Original Research Article

Prediction of gene action, Heterosis and Combining ability to identify superior GMS based hybrids in Asiatic Cotton (*G. arboreum* L.)

Abstract

Nature of gene action and combining ability is valuable in determining whether heterosis is fixable or predictable. Thus, to know the nature of gene action of seed cotton yield and its components and fibre quality parameters, seventeen parents (15 males and two genetic male sterile lines) and 30 F1 crosses (genetic male sterility based) were evaluated in a line x tester mating design of Asiatic cotton (*Gossypium arboreum L*). Sufficient variability among hybrids and their parents was found as the mean squares of genotypes for all the traits including fibre quality parameters investigated were significant. The total genetic variability was partitioned to general combining ability (GCA) and specific combining ability (SCA) effects. GCA was significant for male parents HD-123, RG-270, CISA-59, CISA-64, CISA-65, CISA-66 and LD-694 for seed cotton yield (SCY); HD-123, RG-286 and DLSA-24 for bolls per plant; HD-123, CISA-59, PAIG-8/3, DLSA-9 and LD-694 for boll weight; female parent DS-5, male parents HD-123, RG-18, CISA-65, and PAIG-8/3 for ginning outturn (GOT%); RG--270, RG-286, PAIG-8/3, DLSA-9 and LD-694 for 2.5% span length (mm); RG-286, CISA-59, CISA-66, PAIG-8/3 and LD-694 for lower micronaire value having fineness and HD-400, RG-270, RG-286, RG-341 CISA-60, CISA-66, PAIG-8/3 and LD-694 for tenacity (g/tex) which were considered as good general combiners. Similarly among 30 cross combinations, SCA was positively significant for 10 crosses for seed cotton yield, 10 crosses for boll number, 10 crosses for boll weight, 9 crosses for GOT(%), 10 crosses for 2.5% span length and 8 crosses for fibre strength (gt/tex). Cluster III of Yield attributing traits, consisted of 9 crosses (C3, C6, C18, C20, C26, C22, C23, C24, C30, and C8) showed highest average seed cotton yield where as Cluster II of fibre quality traits consisted of 3 crosses (C2, C12, C15) showed highest average GOT(%) with highest tenacity (g/tex). Cross DS-5 x HD 123 for SCY and bolls per plant, DS-5 x DLSA 9 for boll weight, DS-5 x CISA 65 for GOT % , CISA-2 x CISA 66 for lower micronaire value (fibre fineness) showed significant estimation of heterosis in desirable direction and could be further utilized in future breeding programme for specific trait improvement.

Key words: Gene action, Combining ability, Seed cotton yield, Genetic male sterility, Cluster analysis

Introduction

Cotton is the most important commercial and vital cash crop of India called as “White Gold”, cultivated mainly for its fiber and other by-products important being the edible oil. It influences major economies of countries of the world such as USA, China, India, Pakistan, Uzbekistan, Australia, Africa and others. India is the only country in world where all the four cultivated species of cotton (tetraploid and diploid) viz., *G. hirsutum*, *G. barbadense*, *G. arboreum* and *G. herbaceum* are grown from north to deep south. *G. hirsutum* covers more than 90% of acreage while the diploids the least, however, the diploids are relatively tolerant to biotic as well as abiotic stresses including less inputs as compared to *G. hirsutum* (Verma et al., 2020). Desi or diploid cotton (*Gossypium arboreum* L.; 2n = 26) also known as Asiatic cotton has inherent ability to adapt adverse climatic conditions and well known for resistant to pests and diseases. They are still under cultivation in some part of India as farmers believe the sustainability of the yield in marginal soil and less management practices (Mehetre, 2015). After the introduction of Bt cotton in India, there was significant decrease in area of desi cotton. But there is a big demand of short staple length for denim and surgical cotton. As an alternative the diploid cotton may be taken if they are giving remuneration equal to or higher than *G. hirsutum*. The primary objective for any breeder is to enhance the yield per unit area, the fibre yield and improve its quality length, strength and fineness, particularly in cotton. Parents which are diverse genetically and geographically should be used for genetic gain, enhancement and improvement of yield and fibre quality in cotton per se. Yield being a complex character and components which contribute towards high yield potential in cotton need careful study. The first step in successful breeding program is to select most desired and appropriate parents. Several studies revealed the utility of combining ability analysis in cotton in predicting the prepotency on the basis of the genetic information. The direction of gene action provides a systematic approach for detection of appropriate parents and crosses in terms of estimation of general and specific combining abilities in both self and cross pollinated plants (Kempthorne, 1957). In any breeding programme, the proper choice of parents depending upon their combining ability is a pre-requisite. In the present investigation, Line x Tester mating design was used to obtain information on combining ability and heterosis for yield components and fibre quality traits of genotypes obtained from different eco-geographical regions of India. Findings of early researchers revealed that variation in seed cotton yield and its components were controlled by genes having additive and non-additive gene action. This method has been used by many workers for analysis and identification of potential combiners in early generation (Verma et al. 2004 & 2005; Tuteja and Verma, 2011; Verma et al., 2017). Therefore, seeing the importance of combining ability of parents from diverse eco-geographical regions for various characters in cotton, a total of 30 crosses involving two genetic male sterile lines and 15 male parents of Asiatic cotton (*G. arboreum*) was studied for gene action, heterosis and combining ability estimates.

Materials and Methods

The experimental material utilized for the present study, consisted of 15 genetically diverse male parents belonging to diverse eco-geographical regions, viz. from Northern zone of India: Punjab - LD-694; Haryana- HD-123, HD-400, CISA-59, CISA-60, CISA-64, CISA-65, CISA-66; Rajasthan- RG-270, RG-286, RG-341, RG-18, and from central and southern zone of India: Karnataka- PAIG-8/3, DLSA-24 and DLSA-9) and 2 female GMS lines, viz, DS 5 and CISA 2 and crossed in a line x tester mating design at the ICAR-Central Institute for Cotton Research, Regional Station, Sirsa, Haryana 1250 55, India (29°32′36.1″N and 75°02′18.8″E) during *kharif* seasons (April to October) in the year 2017-18. Fifteen parents and 30 crosses were grown in a Randomized Block Design (RBD) with three replications and crop geometry of 67.5 x 45cm. The details of crosses and their respective codes were given in Table 1. Five random plants were selected to record the data on number of bolls/plant, plant height, monopodia, sympodia and boll weight. The data on seed cotton yield was recorded on per plot of $10.8m^2$ basis and converted to kg/ha. All the seed cotton samples were cleaned and ginned carefully in the laboratory for estimation of GOT % (ginning outturn percentage) and analyzed for fibre quality parameters, viz. 2.5% span length, Micronaire value and tenacity on High Volume Instrument (HVI) as per the standard methods.

