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Research Article

Genetic studies for seed yield and its components in safflower (*Carthamus tinctorius* L.)

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Abstract
General and specific combining ability variances and effects for ten characters related to yield and its contributing traits in safflower were studied using Line x Tester matting design in thirty CMS based hybrids involving 15 lines and two testers along with two checks (AKS 207 & PKV Pink). Combining ability analysis indicated the predominance of non-additive gene action for all the traits under study except seed volume weight for which both additive and non-additive gene actions were found equally important. The parents *viz.,* GMU 2952, GMU 5609 and GMU 3420 among the males and AKS CMS 2A among the females were found good general combiners for seed yield and most of the yield contributing traits whereas for oil content GMU 3420, GMU 3715 and AKS CMS 2A were found good general combiners. For seed yield per plant the cross AKS CMS 3A x GMU 3638 was found significantly superior in addition to number of seeds per capsule. Whereas, AKS CMS 2A x GMU 2900 for seed volume weight, AKS CMS 2A x GMU 3923 for 100 seed weight, AKS CMS 2A x AKS 207 for number of seeds per capsule, AKS CMS 2A x GMU 322 for number of capsule per plant, AKS CMS 3A x GMU 3420 for number of primary branches per plant were identified as good cross combinations. Desired and fertile segregates may be isolated from segregating material of these crosses in the advanced generations if crosses are effected again by using 'B' lines of CMS based females along with same male parents in concerned crosses as these crosses involved CMS line as female parent. Further, early generation segregates may be intermated with each other to break undesirable linkages and obtain desirable segregates for seed yield and its contributing traits due to predominance of SCA variance for almost all the traits.

Key words
Safflower, line x tester, combining ability, seed yield, oil content

Introduction

Safflower is one of the most important oilseed crops. It has been gaining increasing popularity in recent years in several parts of the county because of its adaptability under drought conditions (Sarode *et al.,* 2008). Safflower is known for its cultivation since time immemorial, for orange red dye extracted from its florets and for its much valued oil. Safflower seeds contain 27.5 per cent oil, 15 per cent protein, 41 per cent crude fiber and 2.3 per cent ash. Safflower oil, which on average contains 75 % linoleic acid, also contains tocopherols, known to have antioxidant effect and high vitamin E content (Latha and Prakash, 1984). For this reason, safflower oil is used in the diets of patients with cardiovascular disease, and bears great importance forits anti-cholesterol effect (Jhajhariya *et al*., 2013).

Combining ability studies furnish useful information about selection of suitable parents for effective hybridization programme (Sprague and Tatum, 1942). It is a powerful tool to discriminate good as well as poor combiners and choose appropriate parental material in breeding programmes and it also gives the information about the nature of gene action involved in the inheritance of various characters. The biometrical technique Line x Tester analysis appeared to be most useful tool for screening lines rapidly and with reasonable confidence. It also provides information about the general combining ability (GCA) and specific combining ability (SCA) variances and effects. In addition, it also gives information about additive (D) and dominance (H) components of genetic variances. A good general combiner is characterized by its better breeding value, when crossed with number of other parents. Specific combining ability is due to non-additive genetic effects, which is non-fixable. However, general combining ability is due to additive genetic effects, which is fixable. Therefore, general combining ability contributed much in the improvement of self-pollinated crops (Spargue and Tataum, 1942). It is essential to evaluate newly developed parents in cross combinations for seed yield and its components. Therefore, the present investigation was undertaken to study the combining ability for identification of good combiners and promising crosses for future better accomplishment in safflower.

Materials and methods

Plant Material: Genetically diverse parents deliberately selected on the basis of their distinguishing characters *i.e.* two CMS lines as females and 15 males. The crosses were developed in line x tester scheme for obtaining F_1 seeds of 30 crosses at Oilseeds Research Unit, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola during *rabi*/Summer 2013-14. Emasculation of females was not required due to availability of CMS

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system, only hand pollination using pollens from protected flowers of male parents was done in the protected flowers of CMS based females in the morning hours. The parental seeds were multiplied by selfing.

Field Trial: A field trial of 48 genotypes including. 17 parents, 30 F_1s and two checks *viz*., PKV Pink and AKS 207 were raised in Randomized Complete block Design with three replications during *rabi/*Summer 2014-15. Each genotype was planted in a single row of 4 m length with 45 cm spacing between rows and 20 cm within rows. All the cultivation practices were followed as per recommendations for safflower cultivation to raise healthy crop.

