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Heterosis and combining ability analysis for fiber quality and biochemical parameters in American cotton (*Gossypium hirsutum* L.)

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Abstract
The present experiment was carried out in line × tester fashion during 2018-19 to study heterosis, combining ability and gene action in American cotton for fiber quality and biochemical parameters. Twelve diverse parents, four lines (female) and eight testers (male) were crossed to produce 32 F$_1$ hybrids. A total of 45 (including check) genotypes were evaluated for fiber quality and biochemical parameters to determine the mode of gene action, extent of heterosis, and combining abilities that assisted in formulating an effective breeding strategy for cotton for industrial use. In case of fiber quality parameters, the maximum value of standard heterosis in desired direction was 3.52% (GSHV 199 × SIMA 5) for fiber length and -6.82% (GSHV 199 × SIMA 5, GISV 319 × CPD 1602) for fiber fineness. Whereas, biochemical parameters, the maximum value of standard heterosis in desired direction for oil content was 4.83% (GSHV 199 × PBH 42), for gossypol content -71.33% (GSHV 199 × SIMA 5 and GISV 298 × SIMA 5) and for phenol content 60.71% (GISV 298 × BGDS 1033). As a result, different hybrids demonstrated varying fiber quality and biochemical superiority based on requirements for industrial use. GSHV 199 was found good general combiner for four characters *viz.*, fiber length, fiber strength, fiber fineness and gossypol content and developing hybrids for textile and oil industries products. For fiber fineness, oil percentage, gossypol content and phenol content additive and dominance components were found significant in controlling the traits whereas, the predominance of the additive type of genetic variance found in the inheritance of fiber length, fiber strength and maturity co-efficient. That suggested the simultaneous exploitation of additive gene actions by adopting selective intermating and recurrent selection, which would accumulate more of additive genetic variability whereas, non-additive gene effect can be exploited by heterosis breeding or biparental mating followed by few cycles of recurrent selection.

Keywords: American cotton, standard heterosis, heterobeltiosis, general and specific combining ability

1. Introduction
Cotton is extremely important to India's economy because it contributes significantly to agricultural and industrial development as well as foreign exchange earnings through the export of raw materials and finished products. Cotton is mainly grown for its fiber in the different parts of the world; besides this, it is also important source of edible oil. Its contribution in edible oil production is obvious from the fact that it contributes 65-70% to the local edible oil industry.
India has the unique distinction of being the only country where all the cultivated species and some of their hybrid combinations are commercially grown. The diversity of cotton cultivars and cotton agro climatic zone in India is considerably larger when compared to other major cotton growing countries in the world. The leading cotton growing countries in the world are China, India, United States, Brazil and Pakistan. India ranks first in terms of area (13.47 million hectares) while second in terms of production (12.88 million tonnes) among cotton growing countries in the world after China, whereas, productivity is around 955.7 kg/ha in India. In India among the states, Maharashtra has the highest cotton growing area (4.49 million hectares) while the highest production is in Gujarat (3.07 million tonnes) and productivity is higher in Punjab (1736.8 kg/ha). In Gujarat, cotton is planted on 2.65 million hectares of land with annual production of 3.07 million tonnes and average productivity is about 1159.1 kg/ha (Anon., 2020) [1].
The exploitation of new cotton variety having high yield including good fiber quality and biochemical properties is the new target of all cotton breeders.

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There are many mating designs for estimation of heterosis, GCA and SCA but the simplest method with minimum number of crosses is line × tester mating design where a set of inbreds taken as male are crossed with all inbreds from another set taken as female (Kempthorne, 1957) [12]. Line × tester analysis has been widely used by researchers in the selection of superior parents and crosses.

