0.29	-0.82**	3.62	-0.53	-108.78**
10	CMS 234A× GP6-990	-1.17	0.42	6.62**	-0.83	-88.61**
11	NDCMS 2A× DOR-P-40	-0.33	-0.29	-3.66	0.02	-88.75**
12	NDCMS 2A × GMU-456	-5.04**	-0.56*	0.48	-1.52*	-115.27**
13	NDCMS 2A × GMU-716	1.90*	-0.34	4.45*	-1.07	-23.46
14	NDCMS 2A × GMU-746	-2.20*	0.31	-2.08	0.68	98.80**
15	NDCMS 2A × GMU-759	-0.70	-0.01	1.02	-0.19	-143.58**
16	NDCMS 2A × GMU-773	0.48	-0.19	3.89	0.39	98.40**
17	NDCMS 2A × GMU-785	1.28	0.33	-1.86	0.26	26.96
18	NDCMS 2A × GMU-1092	2.12*	-0.18	0.95	0.04	32.31
19	NDCMS 2A × GP6-952	1.73	0.89**	-1.42	-0.23	19.02
20	NDCMS 2A × GP6-990	0.76	0.03	-1.96	1.64**	95.57**
21	CMS 911A × DOR-P-40	1.08	-0.09	2.29	1.84**	99.13**
22	CMS 911A × GMU-456	2.44**	0.74**	-1.54	-0.36	151.65**
23	CMS 911A × GMU-716	2.62**	-0.46	1.28	-0.50	-134.76**
24	CMS 911A × GMU-746	0.18	-0.41	2.35	-0.91	-143.26**
25	CMS 911A × GMU-759	0.44	-0.25	1.28	-0.42	-32.45
26	CMS 911A × GMU-773	-2.26*	0.24	-1.31	-1.28*	-74.46**
27	CMS 911A × GMU-785	-1.97*	-0.02	1.54	1.34*	-10.30
28	CMS 911A × GMU-1092	-0.93	0.75**	0.93	0.33	61.63**
29	CMS 911A × GP6-952	-2.02*	-0.06	-2.20	0.77	89.76**
30	CMS 911A × GP6-990	0.41	-0.43	-4.65*	-0.81	-6.95
	CD at P=0.05	1.79	0.48	4.04	1.09	43.89
	CD at P=0.01	2.42	0.64	5.44	1.47	65.04

Significant @ P=0.05 \*\*Significant @ P=0.01

**Table 3b:** Promising cross combinations with good specific combining ability for seed yield and its attributing traits in sunflower

Sl. No	Cross combinations	Traits
1	CMS 234A × GMU-716	Stem diameter, seed yield plant-1, hundred seed weight, hull content, oil content and oil yield.
2	CMS 911A × GMU-1092	Days to fifty <i>per cent</i> flowering, head diameter, seed yield plant-1, hundred seed weight, oil yield.
3	NDCMS 2A × GP6-990	Days to fifty <i>per cent</i> flowering, seed yield plant-1, oil content and oil yield.
4	CMS 911A × GMU-456	Seed yield plant-1, Volume weight, hundred seed weight and oil yield.
5	CMS 234A × GMU-456	Plant height, Volume weight and oil content.
6	CMS 911A × DOR-P-40	Seed yield plant-1, oil content and oil yield.
7	CMS 234A × GMU-456	Volume weight and oil yield.
8	CMS 234A × GMU-459	Seed yield plant-1 and oil yield.
9	NDCMS 2A × GMU-746	Seed yield plant-1 and oil yield.

**Table 4:** Per cent heterosis over standard checks KBSH-44 and KBSH-53 for seed yield and yield attributes in sunflower