Observations: The observations were recorded on randomly selected five competitive plants per plot per replication in parents, F_1s and checks for plant height at harvest, number of primary branches per plant, number of capsules per plant, number of seeds per capsule, 100 seed weight (g), seed volume weight (g) and seed yield per plant (g). Whereas, the observations were recorded on plot basis for days to 50 *per cent* flowering, days to maturity and oil content (%). The oil content (%) was determined by following technique on instrument (Bench top Pulse Nuclear Magnetic Resonance (NMR) Spectrometer-Model MQC OXFORD). The samples of 5-10 grams were taken for determination of oil content, before it, calibration had been done in the NMR. The samples were enclosed in a moisture-proof (*i.e.* Ziplock) bag for determination of oil content using NMR.

Statistical Analysis: The analysis of variance was performed as per the procedure given by Panse and Sukthame (1967) from the data obtained in field trials. Further, the line x tester analysis was performed as per the standard procedure given by Kempthorne (1957).

Results and discussion

It has been revealed from the analysis of variance (Table 1) that estimates of mean squares due to genotypes were highly significant for seed yield and its contributing traits indicating presence of substantial genetic variability among the genotypes for all the traits studied. Further, partitioning of genotypic (treatments) variance into components *viz*., parents, crosses and parents v/s crosses naked that the parent differed among them-self significantly for all the characters. Similarly, crosses also showed significant differences for all the traits except plant height. The mean squares due to parents *vs* crosses were significant for all traits except plant height and seed yield indicating the significant differences between parents and crosses for above traits. Line x Tester analysis of 17 parents and 30 crosses (obtained by crossing 15 lines with 2 testers) were carried out of variances attributable to lines and testers were used as a measure of general combining ability effects and the variances due to interaction between lines and testers was used as a measure of specific combining ability effects.

The variances due to lines were highly significant for oil content, seed yield per plant and significant for days to 50 *per cent* flowering, plant height at harvest whereas the variances due to testers were significant only for days to 50 *per cent* flowering. The variances due to crosses were highly significant for all the traits under study except plant height at harvest for which it was found significant. The variances due to lines x testers were highly significant for days to 50 *per cent* flowering, number of capsules per plant, number of seeds per capsule, 100 seed weight, seed volume weight, seed yield per plant and significant for number of primary branches per plant indicated the presence of significant differences between males and females. The SCA variances were found highly significant for all the traits under study whereas GCA variance was found significant only for seed volume weight, as these indicated that the role of dominance gene action was found predominant for all the traits under study, while in the seed volume weight, both additive and non-additive gene action have equally important.

None of the parents recorded the significant GCA effect in desirable direction simultaneously for all the characters studied (Table 2). However, GMU 2952 and GMU 5609 among the lines and AKS CMS 2A among the testers were found to be good general combiners for most of the yield contributing characters. Hence, these genotypes were recognized as the good parental material among the available genotypes for further genetic improvement programme.

For the days to 50 *per cent* flowering and days to maturity the male parents GMU 801 revealed highly significant and negative GCA effects whereas among the females, AKS CMS 2A showed significant GCA effects in desirable direction. Hence, the genotypes *viz.*, GMU 801 and AKS CMS 2A can be used for earliness in safflower. The good GCA was also been recorded by Pahlavani *et al.* (2007) and Sarode *et al.* (2008) for earliness in safflower. The line GMU 2952 exhibited good GCA effects for number of primary branches per plant, number of capsules per plant, seed volume weight and seed yield per plant. Among the testers, AKS CMS 2A exhibited highest, significant and positive GCA effects for seed yield per plant and also recorded highly significant GCA effects in desirable direction for plant height at harvest, number of seeds per capsule, 100 seed weight, seed volume weight and oil content. Hence, the genotypes *viz.*, GMU 2952

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and AKS CMS 2A can be used for genetic improvement of above traits in safflower, similar results were also been reported by Patil *et al.* (1992); Prakash and Prakash (1993). For oil content, GMU 3420 among the lines and the tester, AKS CMS 2A were found to possess good GCA effects. Therefore, these parents can be used for genetic improvement of oil content in safflower. Parents with good GCA effects for above trait were also reported earlier by Prakash and Prakash (1993); Nai *et al*. (2014).

