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Effect of Alien Cytoplasm on Combining Ability for Earliness and Seed Yield in Sunflower under Irrigation and Drought Stress

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Abstract: Nine *CMS* analogues from different cytoplasmic sources and their common maintainer were crossed with four perfect restorers from *PET-1* source to develop of 40 sunflower hybrids. The experiment was conducted during spring season 2011 and 2012 two years continuously, under two different water environments, normal irrigated and water stress environment, where irrigation was stopped after the anthesis. The analysis of variance revealed significant differences among the sources for day to flowering, days to maturity and seed yield under both the environments, both the years and pooled over the years. The variance due to *GCA* and *SCA* showed that gene action was additive for maturity whereas, non-additive genetic effect was observed for days to flowering and seed yield under both the environments. The *CMS* analogues E002-91A (*H. annuus*), PKU-2A (*H. annuus*), and ARG-3A (*H. argophyllus*) were recorded as good combiner for early flowering in both the environments. The *CMS* analogs E002-91A and ARG-3A were observed good combiners for early flowering, early maturity and high seed yield, whereas, NC-41B from conventional *CMS* source *H. petiolaris* (PET-1) was recorded good combiner for late flower and early maturity and poor combiner for seed yield under both the environments. Among testers P69R was recorded good combiner for late flowering under normal water environment while, in water stress it was good combiner for early flowering but it was not good for seed yield. RCR-8297 was recorded for good combiner for late maturity and high seed yield under both the environments. The *SCA* estimates were highest in cross E002-91A × RCR-8297 and PKU-2A × P124R and ARG-6A × RCR-8297 for early flowering and early maturity under both the environments. These new cytoplasmic male sterility sources can be substitute of the classical (PET-1) source with added advantage for early maturing and high yielding.

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Introduction

The discovery of cytoplasmic male sterility (*CMS*) in sunflower by Leclercq (1969) and subsequent identification of genes for fertility restoration have resulted in the development of commercial hybrids since 1972. However, all the sunflower hybrids that are commercially grown have a single source of *CMS* discovered by Leclereq leading to homogeneity and potential risk that was evident in case of maize. *CMS*-T was exclusively used for maize hybrid-seed production in the United States and it became susceptible to Southern corn leaf blight (SCLB), caused by race T of the fungus (Ullstrup, 1972). As a result, in 1970, maize crop suffered colossal yield losses caused by the SCLB epidemic (Ullstrup, 1972). Diversification of *CMS* source is inevitable in heterosis breeding programs as the use of a single *CMS* source involves a potential risk if it became susceptible to a new strain of disease. In order to diversify the cytoplasmic base, attempts have been made and several new cytoplasmic sources have been identified. The present investigation is based on development of a set of nine *CMS* analogues having a common maintainer and identification of four common restorers from *PET-1* source for all these sources. Only a few studies have reported the interactions between cytoplasms and nuclear genes in the expression of several qualitative and quantitative traits in sunflower. In sunflower a unique cytoplasmic nuclear interaction had caused reduction in chlorophyll, photosynthetic rate (Jan, 1990) and positive effects on oil content have been reported (Serieys, 1992; Tyagi and Dhillon, 2014). Sunflower (*Helianthus annuus* L.) as one of the most important sources of vegetable oil in the world, it is moderately tolerant to water stress and its production is affected by drought conditions (Pasda and Diepenbrock, 1990). Although sunflower is moderately tolerant to water stress, its production is greatly affected by drought. Evidence indicates that drought stress during the vegetative phase, flowering and seed-filling period in sunflower causes a considerable decrease in yield and oil content (Ali *et al.*, 2009). Different *CMS* sources in sunflower were developed at Punjab Agricultural University, Ludhiana and evaluated for their performance for different agronomic, physiological, yield and quality traits under normal irrigated environment (Tyagi *et al.*, 2013, 2015a) as well as under water stress conditions (Tyagi *et al.*, 2015b; Tyagi and Dhillon, 2016a). Sunflower hybrids developed and evaluated from these *CMS* sources for combining ability for agronomic and yield traits under different irrigation environments (Dhillon and Tyagi, 2016; Tyagi and Dhillon, 2016b). The present study was therefore aimed to study the effect of cytoplasmic male sterility sources on combining ability for earliness and seed yield under normal irrigated and water stress environments to exploit them in hybrid development program for early maturing high yielding sunflower hybrids.

