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Combining ability and gene action studies for seed yield and its components in sesame (Sesamum indicum L.)

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Abstract

A line x tester analysis using nine lines and five testers was carried out to study the combining ability and gene action in sesame for seed yield and its related 11 quantitative traits. The partitioning of variances due to the crosses showed that the mean squares due to lines were found significant for all the characters except for number of branches per plant and oil content, whereas mean squares due to testers and lines x testers were found significant for all the characters except for the plant height and number of branches per plant. General and specific combining ability variances showed the involvement of both type of gene actions in the inheritance of these characters. Among the parents, two lines *viz.*, AT-472 and AT-483 and three testers *viz.*, GT-2, GT-3 and GT-6 exhibited good general combining ability effect for seed yield per plant. The cross combination, AT-471 x GT-2 showed significant and positive sca effect for seed yield per plant and involved average x good combining parents. It was followed by AT-464 x GT-4 and AT-472 x GT-3 which involved either good x good or poor x poor combining parents. These crosses have been identified as best hybrids for improving seed yield per plant.

Keywords: Sesame, combining ability, gene action, line x tester analysis

Introduction

Sesame (Sesamum indicum L.) is a crop, which is cultivated in diverse agro-ecological situations. It is called as the "Queen of oilseeds" because of its excellent qualities of the seed, oil and meal. Sesame is highly nutritive (oil 50%, protein 25%) and its oil contains an antioxidant called sesamol which imparts a high degree of resistance against oxidative rancidity. It is an important annual oilseed crop in the tropics and warm subtropics, where it is usually grown in small patches (Bedigian and Harlan, 1986)^[1]. Development of short duration varieties in sesame is gaining importance due to their use as catch crop or relay crop. Apart from their wider use, they have several advantages like they require less crop management period, permits multiple cropping system, reduces overall production cost and allows escape from terminal drought. For breaking the present yield barrier and evolving varieties with high yield potential, it is desirable to combine the genes from genetically diverse parents. The success in identifying such parents mainly depends on the gene action that controls the trait under improvement, combining ability and genetic architecture. There are several techniques for evaluating the varieties or cultivars or lines in terms of their combining ability and genetic architecture. Diallel, partial diallel and line × tester techniques are in common use. Among these, Line x Tester analysis technique is more suitable for large number of genotypes for understanding the genetical basis at population level (Kempthorne, 1957)^[3]. An added advantage of this method is that it gives an overall genetic picture of the materials under investigation in a single generation. In a crop like sesame due to epipetalous flower structure there is good scope for exploitation of heterosis. Further, an understanding of the combining ability and gene action is a prerequisite for any successful hybridization programme.

The concept of general and specific combining ability as a measure of gene effects was proposed by Sprague and Tatum (1942)^[7]. The resulting total genetic variance is partitioned into the variances due to general combining ability and specific combining ability. This helps the breeder in knowing the relative proportion of additive and non-additive genetic variances involved in the inheritance of various characters as well as deciding the appropriate breeding methods for effective exploitation of available genetic variation. The presence of non-additive

genetic variance is the primary justification for initiating the hybrid breeding programme (Cockerham, 1961)^[2]. Therefore, the present study was carried out with a view to understand the nature of gene action and combining ability for yield, its attributes and earliness through line x tester analysis in sesame.

Materials and Methods

The experiment was conducted at Cotton Research Station, Junagadh Agricultural University, Junagadh, Gujarat. Nine diverse lines viz., AT-409, AT-464, AT-468, AT-470, AT-471, AT-472, AT-480, AT-482, AT-483 and five testers viz., GT-2, GT-3, GT-4, GT-5 and GT-6 were crossed in a line \times tester mating design during summer 2019 to produce 45 hybrids. The resulting 45 hybrids along with 14 parents and a check variety, GT-6 were evaluated during Kharif 2019 in a Randomized Block Design with three replications. Each entry was accommodated in a single row plot of 2 meters length with row to row and plant to plant distances of 45 cm and 10 cm, respectively. All need based agronomic practices were followed during the crop growth period to raise a good crop. Observations were recorded on randomly selected five plants in each entry for 12 quantitative traits viz., days to 50% flowering, days to maturity, plant height (cm), height to first capsule (cm), number of branches per plant, length of capsule (cm), number of capsules per leaf axil, number of capsules per plant, number of seeds per capsule, 1000-seed weight (g), seed yield per plant (g) and oil content (%) for each replication. The mean values were used for the analysis of variance for experimental design. The days to 50% flowering and days to maturity were recorded on plot basis. The oil content was analysed by using Nuclear Resonance Spectrophotometer as suggested by Tiwari et al. (1974)^[8]. The analysis of variance for combining ability for all 12 characters was carried-out as suggested by Kempthorne (1957)^[3].

