Combining Ability Studies for Development of New Hybrids over Environments in Sunflower (*Helianthus annuus* L.)

B. Satish Chandra
Ph.D. Scholar, Department of Genetics and Plant Breeding
Acharya N.G. Ranga Agricultural University
Rajendranagar, Hyderabad -500030 Andhra Pradesh, India
Tel: 91-939-109-1071 E-mail: chandragene@gmail.com

S. Sudheer Kumar
Department of Genetics and Plant Breeding
College of Agriculture, Acharya N.G. Ranga Agricultural University
Rajendranagar, Hyderabad -500030 Andhra Pradesh, India
Tel: 91-939-109-1071 E mail: sagisudheer@yahoo.com

A.R.G. Ranganadha
Project Coordinator, Sesame and Niger (ICAR)
JNKVV Campus, Jabalpur Madhya Pradesh, India
Tel: 91-0761-268-0254 E-mail: argranga@gmail.com

M. Y. Dudhe (Corresponding author)
Scientist, Crop Improvement (Pl. Breeding)
Directorate of Oilseeds Research, Rajendranagar
Hyderabad -500030 Andhra Pradesh, India
Tel: 91-040-2401-5222 E-mail: mangeshdudhe@rediffmail.com

Received: November 1, 2010 Accepted: November 16, 2010 doi:10.5539/jas.v3n2p230

Abstract

Seven CMS lines were crossed with six inbred lines in Line x Tester fashion to elucidate the information on the nature of gene action involved in the inheritance of important quantitative traits and to select the parents with good *gca* and crosses with good *sca* effects. The resultant 42 hybrids were evaluated along with their parents with three standard checks at three locations in Andhra Pradesh state *viz*., Hyderabad, Tandur, and Jagtial. The pooled analysis of variance for combining ability revealed that *sca* variance was higher in magnitude compared to *gca* variance for all the characters except oil content indicating the preponderance of non-additive gene action for all the characters while additive gene action for oil content. The *gca* effects of the parents in pooled analysis revealed that among the lines ARM 243B and CMS 17B and among the testers RHA-6D-1R, RES-834-1 and 3376R were found to be promising general combiners for seed yield and yield component characters. Based on significant *sca* effects in pooled analysis, five hybrids *viz*., CMS 89A x RES-834-1, CMS 17A x LTRR 341, ARM 243A x R 298, ARM 238A x 3376R and CMS 852A x R-649 were identified as promising for seed yield and other yield contributing characters.

Keywords: Combining ability, Gene action, Pooled analysis, Line x Tester, Sunflower

1. Introduction

Breeding research for genetic enhancement in sunflower has been in progress for more than 3 decades in India. The objective of sunflower breeding is to develop the high yielding hybrids with high oil quality or disease resistance Dudhe *et al*. (2009). Line x Tester analysis provides a systematic approach for detection of appropriate parents and crosses in terms of investigated traits (Kempthorne, 1957). Combining ability studies elucidate the nature and magnitude of gene action involved in the inheritance of character by providing the information on the two components of variance *viz*., additive genetic and dominance variance, which are important to decide upon the parents and crosses to be selected for eventual success. Paying due consideration to genotype x environment interaction during the studies on combing ability may be helpful in identifying desirable genotypes and in understanding the precise nature of inheritance of economic traits. Accordingly, the present investigation was undertaken to have an idea on the nature of gene action involved in the inheritance of important quantitative traits and to select the parents with good *gca* and crosses with good *sca* effects through line x tester analysis over locations in sunflower.

2. Material and methods

Seven CMS lines *viz*., CMS 234A, CMS 17A, CMS 852A, CMS 89A, ARM 238A, ARM 243A and ARM 248A and six inbred lines *viz*., RES-834-1, LTRR 341, RHA-6D-1R, 3376R, R-298 and R-649 were planted during *kharif*, 2008 at Directorate of Oilseeds Research, Rajendranagar, Hyderabad and crossing was performed in line x tester fashion to produce 42 hybrids. During *rabi*, 2008-09 the 42 hybrids along with their parents and three standard checks *viz*., KBSH-1, PAC-1091 and KBSH-44 were evaluated in a Randomized Block Design replicated thrice at three different locations *viz*., Directorate of Oilseeds Research, Hyderabad; Agricultural Research Station, Tandur; and Regional Agricultural Research Station, Jagtial. Observations were recorded on five randomly selected plants in each hybrid combination per replication for ten quantitative characters. Data obtained were subjected to line x tester analysis (Kempthorne, 1957) to estimate general and specific combining ability effects and their respective variances. The result of pooled analysis over locations is presented.

