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# Heterosis and combining ability studies for fibre quality traits in inter-specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.) over environments

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### Abstract

The present study was conducted at three locations during *kharif* 2014-15 with 72 inter-specific hybrids along with their parents and two standard checks to study standard heterosis and combining ability for different fibre quality traits. Combining ability analysis indicated the presence of additive gene action for 2.5% span length and uniformity ratio whereas microneaire value, bundle strength, fibre elongation and lint yield plant<sup>-1</sup> were controlled by non-additive gene action. Among the lines ADB 532 and BS 37 and the testers TCB 37 and SUVIN were found to be good general combiners for 2.5% span length and bundle strength. The hybrid, MCU 5 × GSB 40 for 2.5% span length and bundle strength and H 1442 × GSB 41, TSH 0250 × GSB 40, ADB 542 × DB 16 for lint yield plant<sup>-1</sup> exhibited high *per se* performance, high and significant positive *sca* effects and standard heterosis. The cross combinations which are showing high standard heterosis and *sca* effects may be recommended for commercial cultivation after further confirmation of their stable performance over different locations and years.

**Keywords:** Cotton, inter-specific hybrids, line × tester analysis, fibre quality traits, heterosis, combining ability

### Introduction

Cotton (*Gossypium* spp), the natural plant fibre with unique properties rendering it highly spinnable into yarns for textile use, is considered as “White gold” because of the potential it offers to rural economy, global trade and national GDP. Genetic enhancement is one of the important tools to improve upon the productivity in cotton (Gopikrishnan *et al.*, 2013) [5]. Breeding methods like domestication, germplasm collection, plant introduction, somatic hybridization, genetic engineering, mutation breeding, intra-specific hybridization, inter-specific hybridization and using wild species for introgression are seen in cotton genetic improvement. Among these inter-specific hybridization between *hirsutum* and *barbadense* group is used to develop high yielding genotypes with increased fibre length and strength. Pima cotton or Egyptian cotton, *Gossypium barbadense* is known for its better fibre properties being cultivated in less than 2% in the world (Chen *et al.*, 2007) [2]. In India, long and extra-long staple cotton is widely grown in South Zone states of Tamil Nadu, Andhra Pradesh and Karnataka as the climatic requirement for growing this cotton are more conducive and there has been a heavy demand for this cotton in the recent past in textile industry. To meet the increased demand exploitation of heterosis as hybrids and systemic varietal improvement through hybridization are the main tools. It is an often cross pollinated crop and amenable for both heterosis breeding as well as hybridization followed by selection in subsequent generations. The phenomenon of heterosis has proved to be the most important genetic tool in boosting the yield of self as well as cross pollinated crops and is considered as the most important breakthrough in the field of crop improvement. The exploitation of hybrid vigour in cotton on commercial scale has become feasible and economical due to easy hand emasculation and pollination. The identification of specific parental combination capable of producing the desired level of F<sub>1</sub> heterotic effect is important in improving the yield potential of this crop (Patel *et al.*, 2012) [12]. Hence in the present study 72 inter-specific cross combinations along with their parents and standard checks evaluated over environments to identify best cross combinations for fibre quality traits.

## Material and methods

The present investigation was carried over three locations i.e., Regional Agricultural Research Station (RARS), Lam Farm, Agricultural Research Station (ARS), Jangamaheswarapuram and Agricultural College Farm, Bapatla during *khari* 2014-15. During off-season 2013-14, 12 *hirsutum* lines viz., NDLH 1938, H 1442, ADB 542, ADB 532, WGCV 48, MR 786, TSH 0250, BS 37, SCS 793, MCU 5, L 1058, L 762 and six *barbadense* testers viz., GSB 40, DB 16, DB 11, GSB 41, TCB 37 and SUVIN were mated in line  $\times$  tester fashion and obtained 72 inter-specific cross combinations. The hybrids along with their parents and two checks (DCH 32 and Mahalakshmi) i.e., 96 genotypes were evaluated in a Randomized Complete Block design with three replications. Each plot consisted of two rows of 10 m length spaced at 1.20 m apart with plant to plant distance of 60 cm. All the recommended agronomical practices and plant protection measures were followed as and when required to raise a good crop of cotton. Total seed cotton was harvested from all the selected plants and later it was ginned for obtaining lint. Mean weight of five plants lint recorded as lint yield plant<sup>-1</sup>. All the fibre quality traits i.e., 2.5 % span length (mm), uniformity ratio, micronaire value (10<sup>-6</sup> g/inch), bundle strength (g/tex), fibre elongation measured by using HVT Expert 1201 high volume fibre tester instrument. The data was subjected to statistical analysis for calculating combining ability variances and effects using line  $\times$  tester method suggested by Kempthorne (1957) [6] and detailed by Singh and Chaudhary (1985) [17]. Standard heterosis was calculated over both the checks by adopting methodology suggested by Meredith and Bridge (1972) [8].

