LINE X TESTER ANALYSIS FOR COMBINING ABILITY IN *GOSSYPIUM HIRSUTUM* COTTON

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ABSTRACT

In a combining ability analysis of 28 F1 hybrids developed in a line x tester method in *Gossypium hirsutum* L., non-additive gene action was predominant for number of sympodia per plant, ginning outturn, uniformity ratio and bundle strength. Additive gene action was predominant for number of bolls per plant, seed cotton yield per plant, lint index and 2.5% span length. Preponderance of both additive and non-additive gene action was observed for boll weight and elongation per cent. The genotypes H16, H22; H8 and H12 proved to be best general combiners for more number of characters. H9xH5, H16xH12 and H19xHL34 exhibited favourable sca effects for more number of characters indicating the possibility of utilising these genotypes for further exploitation.

KEY WORDS : *Gossypium hirsutum*, combining ability

A comprehension on the genetic constitution of the population handled is quintessential for the breeders in a hybridisation programme. Various biometrical methods have been successfully employed to assess the genetic make up of different genotypes for developing suitable breeding methodology. One such method is the line x tester analysis which provides valid information on combining ability effect of the genotypes. Accordingly, the present study was undertaken to estimate the combining ability effects for yield, its components characters and fibre traits in *G. hirsutum* genotypes.

MATERIALS AND METHODS

Eleven genetically diverse *G. hirsutum* genotypes were crossed in a 7x4, line x tester fashion to obtain 28 hybrids. The hybrids were evaluated along with their parents in a randomised block design with four replications at the Cotton Breeding Station, Tamil Nadu Agricultural University, Coimbatore during summer, 1995. Each genotype was raised in a single row of 4.5m with a spacing of 90cm x 45cm. Data were recorded from five plants for number of sympodia/plant (SPP), number of bolls per plant (BPP), boll weight (BW), ginning outturn (GOT), lint index (LI), 2.5% span length, uniformity ratio (UR), bundle strength (BS) and elongation per cent. The data were analysed based on the line x tester model for combining ability effects.

RESULTS AND DISCUSSION

Analysis of variance

The mean of squares for different characters studied (Table 1) showed highly significant differences among the parents and hybrids indicating the presence of sufficient variability in the study material. Significant differences were also observed for parents vs crosses component of variance for all the traits. (Table 1).

The specific combining ability variance (SCA) was higher than the general combining ability variance (GCA) for SPP, GOT, UR and BS indicating the importance of additive gene action in controlling these traits. GCA variance was higher than the SCA variance for BPP, seed cotton yield (SCY) per plant, LI and 2.5% span length indicating the preponderance of additive gene action for these traits. For BW weight and elongation per cent, more or less equal role of additive and non additive gene action was observed. These results are in agreement with the reports of Duhoon *et al.*, (1983), Lather (1985), Amalraj (1989). Geen and Culp (1990) Patel and Badaya (1993) and Lloyd and Green (1994).

gca effects

The gca effects of the parents are presented in Table 2.

Among the seven female lines, H22 and H16 exhibited positive and significant *gca* effects for six

Table 1.   Analysis of variance for combining ability for different characters

Source	dt	Sc. Y/P (g)	N.SY/P	NB/P	BW (g)	GOT (%)	LI (g/ 100 seeds)	2.5% SL (mm)	UR (%)	BS (g/tex)	EP (%)
Replication	3	5.95	4.07	3.54	0.10	3.02	0.30	0.25	2.93	1.76	0.03
Parents	10	970.10**	16.01**	38.26**	1.56**	10.19**	1.22**	7.72**	9.09**	6.64**	1.45**
Crosses	27	1626.54**	23.17**	30.16**	2.51**	27.82**	1.39**	4.13**	8.02**	8.23**	0.84**
Parents Vs Crosses	1	130.62**	709.58**	572.97**	2.36**	162.87**	2.70**	1.06*	47.35**	1.26**	0.68**
Lines	6	3359.76**	36.91**	45.33**	0.96**	19.77*	3.60**	9.26**	9.90**	10.17**	1.78**
Testers	3	2510.15**	9.46	23.07**	13.43**	110.62**	6.12**	5.61**	29.85**	8.51**	1.12**
Line x Texters	18	90.53**	20.87**	6.28**	1.21**	16.71**	0.20	0.84**	3.7**	7.54**	0.06**
Error	81	3.10	5.27	2.27	0.12	1.39	0.16	0.31	0.73	0.47	0.01