3. Results and discussion

The pooled analysis of variance revealed significant differences due to environments for all the characters indicating the sufficient diversity among the environments (Table 1). Significant differences for replication x locations were recorded for plant height, number of filled seeds per head, seed yield per plant and oil yield per plant. The differences among the parents, parents *vs* crosses and crosses were observed to be significant for all the characters studied indicating the existence of wider genetic differences among parents and crosses. Partitioning of crosses into lines, testers and lines x testers revealed that the variance due to lines were significant for all the characters except days to maturity, number of filled seeds per head, number of unfilled seeds per head, seed yield per plant and oil yield per plant, whereas for testers, plant height, head diameter, number of unfilled seeds per head, seed yield per plant, oil content and oil yield per plant were found significant, indicates wide variability existing among the genotypes. The interaction due to lines x testers were significant for all the traits studied, suggesting that significant contribution of *sca* effects towards the variation among the crosses. The results are in accordance with the earlier studies Madhavilatha *et al.* (2004), Vishwanath and Shankar Goud (2006) and Gouri Shankar *et al.* (2007). Interaction effects of parents *vs* crosses x locations, parents x locations and crosses x locations were significant for all the characters, except head diameter, number of filled seeds per head and number of unfilled seeds per head in case of (parents *vs* crosses) x locations and oil yield per plant in case of parents vs locations. Further partitioning of crosses x locations indicated that the interaction of lines x locations showed significant differences for plant height, stem diameter and oil content, while testers x locations was significant only for oil content, suggesting the sensitivity of *gca* effects of parents to environmental fluctuations for these characters. Interaction effects of lines x testers x locations were significant for all the characters studied, indicates the *sca* effects of hybrids interacted with the environments for all the characters studied which are contradictory with the earlier reports of Sanket Sharma *et al.* (2003) and Binodh *et al.* (2008). The comparative estimates of variances due to general combining ability (*gca*) and specific combining ability (*sca*) revealed the predominance of *sca* variance in relation to *gca* variance for all the traits except oil content, which implied that all the characters were predominantly under the control of non additive gene action, while additive gene action for oil content. The results corroborates with the findings of Vishwanath and Shankar Goud (2006) and Gouri Shankar *et al*. (2007). Degree of dominance observed to be more than unity for seed yield and other yield components except oil content under study suggesting over-dominance is the major factor for high level of expression of these traits. These results are in accordance with the earlier reports of Satyanarayana (2000) and Madhavilatha *et al.* (2004).

The *gca* effects of the parents revealed that the lines ARM 243B and ARM 248B were good general combiners for most of the traits like head diameter, 100 seed weight, seed yield per plant, oil content and oil yield per plant by exhibiting significant positive *gca* effects (Table 2). These lines also showed negative significant *gca* effects for the traits like days to 50 per cent flowering and days to maturity indicating their usefulness in breeding for early maturing hybrids (Table 4). The line ARM 238B was best general combiner for number of filled seeds per head, head diameter, seed yield per plant, oil content and oil yield per plant. On the contrary, CMS 17B characterized by late maturity by also possessed favourable alleles for tallness, filled seeds per head, 100 seed weight, seed yield per plant and oil yield by recording *gca* effects in the positive direction. The line CMS 89B contributed a large number of favourable alleles for plant height (dwarf stature) and oil content as indicated by their high *gca* effects for these characters. Among the testers, RHA-6D-1R was best general combiner for majority of the important yield components, *i.e*., head diameter, number of filled seeds per head, 100 seed weight, seed yield per plant, oil content and oil yield. It also exhibited high negative *gca* effect in a desired direction for unfilled seeds and days to maturity. The tester LTRR-341 possessed favourable genes for early flowering, maturity and dwarf plant type by recording significant negative *gca* effects. Favourable genes for oil content were predominantly contributed by RES-834-1, RHA-6D-1R, R 649 and R 298 by recording significant positive *gca* effects. For the traits, days to maturity, number of filled seeds per head, seed yield, oil content and oil yield, the tester RES-834-1 was identified as good combiner, as it exhibited significant positive *gca* effects, The line 3376R was a good combiner for number of filled seeds per head, seed yield and oil yield. Hence, among the lines ARM 243B and CMS 17B and among the testers RHA-6D-1R, RES-834-1 and 3376R were proved to be good combiners for seed yield and its most of the related characters and need to be exploited in future breeding programme. The parents which are good general combiners for yield possessed *gca* effects in the desired direction for yield components was also reported earlier by Radhika (1994).