Hybrids	Days to 50% flowering		Plant height (cm)		Head diameter (cm)		Stem diameter (cm)		Seed yield plant-1 (g)	
	KBSH-44	KBSH- 53	KBSH- 44	KBSH-53	KBSH- 44	KBSH- 53	KBSH- 44	KBSH- 53	KBSH- 44	KBSH- 53
CMS 234A× DOR-P-40	-2.46	-9.16**	-0.06	-5.38	-3.38	2.14	30.59**	34.57**	-7.53*	6.22
CMS 234A× GMU-456	-15.57**	-21.37**	-11.45**	-16.17**	2.70	8.57*	27.85**	31.74**	8.00*	24.05**
CMS 234A× GMU-716	-10.66**	-16.79**	1.06	-4.32	-1.01	4.64	22.78**	26.52**	-2.12	12.43**
CMS 234A× GMU-746	-6.56*	12.98**	-0.69	-5.98	6.42	12.50**	-5.91	-3.04	12.00**	28.65**
CMS 234A× GMU-759	-11.48**	-17.56**	-6.64	-11.62**	-0.34	5.36	-10.97	-8.26	7.29*	23.24**
CMS 234A× GMU-773	-13.93**	-19.85**	-9.99**	-14.78**	-0.68	5.00	-4.22	-1.30	-2.35	12.16**
CMS 234A× GMU-785	-5.74*	-12.21**	1.21	-4.18	-5.41	0.00	-0.42	2.61	-8.00*	5.68
CMS 234A× GMU- 1092	-4.92	-11.45**	3.21	-2.28	-16.89**	-12.14*	-5.91	-3.04	-31.53**	-21.35**
CMS 234A× GP6-952	-6.56*	-12.98**	11.94**	5.98	-4.73	0.71	3.38	6.52	-10.12**	3.24
CMS 234A× GP6-990	-7.38**	-13.74**	9.36	3.53	-4.05	1.43	-3.16	-0.22	-25.18**	-14.05**
NDCMS 2A× DOR-P- 40	-6.56*	-12.98**	-8.55*	-13.42**	-6.42	-1.07	-12.66*	-10.00	-29.65**	-19.19**
NDCMS 2A × GMU- 456	-9.02**	-15.27**	2.47	-2.99	-3.72	1.79	9.70	13.04*	0.00	14.86**
NDCMS 2A × GMU- 716	-4.92	-11.45**	-10.73**	-15.49**	-10.14*	-5.00	-21.94**	-19.57**	-24.71**	-13.51**
NDCMS 2A × GMU- 746	-2.46	-9.16**	-10.16*	-14.95**	6.08	12.14**	-8.02	-5.22	8.24*	24.32**
NDCMS 2A × GMU- 759	-7.38**	-13.74**	-13.32**	-17.93**	-8.45*	-3.21	-21.94**	-19.57**	-34.35**	-24.59**
NDCMS 2A × GMU- 773	-8.20**	-14.50**	-18.48**	-22.83**	-6.42	-1.07	-24.05**	-21.74**	4.00	19.46**
NDCMS 2A × GMU- 785	-0.82	-7.63**	-17.05**	-21.47**	-10.81**	-5.71	-20.25**	-17.83**	-16.47**	-4.05
NDCMS 2A× GMU- 1092	0.82	-6.11*	2.35	-3.10	-2.70	2.86	-9.70	-6.96	-25.65**	-14.59**
NDCMS 2A × GP6-952	-0.82	-7.63**	3.04	-2.45	-1.35	4.29	-5.06	-2.17	-4.71	9.46*
NDCMS 2A × GP6-990	-11.48**	-17.56**	3.33	-2.17	-6.08	-0.71	-7.59	-4.78	-17.41**	-5.14
CMS 911A × DOR-P- 40	4.10	-3.05	-3.85	-8.97*	-4.39	1.07	-2.53	0.43	-28.71**	-18.11**
CMS 911A × GMU-456	-4.10	-10.69**	-17.05**	-21.47**	5.41	11.43**	-7.59	-4.78	9.88**	26.22**
CMS 911A × GMU-716	0.82	-6.11**	-18.60**	-22.93**	-10.14*	-5.00	-19.41**	-16.96**	-55.53**	-48.92**
CMS 911A × GMU-746	2.46	-4.58	-13.78**	-18.37**	-6.08	-0.71	-11.81*	-9.13	-31.06**	-20.81**
CMS 911A × GMU-759	3.28	-3.82	-23.08**	-19.63**	-6.08	-0.71	-6.75	-3.91	-38.12**	-28.92**
CMS 911A × GMU-773	0.82	-6.11*	-22.25**	-18.77**	-7.43*	-2.14	-14.35*	-11.74	-28.24**	-17.57**
CMS 911A × GMU-785	4.10	-3.05	-13.19**	-9.30*	-8.11*	-2.86	1.90	5.00	-39.53**	-30.54**
CMS 911A × GMU- 1092	-1.64	-8.40**	-9.81**	-5.77	-2.36	3.21	-7.59	-4.78	-39.29**	-30.27**
CMS 911A × GP6-952	4.10	-3.05	-12.86**	-8.96*	-3.72	1.79	-5.06	-2.17	-15.76**	-3.24
CMS 911A × GP6-990	4.92	-2.29	-14.56**	-10.73**	-4.05	1.43	-8.44	-5.65	-40.71**	-31.89**
CD at P=0.05	3.15		13.17		1.08		0.29		3.09	
CD at P=0.01	4.25		17.54		1.46		0.40		4.17	

