



Evaluation of Diversified Male Sterile and Restorer Lines for Combining Ability in Sunflower (*Helianthus annuus* L.)

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ABSTRACT

The results of the combining ability analysis revealed the importance of non-additive gene action for days to 50% flowering, days to maturity, plant height, head diameter, stem diameter, number of leaves, filled seeds, unfilled seeds, 100 seed weight and oil content, where as both additive and non additive gene action were found to be important for seed yield and oil yield per plant. Most of the characters were controlled by over dominance where, seed yield was controlled by complete dominance and partial dominance was seen to for oil yield. The CMS lines IMS WGA and PFMS 400, were found to be good general combiners for early maturity and dwarf stature. For seed yield, IMS WGA, showed lowest *per se* performance and observed to be good combiner. Though PFMS 400 A and ARM 245 A, recorded high mean seed yield were found to be poor combiners. ARM 245 A showed high *per se* and best general combining for oil content, head diameter and number of leaves. Favorable genes for high oil yield, filled seeds, less number of unfilled seeds and stem diameter were contributed by IMS WGA. Among the testers, 3376 R, was best general combiner for head diameter, 100 seed weight, seed yield, oil content, oil yield and unfilled seeds in desired direction. The tester, R 298, possessed favorable genes for early flowering, maturity and dwarf plant type, while ARM 245 A showed favourable genes for oil content. The cross, IMS WGA x 6D-IR recorded high *per se* performance and SCA effects for seed yield, was also a good specific combiner for 100 seed weight and oil yield, while the cross, PFMS 400 A x R 298, was good sppecific combiner for oil yield, oil content, lower number of unfilled seeds and days to maturity.

Key words : Combining ability, Diversified male sterile lines, Sunflower.

Oil seeds play an important role in the Indian economy. The demand for edible oils is increasing day by day due to increased consumption of oils in India. The solution to overcome the situation, new oil seed crops were introduced in to the country. One such crop is sunflower. Being a versatile crop having photoin sensitivity, short duration, high yield and better quality oil, it can be cultivated in all seasons. A new era opened in sunflower breeding with the discovery of cytoplasmic male sterility (Lecerq, 1969) Most of the presently grown hybrids in the world possess the cytoplasm of *H. petiolaris* (PET-1). Prevalence of genetic uniformity could result in genetic vulnerability of hybrids. Development of hybrids with diverse cytoplasmic background has been one of the priorities in the Indian sunflower breeding programme. The nature and extent of genetic differences and breeding behavior of these sources have to be studied to utilize them in hererosis breeding programmes. The new CMS sources can

be utilized in sunflower improvement if effective restorer lines are identified.

MATERIAL AND METHODS

The new CMS lines were developed under nuclear background of elite inbred lines through back cross breeding. The converted 25 CMS lines includes ten CMS lines with *H. lenticularis*, ten CMS lines with *Helianthus petiolaris sub spp fallax* (branched CMS lines). Two CMS lines with PET-2 cytoplasm (*H. petiolaris*) and 3 CMS lines with PET-1 cytoplasm (*H. annuus*). The material utilized in the crossing programme was obtained from Directorate of Oilseeds Research, Rajendranagar, Hyderabad and Project Coordinating Unit Sunflower Bengaluru. The diversified 25 CMS lines were crossed with 13 testers during *khariif* 2006 and the resultant crosses were evaluated during *rabi* 2006-07 to know the maintainer restorer behavior of the testers. Only 3 x 5 (Line x tester) set could be derived. A set of 15 hybrids along

with parents and two checks APSH-II and KBSH-I were raised in RBD with three replications during *khari* 2007. Each entry was sown in two rows with a row length of 3 m and the spacing adopted was 60 cm between the rows and 30 cm between the plants. Necessary plant protection measures were followed to raise a good crop. Data was collected on ten randomly selected plants from each entry (Parents, F₁S and checks) in each replication for plant height, stem diameter, number of leaves per plant, head diameter, number of filled seeds per head, number of unfilled seeds per head, 100 seed weight, seed yield per plant, oil content and oil yield per plant. The oil content of seeds was determined at 10 per cent moisture level by nuclear magnetic resonance (NMR) Oxford Newport Analyser with a random sample of 10 grams of seeds and expressed in percentage. Analysis of variance was carried out as per the Line x Tester model given by Singh and Chaudhary (1985) and the analysis of combining ability was based on the method of Kempthorne (1957).