Statistical analysis: The data were used for statistical analysis using the method developed by Kempthorne (1957) with the help of OPSTAT computer program which was developed by Chaudhary Charan Singh Haryana Agricultural University, Hissar, Haryana 125 004, India (Sheoran et al., 1998). Heterosis (%) over mid parent or relative heterosis (RH) and better parent (HB) or Heterobeltiosis was calculated after computing heterosis of respective parent by using the following equations:

Heterosis over better parent (%) = (F1-BP) / BP x 100

Here, F1=Mean of F1 individuals

BP=Mean of the better parent values

Heterosis over mid parent (%) = (F1-MP)/ MP x 100

Here, F1=Mean of F1 individuals

MP=Mean of the mid parent values. Significance of heterosis was tested using ‘t’ test.

Cluster analysis: Cluster analysis of 30 crosses were done using JMP PRO 14 (SAS Institute Inc., Cary, NC) software using squared Euclidian distance method.

Results

The analysis of variable (Table. 2) indicated that the mean squares of genotypes for all the traits including fibre quality investigated were significantly different, indicating the presence of sufficient variability among hybrids and their parents. Hence, further analysis for combining ability was possible. The total genetic variability was partitioned to general combining ability (GCA) and specific combining ability (SCA). The variance due to GCA was lower than SCA for all the traits. Which is in accordance with previous results of Ahuja and Dhayal, 2007; Citin Kadeni et al., 2009; Verma et al., 2004, Tuteja and Verma, 2011; Tuteja and Banga, 2013. The results are similar with the findings of Rauf et al., 2006; Kumar et al., 2010; Monaicshree et al., 2013.

General combining ability

The GCA effects of parents are presented in Table 3. Estimates for seed cotton yield, the male parents HD-123, RG-270, CISA-59, CISA-64, CISA-65, CISA-66, LD-694 showed significant positive GCA effect and no female parent showed significant positive GCA effects, where as other RG-286, RG-18, RG-341, CISA-60, PAIG-8/3, DLSA-24, DLSA-9 showed significant negative GCA effects. For seed cotton yield, the male parents HD-123, RG-270, LD-694 and female parent CISA 2 appeared to be good general combiner. For number of bolls/plants, the male parent HD-123, RG-286, DLSA-24, and female parents CISA-2 were general good combiner. For GOT (%) HD-123, RG-18, CISA-65, PAIG-8/3 DS-5 showed significant positive GCA effect, so they may have good combinations. For boll weight male parent HD-123, CISA-59, PAIG-8/3, DLSA-9, LD-694 and no female parent showed significant positive GCA effects. For 2.5% span length the male parents RG-270, RG-286, PAIG-8/3, DLSA-9, LD-694 and CISA-2 female parents recorded significant positive GCA effects and observed to be good general combiner for this trait, this may be due to as the male parents are having blood of genotypes from Central and South zone whereas other male parents HD-123, RG-341, RG-18, CISA-59, CISA-64, CISA-65, andDS-5 female parent were having significant negative GCA effects which may not be advisable to use these parents for improving this trait. For mirconaire value male parents RG-286, CISA-59, CISA-66, PAIG-8/3, LD-694and CISA-2 female parent exhibited significant negative GCA effects and observed to be good general combiner as lower micronaire value increases the fineness of cotton fibre. For Tenacity the male parents HD-400, RG-270, RG-286, RG-341, CISA-60, CISA-66, PAIG-8/3, LD-694 and CISA-2 female parents recorded significant positive GCA effects and appeared to be good general combiner (Table 3). Karademir et al., (2008) also observed high yielding quality hybrids were deducted with significant SCA effects for seed cotton yield and fibre characteristics while crossing 4 lines and 7 testers in line X tester mating system. Kumar et al., (2017) also confirmed that in case of *G. hirsutum* male parents HS180 and PUSA-1803 were best general combiner for seed cotton yield, number of bolls, ginning out turn, seed index, lint index and number of monopods when evaluated through line x tester manner.

Specific combining ability

The positive significant specific combining ability effects for seed cotton yield were predicted from C2, C3, C4, C6, C12, C14, C20, C23, C24, C26 cross combinations while negative significant SCA effects were predicted from C5, C8, C9, C11, C17, C18, CISA C19, C21, C27, C29 cross combinations. For boll number C1, C4, C12, C13, C14, C17, C20, C23, C24C25, C26 crosses had positive and significant estimates for SCA effects, the maximum being in case of C26. In case of GOT (%) C1, C2, C5, C22, C23, C25, C26, C28 recorded significant positive SCA effects. For boll weight positive and significant estimates for SCA effects were predicted from C4, C7, C12, C14, C15, C21, C23, C24, C25, C26. The cross combinations C2, C5, C6, C7, C10, C12, C14, C15, C18, C19, C23, C24, C25, C28 showed positive and significant SCA effects for 2.5% span length. For cotton fibre fineness (micronaire value), negative SCA effects are desirable as lower the micronaire value fine will be the cotton fibre. Negative and significant SCA effects were obtained from C1, C2, C6, C7, C12, C13, C19, C26, C29, C30 cross combinations. The crosses C2, C7, C10, C11, C12, C16, C18, C19, C20, C28 had positive and significant SCA effects for tenacity. The present study based on genetic male sterility in cotton revealed that additive variances were significant for fibre fineness and non-additive as well as additive gene effects for seed cotton yield, boll number, boll weight, ginning percentage. 2.5% span length and Tenacity. Similarly among 30 cross combinations, SCA was positively significant for 10 crosses for seed cotton yield, 11 crosses for boll number, 10 crosses for boll weight, 14crosses for 2.5% span length, and 10 crosses for tenacity (Table 4). Similarly, Combining ability studies were carried out in cotton seed yield and fibre quality traits by utilizing 7 lines, 8 testers and their 56 hybrids significant sca effects for fiber quality traits in desirable direction in upland cotton by Srinivas et al., (2014).