* Significant at 5% level ** Significant at 1% level
Sc.Y/P - Seed cotton yield/Plant, N.Sy/P - Number of sympodia/Plant, NB/P - Number of bolls/Plant, BW - Boll weight. GOT - Ginning Outturn.
LI - Lint index, 2.5% SL - 2.5% span length, UR - Uniformity ratio, BS - Bundle strength, EP - Elongation per cent

characters. H22 evinced to be the best general combiners for BPP, BS and elongation per cent. Highest *gca* effect for SCY was displayed by the line H16 (20.78) and it also showed a significant *gca* effects for quantitative characters such as BW, GOT and LI and for quality characters such as UR and elongation per cent.

Among the pollen parents, H8 and H12 were the most promising general combiners exhibiting favourable and significant heterosis for more number of characters studied. Selection of parents for a hybridisation programmes based on significant and favourable *gca* effects for as many traits as possible is more reliable than selecting

parents based on more mean performance (Nadarajan and Sree Rangasamy, 1990). In the present study H8, H12, H16, and H22 showed significant *gca* effects for more numbers of traits. These genotypes could be used in crossing programmes to bring about recombination of genes to develop better genotypes.

sca effects

Positive and significant *sca* effect was exhibited for SCY by 11 hybrids (Table 3). Among them, the hybrids, H13xHL34, H16xH8, H16xH12. and H22xHL34 had both their parents possessing significant general combining ability for this trait. These crosses may be exploited by adopting

Table 2.   *gca* effects of parents of intra-*hirsutum* hybrids

Particulars		Sc.Y/P (g)	N.SY/P	NB/P	BW (g)	GOT (%)	LI (g 100 seeds)	2.5% SL (mm)	UR (%)	BS (g/tex)	EP (%)
Lines	H9	-18.31**	2.11**	-1.79**	-0.29**	-0.71**	-0.26**	-0.25**	0.82**	-0.34**	0.14**
	H10	-7.04**	1.61**	-1.25**	-0.35**	-0.73**	-0.25**	-0.90**	-0.93**	-0.27*	-0.25**
	H11	-8.02**	-1.64**	-0.38**	0.18**	-0.46**	-0.29**	-0.66**	0.68**	0.01	-0.38**
	H13	16.02**	-1.58**	1.24**	0.04	0.39	0.33**	0.27**	-0.43**	-0.75**	0.11**
	H16	20.78**	-1.08**	0.43	-0.06	2.25**	0.45**	-0.28**	0.82**	-0.35**	0.13**
	H19	-9.35**	0.67	-0.26	0.21**	-0.94**	0.03	-0.13	0.82**	0.84**	0.16**
	H22	5.91**	-0.08	2.01**	0.26**	0.20	0.10	1.14**	-0.43**	0.5**	0.08**
Testers											
	H5	-13.75**	-0.26	0.53	-0.45**	-2.78**	-0.45**	-0.03	0.89**	-0.17	-0.17**
	H8	2.36**	0.13	-0.86*	-0.21*	1.35**	0.48**	-0.49**	0.89**	-0.19	0.11**
	H12	3.52**	-0.62**	0.66	0.03**	1.52**	-1.00**	0.16	-0.82**	-0.28	0.17**
	HL34	7.87**	0.74	-0.34	-0.37**	-0.09	0.07	0.35**	-0.96**	0.64**	-0.14**