RESULTS AND DISCUSSION

The mean squares due to parents and crosses were significant for yield and all the component characters indicating wide genetic variability among CMS lines derived with diverse cytoplasmic sources (Table-1). The lines were found to be diverse for days to 50 per cent flowering, days to maturity, seed yield and oil yield per plant, while testers exhibited substantial differences among themselves for days to 50 per cent flowering, days to maturity, head diameter, number of leaves, seed yield and oil yield. Interaction between lines and testers was also significant for all the yield attributing characters. Non additive gene action was predominant for days to 50% flowering, days to maturity, plant height, head diameter, stem diameter, number of leaves, filled seeds, unfilled seeds, 100 seed weight and oil content whereas equal importance of both additive and non additive components had been reported for seed yield and oil yield. Similar to the present findings the role of non-additive gene action is documented by various researchers in sunflower for various characters such as days to 50% flowering (Govindaraju *et al.*, 1992) plant height (Burli *et al.*, 2001), head diameter, number of leaves, number of filled seeds

(Ashok Kumar *et al.*, 1998 and Burli *et al.*, 2001), seed yield per plant (Gangappa *et al.*, 1997) oil content and oil yield per plant (Rather *et al.*, 1998).

Degree of dominance (Table-2) revealed that over dominance is the cause for expression of all the characters except complete dominance for seed yield and partial dominance for oil yield. The GCA values revealed that (Table-3) among the lines, IMSWGA and PFMS 400 A were good general combiners for early maturity and dwarf stature and 100 seed weight exhibited significant GCA effects in negative direction (desirable for earliness) while ARM 245 A was characterized by late maturity and also possessed favourable alleles for tallness by recording high GCA effects.

For important economic trait like seed yield, IMSWGA line showed lowest per se performance and found to be good combiner. However other lines PFMS 400 A and ARM 245 A which recorded high mean seed yield were found to be poor combiner by recording high negative GCA effects. ARM 245 A showed high per se and best general combiner for oil content, head diameter and number of leaves. Favorable genes for high oil yield, filled seeds, less unfilled seeds and stem diameter were predominantly contributed by IMSWGA by recording significant GCA effect.

Among the testers 3376 R was best general combiner for head diameter, 100 seed weight, seed yield, oil content and oil yield and also exhibited high GCA effect in desirable direction for unfilled seeds. The tester R272-1 possessed high GCA effects in desirable direction for days to 50% flowering, days to maturity, seed yield and 100 seed weight so that earliness coupled with high yield can be obtained by involving R 271-1 as one of the parent in the crossing programme.

Significant SCA effects were observed for seed yield and all the yield components in the present study (Table-4). The crosses with significant negative SCA effects in desirable direction for earliness include ARM 245 A x 89B and ARM 245 A x R298. It is observed that early flowering seems to be dominant over late flowering. Dwarfness is one of the desirable trait in sunflower. The cross ARM 245 A x R 298 was found to be short statured by exhibiting substantial negative SCA effects. This can be attributed to high negative GCA effect of

Table 1. Analysis of variance for combining ability for seed yield and yield components in sunflower.