Sixteen crosses were identified as good specific combinations for seed yield per plant (Table 3). Among these crosses the positive *sca* effect for seed yield also exhibited significant positive *sca* effects for other yield contributing traits. The cross combination CMS 17A x LTRR 341 showed significant positive *sca* effects for seed yield per plant along with number of filled seeds per head, 100 seed weight and oil yield per plant along with negative significant *sca* effect for days to 50% flowering and days to maturity indicating its suitability for commercial exploitation for early maturing hybrids (Table 5). In the crosses *viz*., ARM 238A x RES-834-1, ARM 238A x 3376R and ARM 243A x 3376R, involved parents with high x high *gca* effects suggesting additive x additive type of gene action. This indicated that selection could be effective in F_2 generation and utilized in transgressive breeding. Similar findings as observed in present study were also reported by Sanket Sharma *et al.* (2003), Manivannan *et al.* (2005) and Binodh *et al.* (2008). On the other hand crosses CMS 17A x LTRR 341, ARM 243A x R 298, ARM 248A x R 649 and CMS 89A x RES-834-1 involved parents with high x low *gca* effects indicating the involvement of additive x dominance genetic interaction. Peng and Virmani (1990) also reported about the possibility of interaction between positive alleles from good combiner and negative alleles from poor combiners in high x low crosses in sunflower. The cross combinations CMS 89A x R 649, CMS 852 x LTRR-341 and CMS 852A x R-649 involved low x low combining parents indicating over dominance and epistatic interactions. The results clearly indicated that the high performance of hybrid need not be the ones with high *sca* effect and vice-versa. Similar results were also obtained by Vishwanath and Shankar Goud (2006) and Gouri Shankar *et al.* (2007). In spite of the involvement of both poor general combiners in some crosses or one of the parents as poor general combiner, these cross combinations expressed significant *sca* effects in desirable direction which might be due to concentrations and interaction between favourable genes contributed by parents.

The crosses namely, CMS 89A x LTRR 341 and CMS 852A x R-649 and ARM 238A x R-298 were the best specific combiners for oil content having high x low, low x high and high x high *gca* parental combination, indicating a genetic interaction of the additive and non additive types. Based on significant high *sca* effects, five hybrids *viz*., CMS 89A x RES-834-1, CMS 17A x LTRR 341, ARM 243A x R 298, ARM 238A x 3376R and CMS 852A x R-649 were identified as promising for seed yield and other yield contributing characters. The performance of these crosses needs to be critically evaluated over different seasons and locations to confirm their superiority and stability.

References

Binodh, A. K., Manivannan, N. & Vindhya Varman, P. (2008). Combining ability analysis for yield and its contributing characters in sunflower (*Helianthus annuus* L.). *Madras Agricultural Journal,* 95 (7-12): 295-300.

Dudhe M. Y., Moon, M.K. & Lande, S.S. (2009). Evaluation of restorer lines for heterosis studies on sunflower, (*Helianthus annuus* L.). *J. Oilseeds Res.*, Vol. 26 (Special Issue) 140-142.

Gouri Shankar, V., Ganesh, M., Ranganatha, A. R. G., Suman, A. & Sridhar, V. (2007). Combining ability studies in diverse CMS sources in sunflower (*Helianthus annuus* L.). *Indian Journal of Agricultural Research,* 41(3): 171-176.

Kempthorne, O. (1957). *An introduction to genetic statistics*. John Wiley and Sons, Inc: New York.

