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Estimating combining ability through Line × Tester analysis in upland cotton

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Abstract: Combining ability of the parents was estimated by using line x tester analysis to determine the ability of parents to combine their favourable alleles/ genes during the process of hybridization and transfer those to their progenies. Two types of combining abilities *viz.,* general combining ability (GCA) which is due to additive genes whereas specific combining ability (SCA) is due to dominant and epistatic gene effects were estimated. Twenty seven parents (22 lines and five testers) along with their 110 F_1 hybrids were studied in lattice square design (LSD) with two replications during 2014-15 at ARS Hebballi, University of Agricultural Sciences, Dharwad. The important yield contributing traits *viz.,* number of bolls per plant, boll weight (g), seed cotton yield (q ha^{-1}), ginning outturn percentage and seed index (g) were studied. The results indicated that GCA variances due to lines and testers and SCA variances due to lines x testers interaction were significant for all the characters studied. However, the magnitude of GCA from lines (females) and testers (pollinators) were lesser than the SCA indicating pre dominance of non-additive genes in the expression of all the traits except boll weight. Nonetheless, among the lines, DHS 10-4, MCU 8 and TCH 1457 whereas in testers, DHS T2 and DHS T3 by manifesting maximum GCA effects were regarded as the best general combiners for almost all the traits suggesting the presence of more additive genes in these parents, hence may serve as potential parents to be considered for hybridization and selection programmes to improve the characters studied. Among the F_1 hybrids, DHS 10-4 x DHST1, TCH 1457 x DHS T3 and IC 3584 x DHS T3 were found as the best specific combiners for seed cotton yield. Therefore, these hybrids may be preferred for hybrid crop development.

Key Words: Combining ability, Line × Tester analysis, *Gossypium hirsutum* L.

Introduction

Cotton, the king of fibre is one of the momentous and an important cash crop exercising profound influence on economic and social affairs of the world. Any other fibre crop cannot compare with cotton for its fibre quality. It is also called as "White Gold". In India, cotton is grown in 126.35 lakh ha with a productivity of 537 kg ha^{-1} (AICCIP, 2015). Development of hybrids as a commercial variety is getting importance. Cotton is highly amenable for both heterosis and recombination breeding (Kaliyperumal *et al*., 2013). Heterosis has substantially remained as one of the significant developments in cotton breeding programs (Ranganatha et al., 2013; Choudhary *et al.*, 2014). Hybridization is the most potent technique for breaking yield barriers. Selection of parents on the basis of phenotypic performance alone is not a sound procedure, parents should be chosen on the basis of their combining ability and gene action. The concept of combing ability has been proposed by Sprague and Tautum (1942). It plays a significant role in crop improvement because it helps the breeder to determine the nature and magnitude of gene action involved in the inheritance traits. Combining ability is useful in selection of desirable parents for exploitation of hybrids and transgressive expressions and also to assess the ability of parents to generate potential hybrids with a reasonable level of stability (Ashokkumar and Ravikesavan, 2008; Mehmet Coban and Aydýn Unay, 2015).

The line x tester analysis is one of the important biometrical techniques which provides valuable information about general and specific combining ability variances and effects and thus helps in identification of good general combiners and specific promising cross combinations (Muthuswamy *et al.*, 2003). This helps in detection of appropriate parents and crosses superior in terms of the investigated characters so application of the analysis has been widely used by plant breeders to selection in early generations (Pathak and Kumar, 1975; Kaushik *et al.*, 1984; Jagtap, 1986; El-Feki *et al.*, 1995, Bhardwaj and Kapoor, 1998; Ganapathy *et al.*, 2005; Ahuja and Dhayal, 2007). In this direction, Madhuri Sawarkar (2015), Patil *et al.* (2012) and Patel *et al.* (2012) reported the presence of significant differences among males and females for days to 50 % flowering, days to 50 % boll bursting, number of sympodia per plant, number of bolls per plant, boll weight, seed cotton yield per plant and seed index and fibre strength. Karademir and Gencer (2010) reported additive gene action for ginning percentage and non-additive gene action for seed cotton yield and uniformity ratio, Saravanan et al. (2010) reported non-additive gene action for all fiber quality traits and Karademir *et al.* (2009) reported non-additive gene action for seed cotton yield, uniformity ratio and ginning percentage.