Materials and methods

The present investigation was carried out in the research fields of the oilseeds section, Department of Plant Breeding and Genetics, Punjab Agricultural University, Ludhiana, India. A set of nine *CMS* analogues from different cytoplasmic sources were developed using a common maintainer (for details, see Table 1) and the detailed procedure for the development of all these *CMS* analogs has been reported by Tyagi and Dhillon (2016a). Four common perfect restorers from *PET-1* source for these *CMS* sources were identified. All nine *CMS* analogues along with NC-41B (common maintainer) were crossed with four common restorer lines (to develop the set of 40 hybrids) to study the effect of different cytoplasmic sources on performance of hybrids. Also the efforts were made to identify some good combining *CMS* analogues for early maturity and high seed yield.

Table 1: Information of different *CMS* sources along with common maintainer line (NC-41B) developed at PAU, Ludhiana.

S. No	*CMS*	Origin
1	ARG-2A	*Helianthus argophyllus*
2	ARG-3A	*H. argophyllus*
3	ARG-6A	*H. argophyllus*
4	PKU-2A	*H. annuus*
5	E002-91A	*H. annuus*
6	PRUN-29A	*H. praecox ssp. Runyonii*
7	DV-10A	*H. debilis ssp. Vestitus*
8	PHIR-27A	*H. praecox ssp. Hirtus*
9	*CMS* -XA	Unknown
10.	NC-41B (Common maintainer)	*H. petiolaris* (conventional)

The experiment was conducted during spring season in the year 2011 and 2012. The material was raised in paired rows of 4.5 m length with 0.60 m and 0.30 m inter and intra row spacing respectively, in the randomized block design, with three replication for each treatment. All the agronomic practices recommended for the region were followed to raise a good crop. The data for early maturity like day to flowering and days to maturity were recorded on the basis of total plants per genotype whereas seed yield per plant were recorded for five random plants in the field.

The data recorded was statistically analyzed following standard procedures for the estimation of components of genetic variation for each irrigation level separately and for pooled over the different environments. Combining ability analysis was done in Line × Tester analysis, as suggested by Kempthorne (1957).)

Results and discussion

The combining ability analysis, (pooled over the years) presented in Table 2 reveals that the mean squares due to years were highly significant for days to flowering and seed yield under both the environments, while, mean squares for days to maturity under normal environment were non significant. Mean squares due to restorers were non-significant for days to flowering under stress

Table 2: Analysis of variance for combining ability under normal irrigation and stress environment (individual and pooled over years).

Source of variation	**df**	**Mean squares**					
		Days to Flowering		**Days to maturity**		**Seed yield per plant (g)**	
		N	**S**	**N**	**S**	**N**	**S**
Years	1	1446.04**	725.29**	679.48	2225.07**	2961.48**	372.00**
Rep./years	4	11.42**	8.02*	21.22	16.51**	88.81**	30.93
Females	9	37.26**	48.51**	25.13**	45.38**	543.29**	841.16**
Males	3	14.99**	5.85	12.33**	33.90**	976.08**	158.49**
Female × Male	27	10.15**	16.07**	9.42**	18.45**	379.31**	338.09**
Female × Years	9	27.45**	10.30**	21.23**	64.04**	145.52**	189.12**
Male × Years	3	36.50**	19.69**	104.77**	153.60**	343.09**	693.05**
F × M × Years	27	13.13	10.70**	10.68	19.47**	149.26**	130.24**
Error	146	0.86	2.65	0.94	1.10	13.03	13.30
estimates of genetic components							
σ^2 Females		0.53	1.37	0.22	0.74	6.99	18.51
σ^2 Males		0.21	0.21	1.01	1.32	4.48	8.25
σ^2 Female × Males (*SCA*)		0.99	1.79	0.42	0.34	76.68	69.28
σ^2 *GCA*		0.05	0.11	0.75	1.19	5.00	2.61
σ^2 *GCA*/σ^2 *SCA*		0.05	0.06	1.79	3.50	0.07	0.04
Proportional contribution (Per cent)							
Contribution of Females		52.54	49.50	44.89	42.02	28.74	44.52
Contribution of Males		4.53	1.28	4.72	6.73	11.06	1.80
Contribution of X		42.93	49.21	50.48	51.26	60.20	53.68