Results and Discussion

The partitioning of variances due to the crosses (Table 1) showed that the mean squares due to lines were found significant for all the characters except for number of branches per plant and oil content, whereas mean squares due to testers and lines x testers were found significant for all the characters except for the plant height and number of branches per plant. Mean squares due to lines was found significant when tested against the interaction variance for days to maturity, height to first capsule and number of capsules per leaf axil, while mean squares due to testers was found significant when tested against the interaction variance for days to maturity and height to first capsule. These results indicated that both additive and non-additive genetic variances played a vital role in the inheritance of all the traits under investigation.

The estimated variances due to lines ($\sigma^2 l$) were higher than the corresponding variances due to testers ($\sigma^2 t$) for days to maturity, plant height, height to first capsule, number of branches per plant, length of capsule, number of capsules per leaf axil, number of capsules per plant, number of seeds per capsule and seed yield per plant indicating more diversity among the lines for these characters recorded. For days to 50% flowering and oil content, the variances due to testers ($\sigma^2 t$) were higher than those due to lines ($\sigma^2 l$). The estimates of $\sigma^2 GCA$ were higher than the corresponding $\sigma^2 SCA$ for plant height and height to first capsule. The ratio of $\sigma^2 GCA/\sigma^2 SCA$ was more than unity for plant height and height to first capsule thereby suggesting the presence of additive gene action for the control of these characters. The predominance of additive gene action for plant height and height to first capsule has also been reported by Walter et al. (2016)^[10], Mungala et al. (2017)^[4] and Virani et al. (2018) ^[9]. For days to 50% flowering, days to maturity, number of branches per plant, length of capsule, number of capsules per leaf axil, number of capsules per plant, number of seeds per capsule, 1000-seed weight, seed yield per plant and oil content the sca variance was higher than gca variance which indicated greater role of non-additive gene action in the control of these characters. This was also confirmed by ratio of $\sigma^2 GCA / \sigma^2 SCA$ which is less than unity for these characters. The findings of the present investigation for seed yield per plant and its attributing traits are in close conformity with the findings of Priya et al., 2016 [5]; Saxena and Bisen, 2017^[6] and Virani et al., 2018^[9].

An overall appraisal of gca effects (Table 2) indicated that none of the parents was good general combiner for all the characters studied. Among the parents, two lines viz., AT-472 and AT-483 and three testers viz., GT-2, GT-3 and GT-6 exhibited good general combining ability effect for seed yield per plant. However, among lines, AT-470 was found to be good general combiner for five different characters viz., days to 50% flowering, days to maturity, number of branches per plant, number of capsules per leaf axil and number of seeds per capsule, the line AT-472 showed desired gca effect for four characters viz., plant height, number of capsules per plant, number of seeds per capsule and seed yield per plant. AT-483 had desired gca effects for height to first capsule, number of capsules per leaf axil, number of capsules per plant and seed yield per plant. Among testers, GT-3 had given desired gca effects for six different characters viz., days to 50% flowering, days to maturity, number of capsules per leaf axil, number of seeds per capsules, 1000-seed weight and seed yield per plant. Tester GT-2 had given desired gca effects for height to first capsule, length of capsule, number of capsules per plant and seed yield per plant. While the GT-6 had given desired gca effects for four character viz., days to 50% flowering, number of capsules per plant, number of seeds per capsule and seed yield per plant. The parents which are good general combiners simultaneously for more number of characters are considered as the potential parents and should be preferred in breeding programme in order to combine more number of characters by involving fewer numbers of parents in a crossing programme.

The study also indicated that the parents showing good general combining ability had high *per se* performance for almost all the traits studied. This suggested that while selecting parents for hybridization programme in sesame, *per se* performance of the parents may be given due consideration. High general combining ability effects mostly contribute either additive gene effects or additive x additive interaction effect or both and represent fixable portion of genetic variation. Accordingly, AT-470, AT-472, AT-483 and GT-3 offered the best possibilities of exploitation in breeding programmes as these parents upon crossing, are expected to give desirable segregants in the succeeding generations. Further, the lines showing good general combining ability for particular components may be utilized in component breeding programme for improving specific trait of interest.