## Results and discussion

The pooled analysis of variance for combining ability over three locations recorded significant differences for all the characters studied (Table 1). The differences among the parents, parents *vs* crosses and crosses were observed to be significant for all the characters studied. Partitioning of crosses into lines, testers and line  $\times$  tester revealed that the variance due to lines was significant for all the characters whereas, for testers all the characters were found to be significant except for micronaire value and bundle strength. The interaction due to lines  $\times$  testers were significant for all the traits evaluated.

Interaction effect of locations  $\times$  parents *vs* crosses, locations  $\times$  crosses were significant for all the characters, except for uniformity ratio in locations  $\times$  parents *vs* crosses interaction. Further, locations  $\times$  line effect interaction showed significant differences for micronaire value, and lint yield plant<sup>-1</sup>. While, locations  $\times$  tester effect interaction exhibited non-significant for all the characters except for 2.5% span length. Interaction effects of locations  $\times$  line  $\times$  testers were significant for all the characters studied. General combining ability effects of parents and specific combining ability effects of crosses were estimated and presented in Tables 2 to 3. The  $\sigma^2_{gca}/\sigma^2_{sca}$  ratio was calculated and presented in Table 4.

### 2.5 % span length (mm)

The *gca* effects for 2.5 % span length in pooled analysis varied from -1.54 (MR 786) to 1.56 (MCU 5) in lines and from -0.74 (DB 11) to 0.68 (TCB 37) in testers. The lines, MCU 5, BS 37, L 1058, ADB 532 and TSH 0250 and among the testers, TCB 37 and SUVIN exhibited significant positive *gca* effects in desired direction for this trait. The *sca* effects exhibited variation from -1.50 (TSH 0250  $\times$  GSB 41) to 2.08

(H 1442  $\times$  DB 16) and significant positive *sca* effects was registered in 14 cross combinations. Based on *per se* performance and *sca* effects the hybrids viz., TSH 0250  $\times$  GSB 40 (High  $\times$  Low), H 1442  $\times$  DB 16 (Low  $\times$  Low) and ADB 542  $\times$  SUVIN (Low  $\times$  High) were detected as superior specific cross combinations. Low  $\times$  high and high  $\times$  low *gca* effects resulted in superior cross combinations which may be due to complementary gene action and also revealed the importance of both additive and non-additive gene actions. The superior cross combination between two low combiners mainly due to nicking ability/genetic diversity of their parents. The variance due to *gca* was higher than *sca*. The ratio of *gca* variance to *sca* variance indicated the importance of additive gene action in governing the inheritance of this trait. Hybridization followed by simple selection through pedigree method can be employed for improvement of this character. These results are in accordance with the results of Kumar *et al.* (2013) [7] and Mohammad *et al.* (2013) [3].

All the hybrids exhibited significant positive mid parent heterosis for this character ranging from 5.45 (NDLH 1938  $\times$  GSB 41) to 22.89 (H 1442  $\times$  DB 16). The significant positive heterobeltiosis was recorded in twenty four hybrids with a range of -6.52 (L 762  $\times$  TCB 37) to 11.66 (MCU 5  $\times$  GSB 40). The significant standard heterosis was recorded in 36 hybrids over DCH 32 and it varied from -3.45 (MR 786  $\times$  GSB 40) to 12.30 (MCU 5  $\times$  SUVIN). Heterosis over Mahalakshmi ranged from -5.12 (MR 786  $\times$  GSB 40) to 10.36 (MCU 5  $\times$  SUVIN) and was recorded positive values in twenty six hybrids. These results are in accordance with findings of Amalabalu *et al.* (2012) [1].

### Uniformity ratio

Among the lines *gca* effects ranged from -0.79 (TSH 0250) to MR 786 (0.93) and among the testers it was from -0.62 (SUVIN) to 0.53 (DB 11). Out of 12 lines three lines viz., MR 786 SCS 793 and NDLH 1938 and three testers' viz., DB 11, GSB 40 and GSB 41 exhibited significant positive *gca* effects. For uniformity ratio *sca* effects exhibited a range from -1.16 (MR 786  $\times$  SUVIN) to 1.26 (MR 786  $\times$  TCB 37). The crosses, MR 786  $\times$  TCB 37 (High  $\times$  Low), WGCV 48  $\times$  DB 11 (Low  $\times$  High) and BS 37  $\times$  GSB 40 (Low  $\times$  High) identified as good specific cross combinations based on positive *sca* effects and *per se* performance. The superior cross combinations between low  $\times$  high and high  $\times$  low *gca* effects resulted mainly due to complementary gene action and also revealed the importance of both additive and non-additive gene actions. In pooled analysis this character may be under the control of additive gene action as the variance due to *gca* was higher than the *sca* and both were non-significant. This character can be improved through hybridization followed by simple selection i.e., pedigree method. Similar results were also reported by Nimbalkar *et al.* (2014) [10].