Performance of Parents

The parents showed a significant variation in terms of seed cotton yield, ranged from 1128.60 kg/ha to 1915.17 kg/ha with an mean value of 155.19 kg/ha. The parent CISA-2 (1915.17 kg/ha) showed highest seed cotton yield followed by parent RG-286 (1833.73 kg/ha) on the other hand the parent PAIG-8/36 (1128.60 kg/ha) showed lowest Seed cotton yield. In terms of bolls per plant CISA-2 (43.17) showed best result among all the parents except HD-400 (30.3) which ranged from 30.3 to 43.17 with an mean value of 38.0. The highest Boll weight was observed for the parent RG-34 (3.00 g) followed by CISA-59 (2.67g), CISA-60 (2.47g) and CISA-65 (2.47g). The lowest Boll wt. was observed in the parent RG-18 (1.93g). All the parents showed significant variation in terms of GOT% varied from 32.10 to 39.67 with a mean value of 35.73. The highest GOT % (39.67) was resulted by the parent HD-123 followed by PAIG-8/3 (37.5) and CISA-65 (33.6). The parent HD-123 (39.67) showed highest GOT % where as the CISA-59 (32.1) showed lowest GOT %. In case of 2.5% Span Length except HD-123 (20.7cm) and HD-400 (20.3cm) all other parents showed a significantly higher value for the trait. The highest 2.5% Span Length was resulted in the parent DLSA-24 (25.7cm) followed by CISA-64 (25.4 cm). The trait ranged from 20.30cm to 25.7cm with an average of 23.60cm. The parents showed significant variation in terms of MIC ranged from 5.80 to 8.20 with an average of 6.64. The parent HD-123 (8.20) showed highest MIC followed by RG-270 (7.10) and RG-34 (7.17) where as the parent LD-694 (5.80) and CISA-2 (5.80) showed lowest micronaire value. As micronaire value signifies the fibre fineness, so lower micronaire value of any parent is desirable for the trait improvement. In case of tenacity, parents showed sufficient variation ranged from 16.17 g/tex to 20.33 g/tex with an average value of 18.65 g/tex. The parent DLSA-24 (20.33 g/tex), LD-694 (20.23 g/tex) and CISA-2 (20.23 g/tex) showed the best result in terms of tenacity where as the parents HD-123 (16.17 g/tex) and RG-270 (16.6 g/tex) showed lower performance in terms of tenacity (Table 5).

Performance of the crosses

Thirty cross combination resulted from crossing 15 male and 2 female parents were evaluated for yield traits and fibre quality traits. Cluster analysis for yield traits (Seed cotton Yield, Boll number/ plant and boll weight) showed four cluster with 8, 7, 9 and 6 number of crosses respectively (Table 6 & fig. 1). Cluster III, consisted of 9 crosses (C3, C6, C18, C20, C26, C22, C23, C24, C30, and C8) showed highest average seed cotton yield where as Cluster I consisted of 8 crosses (C1, C4, C16, C12, C14, C7, C25, C15) showed highest average boll no./ plant and boll weight (fig. 1). In case of fibre quality traits, the crosses grouped into four clusters consisted of 8, 3, 3 and 16 crosses respectively (fig. 2). Cluster II consisted of 3 crosses (C2, C12, C15) showed highest average GOT(%) with highest tenacity (g/tex) also. On the other hand Cluster III consisted of 3 crosses (C19, C30, C26) showed highest average 2.5% span length and lowest micronaire value (Table 7 & fig. 2). Crosses with lower micronaire value is desirable as lower the micronaire value higher the fibre fineness of that cross will have (Supplementary Table 1). The crosses with negative significant heterosis value for the trait micronaire were identified through the estimation of heterosis over mid and better parent value. It is not so easy to identify the crosses performed better the traits. To identify the best performing cross for in particular trait magnitude of heterosis was also estimated.

Estimation of Heterosis

Thirty cross combination resulted from crosses among 15 male and 2 female parents were evaluated for heterosis over both mid parent and better parent. The crosses with more than 10% positive heterosis were considered as better performers among all the crosses. The magnitude of heterosis was estimated for three yield attributing (SCY, Boll no. and Boll wt.) and four fibre quality (GOT%, 2.5% span length, micronaire and tenacity) traits. For Seed Cotton Yield six crosses showed more than 10% heterosis over mid parent where as crosses C1 (DS-5x HD-123) and C15 (DS-5 x LD-694) showed more than 10% heterosis over both mid parent and better parent. In case of Boll number/ Plant five crosses (C1, C4, C13, C14, C16) showed significantly higher heterosis value (>10%) over both mid parent and better parent. The similar kind of trend was also shown by the trait boll weight. Four crosses (C12, C14, C15, and C21) showed more than 10% heterosis over both mid and better parent value (Table. 8, Supplementary Table 2)

In case of GOT(%) 9 cross combination (C2, C5, C6, C7, C9, C10, C15, C22, C25) performed better in terms of heterosis over mid parent and 6 (C2, C5, C6, C9, C10, C15) crosses showed significant higher positive heterosis of more than 10% over both mid and better parent. For 2.5% span length no cross combination showed any positive heterosis. The only cross C2 showed only positive heterosis over mid parent in terms of tenacity. In case of Micronaire value, crosses (C1, C2, C7, C16, C19, C26) showed significant negative heterosis over mid parent. For trait fibre fineness lowered micronaire is suitable for the trait improvement (Table. 9 and Supplementary Table 2). Twelve lines of *G. hirsutum* and five testers of *G. barbadense* were crossed in line x tester manner shown desirable heterosis for seed cotton yield along with other yield components in *G. barbadense* (Adsare et al., 2017). Samreen et al., (2008) also observed eighty four crosses obtained by crossing 12 lines with seven testers in line x tester fashion showed significant standard heterosis for most of the yield and fibre quality traits.

Discussion

The present study was done to identify the suitable parents and crosses for higher yield and fibre quality in desi cotton. Female parent CISA-2 showed highest performance in term of seed cotton yield and bolls per plant where as male parent RG-341 showed highest performance in terms of boll weight. Whereas, the cross combinations which involved CISA-2 as female parent showed more than 10% heterosis in terms of SCY, boll weight and bolls per Plant. The crosses, C16 and C26 for SCY, C16 for bolls/ plant, C21 for boll weight showed more than 10% heterosis. On the other hand, the crosses involving DS-5 as female parent and HD-123, HD-450, RG-18 and LD-694 as male parents (C1, C2, C6, C15) showed significant positive heterosis in terms of SCY. Cluster analysis result also confirmed that the crosses C6 and C26 grouped under Cluster III having highest average SCY where as C1, C16, C15 were under Cluster-I having second highest seed cotton yield for the cluster of yield attributing traits (Fig. 1). For Boll/ plant, the crosses involving HD-123, RG-284, DLSA-24, DLSA-9 as male and DS-5 as female (C1, C4, C13, C14) showed >10% positive heterosis and also clustered under Cluster-I (fig. 1) having highest average value of bolls per plant. In case of boll weight, C12, C14, C15 grouped under Cluster-I having highest boll wt. also showed more than 10% heterosis over both mid parent and better parent.

In terms of fibre quality traits HD-123 showed better performance for GOT(%), where as DLSA-24 showed its best performance for 2.5% span length and tenacity traits. Interestingly heterosis result confirmed the crosses involving HD-123 could not show more than 10% heterosis in terms of GOT(%). But the crosses involving HD-400, RG-341, RG-18, CISA-59, CISA-64, CISA-65 and LD-694 as male parent with DS-5 as female parent showed more than 10% heterosis estimation for GOT% over both mid parent and better parent. These crosses (C2, C5, C6, C7, C9, C10, C15) can be used for further improvement of GOT(%). Cluster analysis for fibre quality also confirmed the similar trend that, for GOT% except C7 the crosses with higher estimation (>10%) of heterosis were grouped in Cluster II (with highest GOT%) and in Cluster I (second highest average GOT%) (fig. 2). In case of Micronaire value, crosses (C1, C2, C7, C16, C19, C26) showed significant negative heterosis over mid parent of with C19 and C26 were grouped in Cluster III (fig. 2) with lowest micronaire value. For the trait tenacity the cross C2 (DS-5 x HD-400) only showed significant positive heterosis over mid parent value and also clustered under Cluster II (fig. 2) having highest average value of tenacity. Our result clearly showed that the identified crosses involving the parents can be used for future breeding programme for development of the hybrids.