* Significant at 5% level ** Significant at 1% level
Sc.Y/P - Seed cotton yield/Plant, N.Sy/P - Number of sympodia/Plant, NB/P - Number of bolls/Plant, BW - Boll weight. GOT - Ginning outturn.
LI - Lint index, 2.5% SL - 2.5% span length, UR - Uniformity ratio, BS - Bundle strength, EP - Elongation per cent

Table 3. *sca* effects of crosses for different traits

Particulars	Sc.Y/P (g)	N.SY/P	NB/P	BW (g)	GOT (%)	LI (g/ 100 seeds)	2.5% SL (mm)	UR (%)	BS (g/tex)	EP (%)
H8xB12	24.54**	0.30	-0.51	0.56**	-3.54**	-1.05**	-1.23**	-0.11	-2.57**	-0.20
H9xB10	21.91**	-0.74	-0.04	0.23	-0.88	-0.35	0.53**	0.01	0.20	-0.13
H10xB1	37.11**	-3.16**	3.97**	-0.23	3.80**	0.80**	-4.48**	1.43**	-1.70**	0.06
H10xBT1	3.19**	1.59**	2.99**	0.52**	-3.03**	0.54**	1.06**	-0.43	0.44	-0.48
H11xBT1	25.05**	3.49**	4.63**	0.06	1.17	0.71**	0.78**	-1.23**	2.10**	-0.63**
H11xBT2	2.95**	-1.48**	-6.08**	0.13	3.93**	0.72**	-0.39**	-2.09**	-1.97**	-1.02**
H12xBT1	19.04**	-1.86**	-5.45**	-0.29**	2.69**	0.94**	-0.61**	1.97**	-0.82**	0.38
H12xBT2	23.97**	2.17**	2.45**	0.04	-3.46**	-0.04	-0.63**	-1.89**	-2.19**	-0.06
H13xB1	28.41**	-0.06	-7.26**	0.18	5.55**	0.64**	1.57**	-0.97*	2.69**	-0.03
H13xBT2	8.78**	0.72	5.82**	-0.22	-2.55*	-0.14	0.26*	1.31**	0.26	-0.18
H16xB1	3.75**	-0.41	2.86**	-0.35**	-4.95**	-0.95**	0.75**	0.37	0.94**	-0.18
H16xBT2	12.01**	3.87**	2.28**	0.19	1.53*	-0.04	0.98**	0.91*	4.01**	-0.08

pedigree breeding or applying selection for enhancing the yield. The crosses, H13xH8 and H22xH8 showed a nonsignificant *sca* though both parents involved in these crosses were good general combiners for seed cotton yield. Few other hybrids such as H9xH5, H11xH5 and H19x45 possessed significant and high *sca* effects but the parents involved in these crosses were poor general combiners. The absence of relationship between the *gca* effects of the parents and the *sca* effects of the crosses, indicated the influence of epistatic genes in controlling the complex character, SCY.

Among the eleven crosses which exhibited positive and significant *sca* for SCY (Table 3). H9xH5 and H16xH12 proved to be superior cross combinations possessing significant and positive *sca* for most of the characters under study. The cross H9xH5 could be exploited for simultaneous improvement of BPP, BW, GOT and LI. It is a rewarding feature to notice that there is a possibility fo simultaneous improvement of yield and fibre traits as exhibited by the positive *sca* effects of H16xH12 for SPP, BPP of 2.5% span length, BS and elongation per cent. None of the crosses identified with high *sca* for SCY showed high *sca* for uniformity ratio.

The study revealed that utmost care is essential while selecting suitable parents for any breeding programme. Not all good general combining parents could produce high specific combining crosses. Crosses possessing high *sca* for yield and yield component traits possesed a negative and non-significant *sca* for fibre traits as evidenced in H13xHL34 and H9xH5 indicating the complexity in simultaneous improvement of yield and fibre characters. Future research should, therefore, focus us on these aspects for exploitation of more number of desirable traits in the same breeding programme

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