In view of the importance of knowing the combining ability of the parents, thereby determining the types of gene action involved in the expression of various plant characters in cotton, the line x tester analysis was carried-out to decide for efficient breeding strategies to improve the valuable characters.

Materials and Methods

A trial was conducted at ARS Hebballi, University of Agricultural Sciences, Dharwad, India during 2014-15, to estimate the GCA and SCA of inbred parents through line x tester analysis. The experimental material consisted of F_1 crosses and their parents of upland cotton. The seed was sown in a Lattice square design (LSD) with two replications. There were 27 parents, out of which 22 were used as lines/females and five as testers/pollinators. From these parents, 110 F_1 hybrids were developed and to make it perfect square seven checks were used. Thus a total of 144 genotype were evaluated for important yield contributing traits *viz.,* number of bolls per pant, boll weight (g), seed cotton yield (q ha^{-1}), ginning outturn% (G.O.T. %) and seed index. For recording the observations, five plants from each genotype per replication were randomly tagged. The distance between plant to plant was kept at 40 cm whereas row to row distance was 90 cm. All the recommended agronomic and cultural practices were carried-out properly. At crop maturity, the data for different characters were recorded and the analysis of variance to determine the differences among the genotypes (Parents and F1's) was carried out according to Gomez and Gomez (1984). The variation among the hybrids was partitioned further into sources attributed to general combining ability (gca) and specific combining ability (sca) components in accordance with the procedure suggested by Kempthorne (1957). The mean squares of line x tester design and GCA and SCA effects were calculated by following the statistical procedures as adopted by Singh and Choudhry (1979).

Results and Discussion

For the improvement of any character, plant breeders heavily rely on the availability of genetic variability that could be acquired from different mating designs. Cotton breeders are also well aware of the phenomenon that in hybridization programme certain crosses pass–on more favourable genes in the progeny than the others. Thus, some cross combinations may provide transgressive segregants to improve economic traits in cotton breeding. The present research therefore was designed to estimate the GCA, SCA variances and their effects for different quantitative traits in a set of line x tester crosses. The results obtained are discussed character-wise as under.

Bolls per plant: In cotton plant, as the number of bolls per plant is increased, the yield is correspondingly increased. Thus, there is a close and positive association between these parameters. The analysis of variance (Table-1) revealed significant differences among the genotypes. On an average, maximum number of bolls per plant (41) were set by the cross DHS 10-4 x DHS T1 and MCU 8 x DHS T3 followed by IC 3584 x DHS T3(37.50) as *per se* hybrid performance. Among the parental lines, IC 3584 set highest bolls per plant (24.60) whereas in testers, DHS T2 gave maximum (20.50) bolls per plant (Table-2). The variances due to GCA and SCA were highly significant suggesting that additive and non-additive types of gene actions were involved in the expression of this trait. Line DHS 10-4 gave maximum (8.15) GCA effects whereas among the testers, DHS T3 manifested maximum (1.22) GCA effects (Table III) indicating that both the parents retain more additive genes, thus may be utilized in hybridization programmes for the improved number of bolls per plant in segregating population. The results further revealed that cross MCU 8 X DHS T3 which gave maximum SCA effect of 20.38 may be suitable crosses for hybrid crop development. General predictability ratio indicate the importance of non-additive variance rather than additive variance. Neelima (2002), Subramanian *et al.* (2005), Mohammad Ilyas *et al.* (2007), Wankhade *et al.* (2008), Kumboh *et al.*(2008), Deosarkar *et al.* (2009b), Naqib Ullah *et al.* (2009), Mohammad Reza *et al.*(2010), Imran *et al.* (2012) reported the importance of SCA variance in the inheritance of this trait.

Boll weight (g): In cotton, boll weight and boll number in interspecific and intraspecific hybrids are reported as major components of heterosis in yield (Pavasia *et al.,* 1999b). The higher boll weight observed in the parents DHS 10-6 and DHS 10-14 (4.25g). Among the crosses, the higher boll weight was observed in cross IS 1456x DHS T4 (4.88g).Regarding GCA effects, line MCU 8 and tester DHS T3 revealed maximum effects of 0.62 and 0.19, respectively (Table-3). These higher GCA scoring parents may be suitable for crossing and selection programmes. Among the crosses, IS 1456 x DHS T4 manifested highest (0.68). The crosses showing higher SCA effects may be considered for hybrid crop development. Analysis of variance reveals that magnitude of gca variance was higher than sca variance indicating additive gene action is governing the inheritance of the trait. Present findings are also in consonance with those of Jagtap and Mehetre (1998), Deshpande *et al.* (2004),

