



Line x Tester analysis for Yield and yield contributing traits in sesame (*Sesamum indicum* L.)

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ABSTRACT

The present investigation was undertaken with the objective to assess the combining ability in 21 hybrids obtained by crossing three lines and seven testers in line x tester fashion with their 10 parents and two standard checks (Phule Til-1, JLT-7) replicated twice in randomized block design. Data were recorded on various quantitative characters which contribute to yield and earliness. Analysis of variance for mean revealed significant differences for all ten characters under investigation whereas mean squares due to parents vs. hybrids interaction also significant indicating high amount of variability in parents and hybrids. The line BSG-5, proved to be good general combiner for character viz, plant height , number of capsule per plant , 1000 seed weight and seed yield per plant. While BSG-9 for earlier characters viz. days to 50 percent flowering and days to maturity. These two parents could be utilized in the breeding programme for the further improvement of the specific traits. Combining ability studies indicated the preponderance of non-additive gene action for all the characters except days to maturity and oil content. These are close agreement between per se performance and GCA as well as SCA effects for most of the characters. The best crosses based on heterosis, SCA effect are per se performance were BSG-5 x LT-8, BSG -5 x LT-5 , BSG -5 x IC -413221, BSG-5 x IC-413201 these may be used for further exploitation in breeding programme.

Key words: Line x Tester, Yield, GCA.

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INTRODUCTION

Sesame (*Sesamum indicum* L.) is commonly known as *gingelly*, *til*, *benniseed*, *simsim*. It is called as the "Queen of oil seeds" because of its excellent qualities of the seed, oil and meal. Sesame is a self-pollinated crop, member of the order Tubiflorae and family Pedaliaceae with having ($2n = 26$) chromosome number. 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. India holds a premier position in the global oilseeds scenario accounting for 29 per cent of the total area and 26 per cent of production. The average productivity is very low as compare to other sesame growing countries and almost stagnant during last few years. In India, sesame is cultivated in 19.53 lakh hectare with a production of 8.32 lakh tones and productivity of 426 kg /ha [1]. Development of short duration varieties in sesame is gaining importance due to their use as rice fallow crop, 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 upon that control the trait under improvement, combining ability and genetic makeup. As studies intended to determine the combining ability not only provide necessary information regarding the choice of parents but also illustrate the nature and magnitude of gene action involved. 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 X 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 [7]. 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. Therefore, the present investigation was undertaken on combining ability for seed yield and its components in sesame with a view to identify good general combiners and specific cross combinations which may be used to create a population with favourable genes for seed yield and its component characters of some newly developed crosses through line x tester analysis in sesame.

MATERIAL AND METHODS

The current research work was investigated at the College of Agriculture, Latur, Vasant Rao Naik Marathwada Krishi Vidyapeeth, Parabhani. Ten genetically diverse sesame genotypes comprised of three lines viz., BSG-1, BSG-5, BSG-9 and seven testers viz., IC-413397, IC-413201, IC-413204, IC-413221, LT-4, LT-5, LT-8 were crossed during *rabi* 2013 in line x tester fashion by using hand emasculation and pollination as described by [19]. The resulting 21 F₁ hybrids along with their parents and two checks (Phule Til-1, JLT-7) were raised in randomized block design along with two replications. Each treatment comprised of two rows of 3 m length, row spaced at 45 cm apart, with plant to plant distance of 20 cm. One plant per hill was maintained by thinning 15 days after sowing. The recommended fertilizer doses 30 kg N + 60 kg P₂O₅ + 30 kg K₂O per hectare was applied at the time of sowing and other cultural operations were followed as per schedule so as to maintain the healthy stand of the crop. Observations were recorded on five randomly selected plants for all the characters viz., days to 50 per cent flowering, days to maturity, plant height (cm), number of branches per plant, number of capsules per plant, number of seed per capsule (gm), length of capsule (cm), 1000 seed weight (g), oil content (%), seed yield per plant (kg/ha). The combining ability analysis was done following standard procedure of [7].