The sca effect of the crosses indicated that twelve hybrids manifested significant and positive sca effect for seed yield per plant. Among these, the best three specific combiners were AT-471 \times GT-2, AT-464 \times GT-4 and AT-472 \times GT-3

which positive and significant sca effect for seed yield per plant as well as yield contributing characters (Table 3). A contribution of good general combiners was not necessarily the best cross combination nor a poor x poor cross was always a poor combination. In facts, in most of the cross combinations, the best specific combinations for different characters were either good x good, good x average, poor x poor and *vice versa* general combiners. This suggested that information on gca effect should be supplemented by sca effect and hybrid performance of cross combinations to

predict the transgressive type possibly made available in segregating generations.

It can be concluded that both additive and non-additive genetic effects as well as components were found for seed yield per plant and its contributing traits. The additive component of variance can be exploited by simple selection. However, the presence of non-additive component *viz.*, additive x dominance and dominance x dominance types of interaction suggests the use of breeding methodologies such as heterosis breeding or biparental mating followed by few cycles of recurrent selection.

Table 1: Analysis of varian	ce for combining ability fo	or seed yield and its contributin	g characters in sesame
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Common	df		Mean squares											
Source		DFF	DM	PH	HFC	NBP	LOC	NCLA	NCP	NSC	TSW	SYP	OC	
Line (L)	8	36.67**	99.56 **+	714.59**	472.89**++	0.19	0.21**	2.67**++	636.58**	202.96**	0.12*	30.77**	44.19	
Tester (T)	4	68.65**	132.62**+	189.97	334.02**++	0.02	0.09**	0.52**	305.26**	131.02**	0.17*	29.15**	194.46**	
$\begin{array}{c} Line \times Tester \\ (L \times T) \end{array}$	32	36.59**	42.89**	123.52	58.31*	0.17	0.13**	0.84**	419.72**	92.29**	0.21**	24.30**	189.71**	
Error	88	2.18	9.21	85.56	36.69	0.11	0.02	0.05	34.11	16.87	0.05	1.58	28.78	
				Esti	mates of gene	tic co	mponen	ts of varia	nce					
$\sigma^2 l$		2.30	6.02	41.94	29.08	0.01	0.01	0.17	40.16	12.41	0.01	1.95	1.03	
$\sigma^2 t$		2.46	4.57	3.87	11.01	0.01	0.01	0.02	10.04	4.23	0.01	1.02	6.14	
$\sigma^2 lt (\sigma^2 sca)$		11.50	11.23	12.65	7.21	0.02	0.03	0.27	128.53	25.14	0.05	7.57	53.65	
σ^2 gca		2.40	5.09	17.46	17.47	0.01	0.01	0.07	20.80	7.15	0.01	1.35	4.31	
σ^2 gca/ σ^2 sca		0.21	0.45	1.38	2.42	0.01	0.33	0.26	0.16	0.28	0.01	0.18	0.08	

* and ** significant at 5% and 1% levels when tested against error mean squares, respectively +, ++ Significant at 5% and 1% levels when tested against line × tester interactions mean squares, respectively

DFF :	Days to 50% flowering	DM :	Days to maturity	PH	Plant height
HFC :	Height to first capsule	NBP :	Number of branches per plant	LOC	: Length of capsule
NCLA :	Number of capsules per leaf axil	NCP	Number of capsules per plant	NSC	: Number of seeds per capsule
HSW :	1000-seed weight	SYP	Seed yield per plant	OC	: Oil content

Table 2: General combining ability (gca) effects for lines and testers for seed yield and its contributing characters in sesame