Heterosis over mid parent varied from -6.78 (ADB 532  $\times$  DB 16) to 0.24 (MCU 5  $\times$  GSB 40). Heterobeltiosis ranged from -10.38 (MR 786  $\times$  SUVIN) to -0.53 (BS 37  $\times$  GSB 40). None of the hybrid showed significant positive heterosis over both mid and better parents. Heterosis over DCH 32 and Mahalakshmi varied from -3.56 (MCU 5  $\times$  DB 16) to 4.41 (MR 786  $\times$  TCB 37) and -6.37 (MCU 5  $\times$  DB 16) to 1.36 (MR 786  $\times$  TCB 37), respectively. None of the hybrid exhibited significant positive heterosis over Mahalakshmi whereas, nine hybrids recorded significant heterosis over DCH 32 in desirable direction for this trait. These findings are in conformity with the results of Rajamani *et al.* (2009) and Patil *et al.* (2012) [13].

**Micronaire value ( $10^{-6}$  g/inch)**

In pooled analysis over locations *gca* effects for lines varied from -0.16 (MCU 5) to 0.15 (H 1442) whereas, in testers it was from -0.06 (DB 11 and SUVIN) to 0.08 (DB 16). Estimates of *gca* effects were positive and significant for lines, H 1442, ADB 542, WGCV 48, L 762 and NDLH 1938 and for testers, DB 16, GSB 40 and GSB 41. The *sca* effects ranged from -0.28 (NDLH 1938 × TCB 37 and H 1442 × DB 16) to 0.33 (ADB 542 × DB 16) and significant *sca* effects were recorded in 15 crosses. The general combining ability variance was lower than specific combining ability variance showing the importance of non-additive gene action governing the inheritance of this character. The superior cross combinations found based on *per se* performance and *sca* effects were, ADB 542 × DB 16 (High × High), H 1442 × GSB 41 (High × High) and NDLH 1938 × DB 16 (High × High). The cross combinations involving high × high general combiners revealed additive and additive × additive genetic component of variance where the characters could be easily improved through simple selection procedures in recombination breeding. Further, it was revealed by the ratio of *gca* variance to *sca* variance (0.400). Biparental mating or diallel selective mating or heterosis breeding may be employed for the improvement of this trait. Similar results were also reported by Deosarkar *et al.* (2014)<sup>[3]</sup> and Raja Mani *et al.* (2014)<sup>[15]</sup>.

Heterosis over mid parent varied from -34.03 (MR 786 × SUVIN) to -2.09 (NDLH 1938 × DB 16) whereas, heterobeltiosis varied from -38.29 (L 762 × SUVIN) to -11.21 (NDLH 1938 × DB 16). Heterosis over standard checks, DCH 32 and Mahalakshmi ranged from -0.26 (TSH 0250 × GSB 41) to 34.06 (ADB 542 × DB 16) and -17.46 (TSH 0250 × GSB 41) to 10.94 (ADB 542 × DB 16), respectively. None of the hybrid recorded significant positive relative heterosis and heterobeltiosis for this trait. Sixty six hybrids over DCH 32 and three hybrids over Mahalakshmi possessed significant positive heterosis. These findings are in accordance with the results of Patil *et al.* (2012)<sup>[13]</sup> over mid parent; Deshmukh *et al.* (2014) over better parent; whereas, positive heterosis over standard check was reported by Patil *et al.* (2012)<sup>[13]</sup>.

**Bundle strength (g/tex)**

Estimates of *gca* effects over locations in pooled analysis for this trait varied from -1.15 (MR 786) to 0.82 (ADB 532) in lines and from -0.40 (DB 11) to 0.14 (DB 16) in testers. Significant and positive *gca* effects exhibited by ADB 532, MCU 5, BS 37 and SCS 793 in lines whereas, the testers DB 16 GSB 40, SUVIN and TCB 37 exhibited non-significant and positive *gca* effects. The crosses, BS 37 × SUVIN and MCU 5 × GSB 40 registered lowest and highest *sca* effects, respectively. Out of 72 cross combinations studied, fourteen hybrids possessed significant positive *sca* effects. The variance due to *sca* was high and significant than the *gca* which was low and non-significant revealing the predominant role of non-additive gene action in controlling this character. Based on *per se* performance and positive *sca* effects the crosses, MCU 5 × GSB 40 (High × Low), H 1442 × DB 16 (Low × Low) and BS 37 × GSB 40 (High × Low) were detected as best specific cross combinations for this character. The crosses with high × low combiners resulted in superior combinations which may be due to complementary gene action and the crosses between two low combiners producing superior cross combinations indicating the nicking ability/genetic diversity of their parents. Biparental mating or diallel selective mating or heterosis breeding may be

employed for the improvement of this trait. These results are also confirmed by the findings of Tuteja and Banga (2013)<sup>[18]</sup> and Deosarkar *et al.* (2014)<sup>[3]</sup>.