***, **Significant at 0.05 and 0.01 of probability, N: Normal environment S: Stress environment.**

environment. The differences among the female, female × male, female × years and male × years were observed to be highly significant for days to flowering, days to maturity and seed yield, while mean square due to female × male × years was non-significant for days to flowering and maturity under normal environment indicating the existence of wider genetic differences among parents. The main role in the inheritance was played by the non-additive component of genetic variance as shown by analysis of variance of combining ability and analysis of genetic variance components. *GCA/SCA* ratio for days to flowering and seed yield (g/plant) recorded in F_1 generation was below the value of unity under both normal and stress environment. While, days to maturity recorded in F_1 generation was above the value unity in normal and stress environment showed additive component of genetic variance (Table 2). Combining abilities and gene action for different agronomic traits have been estimated by many researchers (Hladni *et al.*, 2006; Shankar *et al.*, 2007; Chandra *et al.*, 2011; Memon *et al.*, 2015; Dhillon and Tyagi, 2016; Tyagi and Dhillon, 2016b). Additive gene action for these traits has also been reported by Singh *et al.* (1989).

Effect of different cytoplasmic sources on combining ability under different environments (pooled over years)

The importance of combining ability in selection of parents for hybridization has been emphasized by many workers in sunflower (Putt, 1966; Giriraj *et al.*, 1987). The potentiality of any line to be used as a parent in hybridization depends on it is *per se* performance and the performance of F_1 hybrid derived from it and its own *GCA* effect. The estimates of the general combining ability (*GCA*) and specific combining ability (*SCA*) effects for the phenological and yield traits (pooled over the years) under two different water regimes is presented in Table 3, 4 and 5.

Days to flowering

In normal irrigated environment, the *CMS* analogues E002-91A (*H. annuus*), PKU-2A (*H. annuus*), ARG-2A (*H. argophyllus*), ARG-3A (*H. argophyllus*), DV-10A (*H. debilis ssp vestitus*) and PRUN-29A had highly significant negative *GCA* effects (−0.57, −0.45, −1.45, −0.95, −1.37 and −0.70) respectively and were observed as very good combiners for early flowering. Two of the *CMS* analogues

Table 3: Estimation of combining ability effects and mean performance of hybrids for days to flowering under normal and water stress environment. (Pooled over years).

S. No.	Female/Male		RCR-8297		P69R		P124R		P100R		*GCA*	
			N	S	N	S	N	S	N	S	N	S
1	*CMS*-XA	Mean	71.92	71.83	70.67	69.50	70.08	70.33	67.42	69.33	−0.37*	−0.07
		SCA	1.80**	1.35**	0.17	−0.4	0.57*	−0.04	−2.53**	−0.91		
2	E002-91	Mean	68.42	67.67	69.33	68.83	70.58	69.17	70.92	69.00	−0.57**	−1.65**
		SCA	−1.49**	−1.24**	−0.96**	0.52	1.28**	0.38	1.17**	0.34		
3	PKU-2A	Mean	70.75	68.17	69.67	68.67	68.58	66.33	70.75	69.33	−0.45**	−2.19**
		SCA	0.72*	−0.19	−0.75**	0.89	−0.85**	−1.92**	0.88**	1.22*		
4	ARG-2A	Mean	67.58	71.50	70.33	69.17	69.25	71.00	68.58	69.83	−1.45**	0.06
		SCA	−1.45**	0.89	0.92**	−0.86	0.82**	0.5	−0.28	−0.53		
5	ARG-3A	Mean	70.67	68.50	69.75	71.33	68.25	70.33	69.08	68.83	−0.95**	−0.57*
		SCA	1.13**	−1.49**	−0.17	1.94**	−0.68*	0.46	−0.28	−0.91		
6	ARG-6A	Mean	68.17	70.33	70.42	67.50	70.25	66.83	69.92	70.33	−0.32*	0.85**
		SCA	−1.99**	−1.07*	1.04**	0.35	0.86**	−0.12	0.09	0.84		
7	DV-10A	Mean	71.50	70.67	69.75	69.17	69.25	71.17	68.75	69.33	−1.37**	−0.19
		SCA	−0.78**	0.47	0.25	−0.61	0.73**	0.92	−0.2	−0.78		
8	PHIR-27A	Mean	72.17	68.17	74.42	69.33	69.92	71.67	71.83	69.50	1.70**	−0.65*
		SCA	−0.01	−1.74**	1.85**	0.02	−1.66**	1.88**	−0.18	−0.16		
9	PRUN-29A	Mean	70.08	71.83	68.92	70.83	68.92	69.17	70.83	68.17	−0.70**	−0.32
		SCA	0.3	1.60**	−1.25**	1.19*	−0.27	−0.96	1.22**	−1.83**		
10	NC-41B (C)	Mean	71.25	72.50	71.75	74.83	70.92	75.00	72.50	73.17	1.22**	3.56**
		SCA	−0.45	−1.61**	−0.33	1.31**	−0.18	1.00*	0.97**	−0.7		
GCA			0.1	0.24	0.48**	−0.35**	−0.50**	0.12	−0.07	−0.01		

*, ** – significant at 0.05 and 0.01 of provability, N: Normal environment S: Stress environment.