Table-1: Analysis of variance for combining ability involving intra *hirsutum* crosses

SV	df	DF	DBO	PH	NM	NS	BPP	BW	SCY	SI	GOT	LI
Replicates	1	8.800 *	122.255 *	85.152	0.001	0.198	6.016 *	0.284	0.064	3.490	0.110	0.002
Crosses	109	83.777 **	109.146 **	327.581 **	0.474 **	4.693 **	67.274 **	0.419 **	46.056 **	5.610 **	12.045 **	1.326 **
Line effect	21	148.149 **	89.530	901.129 **	0.725 *	8.659 **	110.143 *	0.957 **	63.030	3.693	12.105 *	1.199
Tester effect	4	694.307 **	660.618 **	723.373 *	0.337	11.616 *	34.255	2.013 **	42.716	67.441 **	137.413 **	1.560
Line x tester effect	84	38.612 **	87.790 **	165.347 **	0.418 **	3.372 *	58.129 **	0.208	41.972 **	3.145 **	6.060 *	1.347 **
Error	109	1.699	21.117	35.054	0.022	1.918	0.749	0.161	15.498	0.198	4.225	0.111
σ^2gca	14.14	10.64	23.95	0.004	0.25	0.31	0.04	0.40	1.20	2.54	0.001	
σ^2sca	18.46	34.91	66.25	0.19	0.73	7.50	0.03	14.08	1.48	1.22	0.62	
σ^2gca / σ2sca	0.77	0.30	0.36	0.02	0.34	0.04	1.60	0.02	0.81	2.08	0.01	

*, ** significant at 5% and 1% levels, respectively; DF-Days to 50% flowering; DBO-Days to boll opening; BW-Boll weight; PH-Plant height; NS-Number of sympodia; NM-Number of monopodia; BPP-Bolls per plant; SI-Seed index; GOT-Ginning outturn; LI – Lint index

Table-2: *Per se* performance of parental lines

Lines	BPP	BW (g)	SCY (q ha^{-1})	GOT	SI (%)
IC-3584	24.60	3.10	17.86	35.04	11.96
DHS 10-1	21.00	3.83	19.46	36.49	9.80
DHS 10-4	20.90	3.78	16.53	32.05	9.14
DHS 10-5	21.60	3.65	19.40	40.00	10.32
DHS 10-6	23.60	4.25	22.03	36.82	12.37
DHS 10-7	24.20	3.50	22.49	37.26	8.39
DHS 10-8	22.30	3.33	17.53	37.05	10.83
IC-3571	16.90	2.40	17.60	36.05	9.56
IC-3585	15.15	3.45	21.67	38.32	11.25
AKH 0303	17.60	3.35	21.15	37.45	10.51
AKH 032	22.90	3.58	19.20	33.23	10.09
TCH 1342	18.50	3.80	19.47	34.95	9.65
MCU 6	16.70	3.63	13.55	36.79	10.52
MCU8	15.80	3.85	16.25	35.86	11.17
TCH 1678	15.70	3.63	17.98	32.45	10.84
IS-1456	16.00	3.88	20.04	37.08	10.41
TCH 1458	22.60	3.20	14.75	34.40	10.81
TCH 1457	16.60	3.70	20.82	32.84	11.29
DHS 10-14	17.65	4.05	17.62	36.92	10.85
DHS 10 -17	19.30	2.98	17.01	32.21	10.77
GISV-217	17.60	3.58	19.13	32.50	9.82
DHS 10-18	19.00	3.30	10.47	33.75	10.24
Mean	19.68	3.54	18.27	35.52	10.48
Minimum	15.15	2.40	10.47	32.05	8.39
Maximum	24.6	4.25	22.49	40.00	12.37
Tester					
DHS T1	15.20	3.20	18.77	32.41	10.79
DHS T2	20.50	3.53	18.26	35.65	10.71
DHS T3	17.55	3.68	18.13	36.61	10.51
DHS T4	16.55	3.13	17.78	34.15	11.42
DHS T5	15.00	2.15	16.88	32.00	10.95
Mean	20.5	3.14	17.96	34.16	10.88
Minimum	17.75	2.15	16.88	32.00	10.51
Maximum	15.00	3.68	18.77	36.61	11.42