In case of the specific combining ability, none of the crosses exhibited the significant SCA effects in desirable direction for all the characters studied (Table 3). The cross AKS CMS 3A x GMU 3420 showed good SCA effects for days to 50 *per cent* flowering. For days to maturity, oil content and plant height at harvest, none of the crosses showed significant SCA effect in desirable direction. For number of primary branches per plant the cross AKS CMS 3A x GMU 3420 showed significant SCA effects in desirable direction whereas, the crosses AKS CMS 2A x AKS 322 and AKS CMS 3A x GMU 801 showed good SCA effects for number of capsules per plant and AKS CMS 2A x AKS 207 followed by AKS CMS 3A x GMU 3638 and AKS CMS 3A x GMU 3420 for number of seeds per plant. The crosses AKS CMS 2A x GMU 3420 and AKS CMS 2A x GMU 3923 were found to be best combinations for 100 seed weight. For seed volume weight, AKS CMS 2A x GMU 2900, AKS CMS 2A x GMU 3923, AKS CMS 3A x GMU 5609 and AKS CMS 3A x GMU 3164 were the best cross combinations on the basis of SCA effects. For seed yield per plant, AKS CMS 3A x GMU 3638 was the only cross which exhibited good SCA effect in desirable direction. Earlier workers have also noticed good SCA effects for above traits (Narkhede *et al*., 1984; Patil *et al.*, 1992 and Wandhare *et al.,* 2003). For major yield contributing traits *viz.,* number of primary branches per plant, number of capsules per plant, number of seeds per capsule and 100 seed weight, the high *per se* performance of crosses was observed due to either good GCA effects of their parents or high SCA effects of the respective crosses. These types of finding also have been reported earlier by Pahlavani *et al.* (2007); Parde *et al*. (2010) and Jhajhariya *et al.* (2013) in safflower.

The parents with highest and significant GCA effects *viz.,* GMU 2952 for seed yield per plant along with number of primary branches per plant, number of capsules per plant and seed volume weight, GMU 3420 for oil content, AKS 207 for number of seeds per capsule and GMU 801 for earliness, these genotypes could be used in further breeding programme as donor for genetic improvement of concerned trait. The crosses with high mean performance and good heterosis for seed yield was due to high and significant GCA effect of either of their parents (Parde *et al*., 2010 and Jhajharia *et al*., 2013). It is therefore indicated that selection of parents should be done on the basis of high mean performance and significant GCA effects of one of the parents in cross combination might be effective for seed yield improvement.

Accordingly, five promising crosses were selected *viz.,* AKS CMS 3A x GMU 2952, AKS CMS 2A x GMU 2952, AKS CMS 3A x GMU 5609, AKS CMS 3A x GMU 3420 and AKS CMS 3A x GMU 3638. These selected crosses cannot be directly used further for isolation of fertile segregants, as these crosses involved CMS line as female parent. However, good and fertile segregates may be isolated from segregating material of these crosses in the advanced generations by using 'B' lines of CMS based females along with same male parents in concerned crosses. Further, early generation segregates may be intermated with each other to break undesirable linkages and obtain desirable segregates for seed yield and its contributing traits, as the SCA variance for almost all the traits was found predominant.

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Table 1. Analysis of variance for combining ability in safflower

Sources of variation	d.f.	Mean sum of squares									
		Days to 50 % flowering	Days to maturity	Plant height at harvest	Number of primary branches per plant	Number of capsules per plant	Number of seeds per capsule	100 seed weight	Seed volume weight	Seed yield per plant	Oil content
Replications	2	14.01	0.31	67.84	0.43	12.58	0.05	0.68	1040.04	5.01	3.10
Crosses	29	39.67**	19.72**	63.15*	3.79**	27.77**	21.73**	1.47**	8063.49**	24.18**	2.62**
Line effects	14	56.75*	28.35	93.50*	5.08	38.42	26.39	1.48	9423.47	41.19**	4.74**
Tester effects	1	129.60*	2.50	6.63	7.52	14.13	4.62	0.27	3610.00	0.25	0.24
Line x Tester effects	14	16.17**	12.31	36.84	2.23*	18.10**	18.29**	1.54**	7021.62**	8.87**	0.66
Error	58	5.83	8.60	31.53	0.99	5.37	3.96	0.41	1014.31	3.58	1.09
GCA variance		1.44	0.03	0.07	0.08	0.16	0.05	0.003	40.11*	0.003	0.003
SCA variance		37.73**	28.72**	85.96**	5.21**	42.22**	42.68**	3.60**	16.38**	20.70**	1.55*

(*, ** Significant at P=0.05 and P=0.01, respectively)

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Table 2. Estimates of general combining ability effects of parents for different traits in safflower