Sr. no.	Sources	DFF	DM	PH	HFC	NBP	LOC	NCLA	NCP	NSC	TSW	SYP	OC
	Lines												
1	AT-409	2.793 **	-3.719 **	-1.837	-3.283*	0.106	-0.137**	-0.323**	-7.387 **	-4.990 **	-0.062	-2.196 **	0.494
2	AT-464	-0.007	1.281	6.496 **	1.104	-0.081	-0.041	-0.003	-5.187 **	-2.517 *	-0.137 *	-1.726 **	-1.036
3	AT-468	-0.741	-2.852 **	12.163 **	9.490**	0.006	0.175**	0.384**	-1.693	0.290	-0.003	0.095	1.573
4	AT-470	-2.341**	-1.719 *	-0.837	3.210*	0.219*	-0.171**	0.170**	-2.220	3.236 **	0.073	0.286	1.624
5	AT-471	0.926 *	0.548	-5.237	6.144**	-0.041	-0.051	-0.830**	0.873	-2.350 *	0.088	0.114	-3.074*
6	AT-472	1.526 **	2.081 **	6.963 **	-1.390	0.059	-0.033	-0.363**	6.940 **	7.450**	-0.021	2.744 **	-2.055
7	AT-480	-0.074	1.081	-6.837 **	-4.296**	-0.161	0.129**	0.237**	-7.680 **	1.343	0.133 *	-0.472	0.191
8	AT-482	-1.474 *	4.415 **	-7.037 **	-2.216	-0.061	0.105*	0.357**	6.100 **	-0.684	-0.095	0.368	1.784
9	AT-483	-0.607	-1.119	-3.837	-8.763**	-0.047	0.023	0.370**	10.253 **	-1.777	0.024	0.786 *	0.500
SE	. (gj)	0.381	0.784	2.388	1.564	0.084	0.043	0.055	1.508	1.060	0.058	0.325	1.385
	g _i -g _j)	0.539	1.108	3.378	2.212	0.119	0.061	0.078	2.133	1.500	0.082	0.460	1.959
						Г	esters						
1	GT-2	2.074 **	-0.526	-0.800	-1.967*	0.003	0.082**	-0.163**	2.153 *	0.789	-0.025	0.515 **	-2.560**
2	GT-3	-2.037 **	-1.526 **	0.756	-1.286	-0.019	-0.010	0.163**	1.264	2.204 **	0.125 **	0.956 **	0.477
3	GT-4	0.037	-2.119 **	-2.652	-2.479**	0.010	-0.066**	0.074*	-4.880 **	-2.733 **	-0.032	-1.181 **	3.283**
4	GT-5	0.889 **	3.474 **	4.200 **	6.136**	0.036	-0.040	0.052	-1.924 *	-1.922 **	-0.087	-1.068 **	1.694*
5	GT-6	-0.963 **	0.696	-1.504	-0.404	-0.030	0.035	-0.126**	3.387 **	1.663 **	0.018	0.778 **	-2.894**
SE	. (gj)	0.284	0.584	1.780	1.166	0.063	0.032	0.041	1.124	0.790	0.043	0.242	1.032
SE (g _i -g _j)	0.402	0.826	2.518	1.649	0.088	0.045	0.058	1.590	1.118	0.061	0.343	1.460

* and ** significant at 5% and 1% levels of probability, respectively

DFF :	Days to 50% flowering	DM	Days to maturity	PH :	Plant height
HFC :	Height to first capsule	NBP	: Number of branches per plant	LOC :	Length of capsule
NCLA :	Number of capsules per leaf axil	NCP	: Number of capsules per plant	NSC :	Number of seeds per capsule
TSW :	1000-seed weight	SYP	: Seed yield per plant	OC :	Oil content

Table 3: Specific combining ability effects for various characters of best selected crosses on the basis of seed yield per plant

Hybrids						
AT-471 × GT-2	AT-464 × GT-4	AT-472 × GT-3				
6.259**	-1.770*	-2.230*				
-2.474	-4.948**	-6.007**				
16.860**	32.853**	9.616**				
11.363**	8.560**	-0.059				
0.318*	0.556**	0.354**				
6.823**	6.806**	2.537**				
16.444**	7.693*	11.217**				
	6.259** -2.474 16.860** 11.363** 0.318* 6.823**	$\begin{array}{ c c c c c c c c } \hline \textbf{AT-471} \times \textbf{GT-2} & \textbf{AT-464} \times \textbf{GT-4} \\ \hline & 6.259^{**} & -1.770^{*} \\ \hline & -2.474 & -4.948^{**} \\ \hline & 16.860^{**} & 32.853^{**} \\ \hline & 11.363^{**} & 8.560^{**} \\ \hline & 0.318^{*} & 0.556^{**} \\ \hline & 6.823^{**} & 6.806^{**} \\ \hline \end{array}$				

* and ** significant at 5% and 1% levels of probability, respectively

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