Table-3: General combining ability effects of parental lines

Lines	BPP	BW (g)	SCY (q ha^{-1})	SI (g)	GOT
IC-3584	4.22**	0.27*	1.13	0.20	-0.04
DHS 10-1	2.37**	-0.01	-1.76	0.84**	1.07
DHS 10-4	8.15**	0.05	5.17**	0.076	-0.35
DHS 10-5	2.82**	-0.19	-1.71	-0.207	-0.33
DHS 10-6	3.46**	0.06	2.74*	0.17	-0.20
DHS 10-7	3.52**	0.14	3.04 *	1.23**	0.38
DHS 10-8	-1.28**	0.19	-0.45	-0.46**	-1.28*
IC-3571	1.66**	0.46**	4.60**	0.37**	0.86
IC-3585	-3.53**	-0.02	-1.14	-0.24	-0.04
AKH 0303	-1.22**	-0.20	-0.73	-0.40**	0.03
AKH 032	-1.63**	-0.41**	-0.61	-0.74**	-0.20
TCH 1342	1.13**	-0.17	0.47	-0.92**	2.91**
MCU 6	-2.07**	-0.31*	-1.67	-0.52**	1.60**
MCU8	-0.10	0.62**	3.51**	-0.68**	1.41*
TCH 1678	-1.64**	-0.11	-0.44	-0.48**	-0.43
IS-1456	-3.98**	0.49**	-4.45**	1.10**	-1.35*
TCH 1458	1.79**	-0.02	-2.12	0.44**	0.52
TCH 1457	-2.53**	0.46**	3.19**	-0.73**	-0.96
DHS 10-14	3.13**	-0.01	1.69	-0.07	-0.25
DHS 10 -17	-4.91**	0.20	0.24	0.43**	-1.61**
GISV-217	-1.97**	-0.43**	0.61	0.53**	-0.19
DHS 10-18	-4.01**	0.41**	-2.10	0.06	-1.53*
CD95% GCV (Lines)	0.58	0.24	2.32	0.25	1.19
Testers					
DHS T1	0.42^{**}	0.05	-0.97	0.12	0.14
DHS T2	0.03	0.16^{**}	1.00^{*}	-0.53^{**}	0.76^{**}
DHS T3	1.22^{**}	0.19^{**}	0.94^{*}	-0.98^{**}	1.41^{**}
DHS T4	-0.97^{**}	-0.08	0.03	-0.68^{**}	0.74^{*}
DHS T5	-0.70^{**}	-0.33^{**}	-1.01	2.09^{**}	-3.05^{**}
CD95% GCV (tester)	0.27	0.11	1.11	0.12	0.56

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

Laxman and Ganesh (2003), Maisuria *et al.*(2006), Kalpande *et al.* (2008), Shimna Bhaskaran and Ravikesavan (2008), Kumboh *et al.* (2008), Mohammad Reza *et al.*(2010) and Natera *et al.* (2012).

Seed cotton yield (q ha^{-1}): The parental lines were evaluated along with F$_1$'s for their *per se* performance. The parental lines exhibited high variability (10.47 to 22.49q ha^{-1}) for mean seed cotton yield. The results indicated that the selected parental lines are divergent and are suitable for development of potential hybrids. The crosses *viz.*, DHS 10-4 x DHS T1 followed by cross TCH 1458 x DHS T3 and IC 3584 x DHS T3 recorded highest mean seed cotton yield. However, the highest GCA effects of 5.17 and 1.00 were manifested by the lineDHS 10-4 and tester DHS T2, respectively (Table-3) implying that both the parents were good general combiners hence may be utilized in hybridization and selection programmes to improve the cotton yield. For SCA effects, maximum (11.80) SCA was recorded by the cross MCU 8 x DHS T5 while next ranker (10.44) was IC 3584 x DHS T3 (Table IV). For inheritance of seed cotton yield, SCA variance was higher than GCA variance. The component of variance due to SCA was higher than the GCAfor this trait. The ratio of general combining ability of variance to specific combining ability of variance was low indicating the role of non-additive gene action in governing the inheritance of this trait. Similar results were reported by Mandloi *et al.* (1998), Neelima (2002), Verma *et al.*(2004), Ashok Kumar *et al.* (2013), Kalpande *et al.* (2008), Cetin Karademir *et al.* (2009), Deosarkar *et al.* (2009b), Emine *et al.* (2010), Natera *et al.*(2012), Imran *et al.* (2012) and Yanal *et al.* (2013).