Madhavilatha, K., Reddy, A. V. V., & Devasenamma, V. (2005). Hybrid vigour and combining ability in sunflower (*Helianthus annuus* L.) hybrids involving CMS lines. *Journal of Oilseeds Research,* 22 (2): 309-312.

Manivannan, N., Vidhyavathi, P. and Muralidharan, V. (2005). Diallel analysis in sunflower. *Indian Journal of Agricultural Research,* 39(4): 281-285.

Peng, J. Y. & Virmani, S. S. (1990). Combining ability for yield and yield related traits in relation to breeding in rice. *Oryza,* 27: 1-10.

Radhika, P. (1994). Genetic analysis of yield and certain physiological parameters in sunflower (*Helianthus annuus* L.) M.Sc.(Ag.) thesis, Acharya N.G. Ranga Agricultural University, Hyderabad.

Sanket Sharma, Bajaj, R. K., Narinder Kaur, & Sehgal, S. K. (2003). Combining ability studies in sunflower (*Helianthus annuus* L.). *Crop Improvement,* 30(1): 69-73.

Satyanarayana, K. V. (2000). Genetic analysis of elite inbred lines using L x T design and modified TTC model in Sunflower (*Helianthus annuus* L.) M. Sc. (Ag.) Thesis submitted to Acharya N.G. Ranga Agricultural University, Hydrabad.

Vishwanath, S. J. & Shanker Goud, I. (2006). Combining ability and gene action in sunflower, *Helianthus annuus* L. *Journal of Oilseeds Research,* 23(2): 288-291.

Table 1. Pooled analysis of variance for combining ability (L x T) for yield and yield components in sunflower

		Mean sum of squares									
Source of variation	**d f**	**Days to 50% Flowering**	**Days to maturity**	**Plant height**	**Head diameter**	**No. of filled seeds/head**	**No. of unfilled seeds/head**	**100-seed weight**	**Seed yield per plant**	**Oil content**	**Oil yield**
Locations	2	210.68**	399.04**	1823.96**	99.91**	169063.45**	23208.60**	7.57**	851.27**	163.53**	98.91**
Replications x locations	2	3.52**	3.20**	77.89**	0.15	9926.93**	1040.35	0.01	13.10**	0.08	2.05**
Treatments	54	21.40**	51.35**	1680.44**	13.93**	197184.45**	2454.55**	3.22**	469.63**	23.04**	69.95**
Parents	12	20.41**	36.98**	1943.43**	9.62**	34250.55**	894.33**	6.18**	89.08**	30.64**	13.07**
Parent vs Crosses	1	3.64**	0.94**	22441.68**	345.21**	5569767.50**	3870.31**	16.21**	12963.06**	71.99**	1955.11**
Crosses	41	22.14**	56.78**	1097.10**	7.11**	113833.80**	2876.67**	2.03**	276.29**	19.62**	40.61**
Lines	6	44.44*	90.99	3320.15**	17.91**	92472.91	1115.23	4.18*	279.64	66.71**	30.63
Testers	5	23.87	57.72	1921.79**	13.26*	212343.44	6676.64*	1.62	714.24*	51.80**	120.02**
Line x Tester	30	17.39**	49.79**	515.04**	3.92*	101687.71**	2595.63**	1.67**	202.63**	4.83**	29.37**
Parents x Locations	24	6.54**	6.51**	95.20**	0.70*	3000.02**	1600.73**	0.16**	3.19	3.47**	0.39
Parents vs. Crosses) x Locations	2	14.92**	3.06*	43.03*	0.74	124.03	1024.11	0.06**	36.04**	3.89*	6.14**
Crosses x Locations	82	4.04**	8.27**	113.22**	1.10**	15734.09**	2178.03**	0.54**	12.16**	3.84**	2.21**
Lines x Locations	12	4.70	10.93	383.52**	1.03	10850.07	1386.83	0.75	11.88	5.28*	1.21
Testers x Locations	10	4.18	5.45	69.53	1.02	18766.47	2630.52	0.65	5.74	8.75**	1.88
Lines x Testers x Locations	60	3.89**	8.21**	66.44**	1.13**	16205.50**	2260.86**	0.48**	13.29**	2.73**	2.46**
Error	162	0.79	0.83	13.03	0.43	1506.28	369.93	0.01	2.13	1.20	0.40
σ^2gca		0.85	1.88	36.94	0.29	3862.49	89.52	0.07	12.68	1.49	1.92
σ^2sca		2.76	8.16	94.12	1.06	16652.76	365.14	0.28	33.35	0.59	4.82
σ^2gca/σ^2sca		0.31	0.46	0.80	0.28	0.23	0.25	0.27	0.38	2.52	0.40
Degree of dominance		1.27	1.47	1.12	1.35	1.46	1.42	1.41	1.14	0.44	1.12