Significant @ P=0.05 \*\*Significant @ P=0.01

Hybrids	Volume weight (g/100 ml)		Hundred seed weight (g)		Hull content (%)		Oil content (%)		Oil yield (kg/ha)	
	KBSH- 44	KBSH- 53	KBSH- 44	KBSH- 53	KBSH - 44	KBSH - 53	KBSH - 44	KBSH - 53	KBSH - 44	KBSH - 53
CMS 234A× DOR-P-40	-5.69*	4.92	-1.09	35.66**	-17.15*	1.20	-1.11	-9.48**	-8.56*	-3.86
CMS 234A× GMU-456	4.20	15.93**	-2.73	33.42**	-25.27**	-8.72	14.64**	4.94*	23.83**	30.20**
CMS 234A× GMU-716	- 13.79**	-4.09	8.55	48.88**	-27.46**	-11.39	10.96**	1.56	8.63*	14.21**
CMS 234A× GMU-746	4.88	16.69**	-13.27*	18.95**	-23.92**	-7.07	10.42**	1.07	23.67**	30.02**
CMS 234A× GMU-759	2.93	14.52**	-7.64	26.68**	-22.24**	-5.02	10.53**	1.18	8.70**	24.80**
CMS 234A× GMU-773	-2.12	8.89**	-18.73**	11.47	-14.53	4.40	10.42**	1.07	7.69	13.22**
CMS 234A× GMU-785	-2.31	8.68**	-17.73**	12.84	-12.94	6.34	-1.13	-9.50**	-9.46*	-4.81
CMS 234A× GMU-1092	-9.79**	0.37	-19.91**	9.85	-23.07**	-6.04	7.31**	-1.78	- 26.53**	- 22.75**
CMS 234A× GP6-952	-7.25*	3.19	-25.09**	2.74	-12.30	7.12	6.69**	-2.34	-4.15	0.77
CMS 234A× GP6-990	-5.96*	4.63	0.91	38.40**	-2.67	25.41*	4.31	-4.52*	-21.96**	-17.95**
NDCMS 2A× DOR-P-40	-1.78	9.27**	-14.36*	17.46	-35.99**	-21.82	7.96**	-1.18	-24.04**	-20.13**
NDCMS 2A × GMU-456	-9.49**	0.69	-10.45	22.82*	-33.54**	-18.83	8.26**	-0.91	8.29	13.86**
NDCMS 2A × GMU-716	3.26	14.88**	-13.36*	18.83*	-6.80	13.84	6.75**	-2.29	-19.64**	-15.51**
NDCMS 2A × GMU-746	-1.36	9.74**	-10.18	23.19*	-35.57**	-21.31	15.15**	5.40*	24.62**	31.02**
NDCMS 2A × GMU-759	3.82	15.51**	-13.18*	19.08*	-20.04*	-2.33	11.73**	2.27	-26.64**	-22.87**
NDCMS 2A × GMU-773	-1.97	9.06**	-22.18**	6.73	-4.29	16.91	12.52**	3.00	17.05**	23.07**
NDCMS 2A × GMU-785	1.97	13.45**	-6.36	28.43**	-25.57**	-9.09	7.88**	-1.26	-9.84*	-5.21
NDCMS 2A × GMU-1092	0.45	11.75**	-13.45*	18.70*	-22.20**	-4.97	12.07**	2.58	-16.68**	-12.40**
NDCMS 2A × GP6-952	-1.09	10.04**	5.45	44.64**	-32.63**	-17.71	11.13**	1.73	5.89	11.33*
NDCMS 2A × GP6-990	1.29	12.69**	-6.73	27.93**	-27.16**	-11.03	15.08**	5.34*	-4.95	-0.06
CMS 911A × DOR-P-40	-4.86	5.85	-16.36*	14.71	-15.91*	2.71	13.87**	4.23*	-18.82**	-14.65**
CMS 911A × GMU-456	-0.72	12.06**	7.55	47.51**	-34.22**	-19.65	12.23**	2.73	23.29**	29.63**
CMS 911A × GMU-716	-1.32	9.78**	-21.27**	7.98	-10.54	9.27	9.02**	-0.21	-51.45**	-48.96**
CMS 911A × GMU-746	-2.29	8.71**	-29.00**	-2.62	-18.84*	-0.87	11.09**	1.69	-23.38**	-19.44**
CMS 911A × GMU-759	0.18	11.45**	-23.36**	5.11	-14.54	4.38	11.65**	2.18	-30.92**	-27.37**
CMS 911A × GMU-773	- 14.17**	-4.51	-20.00**	9.73	-13.30	5.89	8.21**	-0.95	- 22.38**	- 18.39**
CMS 911A × GMU-785	- 11.32**	-1.34	-18.18**	12.22	-11.61	7.96	11.63**	2.18	- 32.49**	- 29.02**
CMS 911A × GMU-1092	- 12.42**	-2.56	-2.27	34.04**	-17.46*	0.82	13.52**	3.91	- 31.09**	- 27.55**

CMS 911A × GP6-952	-15.48**	-5.97	-17.64**	12.97	-29.93**	-14.41	14.66*	4.95*	-3.39	1.57
CMS 911A × GP6-990	-5.63*	4.99	-20.91**	8.48	-29.62**	-14.03	8.50**	-0.68	-35.67**	-32.36**
CD at P=0.05	2.54		0.67		5.71		1.55		69.11	
CD at P=0.01	3.42		0.90		7.69		2.09		93.66	

Significant @ P=0.05 \*\*Significant @ P=0.01

## Conclusion

Identification of superior genotypes using empirical estimates of *gca* and *sca* originated by Line × Tester is fundamental strategy in evaluation of breeding value of genotypes involved in breeding program. The present study resulted in the identification of promising hybrids viz., CMS 234A × GMU-456, NDCMS 2A × GMU-746 and CMS 911A × GMU-456 with high seed yield plant<sup>-1</sup> and its attributing traits and these resultant hybrids could be tested in large scale yield trials over locations and seasons to confirm their potentiality for commercial cultivation.

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