Ginning out turn (%): The parent registered the highest GOT (40.00%) followed by AKH-0303 (37.45%). The cross TCH-1342 x DHS T1 exhibited higher *per se* performance (41.33%). Lint % is a complex character which is governed by many genes. Primarily, it depends on lint weight, which has direct effect on seed cotton yield. Among the F1 hybrids *per se*, TCH-1342 x DHS T1 produced top (41.33%) ginning outturn. While among the parents, tester AKH-0303 ginned highest (37.45%) lint % whereas among the females, maximum (40.00%) lint was ginned by the line DCH 10-5 (Table-2). The mean squares due to GCA lines and testers and SCA (lines × tester interaction) (Table-1) indicating that the lint percent was controlled by non-additive genes. Among the lines, TCH 1342(2.91) and tester DHS T3 (1.41) exhibited positive GCA effects. The top three SCA scoring hybrids were IC 3584 x DHS T5(6.70), DHS 10-1 x DHS T5(5.02) and AKH 032 x DHS T4(3.44)SCA. Similar results have also been obtained by Pavasia and Shukla (1997), Surana *et al.* (1997), Mandloi *et al.* (1998), Murthy and Ranganadhacharyulu (1998b), Pavasia*et al.*(1998), Pavasia *et*

Table-4: Specific combining ability effects of intra *hirsutum* hybrids for different quantitative traits