S. No.	Genotype	Days to 50 % flowering	Days to maturity	Plant height at harvest	Number of primary branches per plant	Number of capsules per plant	Number of seeds per capsule	100 seed weight	Seed volume weight	Seeds yield per plant	Oil content
					Lines (Males)						
1.	GMU 3420	3.49*	3.02	3.86	-0.53	0.47	-0.08	0.56	12.14	2.35*	2.26**
2.	GMU 5711	-2.18	-0.31	-0.36	-0.98	-2.97*	0.36	0.02	-37.02*	-2.33*	-1.32*
3.	GMU 801	-5.34**	-3.48*	-1.60	1.58**	4.09**	1.93	-0.80*	-13.52	2.18	0.09
4.	GMU 3715	4.16**	3.19	2.97	-0.70	-0.03	-1.97	0.19	19.14	-1.01	1.23*
5.	GMU 5609	1.16	0.52	5.19	1.19*	2.81*	0.47	0.08	20.64	3.91**	-0.05
6	GMU 2900	3.82**	3.02	-3.75	-0.36	-0.86	2.77*	-0.98*	5.31	-2.05	-0.03
7	GMU 3164	0.32	-0.31	0.69	-0.92	-1.14	-0.94	-0.33	-62.19**	-2.87*	0.28
8	GMU 3923	-0.34	-0.98	-3.28	-0.36	-2.64	-1.14	0.01	-72.69**	-3.38**	-1.19
9	GMU 2952	-2.34	-3.31	5.08	1.80**	5.92**	-0.94	0.27	94.31**	5.98**	0.01
10	GMU 3638	-3.34*	-1.31	2.64	0.53	-0.25	-0.003	0.08	26.64	0.42	-0.60
11	AKS S/41	-2.51	-0.64	-3.64	0.58	0.14	-3.41**	0.69	10.64	-0.84	-0.04
12	AKS 207	-3.34*	-1.64	-6.25	-0.81	-1.80	5.39**	-0.64	16.31	0.43	0.23
13	AKS 322	0.32	-0.48	-5.14	-0.64	-1.31	-1.25	0.28	4.64	-1.69	0.03
14	AKS 325	2.66	-0.14	-1.47	-0.42	-2.64	-0.61	0.61	-9.69	-0.76	-0.01
15	AKDOR 1	3.49*	2.86	5.08	0.02	0.20	-0.56	-0.02	-14.69	-0.35	-0.88
	SE(gi)	0.99	1.20	2.29	0.41	0.95	0.81	0.26	13.00	0.77	0.43
	CD (0.05)	1.97	2.40	4.59	0.81	1.89	1.63	0.52	26.03	1.55	0.85
	CD (0.01)	2.63	3.19	6.11	1.08	2.52	2.17	0.69	34.63	2.06	1.14
					Testers (Females)						
1.	AKS CMS 2A	-1.20**	-0.17**	0.27**	-0.29**	-0.40**	0.23**	0.06**	6.33**	0.05**	0.05**
2.	AKS CMS 3A	1.20**	0.17**	-0.27**	0.29**	0.40**	-0.23**	-0.06**	-6.33**	-0.05**	-0.05**
	SE(gj)	0.36	0.44	0.84	0.15	0.35	0.30	0.09	4.75	0.28	0.16
	CD (0.05)	0.72	0.88	1.68	0.30	0.69	0.59	0.19	9.50	0.57	0.31
	CD (0.01)	0.96	1.16	2.23	0.40	0.92	0.79	0.25	12.64	0.75	0.42

(*, ** Significant at P=0.05 and P=0.01, respectively)

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Table 3. Estimates of specific combining ability effects of crosses for various traits