*: Significant at 5 % level; **: Significant at 1% level

Table 2. Estimates of general combining ability effects for thirteen parents for ten characters in sunflower

Parent	Days to 50% flowering	Days to maturity	Plant height (cm)	Head diameter (cm)	No. of filled seeds/head	No. of unfilled seeds/head	100-seed weight (g)	Seed yield/plant (g)	Oil content (%)	Oil yield (g)
Lines										
CMS-234B	-1.06**	-1.89**	0.61	-0.21*	-62.43**	-9.15**	0.16**	-1.55**	-0.59**	-0.72**
CMS-17B	1.64**	2.02**	-5.27**	-0.03	65.93**	5.05	0.09**	3.74**	-2.80**	0.53**
CMS-852B	0.75**	0.86**	-7.60**	-0.89**	-0.20	6.39	-0.36**	-1.96**	0.16	-0.67**
CMS-89B	0.91**	1.30**	-13.96**	-0.83**	-38.07**	1.72	-0.46**	-4.37**	1.21**	-1.36**
ARM-238B	-0.23	0.69**	10.85**	0.42**	67.84**	-3.00	-0.18**	0.87**	0.55**	0.50**
ARM-243B	-1.28**	-1.75**	3.41**	0.97**	0.35	2.91	0.36**	2.40**	0.95**	1.22**
ARM-248B	-0.73**	-1.23**	11.97**	0.58**	-33.42**	-3.93	0.39**	0.87**	0.52**	0.51**
SE (lines)	0.15	0.15	0.54	0.11	7.01	3.35	0.02	0.27	0.19	0.12
Testers										
RES-834-1	-0.25	-0.33*	-0.61	-0.67**	33.30**	5.22	-0.01	0.75**	0.89**	0.55**
LTRR-341	-1.33**	-1.80**	-1.07*	-0.53**	-64.23**	-5.12	-0.08**	-2.90**	-1.87**	-1.63**
3376R	0.58**	1.17**	2.02**	0.15	51.91**	-6.19*	-0.09**	1.61**	-0.84**	0.35**
RHA-6D-1R	-0.14	-0.52**	8.01**	0.90**	93.31**	-19.41**	0.39**	6.93**	0.78**	2.87**
R-298	0.46**	0.1	3.71**	0.12	-24.64**	11.87**	-0.07**	-1.60**	0.42*	-0.50**
R-649	0.68**	1.37**	-12.06**	0.03	-89.64**	13.62**	-0.14**	-4.79**	0.62**	-1.64**
SE (testers)	0.14	0.14	0.5	0.1	6.45	3.1	0.01	0.25	0.17	0.11

*: Significant at 5% level; **: Significant at 1% level

Table 3. Estimates of specific combining ability effects for forty two crosses for ten characters in sunflower