Table 4: Estimation of combining ability effects and mean performance of hybrids for days to maturity under normal and water stress environment. (Pooled over years).

S. No.	Female/Male		RCR-8297		P69R		P124		P100R		*GCA*	
			N	S	N	S	N	S	N	S	N	S
1	*CMS*-XA	Mean	96.92	98	97.33	97	99.58	97.5	97.67	97	−2.35**	−0.54**
		SCA	−1.38**	−0.25	−0.4	0.03	2.14**	0.57	−0.36	−0.35		
2	E002-91	Mean	97.92	94.5	98.33	98.17	99.75	98.67	100.42	99.83	−1.12**	−0.12
		SCA	−1.61**	−4.17**	−0.63*	0.78*	1.08**	1.32**	1.16**	2.07**		
3	PKU-2A	Mean	101	102	100.42	97.83	96.83	96.33	100.92	96.17	−0.43*	0.17
		SCA	0.78**	3.04**	0.77**	0.15	−2.53**	−1.30**	0.97**	−1.89**		
4	ARG-2A	Mean	99.83	99.33	100.08	95	100.25	98.67	100.83	99	0.03	0.09
		SCA	−0.84**	0.46	−0.02	−2.60**	0.43	1.11**	0.43	1.03**		
5	ARG-3A	Mean	98.92	98.5	100.5	97.33	99.75	97.33	99.33	96.67	−0.60**	−0.46*
		SCA	−1.13**	0.17	1.02**	0.28	0.56	0.32	−0.44	−0.77*		
6	ARG-6A	Mean	100.92	98.67	98.92	96	99	94	97.42	99	0.3	0.42*
		SCA	−0.03	−0.54	−0.38	0.24	−0.67*	−0.39	1.08**	0.69*		
7	DV-10A	Mean	99	97.5	98.25	94.5	100.5	97.17	98.75	95.83	−0.35*	−0.87**
		SCA	1.70**	2.75**	−1.48**	−2.14**	1.06**	0.57	−1.28**	−1.18**		
8	PHIR-27A	Mean	100.92	100.5	103.17	99.5	100.92	100.5	101.83	96.5	1.49**	1.34**
		SCA	−1.22**	0.38	1.60**	0.65*	−0.36	1.70**	−0.03	−2.72**		
9	PRUN-29A	Mean	102.58	96.33	99.17	96.83	97.92	94.83	98.08	94.33	−0.78**	−2.33**
		SCA	2.72**	−0.12	−0.13	1.65**	−1.09**	−0.3	−1.51**	−1.22**		
10	NC-41B (C)	Mean	99.75	94.33	99.5	92.83	100.92	95.17	100	98.83	−0.18	−2.62**
		SCA	−0.72*	−1.83**	−0.4	−2.06**	1.31**	0.32	−0.19	3.57**		
GCA			0.42**	0.88**	−0.14	−0.40**	−0.43**	−0.45**	0.15	−0.03		

*, ** – significant at 0.05 and 0.01 of probability respectively, N: Normal environment S: Stress environment.

Table 5: Estimation of combining ability effects and mean performance of hybrids for seed yield under normal and water stress environment. (Pooled over years).