Source	d.f	Days to 50% flowering	Days to maturity	Plant height (cm)	Head diameter (cm)	Stem diameter (cm)	Number of leaves	Filled seeds / head	Unfilled seeds/ head	100-seed weight (g)	Seed yield / plant (g)	Oil content (%)	Oil yield/ plant (g)
Replications	2	1.65	1.78	2.92	0.013	2.31	0.91	0.44	0.09	1.09	1.17	0.14	3.56
Treatments	22	21.71**	27.71**	74.28**	82.58**	89.57**	19.75**	145.69**	17.75**	25.83**	81.53**	104.16**	107.19**
Parents	7	21.64**	29.38**	22.29**	44.25**	30.80**	22.22**	10.18**	7.36**	15.47**	5.94**	131.86**	7.64**
Parents/Crosses	1	15.44**	13.24**	884.81**	1161.55**	1201.06**	37.88**	1934.30**	0.005	84.86**	807.45**	888.79**	1195.03**
Crosses	14	22.19**	27.91**	42.39**	24.68**	39.56**	17.22**	83.55**	24.21**	26.79**	67.48**	34.25**	79.27**
Lines	2	6.69**	6.83**	0.46	0.06	0.16	2.19	4.90	0.14	2.65	11.71**	1.15	13.28**
Testers	4	3.58*	3.28*	1.32	4.54**	1.12	4.38**	1.82	1.66	1.07	11.33**	0.26	12.89**
Lines x testers	8	8.70**	11.24**	41.85**	13.14**	43.52**	8.06**	46.67**	22.74**	21.37**	12.31**	42.33**	12.88**
Error	44	0.96	0.90	19.95	0.44	0.01	0.97	673.98	263.17	0.03	2.26	0.99	0.30
Total	68												

* Significant at 5 % level

** Significant at 1 % level

Table 2. GCA and SCA variance for seed yield and yield components in sunflower.

Source of variation	Days to 50% flowering	Days to maturity	Plant height (cm)	Head diameter (cm)	Stem diameter (cm)	Number of leaves	Filled seeds / head	Unfilled seeds/ head	100-seed weight (g)	Seed yield / plant (g)	Oil content (%)	Oil yield/ plant (g)
δ^2 GCA (Lines)	0.46	0.53	0.38	0.18	0.0005	0.32	878.78	13.68	0.006	4.41	0.28	0.68
δ^2 SCA (Testers)	2.46	3.06	271.6	1.77	0.0534	2.30	10260.67	1907.22	0.2206	8.53	13.57	1.15
δ^2 GCA / δ^2 SCA	0.19	0.17	0.01	0.11	0.0094	0.14	0.09	0.01	0.0286	0.52	0.04	0.59
Degree of dominance	1.64	1.69	18.90	2.21	7.30	1.91	2.42	8.35	4.29	0.98	4.92	0.92

* Significant at 5 % level

** Significant at 1 % level

Table 3. Estimates of general combining ability effects for seed yield and yield components in sunflower.

Source	Days to 50% flowering	Days to maturity	Plant height (cm)	Head diameter (cm)	Stem diameter (cm)	Number of leaves	Filled seeds / head	Unfilled seeds/ head	100-seed weight (g)	Seed yield / plant (g)	Oil content (%)	Oil yield/ plant (g)
Lines												
IMS WGA	-1.49**	-1.56**	-3.02*	-0.12	0.04*	-0.78**	100.81**	-4.94	0.17**	5.11**	0.18	1.89**
PFMS 400A	-0.69*	-0.89**	-2.80*	-0.06	-0.01	-0.44	-101.97**	-3.68	0.23**	-4.01**	-1.87**	-1.74**
ARM245A	2.18**	2.44**	5.82**	0.18	-0.03*	1.22**	1.16	8.61*	-0.40**	-1.09**	1.69**	-0.15
SEi	0.25	0.24	1.15	0.17	0.02	0.26	6.70	4.18	0.05	0.38	0.28	0.14
SE(gi-gj)	0.36	0.35	1.63	0.24	0.02	0.36	9.48	5.92	0.07	0.54	0.36	0.19
Testers												
6D-1R	1.22**	1.66**	15.97**	0.70**	0.11	-2.02**	-0.64	34.25**	0.12	0.90	-0.17	0.23
R272-1	-2.55**	-2.73**	-1.15	0.86**	0.14*	1.87**	77.96**	37.98**	0.21**	6.28**	-0.76*	2.17**
89B	2.11**	2.27**	1.80	0.02	-0.09	2.31**	-98.30**	33.24**	-0.46**	-7.00**	0.08	-2.60**
R-298	-0.89**	-0.84**	-15.05**	-2.93**	-0.20**	-0.91**	-58.10**	-19.15**	-0.09	-5.13**	-0.96**	-2.13**
3376R	0.11	0.16	-1.57	1.35**	0.04	-1.24**	79.08**	-17.82**	0.23**	4.96**	1.81**	2.33**
SEi	0.33	0.32	1.49	0.22	0.02	0.33	8.65	5.40	0.06	0.50	0.33	0.18
SE(gi-gj)	0.46	0.45	2.10	0.31	0.02	0.47	12.23	7.64	0.08	0.70	0.46	0.25

