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Research Article

Genetic studies for isolation of superior parents and hybrids for a further breeding programme in safflower (*Carthamus tinctorious L*)

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Abstract
Combining ability analysis discriminates the parents and crosses, provides information about the breeding method to be adopted for genetic improvement of a specific character. Thirty hybrids obtained by mating two females with fifteen males in L × T fashion were evaluated in RBD along with parents to estimate the combining ability of parents and crosses for seed yield and yield contributing traits. The parents and hybrids significantly differed amongst themselves for different characters*, viz.,* days to maturity, 100 seeds weight, capsules per plant, branches per plant, seed yield, seed volume weight and oil content. Among the males, GMU-590, GMU-2273, GMU-2830 and GMU-589 and the females, AKS CMS-3B had good *gca* effects for seed yield and some other yield contributing traits. However, GMU-7573 and GMU-2830 were found best general combiners for the trait oil content. All these selected parents may be utilised in a different breeding programme for genetic enhancement of the trait involved. The hybrids AKS CMS-2A × GMU-1731 and AKS CMS-3A × GMU-7448 were identified as good combinations for seed volume weight and capsules per plant. Whereas the hybrids AKS CMS-3A × GMU-2273 and AKS CMS-2A × GMU-6891 were effective for seed filling percentage and seed yield per plant. Three promising hybrids *viz*., AKS CMS-3A × GMU-7448, AKS CMS-3A × GMU-2273 and AKS CMS-2A × GMU-6891 were designated as promising hybrids as they had good *per se* performance and significant *sca* effects for seed yield per plant and most of its contributing characters which can be utilized for heterosis breeding and release of new hybrids at commercial level after thorough multilocation testing. Further, the hybrids AKS CMS-3A × GMU-7448, AKS CMS-3A × GMU-590 and AKS CMS-3A × AKS-589 involving one or both good general combining parents with non-significant *sca* effects for many studied characters which may be utilized to isolate desirable segregants in progressive generations for identification and release of new varieties by hybridizing the 'B' lines of concerned CMS line with similar males again.

Keywords*:* Safflower, line × tester, general combining ability, specific combining ability, seed yield

INTRODUCTION

Among the various oilseed crops, safflower (*Carthamus tinctorius* L.) is the most prominent *rabi* oilseed crop, possessing resistance to heat, drought and salinity. Amongst the 36 members of the Carthamus genus, only one species, *viz., Carthamus tinctorius* L., is the cultivated species of safflower, which is utilized for oil extraction, whereas other related species are wild ones. Safflower is being cultivated in different seasons, *i.e.*, during winter in southern India, as a late spring crop in California and as a mid-summer crop in the northern Great Plains of the United States (Knowles *et al*., 2015). Safflower seeds contain 26-30 per cent high quality oil used for cooking. It contains about 75 % of linoleic acid, tocopherols too and is considered to possess antioxidant properties and high levels of vitamin E. Hence, safflower oil is most suitable for cardiovascular disease patients, because it invigorates blood circulation (Jhajhariya *et al*., 2013). Furthermore, safflower blossoms

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have numerous therapeutic properties for relieving a few persistent infections. They are broadly utilized in Chinese natural arrangements (Li and Mundel, 1996).

Combining ability evaluation can help to isolate appropriate parents to be used in the hybridization programme (Sprague and Tatum, 1942). Further, it proved to be useful for identifying good and poor combiners and selecting suitable parents for hybridization programmes. It also gives an idea about the mechanism of gene action controlling the inheritance of certain traits. Therefore, the combing ability study helps to choose the desired combinations as well as the desired parents for a further breeding programme.

Using biometrical techniques such as the line × tester design is an effective and reliable approach for easy and quick assessment of parental lines. The evaluation of F_1s and their parents is necessary to judge the worth of F_1 hybrids. This design discriminates the good combining parents and specific hybrid combinations and generates ideas about predominant gene action controlling the characters. This technique is one of the powerful tools to assess parental lines in all possible combinations for seed yield and other associated characters. Hence, the present study was carried out to discriminate parents with a good combining ability and promising hybrids for future breeding programmes and improving economically important traits in safflower.