Pooled analysis for heterosis over locations revealed that 71 hybrids recorded significant average heterosis and it ranged from -1.10 (BS 37 × SUVIN) to 25.89 (H 1442 × DB 16). The significant heterobeltiosis was recorded in nine hybrids with a range of -12.65 (MR 786 × SUVIN) to 13.80 (MCU 5 × GSB 40). The significant positive heterosis registered in 49 hybrids over DCH 32 and it ranged from -2.65 (MR 786 × DB 11) to 17.50 (MCU 5 × GSB 40) and 25 hybrids over Mahalakshmi and it ranged from -5.71 (MR 786 × DB 11) to 13.80 (MCU 5 × GSB 40). These findings are in agreement with the results of heterosis over mid parent reported by Punitha *et al.* (2012); over better parent by Deshmukh *et al.* (2014) whereas, heterosis over standard check was reported by Tuteja *et al.* (2013)<sup>[19]</sup> and Tuteja (2014)<sup>[20]</sup>.

**Fibre elongation (%)**

The *gca* effects for lines in pooled analysis ranged from -0.14 (TSH 0250) to 0.08 (NDLH 1938) and from -0.07 (TCB 37) to 0.09 (DB 16) in testers. Among the lines, NDLH 1938, ADB 542, BS 37 and L 762 whereas, in testers, DB 16 and GSB 41 possessed significant positive *gca* effects. Estimates of *sca* effects varied from -0.23 (MR 786 × DB 11) to 0.20 (MR 786 × GSB 41). Thirteen crosses recorded significant *sca* effects. The crosses, BS 37 × GSB 40 (High × Low), MR 786 × GSB 41 (Low × High) and TSH 0250 × DB 16 (Low × High) were identified as best specific cross combinations based on their *per se* performance and *sca* effects. The crosses involving high × low and low × high *gca* effects resulted in superior combinations which may be due to complementary gene action. The component of variance due to specific combining ability was greater than the general combining ability. The ratio of *gca* variance to *sca* variance exhibiting the operation of non-additive gene action and it can be exploited by bi-parental mating or diallel selective mating or heterosis breeding. Similar results were also reported by Vineela *et al.* (2012)<sup>[21]</sup> and Deosarkar *et al.* (2014)<sup>[3]</sup>.

Relative heterosis for this trait varied from -9.38 (MR 786 × DB 11) to 2.69 (NDLH 1938 × DB 16) while, heterobeltiosis ranged from -11.50 (MR 786 × DB 11) to 0.02 (MR 786 × GSB 41). Heterosis over DCH 32 and Mahalakshmi varied from -1.82 (TSH 0250 × SUVIN) to 13.26 (NDLH 1938 × DB 16) and -7.54 (TSH 0250 × SUVIN) to 6.66 (NDLH 1938 × DB 16), respectively. One hybrid (NDLH 1938 × DB 16) over mid parent and none of the hybrid over better parent exhibited significant positive values. Sixty four hybrids over DCH 32 and nine hybrids over Mahalakshmi recorded significant heterosis in desirable direction. These findings are in conformity with the results of heterosis over mid parent reported by Patil *et al.* (2012)<sup>[13]</sup>; over better parent was reported by Patil *et al.* (2012)<sup>[13]</sup> and Deshmukh *et al.* (2014)<sup>[3]</sup>, while, heterosis over standard check was reported by Patil *et al.* (2012)<sup>[13]</sup>.

**Lint yield Plant<sup>-1</sup> (g)**

Range of *gca* effects for lint yield plant<sup>-1</sup> varied from -19.40 (MCU 5) to 9.87 (H 1442) in lines and from -8.50 (SUVIN) to 7.26 (DB 16) in testers. Out of twelve lines, H 1442, NDLH 1938, MR 786, L 762 and ADB 542 and three tester's *viz.*, DB 16, GSB 41 and GSB 40 exhibited significant and positive *gca* effects in desirable direction for this character. Specific combining ability effects ranged from -14.25 (L 762 × GSB 41) to 33.18 (TSH 0250 × GSB 40) and significant

positive *sca* effects were exhibited by 21 cross combinations. The top five superior cross combinations identified were, TSH 0250 × GSB 40, L 762 × TCB 37, H 1442 × GSB 41, ADB 542 × DB 16 and BS 37 × SUVIN.