* Significant at 5 % level

** Significant at 1 % level

the male parent and significant effect of the female parent involved in the cross combination, while IMG WGA x R 298 exhibited significant positive SCA effect and the parents involved were poor combiners.

For head diameter high magnitude of SCA effects was observed in cross combinations PFMS 400 A x R 298 (LxL), IMS WGA x 3376R (L x H) IMS WGA x 89 B (L x L). The crosses IMS WGA x R 298, ARM 245A x 3376R, ARM 245A x R272-1 and IMS WGA x 89B were good specific combiners and also recorded high mean values for the trait filled seeds per head. High magnitude of negative SCA effects for unfilled seeds per head was exhibited by the crosses PFMS 400 A x R 272-1, IMS WGA x 89B, PFMS 400 A x 3376 R and ARM 245A x 6D-IR. These cross combinations involved at least one parent with high GCA effect and the other with a poor combiner.

Seed yield and oil content are the two most important characters in sunflower crop. It is desirable to evolve a hybrid that will produce high seed yield with high oil percent. For the economic trait, seed yield, the cross IMS WGA x 6D-IR showed high mean and significant positive SCA effect involving parents with high x low GCA effects. The hybrid combinations IMS WGA x 3376R and IMS WGA x R 272-1 showed high mean seed yield but exhibited significant negative SCA effects probably because of antagonistic effects of cytoplasmic nuclear interactions.

High SCA effects for oil content were observed in crosses ARM 245A x 89B, PFMS 400 A x R-272-1, PFMS 400 A x R 298, IMS WGA x 89 B and PFMS 400 A x 6D-IR. The first cross had one parent as a good general combiner while in rest of the four crosses, the parents involved were poor combiners

Table 4. Estimates of specific combining ability effects for seed yield and yield components in sunflower.

Source	Days to 50% flowering	Days to maturity	Plant height (cm)	Head diameter (cm)	Stem diameter (cm)	Number of leaves	Filled seeds / head	Unfilled seeds/ head	100-seed weight (g)	Seed yield / plant (g)	Oil content (%)	Oil yield/ plant (g)
IMS WGA x 6D-IR	-0.62	-0.56	4.08	-0.86*	-0.06	1.56**	-22.16	-4.29	0.63**	4.81**	-2.16**	1.29**
IMS WGA x R272-1	-0.18	-0.01	-5.44**	-0.92*	-0.23**	-1.00	-90.12**	11.73	0.21	-2.10*	-0.17	-0.79*
IMS WGA x 89B	-0.18	-0.01	-18.26**	0.85*	-0.13**	0.56	63.71**	-50.54**	-0.22*	-0.45	2.27**	0.23
IMS WGA x R298	0.82	0.11	17.30**	0.04	0.19**	-1.89**	113.37**	25.33**	-0.53**	0.12	-0.02	0.02
IMS WGA x 3376R	0.16	0.44	2.32	0.89*	0.22**	0.78	-64.80**	17.77	-0.10	-2.37**	0.08	-0.76*
PFMS 400A x 6D-IR	-1.09	-1.56**	-14.01**	-0.45	-0.13**	-0.78	12.12	37.12**	-0.67**	-5.26**	1.29*	-1.77**
PFMS 400A x R272-1	-0.98	-1.00	-4.49	0.83*	0.08*	-1.00	-11.69	-55.66**	-0.18	1.04	3.8**	1.00**
PFMS 400A x 89B	2.36**	2.33**	14.16**	-0.30	0.23**	1.56**	67.58**	56.00**	-0.03	1.48	-6.39**	-0.13
PFMS 400A x R298	0.69	1.44**	10.24**	1.65**	0.07	0.11	-25.71	-5.52	0.66**	1.49	3.12**	0.97**
PFMS 400A x 3376R	-0.98	-1.22*	-5.90*	-1.73**	-0.24**	-0.89	-42.30**	-31.93**	0.22*	1.25	-1.19*	-0.07
ARM245A x 6D-IR	1.71**	2.11**	9.94**	-1.31**	0.19**	-0.78	10.05	-32.83**	0.04	0.45	0.87	0.48
ARM245A x R272-1	1.16**	1.00	9.92**	0.09	0.16**	1.00	101.81**	43.94**	-0.03	1.06	-3.01**	-0.22
ARM245A XR298	-2.18**	-2.33**	4.10	-0.54	-0.10**	-2.11**	-131.29**	-5.46	0.25*	-1.03	4.12**	-0.10
ARM245A x 89B	-1.51*	-1.56**	-27.54**	-1.69**	-0.26**	1.78**	-87.66**	-19.80*	-0.14	-1.60	-3.09**	-1.00**
ARM245A X3376R	0.82	0.78	3.58	0.83	0.02	0.11	107.10**	14.15	-0.12	1.12	1.11	0.83*
SEij	0.80	0.77	3.65	0.54	0.05	0.81	21.20	13.25	0.15	1.23	0.81	0.44