Conclusion

The identified crosses viz. DS-5 x HD 123 for Seed Cotton Yield and bolls/plant, DS-5 x DLSA 9 for boll weight, DS-5 x CISA 65 for GOT (%), CISA-2 x CISA 66 for micronaire (fibre fineness) showed significant estimation of heterosis in desirable direction and could be further utilized in future breeding programme for specific trait improvement.

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Table 1 Details of the crosses and their respective codes.

Crosses	Code	Crosses	Code	Crosses	Code
DS 5 x HD 123	C1	DS 5 x CISA 66	C11	CISA 2 x RG 18	C21
DS 5 x HD 400	C2	DS 5 x PAIG 8/3	C12	CISA 2 x CISA 59	C22
DS 5 x RG 270	C3	DS 5 x DLSA 24	C13	CISA 2 x CISA 60	C23
DS 5 x RG 286	C4	DS 5 x DLSA 9	C14	CISA 2 x CISA 64	C24
DS 5 x RG 341	C5	DS 5 x LD 694	C15	CISA 2 x CISA 65	C25
DS 5 x RG 18	C6	CISA 2 x HD 123	C16	CISA 2 x CISA 66	C26
DS 5 x CISA 59	C7	CISA 2 x HD 400	C17	CISA 2 x PAIG 8/3	C27
DS 5 x CISA 60	C8	CISA 2 x RG 270	C18	CISA 2 x DLSA 24	C28
DS 5 x CISA 64	C9	CISA 2 x RG 286	C19	CISA 2 x DLSA 9	C29
DS 5 x CISA 65	C10	CISA 2 x RG 341	C20	CISA 2 x LD 694	C30

Table 2 Analysis of Variance for Line x Tester mating design for various traits in *G. arboreum L.*

Source of Variation	**DF**	**Seed Cotton Yield (kg/ha)**	**Bolls/ Plant**	**Boll wt(g)**	**GOT (%)**	**2.5%Span length (cm)**	**MIC**	**Tenacity (g/tex)**
Blocks	2	9,770.953	86.019	0.070	1.982	1.384	0.004	0.628
Parents	16	241,035.502**	31.468*	0.157**	7.706**	6.195**	0.890**	4.891**
Males	14	239,648.578**	29.371	0.177**	8.757**	6.902**	0.837**	4.851**
Female	1	62,201.553	73.500	0.000	0.375	0.060	0.540	1.042
Male vs Female	1	439,286.381	18.791	0.025	0.320	2.428	1.991	9.302
Crosses	29	282,756.126**	113.805**	0.253**	9.752**	7.295**	0.662**	3.877**
Parents vs. Crosses	1	137,023.199	49.785	0.841	191.239	89.424	0.051	37.511
Error	92	2,344.036	12.259	0.026	0.253	0.111	0.038	0.071
Total	140	12,428,712.123	5,153.447	13.183	624.582	413.108	22.151	236.032
σ^2_{gca}		642.389	2.172	-0.000	1.435	0.173	0.051	0.011
σ^2_{sca}		62,834.380	25.174	0.080	2.447	1.376	0.128	0.922
σ^2_A		1,284.778	4.343	-0.000	2.869	0.345	0.102	0.022
σ^2_D		62,834.380	25.174	0.080	2.447	1.376	0.128	0.922
$\sigma^2_{gca} / \sigma^2_{sca}$		0.010	0.086	0.000	0.586	0.126	0.398	0.012
$(\sigma^2_D / \sigma^2_A)^{½}$		48.907	5.796	0.000	0.853	3.988	1.255	41.909
Contribution of lines		67.13	61.30	45.92	32.86	68.32	54.11	63.25
Contribution of testers		0.26	3.94	3.79	28.98	3.33	14.26	1.07
Contribution of lines x testers		32.61	34.75	50.31	38.16	28.34	31.63	35.68

**Significant at 1% and 5% probability level of significant, DF: degree of freedom

Table 3 Estimates of general combining ability (GCA) effects for various traits in *G. arboreum* L.

Entry	SCY (kg/ha)	Bolls/ Plant	Boll wt. (g)	GOT (%)	2.5% Span Length (cm)	MIC	Tenacity (g/tex)
Lines							
DS5	-15.50	-1.20	0.056	0.954**	-0.280*	0.174*	-0.116
CISA 2	15.50	1.20	-0.056	-0.954**	0.280*	-0.174*	0.116
SE±	**5.267**	**0.267**	**0.017**	**0.064**	**0.041**	**0.024**	**0.033**
Testers							
HD-123	446.43**	14.74**	0.217**	0.879**	-2.394**	0.166*	-1.590**
HD-400	-12.07	-4.19**	-0.267**	-0.004	-0.011	0.132	1.010**
RG-270	211.21**	0.33	-0.200**	-1.588**	1.256**	0.116	1.110**
RG-286	-65.77**	4.38**	0.050	0.229	1.939**	-0.501**	0.610**
RG-341	-26.16	-1.99*	-0.200**	-0.621**	-0.528**	0.216**	0.110**
RG-18	-36.76*	-0.99	0.000	1.546**	-1.778**	0.532**	-1.640**
CISA-59	146.64**	-0.56	0.133**	0.346	-1.744**	-0.234**	-0.473**
CISA-60	-157.71**	-1.56	-0.100*	0.079	-0.011	0.166*	0.643**
CISA-64	158.78**	-2.11**	-0.117*	0.312	-0.411**	0.032	-0.707**
CISA-65	114.89**	-2.07**	-0.117*	1.529**	-0.344**	0.566**	-0.573**
CISA-66	53.56**	-7.37**	-0.250**	-0.638**	0.006	-0.551**	0.543**
PAIG-8/3	-322.87**	-0.54	0.250**	1.212**	0.989**	-0.184**	0.843**
DLSA-24	-532.09**	2.71**	0.000	-1.688**	0.172	0.166*	-0.623**
DLSA-9	-298.64**	1.08	0.283**	-1.438**	0.672**	-0.051	-0.290**
LD-694	320.58**	-1.86*	0.317**	-0.154	2.189**	-0.568**	1.027**
SE±	**19.706**	**0.999**	**0.062**	**0.239**	**0.155**	**0.088**	**0.124**

**Significant at 1% and 5% probability level of significant

Table 4 Estimates of specific combining ability (SCA) effects for various traits in *G. arboreum* L.