Based on *per se* performance and *sca* effects H 1442 × GSB 41 (High × High), TSH 0250 × GSB 40 (Low × High) and ADB 542 × DB 16 (High × High) were identified as best specific cross combinations. The cross combinations involving high × high general combiners revealed additive and additive × additive genetic component of variance which could be easily improved through simple selection procedures in recombination breeding. Low × high *gca* effects resulted in superior cross combinations which may be due to complementary gene action and revealed the importance of both additive and non-additive gene actions. The variance due to specific combining ability was greater than the general combining ability. The ratio of *gca* variance to *sca* variance revealed the importance of non-additive gene action in the inheritance of this character. Biparental mating or diallel selective mating or heterosis breeding can be employed for the improvement of this trait. These results are in agreement with the findings of Patel *et al.* (2012) [12] and Vineela *et al.* (2012) [21].

Average heterosis for this character varied from -20.39 (TSH 0250 × TCB 37) to 112.76 (TSH 0250 × GSB 40) and heterobeltiosis ranged from -32.88 (TSH 0250 × TCB 37) to 101.38 (ADB 542 × DB 16). Heterosis over DCH 32 and Mahalakshmi ranged from -47.27 (TSH 0250 × TCB 37) to 57.03 (H 1442 × GSB 41) and -52.87 (TSH 0250 × TCB 37) to 40.36 (H 1442 × GSB 41), respectively. Significant positive average heterosis was observed in sixty two hybrids whereas, forty nine hybrids recorded significant positive heterobeltiosis. Twenty five hybrids over DCH 32 and eleven hybrids over Mahalakshmi exhibited significant positive heterosis in desirable direction. Similar findings were earlier reported by Seoudy *et al.* (2014) [16] for heterosis, over mid parent and heterobeltiosis; Patel *et al.* (2014) [11] over standard check.

Based on overall performance (*per se* performance, significant *sca* effects and standard heterosis) for 2.5% span length and bundle strength in pooled analysis the hybrid, MCU 5 × GSB 40 recorded high *per se* performance, significant *sca* effects and standard heterosis over DCH 32 and Mahalakshmi. The best heterotic cross combinations identified based on overall performance for different characters are presented in the Table 5.

**Table 1:** Analysis of variance of combining ability for different characters in inter-specific hybrids of cotton (*G. hirsutum* × *G. barbadense*) over three locations (pooled) during *kharif*, 2014-15.

Source of variation	d.f	2.5% span length (mm)	Uniformity ratio	Micronaire value (10 <sup>-6</sup> g/inch)	Bundle strength (g/tex)	Fibre elongation (%)	Lint yield plant <sup>-1</sup> (g)
Replications	2	0.13	0.79	0.01	0.39	0.03	2.60
Environments	2	692.79**	6.97*	31.88**	514.82**	5.55**	10799.23**
Rep × Env.	4	0.97	0.51	0.01	1.10	0.01	9.46
Treatments	89	66.82**	15.70**	1.69**	47.17**	0.20**	1495.51**
Parents	17	107.59**	22.83**	1.75**	108.06**	0.41**	463.16**
Parents (Line)	11	18.23**	21.53**	1.48**	11.03**	0.16**	238.17**
Parents (Testers)	5	16.88**	4.04*	0.86**	13.51**	0.04	246.46**
Parents (L vs T)	1	1544.10**	131.12**	9.07**	1648.09**	5.05**	4021.53**
Parent vs Crosses	1	3137.13**	556.85**	100.57**	1695.58**	0.09	27031.85**
Crosses	71	13.81**	6.38**	0.29**	9.37**	0.15**	1383.02**
Line effect	11	43.95**	15.84**	0.78**	17.77*	0.24*	3511.55**
Tester effect	5	35.63**	22.27**	0.35	4.92	0.38**	4095.10**
Line × Tester effect	55	5.80**	3.04**	0.18**	8.09**	0.11**	710.76**
Env × Treatments	178	3.72**	2.37**	0.14**	3.56**	0.04**	311.68**
Env × Parents	34	5.84**	2.44*	0.27**	5.02**	0.04**	78.56**
Env × Parents (L)	22	3.85**	2.38	0.26**	2.13**	0.03	94.83**
Env × Parents (T)	10	5.97**	2.48	0.24**	7.03**	0.06**	44.49*
Env × PAR (L vs T)	2	27.15**	3.03	0.52**	26.77**	0.03	69.84*
Env × Parent vs Cross	2	20.05**	0.11	0.20**	6.96**	0.17**	1533.48**
Env × Crosses	142	2.98**	2.39**	0.11**	3.17**	0.04**	350.29**
Env × Line effect	22	2.03	1.71	0.23**	2.88	0.04	615.49**
Env × Tester effect	10	6.85*	2.10	0.03	5.54	0.05	478.99
Env × L × T effect	110	2.82**	2.55**	0.09**	3.01**	0.04**	285.55**
Error	534	1.07	1.53	0.01	0.71	0.02	19.88