* Significant at 5 % level

** Significant at 1 % level

indicating the predominance of non-additive gene action. Two poor combiners also resulted into high positive SCA effects which might be due to the better nicking ability of the parents. The poor combiners tended to produce significant SCA effects in the hybrids, wherein the parental combination provided environment for the full expression of the genes controlling this trait, though the parents themselves would not express any superiority for this trait, accumulation of favourable genes may be cause for parents with poor GCA giving rise to hybrids with higher SCA effect.

With regard to oil yield, significant SCA effects were observed in IMS WGA x 6D-IR, PFMS 400 A x R 272-1, PFMS 400 A x R 298 and ARM 245 A x 3376 R involved parents with high x low or low x low GCA effects of the parents. Presence of positive interaction between parents was noticed in these combinations. Dua (1979) reported non involvement of two good combining parents for high SCA effect of the cross indirectly indicating the non occurrence of additive gene action. Which was in agreement with the present study. The cross IMSWGA x 6D-IR with high SCA effects for seed yield per plant was also possessed best specific combinations for other important yield attributes i.e 100 seed weight and oil yield per plant indicating the possibility of exploiting this cross combinations, for yield improvement in sunflower through heterosis breeding. Similar results were also observed by Giriraj *et al.* (1987), Rudranaik *et al.* (1990), Govindaraju *et al.* (1992) and Gourishankar *et al.* (2007) for plant height, head diameter, number of filled seeds, 100 seed weight, oil content, seed yield and oil yield.

The cross PFMS 400 A x R 298 possessed PEF cytoplasm was found to be good specific

combiners for oil yield, oil content, unfilled seeds and days to maturity while ARM 245A x 89B with traditional PET 1 cytoplasm recorded high magnitude of SCA effects for oil content, 100 seed weight, days to 50% flowering and day to maturity. The hybrid IMS WGA x 89B (*H.lenticularis* cytoplasm) showed significant SCA effect for unfilled seeds, filled seeds, head diameter and oil content, while IMS WGA x R 298 for early flowering and number of leaves per plant, respectively.

The overall perusal of the SCA effects of different characters in the present investigation reveals that the parents, involved in the cross combination should have high GCA effect to get significant SCA effect, however high x low, low x low general combiners which resulted in high specific combining ability effects among the top ranking crosses are of great importance as these combinations would throw desirable transgressive segregants if the additive effect of one parent and complementary epistatic effect of other parent act in the same direction for maximum expression of the trait. Diversified CMS PF and CMS I sources used in the present investigation are equally efficient in expressing their fullest potential of yield and yield contributing characters for yield improvement in sunflower. The breeder can be safely use these sources to broaden the genetic base of CMS source and sunflower crop can safeguarded from any eventuality of biotic and abiotic threats in future.

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