Cross	Days to 50% flowering	Days to maturity	Plant height (cm)	Head diameter (cm)	No. of filled seeds/head	No. of unfilled seeds/head	100-seed weight (g)	Seed yield/plant (g)	Oil content (%)	Oil yield (g)
CMS-234A X RES-834-1	0.06	0.46	2.53	-0.35	-141.15**	-2.99	0.44**	-3.23**	0.04	-1.29**
CMS-234A X LTRR-341	1.63**	1.77**	4.77**	-0.86**	-81.79**	4.63	0.11**	-3.18**	-0.46	-1.13**
CMS-234A X 3376R	-2.77**	-4.70**	4.53**	0.75**	-91.11**	21.17*	0.80**	0.83	1.29**	0.65*
CMS-234A X RHA-6D-1R	-0.73	0.65	0.8	-0.28	160.97**	-21.61**	-0.46**	3.90**	-0.04	1.48**
CMS-234A X R-298	0.18	0.54	4.83**	1.71**	142.71**	5.21	-0.20**	4.69**	-1.26**	1.36**
CMS-234A X R-649	1.63**	1.27**	-17.48**	-0.97**	10.38	-6.41	-0.69**	-3.00**	0.42	-1.07**
CMS-17A X RES-834-1	2.53**	3.71**	3.16*	0.64*	-29.8	19.16*	0.04	-0.48	-0.72	-0.38
CMS-17A X LTRR-341	-3.06**	-5.14**	0.58	0.01	163.53**	-17.09*	0.28**	8.87**	0.01	3.05**
CMS-17A X 3376R	-0.13	-0.29	3.79**	-0.17	-2.76	-12.44	0.14**	-0.31	0.34	-0.07
CMS-17A X RHA-6D-1R	-0.75*	-1.26**	7.22**	0.93**	15.19	-8.07	0.41**	3.92**	0.29	1.39**
CMS-17A X R-298	-0.02	1.12**	-0.47	-0.44	-85.03**	-5.45	0.13**	-3.11**	0.67	-0.85**
CMS-17A X R-649	1.44**	1.86**	-14.28**	-0.97**	-61.12**	23.90**	-1.00**	-8.88**	-0.59	-3.14**

CMS-852A X RES-834-1	-3.58**	-6.12**	-7.16**	-0.54*	-70.25**	-0.82	-0.49**	-5.64**	-0.8	-2.41**
CMS-852A X LTRR-341	-0.17	-1.31**	0.46	0.03	83.19**	26.01**	0.21**	4.37**	0.75	1.91**
CMS-852A X 3376R	1.92**	3.38**	11.40**	-0.2	-92.06**	11.44	-0.01	-3.97**	-0.46	-1.64**
CMS-852A X RHA-6D-1R	0.80*	1.57**	-2.58	1.54**	70.89**	-7.04	0.17**	3.91**	0.45	1.67**
CMS-852A X R-298	1.71**	2.79**	-15.01**	-0.69**	-38.21*	-16.94*	-0.23**	-3.03**	-1.53**	-1.52**
CMS-852A X R-649	-0.67	-0.31	12.89**	-0.15	46.43**	-12.63	0.36**	4.36**	1.60**	1.99**
CMS-89A X RES-834-1	0.92*	2.77**	8.94**	0.95**	56.07**	-10.14	1.28**	10.11**	0.59	4.13**
CMS-89A X LTRR-341	1.16**	3.08**	-10.35**	-1.06**	-138.46**	20.13*	-0.40**	-6.75**	1.81**	-2.14**
CMS-89A X 3376R	1.09**	0.94*	-8.34**	-0.34	-84.40**	22.92**	-0.56**	-6.77**	-0.79	-2.69**
CMS-89A X RHA-6D-1R	0.63	0.46**	4.44**	-0.70**	86.45**	-4.74	0.28**	4.42**	-1.19*	1.43**
CMS-89A X R-298	-2.46**	-4.99**	1.59	0.46	-91.95**	-8.55	-0.31**	-5.69**	0.62	-2.17**
CMS-89A X R-649	-1.34**	-2.25**	3.72**	0.68*	172.30**	-19.61*	-0.30**	4.69**	-1.03*	1.44**
ARM-238A X RES-834-1	-0.11	1.55**	-6.99**	0.07	291.38**	-23.50**	-0.63**	6.24**	0.57	2.65**
ARM-238A X LTRR-341	-0.54	-1.81**	-10.32**	1.08**	52.09**	-36.04**	-0.40**	-0.18	-1.08*	-0.32
ARM-238A X 3376R	0.39	-0.29	-4.36**	-0.09	118.94**	-15.46	0.07	6.02**	-0.82	2.03**
ARM-238A X RHA-6D-1R	-1.06**	-3.26**	2.80*	-0.87**	-302.34**	52.96**	-0.05	-12.74**	0.12	-4.86**
ARM-238A X R-298	0.35	1.29**	4.60**	-0.66*	-5.72	17.65*	0.10**	1.35*	1.36**	0.89*
ARM-238A X R-649	0.96*	2.52**	14.27**	0.46	-154.35**	4.39	0.90**	-0.68	-0.14	-0.39
ARM-243A X RES-834-1	0.95*	-0.34	-5.75**	-0.63*	-8.47	-4.26	-0.39**	-2.12**	0.29	-0.76**
ARM-243A X LTRR-341	1.02**	3.30**	1.48	0.26	-52.87**	16.72*	-0.18**	-3.92**	-0.31	-1.52**
ARM-243A X 3376R	-0.88*	0.49	4.16**	-0.33	76.79**	-14.87	0.10*	4.57**	-0.17	1.66**
ARM-243A X RHA-6D-1R	-1.00**	-1.32**	-3.75**	0.08	-83.35**	-5.82	0.01	-3.65**	0.04	-1.37**
ARM-243A X R-298	-0.93*	-1.94**	-3.22*	0.37	141.48**	-11.38	0.11**	6.41**	0.27	2.59**
ARM-243A X R-649	0.85*	-0.2	7.09**	0.26	-73.59**	19.61*	0.36**	-1.30*	-0.12	-0.60*
ARM-248A X RES-834-1	-0.77*	-2.04**	5.27**	-0.14	-97.79**	22.56**	-0.24**	-4.88**	0.04	-1.93**
ARM-248A X LTRR-341	-0.04	0.11	13.37**	0.53*	-25.69	-14.34	0.38**	0.79	-0.71	0.15
ARM-248A X 3376R	0.39	0.46	-11.18**	0.37	74.60**	-12.76	-0.54**	-0.36	0.61	0.05
ARM-248A X RHA-6D-1R	2.11**	3.15**	-8.94**	-0.71**	52.20**	-5.68	-0.36**	0.23	0.34	0.26
ARM-248A X R-298	1.18**	1.20**	7.68**	-0.74**	-63.28**	19.46*	0.40**	-0.61	-0.14	-0.3
ARM-248A X R-649	-2.87**	-2.89**	-6.21**	0.69*	59.95**	-9.23	0.36**	4.82**	-0.14	1.78**
SEij	0.37	0.38	1.31	0.26	17.18	8.21	0.04	0.65	0.46	0.28