\* Significant at 5% level

\*\*Significant at 1% level

**Table 2:** General combining ability effects of parents for different characters in cotton over three locations (pooled) during *kharif*, 2014-15

	2.5% span length (mm)	Uniformity ratio	Micronaire value (10 <sup>-6</sup> g/inch)	Bundle strength (g/tex)	Fibre elongation (%)	Seed cotton yield plant <sup>-1</sup> (g)	Lint yield plant <sup>-1</sup> (g)
<b>Lines</b>							
NDLH 1938	-0.92**	0.52**	0.11**	0.17	0.08**	25.23**	8.97**
H 1442	-0.24	0.32	0.15**	0.15	-0.01	25.40**	9.87**
ADB 542	0.17	0.10	0.14**	-0.23*	0.06**	11.21**	4.16**
ADB 532	0.48**	-0.26	-0.13**	0.82**	0.03	4.22*	-0.47
WGCV 48	0.01	-0.03	0.12**	-0.06	-0.01	-7.19**	-1.64*
MR 786	-1.54**	0.93**	-0.02	-1.15**	-0.01	16.75**	6.08**

TSH 0250	0.42**	-0.79**	-0.13**	0.05	-0.14**	-20.20**	-6.12**
BS 37	0.90**	-0.02	-0.03*	0.34**	0.05*	10.51**	-0.39
SCS 793	-0.54**	0.61**	-0.10**	0.34**	0.02	-7.09**	-5.75**
MCU 5	1.56**	-0.78**	-0.16**	0.42**	-0.11**	-55.60**	-19.40**
L 1058	0.76**	-0.55**	-0.07**	0.19	-0.02	-10.81**	-1.00
L 762	-1.07**	-0.05	0.12**	-1.03**	0.05*	7.56**	5.69**
SE (gi)	0.15	0.16	0.01	0.11	0.02	2.03	0.64
<b>Testers</b>							
GSB 40	0.07	0.36**	0.03**	0.12	0.01	7.58**	2.12**
DB 16	-0.06	-0.11	0.08**	0.14	0.09**	16.62**	7.26**
DB 11	-0.74**	0.53**	-0.06**	-0.40**	0.01	4.83**	0.75
GSB 41	-0.54**	0.25*	0.03**	-0.08	0.03*	8.90**	4.58**
TCB 37	0.68**	-0.41**	-0.03**	0.11	-0.07**	-15.20**	-6.21**
SUVIN	0.59**	-0.62**	-0.06**	0.12	-0.06**	-22.73**	-8.50**
SE (gj)	0.10	0.12	0.01	0.08	0.01	1.43	0.45

\* Significant at 5% level

\*\*Significant at 1% level

**Table 3:** Specific combining ability effects of 72 inter-specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.) for 2.5% span length, uniformity ratio, micronaire value, bundle strength, fibre elongation and lint yield plant<sup>-1</sup> over three locations (pooled) during *khariif*, 2014-15