S. No.	**Female/Male**		**RCR-8297**		**P69R**		**P124R**		**P100R**		***GCA***	
			N	**S**	**N**	**S**	**N**	**S**	**N**	**S**		
1	*CMS*-XA	Mean	51.15	56.13	37.54	30.18	52.8	48.28	59.05	53.32	−1.3*	6.60**
		SCA	−2.14	7.46**	−9.1	−15.76	4.76**	2.37*	6.47**	5.93**		
2	E002-91	Mean	56.99	55.42	51.71	36.43	51.72	47.02	52.3	29.92	1.75**	1.82**
		SCA	0.66	11.52**	2.03	−4.72	0.64	5.88**	−3.32	−12.69		
3	PKU-2A	Mean	47.67	40.63	42.32	34.12	57.8	45.97	58.58	37.58	0.16	−0.8
		SCA	−7.07	−0.64	−5.78	−4.41	8.31**	7.46**	4.54**	−2.4		
4	ARG-2A	Mean	64.97	39.63	26.29	31	41.93	27.92	60.95	47.67	−2.9**	−3.82**
		SCA	13.28**	1.38	−18.75	−4.51	−4.51	−7.57	9.97**	10.70**		
5	ARG-3A	Mean	55.51	51.33	51.9	38.77	57.9	47.63	61.1	42.97	5.17**	4.80**
		SCA	−4.25	4.46**	−1.2	−5.36	3.39**	3.52**	2.06	−2.62		
6	ARG-6A	Mean	62.17	42.7	42.34	21.53	44.02	31.08	51.91	48.18	7.21**	3.78**
		SCA	0.37	−3.16	5.46**	4.99**	0.99	4.77**	−6.82	−6.6		
7	DV-10A	Mean	66.27	48.62	43.52	37.3	49.3	37.98	57.28	48.64	0.21	−0.04
		SCA	1.67	−4.62	−4.63	−1.99	−0.25	−1.29	3.20**	7.90**		
8	PHIR-27A	Mean	57.29	39.08	47.08	37.6	50.63	33	54.72	48.65	1.0	−0.79
		SCA	1.71	−2.2	−1.85	−0.94	0.3	−5.52	−0.15	8.65**		
9	PRUN-29A	Mean	62.36	53.88	46.45	56.52	48.72	41.35	52.49	45.68	1.07	8.98**
		SCA	6.70**	2.83**	−2.56	8.21**	−1.69	−6.94	−2.45	−4.09		
10	NC-41B (C)	Mean	42.02	29.62	45.72	20.63	46.97	26.27	50.06	23.03	−5.24**	−15.49**
		SCA	−7.33	3.03**	3.03**	−3.21	2.87**	2.44*	1.43	−2.27*		
GCA			3.15**	1.70**	−3.5**	−1.05*	−2.1**	−1.06*	2.44**	0.41		

*, ** – significant at 0.05 and 0.01 of probability respectively, N: Normal environment S: Stress environment.

CMS-XA and ARG-6A having *GCA* effects of −0.37 and −0.32 (significant at 5 per cent) were identified as good combiner for early flowering. Whereas *CMS* PHIR-27A (*H. praecox ssp hirtus*) had highly significant positive *GCA* effects (1.70) and hence was recorded as very good combiner for late flowering. The maintainer line NC-41B (1.22) from *PET-1* source was very good combiner for late flowering.

In stress environment the *CMS* analogues E002-91A, PKU-2A and ARG-6A (*GCA* effects of −1.65, −2.19 and −0.85) were recorded as very good combiner while ARG-3A (*H. argophyllus*) and PHIR-27A (*H. praecox ssp hirtus*) (−0.57 and −0.65) were good combiner for early flowering. The *CMS* analogue ARG-6A (0.85) and NC-41B (3.56) from *PET-1* source had significant positive *GCA* effects under stress environment and were recorded as very good combiner for late flowering. The *CMS* analogues E002-91A, PKU-2A and ARG-3A (*H. argophyllus*) were recorded as good combiner for early flowering in both the environments. Among restorers the male parent P124R was recorded as very good combiner for early flowering under normal environment, whereas P69R was very good combiner for late flowering in normal environment while very good combiner under water stress environment for early flowering.

The cross combinations viz. E002-91A × RCR-8297 (−1.49 and −1.24), PKU-2A × P124R (−0.85 and −1.92) and ARG-6A × RCR-8297 (−1.99 and −1.07) having highly significant *SCA* effects were identified for early flowering under both the environments. The cross PKU-2A × P100R (0.88 and 1.22) recorded highly positive *SCA* effects under both the environments for late flowering.

Days to maturity

The *CMS* analogues *CMS*-XA, E002-91A, ARG-3A (*H. argophyllus*) and PRUN-29A were observed as very good combiner for early maturity due to their highly significant negative *GCA* effects (−2.35, −1.12, −0.60 and −0.78 respectively) whereas PKU-2A and DV-10A (*H. debilis ssp vestitus*) was recorded as good combiner due to their significant *GCA* effects (−0.43 and −0.35) for earliness under normal environment. Only the *CMS* line PHIR-27 was recorded as very good combiner (1.49 and 1.34) for late maturity under both environments respectively. Under stress environment highly significant negative *GCA* effects (−0.54, −0.87 and −2.33) were recorded for *CMS*-XA, DV10A, PRUN-29A respectively and were recorded very good combiners for early maturity in stress environment, whereas, ARG-3A and ARG-6A from (*H. argophyllus*) were recorded as a good combiner (−0.46 and 0.42) for earliness and late maturity respectively. The *CMS* lines from *PET-1* source NC-41B (−2.62) was observed very good combiner for early maturity. The male parent RCR-8297 with *GCA* value of 0.42 and