MATERIALS AND METHODS

Diverse parental lines were intentionally selected in accordance with their distinctive traits, *i.e.*, two cytoplasmic male sterile lines *viz*., AKS CMS-2A/B and AKS CMS-3A/B as female parents and GMU-1758, GMU-7355, GMU-1654, GMU-7448, GMU-1397, GMU-7573, GMU-1731, GMU-590, GMU-7612, GMU-589, GMU-2928, GMU-2273, GMU-6691, GMU-2830 and GMU-579 as male parents. The hybridization was performed between two female and fifteen male parents in L × T fashion to yield an adequate quantity of F_0 seeds of 30 hybrids by transferring the pollens from protected flowers of males to protected flowers of male-sterile female lines.

A field experiment of 50 entries comprised of 17 parental lines, 30 hybrids and three standard check varieties *viz*., PKV-PINK, A-1 and PBNS-12 was conducted in Randomized Block Design during *rabi,* 2019-20 season. All the entries were replicated thrice and every entry was grown in a single row of 3 m length and maintained the recommended spacing of 45 and 20 cm between and within rows, respectively. In addition, all the recommended packages of practices were applied timely for the healthy growth of safflower plants in all the entries in the experiment.

Five competitive plants were randomly selected in each entry in every replication for recording observations as shown in **Table 1**, except for days to 50 % flowering and days to maturity for which all the plants in a plot were considered. To determine the oil content in all the entries in all three replications, Benchtop Pulse Nuclear Magnetic Resonance (NMR) Spectrometer (Model MQC OXFORD) was used.

The data obtained from the field experiment were subjected to analysis of variance following the procedure specified by Panse and Sukthame (1985). Further, Kempthorne (1957) developed the procedure to calculate the mean sum of squares from L × T design and general and specific combining ability effects of the parents and hybrids, respectively.

RESULTS AND DISCUSSION

The analysis of variance performed for various characters studied is presented in **Table 1**. The mean squares due to hybrids were found to be highly significant for all the characters except for days to 50 % flowering and days to maturity, indicating the presence of considerable genetic variability among all the hybrids. The variation between all the hybrids was partitioned into different components of variation representing the mean sum of squares due to males, females and males v/s females interaction. The mean sum of squares due to males showed that significantly differed for the number of primary branches per plant and the number of capsules per plant. Whereas, the females differed for all the characters studied except for days to 50% flowering, 100 seeds weight, volume per weight and oil content. Further, the interaction was highly significant for all the characters except for days to 50% flowering, days to maturity and primary branches per plant. Pandya and Patil (1994), Sarode *et al.* (2008), Kose (2017) and Patel *et al.* (2018) also noticed significant differences amongst the hybrids, males, females and interaction. As per the analysis of variation for combining ability, the variance for specific combining ability was greater than the variation due to general combining ability for all the characters under study, revealing the prevalence of SCA variance, *i.e.* non-additive gene action, for controlling all the characters under study. Parde *et al*. (2010), Patel *et al.* (2018) and Rathod *et al.* (2020) also reported a predominance of SCA variance for the characters studied.

The specific combining ability results from non-additive genetic effects and is a non-fixable type of variation. Whereas, general combining ability is the result of additive genetic effects and it is a fixable one. Spargue and Tataum (1942) stated that the general combining ability, *i.e*., additive variation has a major role in the genetic improvement of self-pollinated crops. In the present investigation, none of the parental lines could be a good general combiner for all the characters under study (**Table 2**). However, some of the parental lines (males and females) found to have good *gca* effects in a favourable direction for one or more characters under study, such as GMU-590, GMU-589 and GMU-2273 divulged significant and positive *gca* effects in a favourable direction each for seed yield per plant, primary branches per plant, capsules per plant and seed filling percentage in addition to positive and significant *gca* effects by GMU-590 for the trait volume per weight.

Further, a male parent GMU-2830 displayed good *gca* effects for seed yield per plant, primary branches per plant, volume per weight, seed filling percentage and oil content as well. Some of the male parents could not exhibit good *gca* effects for seed yield per plant in a desirable