	2.5% span length (mm)	Uniformity ratio	Micronaire value (10 <sup>-6</sup> g/inch)	Bundle strength (g/tex)	Fibre elongation (%)	Lint yield plant <sup>-1</sup> (g)
NDLH 1938 × GSB 40	-0.08	0.11	0.04	-0.06	0.03	1.04
NDLH 1938 × DB 16	-0.44	0.61	0.22**	0.07	0.14**	-1.97
NDLH 1938 × DB 11	-0.28	-0.47	0.23**	-0.62*	-0.03	6.61**
NDLH 1938 × GSB 41	0.02	-0.04	-0.25**	-0.07	-0.09	2.86
NDLH 1938 × TCB 37	0.07	-0.02	-0.28**	-0.11	-0.15**	2.19
NDLH 1938 × SUVIN	0.74*	-0.20	0.05	0.80**	0.10	-10.72**
H 1442 × GSB 40	-0.45	-0.06	0.02	-0.80**	-0.01	-5.67**
H 1442 × DB 16	2.08**	0.29	-0.28**	2.36**	-0.04	7.33**
H 1442 × DB 11	-0.71	-0.51	-0.10**	-0.64*	0.05	-5.90**
H 1442 × GSB 41	-0.18	0.15	0.28**	-0.16	-0.01	15.37**
H 1442 × TCB 37	-0.40	0.24	0.02	-0.48	-0.11*	-5.39**
H 1442 × SUVIN	-0.34	-0.10	0.06	-0.27	0.11*	-5.72**
ADB 542 × GSB 40	-1.08**	-0.32	0.02	-1.32**	-0.05	-1.63
ADB 542 × DB 16	-0.04	0.24	0.33**	0.32	0.07	14.28**
ADB 542 × DB 11	0.48	-0.05	-0.21**	0.48	-0.11*	4.94**
ADB 542 × GSB 41	0.34	-0.02	-0.18**	1.09**	0.03	-6.44**
ADB 542 × TCB 37	-0.69	0.32	-0.12**	-0.88**	-0.07	-0.07
ADB 542 × SUVIN	0.99**	-0.17	0.18**	0.31	0.13*	-11.08**
ADB 532 × GSB 40	-0.70	0.27	-0.18**	0.23	-0.09	8.34**
ADB 532 × DB 16	0.28	-0.31	0.02	0.35	0.08	-4.25**
ADB 532 × DB 11	-0.72*	0.33	0.03	-1.29**	0.03	-0.68*
ADB 532 × GSB 41	0.64	0.05	-0.04	0.73**	0.04	-3.17*
ADB 532 × TCB 37	-0.15	-0.19	0.21**	0.50	0.02	-2.35
ADB 532 × SUVIN	0.65	-0.15	-0.05	-0.52	-0.03	2.11
WGCV 48 × GSB 40	0.76*	-0.72	-0.04	0.08	-0.05	-2.92
WGCV 48 × DB 16	-0.17	-0.34	-0.14**	0.27	-0.06	-3.38*
WGCV 48 × DB 11	0.16	1.20**	0.09**	-0.19	0.03	9.56**
WGCV 48 × GSB 41	-0.54	-0.06	0.06	-0.76**	0.12*	-3.06*
WGCV 48 × TCB 37	0.53	-0.73	-0.04	0.45	-0.07	1.17
WGCV 48 × SUVIN	-0.74*	0.64	0.07*	0.15	0.03	-1.36
MR 786 × GSB 40	-0.80*	0.25	-0.06	-0.78**	-0.11*	-7.62**
MR 786 × DB 16	-0.24	-0.17	0.03	0.30	0.09	-1.48
MR 786 × DB 11	0.08	-0.74	-0.07*	-0.47	-0.23**	-7.33**
MR 786 × GSB 41	0.99**	0.57	0.17**	0.69*	0.20**	10.21**
MR 786 × TCB 37	0.16	1.26**	0.12**	1.18**	0.18**	0.90
MR 786 × SUVIN	-0.19	-1.16**	-0.19**	-0.92**	-0.13*	5.31**
TSH 0250 × GSB 40	1.38**	-0.49	0.25**	0.48	0.02	33.18**
TSH 0250 × DB 16	0.18	0.49	0.01	0.30	0.16**	-5.33**
TSH 0250 × DB 11	-0.07	0.36	0.01	0.18	0.06	-3.10*
TSH 0250 × GSB 41	-1.50**	-0.17	-0.22**	-0.57*	0.02	-4.05**
TSH 0250 × TCB 37	0.57	-0.08	0.03	-0.09	-0.07	-13.46**
TSH 0250 × SUVIN	-0.56	-0.11	-0.06	-0.30	-0.19**	-7.24**
BS 37 × GSB 40	0.75*	1.16**	-0.01	1.78**	0.19**	8.00**
BS 37 × DB 16	-0.31	-0.76	0.06	-1.08**	-0.21**	-8.52**
BS 37 × DB 11	0.54	0.16	-0.07*	0.42	-0.02	-9.10**
BS 37 × GSB 41	-0.13	-0.12	0.03	0.44	-0.01	5.72**
BS 37 × TCB 37	0.41	-0.44	-0.11**	0.30	0.10*	-6.84**