Crosses	SCY (kg/ha)	Bolls/ Plant	Boll wt. (g)	GOT (%)	2.5% Span Length (cm)	MIC	Tenacity (g/tex)
DS 5 x HD 123	-15.60	1.62**	-0.039	0.746**	-0.037	-0.208**	-1.001**
DS 5 x HD 400	177.33**	-3.08**	0.011	1.129**	1.180**	-0.441**	1.166**
DS 5 x RG 270	35.68**	0.00	-0.022	0.312	-0.220*	0.009	-0.734**
DS 5 x RG 286	113.07**	5.62**	0.228**	0.162	-0.470**	0.426**	-0.734**
DS 5 x RG 341	-109.72**	-1.68**	-0.056	2.312**	0.430**	0.009	-0.968**
DS 5 x RG 18	192.52**	1.02	-0.222**	-0.288	0.713**	-0.174**	0.049
DS 5 x CISA 59	12.08	-0.88	0.144**	-1.221**	0.647**	-0.141**	1.082**
DS 5 x CISA 60	-347.27**	-2.68**	-0.156**	-0.588**	-0.953**	-0.074	-0.101
DS 5 x CISA 64	-36.95**	-1.56*	-0.239**	0.312	-1.620**	-0.008	0.016
DS 5 x CISA 65	-20.30	-2.53**	-0.406**	-0.404**	0.780**	-0.108	0.782**
DS 5 x CISA 66	-388.87**	-9.06**	-0.106**	-2.204**	-1.070**	0.642**	0.232**
DS 5 x PAIG 8/3	166.50**	3.27**	0.261**	-0.288	0.713**	-0.158**	0.532**
DS 5 x DLSA 24	14.78	2.82**	0.078	-1.321**	-1.003**	-0.141**	-0.368**
DS 5 x DLSA 9	221.20**	4.09**	0.361**	-0.004	0.430**	0.209**	0.166
DS 5 x LD 694	-14.45	3.0588	0.161**	1.346**	0.480**	0.159**	-0.118
CISA 2 x HD 123	15.60	-1.62**	0.039	-0.746**	0.037	0.208**	1.001**
CISA 2 x HD 400	-177.33**	3.08**	-0.011	-1.129**	-1.180**	0.441**	-1.166**
CISA 2 x RG 270	-35.68**	0.00	0.022	-0.312	0.220*	-0.009	0.734**
CISA 2 x RG 286	-113.07**	-5.62**	-0.228**	-0.162	0.470**	-0.426**	0.734**
CISA 2 x RG 341	109.72**	1.68**	0.056	-2.312**	-0.430**	-0.009	0.968**
CISA 2 x RG 18	-192.52**	-1.02	0.222**	0.288	-0.713**	0.174**	-0.049
CISA 2 x CISA 59	-12.08	0.88	-0.144**	1.221**	-0.647**	0.141**	-1.082**
CISA 2 x CISA 60	347.27**	2.68**	0.156**	0.588**	0.953**	0.074	0.101
CISA 2 x CISA 64	36.95**	1.56*	0.239**	-0.312	1.620**	0.008	-0.016
CISA 2 x CISA 65	20.30	2.53**	0.406**	0.404**	-0.780**	0.108	-0.782**
CISA 2 x CISA 66	388.87**	9.06**	0.106**	2.204**	1.070**	-0.642**	-0.232**
CISA 2 x PAIG 8/3	-166.50**	-3.27**	-0.261**	0.288	-0.713**	0.158**	-0.532**

CISA 2 x DLSA 24	-14.78	-2.82**	-0.078	1.321**	1.003**	0.141**	0.368**
CISA 2 x DLSA 9	-221.20**	-4.09**	-0.361**	0.004	-0.430**	-0.209**	-0.166
CISA 2 x LD 694	14.45	-3.05**	-0.161**	-1.346**	-0.480**	-0.159**	0.118
SE±	**19.706**	**0.999**	**0.062**	**0.239**	**0.155**	**0.088**	**0.124**

**Significant at 1% and 5% probability level of significant

Table 5 Mean Performance of Parents (males and females)

Entry	**SCY (kg/ha)**	**Bolls/ Plant**	**Boll wt (g)**	**GOT (%)**	**2.5%Span Length (cm)**	**MIC**	**Tenacity (g/tex)**
DS5	1,711.53	36.17	2.30	36.20	24.10	6.40	19.40
CISA 2	1,915.17	43.17	2.30	35.70	24.30	5.80	20.23
HD-123	1,517.90	38.73	2.17	39.67	20.70	8.20	16.17
HD-400	1,146.73	30.30	2.40	36.00	20.30	6.80	18.80
RG-270	1,700.53	36.10	2.20	34.70	23.50	7.10	16.60
RG-286	1,833.73	36.33	2.37	36.10	24.70	6.50	18.13
RG-341	1,733.03	39.90	3.00	36.70	24.10	7.17	17.33
RG-18	1,147.07	41.50	1.93	35.60	22.50	6.43	17.63
CISA-59	1,777.67	35.80	2.67	32.10	22.60	6.73	19.73
CISA-60	1,765.57	38.50	2.47	36.27	23.50	6.60	18.70
CISA-64	1,747.77	39.27	2.43	35.20	25.40	6.70	19.80
CISA-65	1,500.73	37.57	2.47	33.60	23.50	6.77	18.73
CISA-66	1,788.63	37.40	2.40	35.70	24.53	6.70	17.93
PAIG-8/3	1,128.60	41.03	2.20	37.50	23.40	6.53	17.83
DLSA-24	1,244.13	34.97	2.23	34.50	25.70	6.20	20.33
DLSA-9	1,136.47	36.17	2.30	36.20	24.10	6.47	19.40
LD-694	1,710.93	43.17	2.30	35.70	24.30	5.80	20.23
Mean	**1,559.19**	**38.00**	**2.36**	**35.73**	**23.60**	**6.64**	**18.65**
C.D.	**77.479**	**3.814**	**0.175**	**0.228**	**0.152**	**0.197**	**0.248**

SE(m)	**26.775**	**1.318**	**0.060**	**0.079**	**0.052**	**0.068**	**0.086**
C.V.	**2.974**	**6.007**	**4.435**	**0.382**	**0.385**	**1.776**	**0.795**
Range	1128.60-1915.17	30.30-43.17	1.93-3.00	32.10-39.67	20.30-25.70	5.80-8.20	16.17-20.33

Table 6 Cluster analysis for yield attributing traits

Cluster no.	**No. of Crosses**	**Cluster colour**	**SCY (kg/ha)**			**Boll no.**			**Boll weight.**		
			Mean	**SD**	**Range**	**Mean**	**SD**	**Range**	**Mean**	**SD**	**Range**
1	8	🟥	1779.65	231.10	1452.23-2101.63	44.59	6.67	36.60-51.40	2.59	0.19	2.40-2.90
2	7	🟩	1552.07	185.55	1273.3-1773.87	33.30	6.01	21.6-39.33	1.91	0.09	1.73-2.00
3	9	🟦	1850.39	112.05	1723.17 - 2082.03	39.69	2.05	35.53-42.13	2.10	0.13	1.97-2.3
4	6	🟨	1161.33	123.93	1091.30-1410.33	38.37	3.34	33.80-43.57	2.16	0.15	2.00-2.37