S. No.	Genotype	Days to 50 % flowering	Days to maturity	Plant height at harvest	No. of primary branches / plant	No. of capsules/ plant	No. of seeds/ capsule	100 seed weight	Seed volume weight	Seeds yield/ plant	Oil content
1	AKS CMS 2A x GMU 3420	3.53*	2.33	-1.05	-1.43*	-2.33	-2.31*	0.90*	-25.17	-1.51	-0.09
2	AKS CMS 2A x GMU 5711	-2.47	-1.00	-3.50	0.57	2.01	0.64	-0.72	-6.00	0.04	0.39
3	AKS CMS 2A x GMU 801	-2.30	-0.83	1.39	-0.65	-3.05*	1.32	0.37	-8.50	0.61	0.04
4	AKS CMS 2A x GMU 3715	0.20	-0.50	-4.72	0.29	0.06	0.09	-0.16	-6.50	-0.39	-0.04
5	AKS CMS 2A x GMU 5609	-0.47	-1.50	-1.49	-0.04	-0.77	-0.26	0.07	-39.33*	-0.69	-0.69
6	AKS CMS 2A x GMU 2900	-1.13	-2.00	3.34	0.95	0.12	-1.37	0.35	82.33**	0.52	0.18
7	AKS CMS 2A x GMU 3164	1.37	0.33	1.23	0.51	1.06	1.40	-0.38	-60.83**	0.82	-0.004
8	AKS CMS 2A x GMU 3923	-0.97	-2.00	-0.80	-0.27	0.23	-1.45	0.97*	45.67*	1.98	0.17
9	AKS CMS 2A x GMU 2952	0.03	-0.67	-3.72	-0.21	0.12	0.80	-0.31	-21.33	-0.11	-0.13
10	AKS CMS 2A x GMU 3638	0.37	2.00	2.06	-0.27	-1.49	-2.61*	0.25	-1.00	-3.16**	-0.02
11	AKS CMS 2A x AKS S/41	-1.47	0.00	1.67	-0.32	-0.66	0.43	0.17	24.00	0.49	0.50
12	AKS CMS 2A x AKS 207	0.70	2.00	-0.38	0.18	0.62	3.58**	-0.51	13.67	1.23	-0.09
13	AKS CMS 2A x AKS 322	2.37	1.50	2.28	0.90	4.12**	-2.29	-0.49	10.00	-0.05	0.32
14	AKS CMS 2A x AKS 325	-0.63	0.50	1.84	-0.10	0.90	0.12	-0.08	5.00	0.74	0.14
15	AKS CMS 2A x AKDOR 1	0.87	-0.17	1.84	-0.10	-0.94	1.87	-0.43	-12.00	-0.52	-0.67
16	AKS CMS 3A x GMU 3420	-3.53*	-2.33	1.05	1.43*	2.33	2.31*	-0.90*	25.17	1.51	0.09
17	AKS CMS 3A x GMU 5711	2.47	1.00	3.50	-0.57	-2.01	-0.64	0.72	6.00	-0.04	-0.39
18	AKS CMS 3A x GMU 801	2.30	0.83	-1.39	0.65	3.05*	-1.32	-0.37	8.50	-0.61	-0.04
19	AKS CMS 3A x GMU 3715	-0.20	0.50	4.72	-0.29	-0.06	-0.09	0.16	6.50	0.39	0.04
20	AKS CMS 3A x GMU 5609	0.47	1.50	1.49	0.04	0.77	0.26	-0.07	39.33*	0.69	0.69
21	AKS CMS 3A x GMU 2900	1.13	2.00	-3.34	-0.95	-0.12	1.37	-0.35	-82.33**	-0.52	-0.18
22	AKS CMS 3A x GMU 3164	-1.37	-0.33	-1.23	-0.51	-1.06	-1.40	0.38	60.83**	-0.82	0.004
23	AKS CMS 3A x GMU 3923	0.97	2.00	0.80	0.27	-0.23	1.45	-0.97*	-45.67*	-1.98	-0.17
24	AKS CMS 3A x GMU 2952	-0.03	0.67	3.72	0.21	-0.12	-0.80	0.31	21.33	0.11	0.13
25	AKS CMS 3A x GMU 3638	-0.37	-2.00	-2.06	0.27	1.49	2.61*	-0.25	1.00	3.16**	0.02
26	AKS CMS 3A x AKS S/41	1.47	0.00	-1.67	0.32	0.66	-0.43	-0.17	-24.00	-0.49	-0.50
27	AKS CMS 3A x AKS 207	-0.70	-2.00	0.38	-0.18	-0.62	-3.58**	0.51	-13.67	-1.23	0.09
28	AKS CMS 3A x AKS 322	-2.37	-1.50	-2.28	-0.90	-4.12**	2.29	0.49	-10.00	0.05	-0.32
29	AKS CMS 3A x AKS 325	0.63	-0.50	-1.84	0.10	-0.90	-0.12	0.08	-5.00	-0.74	-0.15
30	AKS CMS 3A x AKDOR 1	-0.87	0.17	-1.84	0.10	0.94	-1.87	0.43	12.00	0.52	0.67
SE (Sij) ±		1.39	1.69	3.24	0.58	1.34	1.15	0.37	18.39	1.09	0.60
CD (0.05)		2.790	3.39	6.49	1.15	2.69	2.30	0.74	36.81	2.19	1.21
CD (0.01)		3.71	4.51	8.63	1.53	3.56	3.06	0.98	48.97	2.91	1.61

(*, ** Significant at P=0.05 and P=0.01, respectively)