BS 37 × SUVIN	-1.27**	-0.01	0.12**	-1.86**	-0.06	10.73**
SCS 793 × GSB 40	1.25**	-0.76	0.09**	-0.14	0.07	-9.40**
SCS 793 × DB 16	-0.61	0.14	-0.06	-0.62*	-0.03	5.26**
SCS 793 × DB 11	0.21	0.25	-0.03	1.46**	0.04	6.34**
SCS 793 × GSB 41	-0.52	0.67	0.03	-0.54	0.01	-0.31
SCS 793 × TCB 37	0.84*	0.22	0.03	0.10	0.02	-4.15**
SCS 793 × SUVIN	-1.16**	-0.52	-0.06	-0.25	-0.11*	2.27
MCU 5 × GSB 40	0.75*	0.80*	-0.05	2.61**	0.13*	-7.65**
MCU 5 × DB 16	0.16	-0.96*	-0.12**	-0.88**	-0.15**	0.11
MCU 5 × DB 11	-1.24**	0.21	-0.01	-0.66*	-0.05	-4.60**
MCU 5 × GSB 41	-0.33	-0.01	0.03	-1.04**	-0.11*	-1.43
MCU 5 × TCB 37	-0.23	-0.58	0.13**	-0.72*	0.11*	8.28**
MCU 5 × SUVIN	0.90*	0.54	0.02	0.69*	0.07	5.30**
L 1058 × GSB 40	-1.00**	0.03	0.01	-1.39**	-0.01	-7.36**
L 1058 × DB 16	-1.00**	-0.15	-0.10**	-1.19**	-0.10	-1.74
L 1058 × DB 11	0.92*	0.20	0.06	0.97**	0.13*	4.13**
L 1058 × GSB 41	0.73*	-0.72	0.06	0.58*	-0.14**	-1.43
L 1058 × TCB 37	-0.40	-0.21	-0.04	-0.19	0.02	2.36
L 1058 × SUVIN	0.76*	0.85*	0.02	1.23**	0.09	4.04**
L 762 × GSB 40	-0.76*	-0.28	-0.07*	-0.69*	-0.13*	-8.31**
L 762 × DB 16	0.10	0.93*	0.05	-0.19	0.04	-0.31
L 762 × DB 11	0.63	-0.94*	0.09**	0.37	0.13*	-0.87
L 762 × GSB 41	0.50	-0.31	0.03	-0.37	-0.06	-14.25**
L 762 × TCB 37	-0.69	0.22	0.05	-0.05	0.02	17.38**
L 762 × SUVIN	0.22	0.38	-0.14**	0.94**	-0.01	6.36**
SE (s <sub>ij</sub> )	0.36	0.40	0.03	0.28	0.05	1.56

**Table 4:** Estimates of *gca* and *sca* variances for different characters in inter- specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.) over three locations (pooled) during *kharif*, 2014-15

	2.5% span length (mm)	Micronaire value (10 <sup>-6</sup> g/inch)	Bundle strength (g/tex)	Uniformity ratio	Fibre elongation (%)	Lint yield plant <sup>-1</sup> (g)
$\sigma^2_{gca}$	0.399**	0.004**	0.025	0.205	0.002**	34.949**
$\sigma^2_{sca}$	0.331**	0.010**	0.564**	0.054	0.008**	47.246**
$\sigma^2_{gca}/\sigma^2_{sca}$	1.205	0.400	0.044	3.796	0.300	0.739

\*Significant at 5% level

\*\*Significant at 1% level

**Table 5:** The best heterotic inter-specific cotton hybrids identified for different quality characters based on overall performance over three locations during *kharif*, 2014-15

Character	hybrids	<i>Per se</i> performance	SCA effect	Standard heterosis	
				DCH 32	Mahalakshmi
2.5% span length (mm)	MCU 5 × SUVIN	37.97	0.90*	12.30**	10.36**
	MCU 5 × GSB 40	37.29	0.75*	10.29**	8.39**
	L 1058 × SUVIN	37.02	0.76*	9.51**	7.62**
Uniformity ratio	MR 786 × TCB 37	47.50	1.26**	4.41**	1.36
	WGCV 48 × DB 11	47.42	1.20**	4.22**	1.18
	BS 37 × GSB 40	47.22	1.16**	3.79**	0.77
Micronaire value (10 <sup>-6</sup> g/inch)	ADB 542 × DB 16	3.40	0.33**	34.06**	10.94**
	H 1442 × GSB 41	3.32	0.28**	30.65**	8.12**
	NDLH 1938 × DB 16	3.26	0.22**	28.28**	6.16**
Bundle strength (g/tex)	MCU 5 × GSB 40	30.17	2.61**	17.50**	13.80**
	H 1442 × DB 16	29.66	2.36**	15.51**	11.87**
	BS 37 × GSB 40	29.26	1.78**	10.35**	2.18
Fibre elongation (%)	NDLH 1938 × DB 16	5.25	0.14**	13.26**	6.66**
	BS 37 × GSB 40	5.19	0.19**	12.09**	5.56**
	MR 786 × GSB 41	5.15	0.20**	11.20**	4.72**
Lint yield plant <sup>-1</sup> (g)	H 1442 × GSB 41	83.71	15.37**	57.03**	40.36**
	TSH 0250 × GSB 40	83.08	33.18**	55.85**	39.31**
	ADB 542 × DB 16	79.60	14.28**	49.32**	33.47**

\*Significant at 5% level

\*\*Significant at 1% level

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