Table 7 Cluster analysis for fibre quality traits

Cluster no.	**No. of Crosses**	**Cluster Colour**	**GOT (%)**			**2.5% span Length**			**Mic**			**Tenacity (g/tex)**		
			Mean	**SD**	**Range**	**Mean**	**SD**	**Range**	**Mean**	**SD**	**Range**	**Mean**	**SD**	**Range**

1	8	🟥	39.85	0.80	38.77-40.8	20.47	1.03	19.23-22.1	6.93	0.30	6.33-7.23	16.28	0.80	14.87-17.67
2	3	🟩	40.19	0.14	40.03-40.3	23.51	0.76	22.83-24.33	6.42	0.05	6.37-6.47	18.94	0.64	18.37-19.63
3	3	🟦	37.24	1.54	35.7-38.77	23.95	0.67	23.3-24.63	5.48	0.24	5.23-5.7	18.62	0.55	18-19.03
4	16	🟨	37.09	1.40	34.27-39.5	22.01	1.27	19.87-23.7	6.68	0.23	6.17-7	17.77	0.76	16.47-19.53

Table 8 Estimation of Heterosis over mid parent and better parent (>10%) yield attributing traits

SCY (kg/ha)	**Bolls/ Plant**	**Boll wt. (g)**
(MP, BP)	(MP, BP)	(MP, BP)
C1 (26.30**,19.16**)	C1 (45.26**, 40.45**)	C1 (8.96**, 5.80**)
C2 (24.12**, 3.64**)	C3 (6.18**, 6.08**)	C4 (8.57**, 7.04**)
C3 (8.76**, 8.41**)	C4 (32.51**, 32.20**)	C12 (22.963, 20.29**)
C6 (23.44**,3.09**)	C13 (22.49**, 20.46**)	C13 (2.941, 1.45)
C15 (11.82**,11.87**)	C14 (19.45**, 19.45**)	C14 (26.087, 26.09**)
C16 (22.44**, 9.74**)	C16 (30.81**, 24.09**)	C15 (18.841, 18.84**)
C26 (12.43**, 8.71**)		C16 (7.463, 4.35**)
C30 (8.91**, 3.11**)		C21 (11.811, 2.90**)

Table 9 Estimation of Heterosis over mid parent and better parent for fibre quality traits

GOT (%)	**MIC**
(MP,BP)	(MP,BP)

C1 (7.38**, 2.69**)	C4 (3.88**, 3.08**)
C2 (11.45**, 11.14**)	C6 (11.17**, 10.88**)
C3 (6.72**, 4.51**)	C8 (5.64**, 4.04**)
C4 (9.27**, 9.12**)	C9 (3.82**, 1.49
C5 (11.93**, 11.17**)	C10 (9.87**, 6.90**)
C6 (12.44**, 11.51**)	C11 (4.84**, 2.49**)
C7 (11.96**, 5.62**)	C13 (7.94**, 6.25**)
C8 (6.53**, 6.43**)	C14 (7.77**, 7.22**)
C9 (11.30**, 9.76**)	C17 (11.11**, 2.94**)
C10 (15.28**, 11.14**)	C21 (16.62**, 10.88**)
C12 (8.64**, 6.76**)	C23 (7.53**, 1.01)
C14 (4.05**, 4.05**)	C25 (13.00**, 4.93**)
C15 (12.10**, 11.33**)	C28 (12.22**, 8.60**)
C19 (3.81**, 3.23**)	**Tenacity (g/tex)**
C21 (9.49**, 9.34**)	C2 (2.79**, 1.20)
C22 (14.36**, 8.59**)	
C23 (5.23**, 4.41**)	
C24 (4.94**, 4.20**)	
C25 (12.94**, 9.62**)	
C26 (8.59**, 8.59**)	
C27 (5.74**, 3.20**)	
C28 (4.94**, 3.18**)	

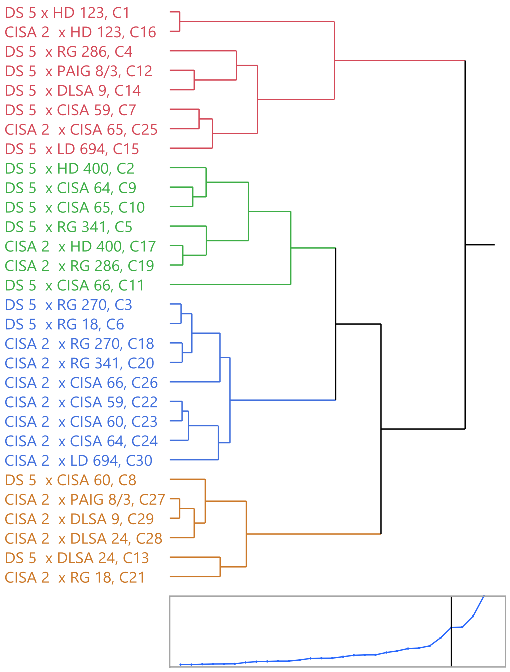

Figure 1. Cluster analysis of the crosses for yield attributing traits involving thirty cross combinations

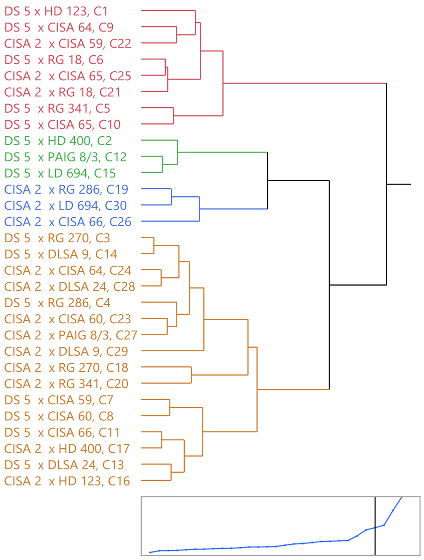

Figure 2. Cluster analysis of the crosses for fibre quality traits involving thirty cross combinations