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/ plants	Number of capsules/ plants	100 seed weight	Volume/ weight	Seed yield / plant	Seed filling percentage	Oil content
Replications	2	201.67	154.71	44.61	1.48	0.17	12.33	20.99	27.43	2.649	4.98
Hybrids	29	15.90	10.66	101.20**	6.07**	51.05**	0.73**	145.31**	63.38**	367.26**	26.67**
Males	14	14.78	3.89	87.06	9.02**	57.46*	0.78	207.02	81.79	471.88	32.44
Females	1	21.51	117.88**	578.61*	16.47*	356.01**	0.04	34.47	193.60*	1199.02*	5.04
Males × females	14	16.63	9.76	81.24**	2.39	22.86**	0.72*	91.51**	35.67**	203.24**	22.44**
Error	58	17.93	14.66	28.77	1.69	5.80	0.35	5.82	4.67	16.38	4.46
GCA variance		0.24	1.31	6.43	0.18	3.96	0.00	0.38	2.15	13.32	0.06
SCA variance		38.80	22.77	189.55	5.57	53.33	1.69	213.52	83.24	474.23	52.37
GCA/SCA		0.006	0.058	0.034	0.032	0.074	0.000	0.002	0.026	0.028	0.001

* =Significant at 5 *per cent* level of significance; ** =Significant 1 *per cent* level of significance; d.f.=degrees of freedom

Table 2. Estimates of *gca* effects of parents for different traits

S. No.	Genotypes	Days to 50% flowering	Days to maturity	Plant height at harvest	Number of primary branches/ plants	Number of capsules/ plants	100 seed weight	Volume/ weight	Seed yield / plant	Seed filling percentage	Oil content
Lines											
1	GMU-1758	-0.86	-0.32	0.13	-0.80	-0.58	-0.22	3.03**	-0.5	-2.70	-1.62
2	GMU-7355	-0.19	0.18	4.25*	-1.20 *	-1.83	0.38	-9.57**	-1.44	-3.95	0.39
3	GMU-1654	0.98	-0.82	-2.95	-1.08*	-1.46	0.11	3.00**	-3.45**	-9.90**	1.98*
4	GMU-7448	2.81	0.01	8.47**	1.38**	2.62**	-0.06	-0.69	0.26	1.00	0.39
5	GMU-1397	1.98	1.01	-0.02	-0.90	-0.74	0.46	5.98**	-0.57	-1.25	-0.28
6	GMU-7573	-2.69	0.68	5.43**	0.15	-1.33	0.19	-4.79**	-0.55	-1.60	4.95**
7	GMU-1731	-1.02	-1.99	0.97	-1.31**	-3.58**	-0.31	-0.09	-3.79**	-9.40**	0.70
8	GMU-590	0.98	0.18	-2.37	1.34**	3.76**	0.53	4.68**	3.86**	10.60**	-1.38
9	GMU-7612	0.81	0.84	-5.52**	-0.35	-2.36*	-0.64*	-15.30**	-3.34**	-6.40**	0.27
10	GMU-589	-0.36	0.34	-1.52	1.35**	3.39**	0.19	1.46	5.76**	13.80**	-1.79*
11	GMU-2928	1.64	0.34	-1.58	0.74	-3.83**	-0.14	6.66**	-3.80**	-9.50**	-1.59
12	GMU-2273	-1.02	0.68	-2.27	2.45**	7.41**	0.44	0.73	8.43**	18.05**	-4.71**
13	GMU-6891	-0.86	-1.16	-0.27	-0.83	-1.46	-0.47	1.13	-1.97*	-3.80	0.47
14	GMU-2830	-2.52	-0.16	2.12	1.50**	1.31	0.22	3.03**	3.05**	9.60**	3.48**
15	GMU-579	0.31	0.18	-4.87*	0.32	-1.33	0.22	0.73	-1.87*	-4.50*	-1.30
	SE ± (gi)	1.72	1.47	1.99	0.47	0.93	0.28	0.95	0.93	2.09	0.88
	CD (0.05 %)	3.44	2.93	3.98	0.93	1.87	0.57	1.83	1.86	4.18	1.77
	CD (0.01 %)	4.58	3.90	5.30	1.24	2.49	0.75	2.44	2.48	5.56	2.3509
Testers											
16	AKS CMS-2B	0.49	1.14*	-2.54**	-0.43*	-1.99**	0.02	0.62	-1.47**	-3.65**	0.24
17	AKS CMS-3B	-0.49	-1.14*	2.54**	0.43*	1.99**	-0.02	-0.62	1.47**	3.65**	-0.24
	SE ± (gi)	0.63	0.54	0.73	0.17	0.34	0.10	0.33	0.34	0.76	0.32
	CD (0.05 %)	1.26	1.10	1.45	0.34	0.68	0.21	0.67	0.68	1.53	0.65
	CD (0.01 %)	1.67	1.42	1.93	0.45	0.91	0.27	0.89	0.91	2.03	0.86