RESULT AND DISCUSSION

The analysis of variance revealed that, all the characters had significant treatments variances indicating the presence of considerable amount of variability in the experiment material used in the present study. The analysis of variance due to crosses, lines, testers and line x tester were significant for plant height, number of capsules per plant and oil content for lines and all the characters except days to 50% flowering, number of primary branches per plant, 1000 seed weight and oil content for testers and variances due to line x tester were significant to oil content. The significant variance due to lines, testers and line x tester showed the involvement of non-additive gene action in controlling the traits except days to maturity and oil content. However all these characters except days to maturity/oil content appeared to be controlled predominantly by non-additive gene action as judge from high SCA variance compared to GCA variance. For days to maturity/oil content, the estimate of GCA was higher than SCA indicating the predominance of additive gene action for this trait. Governing of such characters non additive gene action was reported earlier by [17] [9] and [14]. A perusal of GCA effects revealed that among the lines, BSG-1 (0.038) was good general combiner for number of capsule per plant and BSG-5 also exhibited desirable and significant gca for plant height (4.338), number of capsule per plant (12.914), 1000 seed weight (0.231) and seed yield per plant (3.231) significant positive gca effects for seed yield. The female BSG-9 showed desirable high gca effects for days to 50 per cent flowering (-0.619), days to maturity (-0.714), number of branches per plant (0.190) and oil content (0.586) significant positive GCA effects for seed yield. Among the male parents viz., IC-413197 (5.255) showed positive gca effects for plant height. The parent IC-413204 was the best general combiner for plant height (4.888) and 1000 seed weight (0.360). The parent IC-413221 was the best general combiner for number of capsule per plant (4.436) and number of seed per capsule (4.314) also had significant GCA effects. The parent LT-4 was the best general combiner for number of capsule per plant (4.236). The parent LT-5 was the best general combiner for length of capsule (0.058) had significant gca effects. The parent LT-8 was the best general combiner for number of capsule (2.948) and seed yield per plant (1.949) also had significant gca effects. These observations clearly indicate that there appeared to be close relationship between gca and per se performance of most of the characters expressed by parent. In turns it will help as criteria to select the parents for breeding programmes. Similar results on general combining ability were reported previously by [8], Suresh Kumar *et al.*, (2004), [17], [10], [9], [8], [12] and [14]. The performance of F₁s derived from crosses BSG-5 X LT-5, BSG-9 X LT-8 showed better performance for days to 50% flowering. The F₁s derived from BSG-1 x LT-5 showed better performance for days to maturity. The F₁s derived from BSG-9 x LT-8, BSG-9 x IC-413204, BSG-1 x LT-8 for number of capsule per plant. The F₁s derived from BSG-1 x LT-8 for number of capsule per plant and number of seed per capsule, showed highly significant positive sca effects. Similarly crosses BSG-1 x LT-4, BSG-1 x LT-5, BSG-5 x LT-4 and BSG-5 x LT-5 were good specific combiner for seed yield/plant. Similar results were also obtained by [17], [10], [9], [8], [12] and [14]. The estimation of sca effects of 5 crosses showed significant positive effects for seed yield. The cross BSG-5 x

LT-8 had significant desirable sca effects for 2 out 10 characters, number of seed per capsule and seed yield per plant. The cross BSG-5 x LT-5 had desirable sca effects for plant height, number of branches per plant and seed yield per plant. The crosses BSG-5 x IC-413221 for seed yield per plant, BSG-5 x IC-413204 for plant height and seed yield per plant and BSG-5 x IC-413201 had significant desirable sca effects for seed yield per plant.

CONCLUSION

From this study it was noted that, while selecting the potential crosses for future use in breeding programme *per se* performance of parents and hybrids for various attributes must be taken in to consideration in addition to per cent heterosis. Non-additive gene action was found to be important for eight characters except the traits days to maturity and oil content. The ratio of δ^2 gca / δ^2 sca was less than unity for the characters indicating predominance of sca variance and their by non-additive gene action (dominance and epistasis). The character days to maturity and oil content showed additive type gene action. The best 5 crosses *viz.* BSG-5 x LT-8, BSG-5 x LT-5, BSG-5 x IC-413221, BSG-5 x IC-413204, BSG-5 x IC-413201, produced significant and desirable sca effects for most of the traits studied. Among the 5 best hybrid combinations crosses showed the higher magnitude of standard heterosis indicating good potential for their exploitation of hybrid vigour commercially.

Table 1: Variances for General and Specific Combining ability for different characters in sesame.

Sr.No.	Character	δ^2 GCA	δ^2 SCA	δ^2 GCA / δ^2 SCA
1	Days to 50 % flowering	0.593	0.621	0.955
2	Days to maturity	0.704	0.622	1.131
3	Plant height (cm)	4.3907	16.364	0.268
4	Number of branches / plant	0.042	0.066	0.636
5	Number of capsule / plant	6.995	97.663	0.071
6	Number of seed / capsule	0.120	2.850	0.042
7	Length of capsule (cm)	0.0038	0.0052	0.723
8	1000 seed weight (g)	0.063	0.102	0.617
9	Oil content (%)	5.033	0.561	8.91
10	Seed yield / plant (g)	0.681	0.975	0.698

Table 2 Analysis of variance for combining ability of various quantitative characters

Source	D.f	Days to 50% Flowering	Days to maturity	Plant Height (cm)	No. of branches / plant	No. of Capsule / plant	No. of Seed / capsule	Length of capsule (cm)	1000 seed Weight (gm)	Oil content (%)	Seed yield / plant (gm)
Replication	1	7.112	2.322	13.979	0.117	0.258	30.100	0.003	0.041	3.161	0.412
Crosses	20	4.845**	3.507	73.050*	0.361**	241.214*	23.921	0.005**	0.465**	12.688**	21.326**
Tester	2	2.000	6.500	118.652**	0.286	1105.251**	10.106	0.002	0.011	26.086**	16.240**
Line	6	3.404	7.404*	163.6057**	0.233	331.306**	57.356**	0.018**	0.001	4.524	7.541
L x T	12	3.123	1.111	9.987	0.196	9.001	8.556	0.002	0.259	14.761**	3.507
Error	30	1.879	2.355	18.781	0.111	22.992	8.797	0.002	0.131	4.694	2.143

* and ** indicated significance at 5 and 1 % level respectively

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