Supplementary table 1: Mean Performance of Crosses

Crosses	SCY (Kg/ha)	Plant ht (cm)	Mono pods	Sym pods	Bolls/ Plant	Boll wt (g)	GOT (%)	2.5% Span length (cm)	MIC	Tenacity (g/tex)
DS 5 x HD 123	2,039.43	168.30	4.57	22.47	54.40	2.43	40.73	19.23	6.73	14.87
DS 5 x HD 400	1,773.87	189.83	4.63	13.73	30.77	2.00	40.23	22.83	6.47	19.63
DS 5 x RG 270	1,855.50	168.37	3.93	14.87	38.37	2.03	37.83	22.70	6.90	17.83
DS 5 x RG 286	1,655.90	206.87	4.20	19.03	48.03	2.53	39.50	23.13	6.70	17.33
DS 5 x RG 341	1,472.73	213.90	4.80	14.40	34.37	2.00	40.80	21.57	7.00	16.60
DS 5 x RG 18	1,764.37	218.17	4.13	17.93	38.07	2.03	40.37	20.60	7.13	15.87
DS 5 x CISA 59	1,767.33	158.57	3.43	15.53	36.60	2.53	38.23	20.57	6.40	18.07
DS 5 x CISA 60	1,103.63	218.00	4.13	11.63	33.80	2.00	38.60	20.70	6.87	18.00
DS 5 x CISA 64	1,730.43	215.67	4.67	15.13	34.37	1.90	39.73	19.63	6.80	16.77
DS 5 x CISA 65	1,703.20	180.03	3.60	15.60	33.43	1.73	40.23	22.10	7.23	17.67
DS 5 x CISA 66	1,273.30	118.67	3.43	8.83	21.60	1.90	36.27	20.60	6.87	18.23
DS 5 x PAIG 8/3	1,452.23	196.20	4.03	13.07	40.77	2.77	40.03	23.37	6.43	18.83
DS 5 x DLSA 24	1,091.30	180.67	3.27	14.63	43.57	2.33	36.10	20.83	6.80	16.47
DS 5 x DLSA 9	1,531.17	166.33	3.50	20.87	43.20	2.90	37.67	22.77	6.93	17.33

DS 5 x LD 694	1,914.73	218.23	3.60	15.43	39.23	2.73	40.30	24.33	6.37	18.37
CISA 2 x HD 123	2,101.63	217.27	4.73	12.10	53.57	2.40	37.33	19.87	6.80	17.10
CISA 2 x HD 400	1,450.20	224.73	4.77	15.57	39.33	1.87	36.07	21.03	7.00	17.53
CISA 2 x RG 270	1,815.13	199.90	4.63	15.53	40.77	1.97	35.30	23.70	6.53	19.53
CISA 2 x RG 286	1,460.77	216.13	4.20	13.87	39.20	1.97	37.27	24.63	5.50	19.03
CISA 2 x RG 341	1,723.17	207.40	4.23	12.87	40.13	2.00	34.27	21.27	6.63	18.77
CISA 2 x RG 18	1,410.33	178.83	4.30	12.33	38.43	2.37	39.03	19.73	7.13	16.00
CISA 2 x CISA 59	1,774.17	224.40	4.47	16.67	40.77	2.13	38.77	19.83	6.33	16.13
CISA 2 x CISA 60	1,829.17	203.23	4.73	14.53	41.57	2.20	37.87	23.17	6.67	18.43
CISA 2 x CISA 64	1,835.33	193.80	4.77	10.20	39.90	2.27	37.20	23.43	6.47	16.97
CISA 2 x CISA 65	1,774.80	198.00	4.73	11.73	40.90	2.43	39.13	21.10	7.10	16.33
CISA 2 x CISA 66	2,082.03	199.70	3.23	11.30	42.13	2.00	38.77	23.30	5.23	18.00
CISA 2 x PAIG 8/3	1,150.23	203.17	4.33	13.43	36.63	2.13	38.70	22.50	6.40	18.00
CISA 2 x DLSA 24	1,092.73	222.80	4.13	12.27	40.33	2.07	36.83	23.40	6.73	17.43
CISA 2 x DLSA 9	1,119.77	215.00	4.57	13.97	37.43	2.07	35.77	22.47	6.17	17.23
CISA 2 x LD 694	1,974.63	199.67	4.00	12.83	35.53	2.30	35.70	23.93	5.70	18.83
C.D.	**81.86**	**25.31**	**1.04**	**1.77**	**4.15**	**0.259**	**0.992**	**0.645**	**0.367**	**0.516**
SE(m)	**28.842**	**8.917**	**0.368**	**0.623**	**1.462**	**0.091**	**0.349**	**0.227**	**0.129**	**0.182**
C.V.	**3.076**	**7.824**	**15.184**	**7.486**	**6.451**	**7.177**	**1.586**	**1.793**	**3.390**	**1.791**

Supplementary table 2: Estimation of Heterosis over mid parent and better parent for seed cotton yield and fibre quality traits.

Crosses	**SCY (Kg/ha)**		**Plant ht. (cm)**		**Monopods**		**Sympods**		**Bolls/ Plant**		**Boll wt. (g)**		**GOT (%)**		**2.5% Span length (cm)**		**MIC**		**Tenacity (g/tex)**	
	MP	BP	MP	BP	MP	BP	MP	BP	MP	BP	MP	BP	MP	BP	MP	BP	MP	BP	MP	BP
DS 5 x HD 123	26.30**	19.16**	1.071	-3.42**	45.75**	44.21**	79.02**	70.63**	45.26**	40.45**	8.96**	5.80**	7.38**	2.69**	-14.14**	-20.19**	-7.76**	-17.89**	-16.40**	-23.37**
DS 5 x HD 400	24.12**	3.64**	26.49**	8.93**	40.40**	32.38**	1.85	-0.483	-7.42**	-14.93**	-14.89**	-16.67**	11.45**	11.14**	2.85**	-5.26**	-2.02	-4.90**	2.79**	1.20
DS 5 x RG 270	8.76**	8.41**	-2.32*	-3.39**	33.33**	26.88**	20.22**	12.91**	6.18**	6.08**	-9.63**	-11.59**	6.72**	4.51**	-4.62**	-5.81**	2.22**	-2.82**	-0.93	-8.08**
DS 5 x RG 286	-6.59**	-9.70**	19.32**	18.71**	35.48**	35.49**	50.26**	44.56**	32.51**	32.20**	8.57**	7.04**	9.27**	9.12**	-5.19**	-6.34**	3.88**	3.08**	-7.64**	-10.65**
DS 5 x RG 341	-14.49**	-15.02**	25.61**	22.74**	47.69**	41.18**	16.29**	9.37**	-9.64**	-13.87**	-24.53**	-33.33**	11.93**	11.17**	-10.51**	-10.51**	3.19**	-2.33*	-9.62**	-14.43**
DS 5 x RG 18	23.44**	3.09**	17.84**	11.31**	5.98**	-12.06**	31.70**	27.49**	-1.974	-8.27**	-3.94**	-11.59**	12.44**	11.51**	-11.59**	-14.52**	11.17**	10.88**	-14.31**	-18.21**
DS 5 x CISA 59	1.30	-0.58	-2.90**	-9.01**	6.74**	3.00**	20.41**	17.98**	1.71	1.20	2.01	-5.00**	11.96**	5.62**	-11.92**	-14.66**	-2.54**	-4.95**	-7.67**	-8.45**
DS 5 x CISA 60	-36.52**	-37.49**	24.95**	24.81**	35.52**	33.33**	-11.08**	-11.65**	-9.46**	-12.21**	-16.08**	-18.92**	6.53**	6.43**	-13.03**	-14.11**	5.64**	4.04**	-5.51**	-7.22**
DS 5 x CISA 64	0.05	-0.99	28.28**	23.76**	60.00**	50.54**	10.19**	5.83**	-8.88**	-12.48**	-19.718	-21.92**	11.30**	9.76**	-20.67**	-22.70**	3.82**	1.49	-14.46**	-15.32**
DS 5 x CISA 65	6.04**	-0.49	35.16**	3.31**	-27.27**	-47.059	31.28**	18.48**	-9.31**	-11.00**	-27.273	-29.73**	15.28**	11.14**	-7.14**	-8.30**	9.87**	6.90**	-7.34**	-8.94**
DS 5 x CISA 66	-27.24**	-28.81**	-32.10**	-32.29**	8.42**	6.19**	-29.14**	-32.91**	-41.28**	-42.25**	-19.149	-20.83**	0.88	0.18	-15.28**	-16.03**	4.84**	2.49**	-2.32**	-6.01**
DS 5 x PAIG 8/3	2.27*	-15.15**	6.70**	1.40	12.04**	-1.63	2.89**	-0.76	5.61**	-0.65	22.963	20.29**	8.64**	6.76**	-1.61	-3.043	-0.52	-1.53**	1.16**	-2.92**
DS 5 x DLSA 24	-26.16**	-36.24**	3.88**	3.67**	6.52**	5.38**	23.84**	11.14**	22.49**	20.46**	2.941	1.45	2.12*	-0.28	-16.33**	-18.94**	7.94**	6.25**	-17.11**	-19.02**
DS 5 x DLSA 9	7.53**	-10.54**	-4.55**	-4.55**	12.90**	12.90**	58.48**	58.48**	19.45**	19.45**	26.087	26.09**	4.05**	4.05**	-5.53**	-5.53**	7.77**	7.22**	-10.65**	-10.65**