* =Significant at 5 *per cent* level of significance; ** =Significant 1 *per cent* level of significance

direction. However, those parents were found to possess good *gca* effects for the rest of the yield contributing traits, *i.e*., the parent GMU-7448 for plant height, primary branches per plant and capsules per plant; GMU-1654 for volume per weight and oil content, whereas, a male parent GMU-7573 found better general combiner for plant height and oil content. Amongst the female parents, AKS CMS-3B displayed positively significant *gca* effects for seed yield per plant. The same female parent is also recognised as a better general combiner for earliness, plant height, primary branches per plant, capsules per plant and seed filling percentage. Shivani *et al*. (2011), Ahmed *et al.* (2016), Patel *et al.* (2018), Rathod *et al.* (2020), Thorat and Gawande (2021) also reported significant *gca* effects for yield per plant and its contributing traits in safflower. Therefore, these parents having good *gca* effects for various characters can be utilised to improve the concerned trait in safflower in the future. In the present investigation, none of the male parents was found to possess good *gca* for earliness i.e. for days to 50% flowering and days to maturity. However, Ahmed *et al.* (2016) and Thorat and Gawande (2021) identified good general combining parents (males) for earliness in safflower.

In the case of the specific combining ability (**Table 3**), a hybrid AKS CMS-3A × GMU-2273 displayed significant *sca* effects in the direction of interest for plant height at harvest and seed yield per plant. Whereas, two hybrids *viz.,* AKS CMS-2A × AKS-1731 and AKS CMS-3A × GMU-7448 were significantly superior for the traits seed volume weight and the number of capsules per plant. A similar result has also been reported earlier by Ahmad *et al.* (2016) and Thorat and Gawande (2021) for both traits in safflower. A hybrid AKS CMS-2A × AKS-6891 followed by AKS CMS-3A × GMU-2273 exhibited good *sca* effects for the trait seed yield per plant in a desirable direction. Whereas, the hybrids *viz.,* AKS CMS-2A × GMU-1731 and AKS CMS-2A × GMU-6891 were also found to possess significant *sca* effects in case of oil content in a desirable direction as also reported earlier by Thorat and Gawande (2021). For seed yield per plant and its important contributing traits *viz.,* primary branches per plant, capsules per plant, 100 seed weight, the high mean performance of hybrids were detected either due to good general combining ability of their parents or high *sca* effects of respective hybrids. A similar fact has also been observed by Pahlavani *et al.* (2007), Parde *et al.* (2010), Golkar *et al.* (2011) and Thorat and Gawande (2021) in safflower. In the present study, none of the hybrids performed significantly superior in the desired direction for the characters days to 50% flowering, days to maturity and primary branches per plant. However, Thorat and Gawande (2021) noticed some good specific combinations for these traits in safflower, which may be due to the difference in parental lines used for the study.

The hybrids *viz.* AKS CMS-3A × GMU-590, AKS CMS-3A × GMU-589 and AKS CMS-3A × GMU-2830 displayed non-significant specific combining ability effects for seed yield per plant. Similar situation was also noticed in AKS CMS-3A × GMU-7355, AKS CMS-3A × GMU-7448 and AKS CMS-3A × GMU-7573 for plant height; AKS CMS-3A × GMU-7448, AKS CMS-3A × GMU-590, AKS CMS-3A × GMU-589, AKS CMS-3A × GMU-2273 and AKS CMS-3A × GMU-2830 for the trait primary branches per plant; AKS CMS-3A × GMU-590, AKS CMS-3A × GMU-589 and AKS CMS-3A × GMU-2273 for capsules per plant; AKS CMS-2A × GMU-1758, AKS CMS-2A × GMU-1654, AKS CMS-2A × GMU-590, AKS CMS-2A × GMU-2830, AKS CMS-3A × GMU-1758, AKS CMS-3A × GMU-1397, AKS CMS-3A × GMU-590, AKS CMS-3A × GMU-2928 and AKS CMS-3A × GMU-2830 for the character volume per weight; AKS CMS-3A × GMU-590, AKS CMS-3A × GMU-589, AKS CMS-3A × GMU-2273 and AKS CMS-3A × GMU-2830 for seed filling percentage. However, all these hybrids were found to involve both the parents with good general combining ability for the concerning traits. Thus, it revealed that the parents possessing high x high or high x low *gca* effects do not necessarily produce hybrids with high *sca* effects. This may be either due to the internal cancellation of gene effects in the parents involved or lack of good co-ordination between favourable alleles contributed by both the parents in these hybrids for the concerned trait.