*: Significant at 5% level; **: Significant at 1% level

Table 4. Promising general combiners identified for yield and yield contributing traits in sunflower

S.NO.	Parents	Characters
1	CMS 17B	Seed yield per plant, plant height, number filled seeds per head, 100 seed weight, oil yield per plant
2	ARM 238B	Seed yield per plant, head diameter, stem diameter, number filled seeds per head, oil content, oil yield per plant
3	ARM 243B	Seed yield per plant, days to 50% flowering, days to maturity, head diameter, stem diameter, 100 seed weight, oil content, oil yield per plant
4	ARM 248B	Seed yield per plant, days to 50% flowering, days to maturity, head diameter, stem diameter, 100 seed weight, oil content, oil yield per plant
5	RHA-6D-1R	Seed yield per plant, days to maturity, head diameter, number filled seeds per head, 100 seed weight, oil content, oil yield per plant
6	RES-834-1	Seed yield per plant, days to maturity, stem diameter, number filled seeds per head, oil content, oil yield per plant
7	3376R	Seed yield per plant, number filled seeds per head, oil yield per plant

Table 5. Promising specific combiners identified for yield and yield contributing traits in sunflower

S.No.	Cross	Characters
1	CMS 89A x RES-834-1	Seed yield per plant, head diameter, number of leaves per plant, number of filled seeds per head, 100 seed weight, oil content, oil yield per plant
2	CMS 17A x LTRR 341	Seed yield per plant, days to 50% flowering, days to maturity, number of leaves per plant, number of filled seeds per head, 100 seed weight, oil content, oil yield per plant
3	ARM 243A x R 298	Seed yield per plant, days to 50% flowering, days to maturity, plant height, number of filled seeds per head, 100 seed weight, oil content, oil yield per plant
4	ARM 238A x RES-834-1	Seed yield per plant, plant height, number of filled seeds per head, oil content, oil yield per plant
5	ARM 238A x 3376R	Seed yield per plant, plant height, stem diameter, number filled seeds per head, oil content, oil yield per plant