0.88 was recorded as a very good combiner for late maturity, while P124R with *GCA* value of (−0.43 and −0.45) was observed as very good combiner for earliness under both the environments respectively. The male parent P69R average combiner under normal environment due to its non-significant negative *GCA* effect (−0.14) under normal environment whereas, very good combiner (−0.40) for earliness under stress environment. Significantly negative *GCA* effects for maturity were also reported by Kang *et al.* (2013) and Saleem *et al.* (2014). These *CMS* lines and male lines may also be used in sunflower heterosis breeding to get early matured hybrids.

The cross combinations E002-91A × RCR-8297 (−1.61 and −4.17), PKU-2A × P124R (−2.53 and −1.30), DV10A × P69R (−1.48 and −2.14), DV-10A × P100R (−1.28 and −1.18) and PRUN-29A × P100R (−1.51 and −1.22) were recorded as having high *SCA* effects for earliness under both the environments. While cross combinations E002-91A × P124R (1.08 and 1.32), E002-91A × P100R (1.16 and 2.07), PKU-2A × RCR-8297 (0.78 and 3.04) and DV-10A × RCR-8297 (1.70 and 2.75) were recorded high *SCA* effect for late maturity under both the environments. The earlier findings of Limbore *et al.* (1997) and Bajaj *et al.* (1997) were in conformity with the present findings.

Seed yield

The *CMS* analogues E002-91A (1.75), ARG-3A (5.17) and ARG-6A (7.21) from (*H. argophyllus)* having highly significant positive *GCA* effects were recorded as very good combiner, whereas, NC-41B from *PET-1* (−5.24) with negative *GCA* effects was poor combiner for seed yield under normal environment. Under stress environment the *CMS* analogues *CMS*-XA (6.60), E002-91A (1.82), ARG-3A (*H. argophyllus*) (4.80), ARG-6A (*H. argophyllus*) (3.78) and PRUN-29A (8.98) were recorded as very good combiner because these had highly significant *GCA* effects for seed yield. The *CMS* analogues E002-91A (*H. annuus*), ARG-3A (*H. argophyllus*) and ARG-6A (*H. argophyllus*) recorded very good combining ability under both the environments. The testers RCR-8297 was recorded very good combiner (3.15 and 1.70) under both the environments, while P100R appeared to be very good general combiner (2.44) for seed yield per plant under normal environment only. While, the maintainer line NC-41B (−5.24 and −15.49) and *CMS* line ARG-2A (−2.9 and −3.82) performed negative general combining ability effects for seed yield under both the environments respectively. Among the testers P69R (−3.5) and P124R (−2.1) showed highly significant negative *GCA* effects under normal environment whereas, significant negative *GCA* under stress environment. Results indicate these newly identified divers *CMS* sources may be use in future sunflower hybrid breeding programs due to its high positive *GCA* performance for seed yield under both the environments. For seed yield good general combing lines have been reported by Kandhola *et al.* (1995), Reddy and Madhavi (2005), Hladni *et al.* (2006), Parameshwarappa *et al.* (2008).

Hybrid combinations *CMS*-XA × P100R (6.47 and 5.93), ARG-2A × P100R (9.97 and 10.70), ARG-6A × P69R (5.46 and 4.99), DV-10A × P100R (3.20 and 7.90) and PRUN-29A × RCR-8297 (6.70 and 2.83) were identified with high *SCA* effects for seed yield per plant under both the environments. Khan *et al.* (2009), Karasu *et al.* (2010) were reported significant positive *SCA* effects for oil content, seed yield and yield associated traits.

The *CMS* analogs E002-91A (*H. annuus*) and ARG-3A (*H. argophyllus*) were observed good combiners for early flowering, early maturity and high seed yield derived from different wild *CMS* sources performed good for these traits as compared to NC-41B from classical (*H. petiolaris*) PET-1 source under both the environments, these new sources can be utilize for development of high yielding and early maturing sunflower hybrids with stable performance under normal and water stress environment. These new cytoplasmic male sterility sources derived from different wild spp. can be substitute of the classical (PET-1) source with added advantage for early maturing and high yielding.

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