Crosses	BPP	BW (g)	SCY (q ha^{-1})	SI (g)	GOT(%)
L1 x T1	-1.25	-0.08	-6.55 *	-0.46	-1.05
L1 x T2	0.05	-0.36	-2.95	0.19	-2.94 *
L1 x T3	4.7	0.42	10.44 **	1.16 **	-0.38
L1 x T4	3.4	0.32	0.57	-0.34	-2.32
L1 x T5	-1.85	-0.30	-1.504	-0.551	6.69 **
L2 x T1	-0.12	-0.25	0.80	0.25	-2.58
L2 x T2	-0.6	0.06	0.398	-0.50	-0.37
L2 x T 3	-3.4	0.28	2.490	0.725 *	0.426
L2 x T4	-0.3	-0.12	0.98	-0.95 **	-2.49
L2 x T5	1.25	-0.05	-4.67	0.48	5.02 **
L3 x T1	2.5	-0.01	8.69 **	-0.52	-2.14
L3 x T 2	3.35	0.15	-2.49	0.39	-1.58
L3 x T3	-1.25	-0.04	1.52	0.48	1.56
L3 x T4	3.15	-0.42	-2.23	-0.74 *	2.29
L3 x T5	-0.15	0.34	-5.49 *	0.39	-0.12
L4 x T1	4.1	0.40	-6.44 *	0.49	-1.37
L4 x T2	-3.5	-0.34	-0.204	-0.98 **	0.516
L4 x T3	0.1	-0.16	-8.38 **	1.28 **	0.71
L4 x T4	-4.35	-0.01	10.15 **	0.65 *	0.06
L4 x T5	-3.75	0.12	4.87	-1.44**	0.08
L5 x T1	-1.7	0.03	-1.47	-0.32	0.59
L5 x T2	-1.7	0.37	-2.43	-0.24	-0.65
L5 x T3	-2.85	0.41	0.33	-1.46 **	0.09
L5 x T4	2.85	-0.06	1.29	-0.56	0.33
L5 x T5	-3.85	0.09	2.28	-0.33	-0.37
L6 x T1	1.45	-0.11	0.71	-1.36 **	-0.96
L6 x T2	-0.6	-0.04	-3.14	-1.57 **	-0.41
L6 x T3	2.3	0.13	-1.99	-0.34	1.98
L6 x T4	1.5	0.31	-0.52	2.84 **	1.11
L6 x T5	1.25	-0.29	4.94	0.43	-1.73
L7 x T1	-2.3	0.11	-0.71	-1.36 **	-0.96
L7 x T2	0.6	-0.19	-0.91	1.75 **	1.11
L7 x T3	4.05	-0.02	-8.83 **	1.86 **	-2.98 *
L7 x T4	1.7	-0.02	0.71	-0.79 **	0.66
L7 x T5	1.45	0.01	5.66 *	-2.93 **	-0.16
L8 x T1	3.45	-0.02	4.92	0.03	2.06
L8 x T2	4	-0.16	2.45	0.34	-1.12
L8 x T3	-1.05	-0.14	-5.73 *	0.16	0.69
L8 x T4	0.3	0.46	-5.20	-1.09 **	-0.22
L8 x T5	1.25	-0.14	3.56	0.55	-1.42
L9 x T1	-1.25	-0.29	0.47	-0.95 **	-0.42
L9 x T2	-3.15	-0.37	-3.19	-0.85 **	1.59
L9 x T3	0.15	0.546	-1.195	1.376 ***	1.209
L9 x T4	-3.6	-0.15	-1.07	0.47	-1.22
L9 x T5	-1.45	0.27	4.98	-0.04	-1.16
L10 x T1	2.2	0.52	6.64 *	0.34	1.01
L10 x T2	-2.55	-0.51	0.94	1.26 **	-0.51
L10 x T3	0.6	0.06	0.68	-2.24 **	0.98
L10 x T4	-1.2	0.23	-0.57	-0.76 *	-0.86
L10 x T5	-0.3	-0.29	-7.68 **	1.40 **	-0.62
L11 x T1	4.6	0.23	3.03	-0.21	-1.11
L11 x T2	-1.5	-0.01	1.82	-0.73*	-0.85
L11 x T3	2.15	-0.14	-2.11	0.56	1.31
L11 x T4	1.9	0.01	-2.30	1.05 **	3.44 *
L11 x T5	-2.35	-0.09	-0.43	-0.67 *	-2.79 *
L12 x T1	2.55	-0.39	1.56	-2.14 **	1.00
L12 x T2	0.85	0.31	2.72	0.05	0.38
L12 x T3	1.3	-0.35	-1.18	1.48 **	-1.78
L12 x T4	0.12	0.18	-2.51	0.78 **	-0.33
L12 x T5	3.5	0.25	-0.58	-0.17	0.73
L13 x T1	-2.55	-0.25	3.66	0.90**	0.84
L13 x T2	1.7	-0.20	2.08	-1.08 **	-0.55
L13 x T3	3.6	0.59*	-1.52	-1.06 **	-0.56
L13 x T4	-1.9	-0.01	-1.11	0.89 **	0.37
L13 x T5	3.15	-0.14	-3.11	0.33	-0.11
L14 x T1	2.35	0.41	-4.72	0.18	0.09
L14 x T2	4.35	-0.01	7.36 **	-2.63 **	1.38
L14 x T3	-4.7	0.13	7.98 **	0.65 *	-0.06
L14 x T4	-2.2	-0.17	1.18	0.92**	1.06
L14 x T5	1.05	-0.35	-11.81 **	0.87**	-2.47
L15 x T1	-2.35	-0.18	-0.05	-0.38	0.64
L15 x T2	1	0.07	-0.52	-0.16	1.42
L15 x T3	0.35	-0.01	0.06	0.02	1.88
L15 x T4	1.25	-0.29	-1.07	0.31	-3.37 *
L15 x T5	0.55	0.41	1.58	0.21	-0.58
L16 x T1	-4.1	0.22	-3.51	-0.71 *	0.85
L16 x T2	3.3	-0.17	3.04	0.29	0.28
L16 x T3	1.2	-0.22	2.34	-0.07	-1.81
L16 x T4	1.2	0.68 *	-4.38	0.26	1.02
L16 x T5	2.15	-0.50	2.51	0.23	-0.33
L17 x T1	-0.1	-0.06	-6.07 *	2.45 **	-0.08
L17 x T2	-0.55	0.61*	1.17	2.47 **	2.03
L17 x T3	-0.85	-0.12	5.69 *	-2.42 **	-1.34
L17 x T4	0.75	-0.42	4.65	-1.47**	1.16
L17 x T5	3.05	0.00	-5.44 *	-1.03 **	-1.77
L18 x T1	4.25	0.23	-2.57	0.63 *	1.54
L18 x T2	-1.45	-0.13	-0.01	0.53	-1.46
L18 x T3	-2.5	-0.36	8.68 **	-3.77**	-0.41
L18 x T4	2.55	-0.16	-2.16	0.40	0.82
L18 x T5	-2.15	0.44	-3.95	2.21**	-0.49
L19 x T1	0.3	0.05	-1.40	0.29	0.19
L19 x T2	-3.45	0.17	-3.18	0.29	0.70
L19 x T3	-0.75	-0.36	-0.07	0.45	-0.83
L19 x T4	3.85	-0.09	2.13	-1.20**	0.97
L19 x T5	-3.15	0.24	2.53	0.18	-1.05
L20 x T1	-1.25	-0.12	-1.29	-0.29	-0.92
L20 x T2	-0.05	0.19	-2.06	0.42	0.99
L20 x T3	3.75	0.39	0.91	0.62 *	-0.05
L20 x T4	9.15**	-0.41	-2.08	-0.93 **	0.08
L20 x T5	-3.35	-0.06	4.53	0.19	-0.11
L21 x T1	1.85	-0.80 **	-0.48	0.30	-1.06
L21 x T2	-1	0.37	-1.34	-0.08	-0.11
L21 x T3	-0.35	-0.06	-2.30	-1.18**	-0.12
L21 x T4	2.35	0.11	1.26	0.17	0.11
L21 x T5	-1.3	0.39	2.87	0.78 **	1.18
L22 x T1	3.05	0.22	0.73	1.38**	1.51
L22 x T2	-3.3	0.24	0.45	0.83 **	0.12
L22 x T3	-4	-0.12	-7.81 **	-1.19 **	-0.54
L22 x T4	-3.05	0.01	2.28	0.08	-2.66 *
L22 x T5	-2.15	-0.35	4.36	-1.09**	1.57
CD95% SCA	5.61	0.54	5.01	2.66	0.57