DS 5 x LD 694	11.82**	11.87**	20.85**	16.77**	16.13**	16.13**	15.32**	13.48**	-1.09	-9.11**	18.841	18.84**	12.10**	11.33**	0.55	0.14	4.37**	-0.52	-7.32**	-9.23**
CISA 2 x HD 123	22.44**	9.74**	25.71**	16.25**	51.06**	49.47**	-5.22**	-11.03**	30.81**	24.09**	7.463	4.35**	-0.93	-5.88**	-11.70**	-18.24**	-2.86**	-17.07**	-6.04**	-15.49**
CISA 2 x HD 400	-5.28**	-24.28**	43.69**	20.24**	44.44**	36.19**	13.63**	12.80**	7.08**	-8.88**	-20.567	-22.22**	0.60	0.19	-5.68**	-13.44**	11.11**	2.94**	-10.16**	-13.34**
CISA 2 x RG 270	0.40	-5.22**	11.87**	6.96**	57.06**	49.46**	23.44**	14.22**	2.86**	-5.56**	-12.593	-14.49**	0.28	-1.12	-0.84	-2.47*	1.29	-7.98**	6.06**	-3.46**
CISA 2 x RG 286	-22.07**	-23.73**	20.29**	15.64**	35.48**	35.48**	7.63**	1.96**	-1.38	-9.19**	-15.714	-16.90**	3.81**	3.23**	0.54	-0.27	-10.57**	-15.39**	-0.78	-5.93**
CISA 2 x RG 341	-5.53**	-10.03**	17.44**	10.97**	30.26**	24.51**	2.12*	-5.39**	-3.37**	-7.03**	-24.528	-33.33**	-5.34**	-6.63**	-12.12**	-12.48**	2.31*	-7.44**	-0.09**	-7.25**
CISA 2 x RG 18	-7.89**	-26.36**	-6.59**	-8.76**	10.26**	-8.51**	-10.84**	-12.32**	-9.213	-10.97**	11.811	2.90**	9.49**	9.34**	-15.67**	-18.79**	16.62**	10.88**	-15.49**	-20.92**
CISA 2 x CISA 59	-3.93**	-7.36**	32.30**	20.06**	38.86**	34.00**	27.07**	22.55**	3.25**	-5.56**	-14.094	-20.00**	14.36**	8.59**	-15.42**	-18.38**	1.06	-5.94**	-19.27**	-20.26**
CISA 2 x CISA 60	-0.61	-4.49**	12.42**	8.74**	55.19**	52.69**	9.27**	6.86**	1.80	-3.71**	-7.692	-10.81**	5.23**	4.41**	-3.07**	-4.66**	7.53**	1.01	-5.31**	-8.90**
CISA 2 x CISA 64	0.21	-4.17**	11.10**	3.69**	63.43**	53.76**	-26.88**	-28.67**	-3.20**	-7.57**	-4.225	-6.85**	4.94**	4.20**	-5.70**	-7.74**	3.47**	-3.48**	-15.27**	-16.15**
CISA 2 x CISA 65	3.91**	-7.33**	41.92**	5.94**	-4.38**	-30.39**	-3.03**	-13.73**	1.32	-5.25**	2.10*	-1.35	12.94**	9.62**	-11.72**	-13.17**	13.00**	4.93**	-16.17**	-19.28**
CISA 2 x CISA 66	12.43**	8.71**	10.28**	6.85**	2.11*	-0.000	-10.91**	-16.91**	4.59**	-2.39*	-14.89**	-16.67**	8.59**	8.59**	-4.57**	-5.03**	-16.27**	-21.89**	-5.68**	-11.04**
CISA 2 x PAIG 8/3	-24.42**	-39.94**	6.82**	5.00**	20.37**	5.69**	4.00**	-1.23	-12.99**	-15.14**	-5.18**	-7.25**	5.74**	3.20**	-5.66**	-7.41**	3.78**	-2.04	-5.43**	-11.04**
CISA 2 x DLSA 24	-30.82**	-42.94**	23.62**	19.21**	34.78**	33.33**	1.94	-9.80**	3.24**	-6.56**	-8.82**	-10.15**	4.94**	3.18**	-6.40**	-8.95**	12.22**	8.60**	-14.05**	-14.26**
CISA 2 x DLSA 9	-26.61**	-41.53**	19.06**	15.04**	47.31**	47.31**	4.36**	2.70*	-5.63**	-13.28**	-10.15**	-10.15**	-0.51	-1.20	-7.16**	-7.55**	0.54	-4.64**	-13.04**	-14.83**
CISA 2 x LD 694	8.91**	3.11**	6.83**	6.83**	29.03**	29.03**	-5.64**	-5.64**	-17.68**	-17.68**	0.00	0.00	-0.00	-0.00	-1.51	-1.51	-1.72	-1.72	-6.92**	-6.92**

**, *Significant at 1% and 5% probability level of significance. MP- Heterosis over mid parent, BP- Heterobeltiosis or Heterosis over better parent