Similarly, the hybrid AKS CMS-2A × GMU-6891 revealed the highest and positively significant *sca* effects for the trait seed yield per plant, AKS CMS-2A × GMU-1731 for capsules per plant, AKS CMS-2A × GMU-7573, AKS CMS-2A × GMU-1731, AKS CMS-3A × GMU-7448 and AKS CMS-3A × GMU-589 for the trait volume per weight, AKS CMS-2A × GMU-6891 for seed filling percentage, AKS CMS-2A × GMU-6891 and AKS CMS-3A × GMU-1731 for oil content. However, the parents involved in these hybrids were poor general combiners for the same character. This may be due to the presence of genetic diversity in the form of dispersed alleles for these characters.

The parents *viz*., GMU-2273, GMU-589, GMU-590, GMU-2830 and AKS CMS-3A/B were selected as promising parents based on their general combining ability effects and mean performance. Hence, desirable segregants may be isolated from advanced segregating generations of the hybrids which involve any one or two of the above selected genotypes as parents and can be released for commercial cultivation as a variety after thorough multilocation testing. Three promising hybrids *viz*., AKS CMS 3A × GMU 7448, AKS CMS 3A × GMU 2273, AKS CMS 2A × GMU 6891 were selected based on significant *sca* effects for seed yield and most of its contributing characters. These hybrids can be utilised for heterosis breeding and development and release of new hybrids in safflower at a commercial level after thorough multilocation testing. Further, the hybrids *viz*., AKS CMS-3A × GMU-7448, AKS CMS-3A × GMU-590 and AKS CMS-3A × AKS-589 had low SCA effects for most of the characters under study and involving parents with highly significant *gca* effects in a favourable direction for most of the traits studied. These hybrids may be reconstructed using 'B' line of male sterile line as female to cross with same male parents and advancing the generations to isolate promising segregants after achieving virtual homozygosity for releasing as a variety after multilocation testing. As per Clegg *et al.* (1972), the hybridization followed by the conventional pedigree method or SSD or bulk method is correlated with weakness of resulting speedy homozygosity and low genetic variation in segregating generations particularly in the presence

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Table 3. Estimates of *sca* effects of crosses for various traits