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

al. (1999) and Patel *et al.* (2005), Pole *et al.* (2008), Kalpande *et al.* (2008), Shimna Bhaskaran and Ravikesavan (2008), Patel *et al.*(2009). Emine *et al.* (2010) and Natera *et al.* (2012) being good general combiners may be potential parents for hybridization and selection programmes whereas among the F1 hybrids IC 3584 x DHS T5, DHS 10-1 x DHS T5 and AKH 032 x DHS T4 being best specific cross combinations are worth to be exploited for hybrid crop development to improve the lint percent.

Seed Index: Seed index and seed cotton yield are positively correlated that means increase in seed index will simultaneously increase the seed cotton yield. The mean performance of F1 hybrids *per se* showed that hybrid manifested highest (13.59 g) seed index was given by DHS 10-7 x DHS T5 (Table II). Among the lines, DHS 10-7 (12.37 g) and testers, DHS T4 (11.42 g) recorded maximum seed index (Table-2). Mean squares due to GCA and SCA were significant (Table-1). Among the lines, *gca* effect ranges from -0.06 (DHS 10-18) to 1.23 (DHS 10-7) in which only seven showed significant positive *gca* effect but eleven lines exhibited *gca* effect in negative direction. While the tester DHS T5 (2.09) and exhibited significantly positive *gca* effect. As non-additive gene action was predominant, breeding methods involving selection, intermating among selected ones and reselection may help to improve this trait besides exploiting through heterosis breeding. Similar results were reported by Kajjidoni (1982), Mohiuddin (1997), Mandloi*et al.* (1998), Laxman and Ganesh (2003), Patel *et al.* (2005), Maisuria *et al.* (2006), Paulo Antnio de Aguiar *et al.* (2007) and Deosarkar *et al.* (2009b).

The GCA and SCA mean squares were significant, however the magnitude of variances due to GCA for both lines (females) and testers (pollinators) was lesser than SCA (lines x tester interaction) for all the traits except boll weight (g) indicating preponderance of non-additive genes as compared to additive genes. Among the lines, DHS 10-4 and in testers, DHS T3 were found to be the best general combiners for all the traits studied and thus can reliably be used in hybridization programmes so as to select the desirable plants from segregating populations. Among the F_1 hybrids, crosses *viz.,* DHS 10-4 x DHS T1, TCH 1458 x DHS T3 and IC 3584 x DHS T3 were best specific combiners for seed cotton yield and also comparably good for all other yield attributing traits. Therefore, these crosses could be promising to be exploited for hybrid cotton development for different characters.

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