S. No.	Genotypes	Days to 50% flowering	Days to maturity	Plant height at harvest	Number of primary branches/ plant	Number of capsules/ plant	100 seeds weight	Volume/ weight	Seed yield/ plant	Seed filling percent-age	Oil content
1	AKS-CMS 2A × GMU-1758	-0.32	-1.48	4.05	-0.59	-1.328	0.478	0.05	2.47	4.55	0.98
2	AKS-CMS 2A × GMU-7355	-1.32	-0.64	2.34	0.28	1.16	-0.79	-1.05	1.32	2.50	-1.60
3	AKS-CMS 2A × GMU-1654	0.51	-1.31	5.50	-0.04	-0.88	0.48	-3.45**	1.40	3.15	-0.06
4	AKS-CMS 2A × GMU-7448	1.34	-0.48	-0.75	-0.44	-4.46**	-0.36	-4.14**	-2.12	-7.55*	-1.59
5	AKS-CMS 2A × GMU-1397	0.84	1.19	3.94	0.14	-1.93	0.16	3.66**	2.08	4.80	0.19
6	AKS-CMS 2A × GMU-7573	-1.16	2.19	-3.48	0.57	-0.11	-0.12	3.46**	-1.50	-5.25	0.50
7	AKS-CMS 2A × GMU-1731	-1.49	1.86	3.75	0.23	3.94**	0.23	3.50**	-0.47	-0.75	-4.82**
8	AKS-CMS 2A × GMU-590	0.18	1.36	-4.88	0.64	-0.93	-0.11	-0.10	-0.85	-1.35	1.39
9	AKS-CMS 2A × GMU-7612	-0.32	1.36	1.30	0.33	0.52	-0.11	2.38	-2.52	-9.85**	-1.27
10	AKS-CMS 2A × GMU-589	-1.16	-0.81	-4.13	0.46	-1.16	-0.11	-6.91**	-1.95	-2.85	-1.41
11	AKS-CMS 2A × GMU-2928	1.51	-0.81	-2.26	0.31	1.29	0.06	8.88**	-0.38	0.65	1.63
12	AKS-CMS 2A × GMU-2273	-1.49	-0.14	-6.08*	-0.44	0.86	-0.19	-2.45	-4.18**	-3.50	0.59
13	AKS-CMS 2A × GMU-6891	3.34	-1.31	-0.01	-0.32	1.72	-0.27	-0.02	5.52**	13.85**	3.48**
14	AKS-CMS 2A × GMU-2830	2.34	0.36	-1.90	1.31	0.24	0.14	-2.05	-0.53	-1.15	0.87
15	AKS-CMS 2A × GMU-579	-2.82	-1.31	2.62	-1.31	1.56	0.48	-1.75	1.72	4.05	1.02
16	AKS-CMS 3A × GMU-1758	0.32	1.48	-4.05	0.59	1.33	-0.48	-0.05	-2.47	-4.55	-0.97
17	AKS-CMS 3A × GMU-7355	1.32	0.64	-2.33	-0.28	-1.16	0.79	1.05	-1.32	-2.50	1.60
18	AKS-CMS 3A × GMU-1654	-0.51	1.31	-5.50	0.04	0.88	-0.48	3.45**	-1.40	-3.15	0.07
19	AKS-CMS 3A × GMU-7448	-1.34	0.48	0.75	0.44	4.46**	0.36	4.14**	2.12	7.55*	1.59
20	AKS-CMS 3A × GMU-1397	-0.84	-1.19	-3.94	-0.14	1.92	-0.16	-3.66**	-2.08	-4.80	-0.11
21	AKS-CMS 3A × GMU-7573	1.16	-2.19	3.48	-0.57	0.11	0.11	-3.46**	1.50	5.25	-0.50
22	AKS-CMS 3A × GMU-1731	1.49	-1.86	-3.75	-0.23	-3.94**	-0.23	-3.49**	0.47	0.75	4.82**
23	AKS-CMS 3A × GMU-590	-0.18	-1.36	4.88	-0.64	0.93	0.11	0.10	0.85	1.35	-1.39
24	AKS-CMS 3A × GMU-7612	0.32	-1.36	-1.30	-0.33	-0.52	0.11	-2.38	2.52	9.85**	1.27
25	AKS-CMS 3A × GMU-589	1.16	0.81	4.13	-0.46	1.16	0.11	6.92**	1.95	2.85	1.41
26	AKS-CMS 3A × GMU-2928	-1.51	0.81	2.26	-0.31	-1.29	-0.06	-8.88**	0.38	-0.65	-1.63
27	AKS-CMS 3A × GMU-2273	1.49	0.14	6.08*	0.44	-0.86	0.19	2.45	4.18**	3.50	-0.59
28	AKS-CMS 3A × GMU-6891	-3.34	1.31	0.01	0.32	-1.72	0.27	0.02	-5.52**	-13.85**	-3.48**
29	AKS-CMS 3A × GMU-2830	-2.34	-0.36	1.90	-1.31	-0.24	-0.14	2.05	0.53	1.15	-0.87
30	AKS-CMS 3A × GMU-579	2.82	1.31	-2.62	1.31	-1.56	-0.48	1.75	-1.72	-4.05	-1.02
	SE ±	2.43	2.06	2.81	0.66	1.32	0.40	1.29	1.32	2.95	1.25
	CD (0.05 %)	4.86	4.14	5.63	1.31	2.64	0.79	2.59	2.63	5.91	2.50
	CD (0.01 %)	6.47	5.50	7.49	1.75	3.52	1.05	3.45	3.50	7.86	3.32

* =Significant at 5 *per cent* level of significance; ** =Significant 1 *per cent* level of significance

of linkage blocks and negative association among the desirable traits. In the present study, the genetic material used have the preponderance of SCA (non-additive) variance than GCA (additive) variance for all the characters under study. Therefore, biparental mating or diallel selective mating is suggested to isolate superior transgressive segregants from this material, as reported earlier by Jensen (1970). Further, Malhotra *et al*. (1980) also suggested that diallel selective mating among the parents can break up some undesirable linkages and thereby discharge more significant genetic variability for all the traits.

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