Knowledge about heterosis, combing ability and gene action are important for plant breeder to select better parental combination and design breeding method for further enhancement. Simpson (1954) [28] classified cotton as often cross-pollinated crop which is amenable for heterosis breeding. Dr. C. T. Patel (1971) [19] at Main Cotton Research Station, Gujarat Agricultural University, Surat demonstrated the heterosis at commercial level and the first intra hirsutum hybrid H-4 (G-67 × American Nectariless) was developed by him. In the same year, Katarki (1971) [11] also developed an interspecific tetraploid hybrid, Varalaxmi (Laxmi × SB 289 E). These two events changed the entire cotton production scenario of India and played significant role to attain self-sufficiency in cotton production. India was the first country to commercially exploit heterosis in cotton. The magnitude of heterosis depends on the choice of appropriate parental lines. The introgression of *Bt* gene in cotton has increased the importance of hybrid cotton as it offers high yield potential, good fiber properties, wider adaptability with high degree of resistance to biotic and abiotic stresses. Estimating combining ability effects is a method of choice for breeders to screen and select parents for heterosis breeding (Sandhu and Chahal, 1995) [25]. The general combining ability and specific combining ability describes the breeding value of parental lines and hybrids, respectively. GCA effect due to additive and SCA effect due to non-additive gene action (Sprague and Tatum, 1942) [29] provides guidelines to the plant breeder in selecting the elite parents and desirable cross combinations to be used in the formulation of the systematic breeding programmes and at the same time reveals the nature of gene actions involved in the inheritance of various traits.

2. Materials and methods
2.1 Parent material
The present investigation was carried out to elicit information on magnitude of heterosis (heterobeltiosis and standard heterosis), combining ability and gene action for cotton fiber quality and biochemical traits. The experiment was conducted during 2018-19 at Main Cotton Research Station, Navsari Agricultural University, Surat. The experimental materials comprised of 45 diverse genotypes of cotton including four female parents *viz.*, GSHV 191, GSHV 199, GISV 298 and GISV 319 as well as eight male parents *viz.*, CPD 1602, SIMA 5, RAH 1071, RHC 1217, PBH 42, HS 298, F 2453 and BGDS 1033 of *Gossypium hirsutum* L. and their resultant 32 hybrids (line × tester) along with GN. Cot. Hy-14 as standard check. The crossing programme was carried out using four lines and eight testers by Doak's (Doak, 1934) [6] method at MCRS, NAU, Surat during 2017-18 through line × tester design of mating. One plant of each parent was also selfed to obtain selfed parental seeds to be used for final evaluation. All the F₁'s and selfed seeds of parents were stored properly in seed packets for sowing in the next season. The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications. Each plot consisted of single row of 5.4 m length spaced at 1.20 m

apart. Plant to plant distance was 45 cm. One guard row was planted on both sides of the experiments. All recommended packages of practices were adopted for raising a successful and healthy crop.

2.2 Trait phenotyping
Five competitive plants excluding border plant were randomly selected to record the observation on fiber quality and biochemical parameters *viz.,* fiber length (mm), fiber strength (g/tex), maturity co-efficient, fiber fineness (mv), oil content (%), gossypol content (%) and phenol content (%).
The following fiber quality parameters were measured using High Volume Instrument (HVI) at Central Institute for Research on Cotton Technology (CIRCOT), Mumbai. The oil content in cotton seed was determined by NMR (Nuclear Magnetic Resonance) machine of each sample at Main Cotton Research Station, Navsari Agricultural University, Surat. The gossypol extraction and estimation elucidated by the method of Bell (1967) [3]. The phenol extraction and estimation elucidated by the method of Malick and Singh (1980) [15].

2.3 Statistical analysis
To test the significant differences between the genotypes for all the characters, analysis of variance (ANOVA) was performed (Panse and Sukhatme, 1978). Heterobeltiosis (%) was calculated according to Fonseca and Patterson (1968) [7]. Standard heterosis (SH%) was measured as suggested by Meredith and Bridge (1972) [6]. The variation among the hybrids were partitioned further into sources attributed to general combining ability (GCA) and specific combining ability (SCA) components by the procedure suggested by Kempthorne (1957) [12].

3. Results and discussion
3.1 Analysis of variance for experimental design
The analysis of variance was performed to test the differences among parents and hybrids. Analysis of variance depicting mean sum of squares for seven fiber quality and biochemical parameters are presented in Table 1. The analysis of variance showed highly significant differences among the genotypes for all the traits except oil percentage revealed that the considerable amount of variability was observed among experimental material. This validated that the material was appropriate for present study. The genotypic variance was further partitioned into parents, hybrids and parents *vs* hybrids. The differences among parents significant for all characters under investigation except oil percentage and hybrids were also found highly significant for all characters except oil percentage. Differences due to parents *vs* hybrids were also found highly significant for all the traits under study except oil percentage.

3.2 Magnitude of heterosis
3.2.1 Fiber length (mm)
Fiber length is the most important among fiber properties. Depending upon the species, the character is controlled by multiple gene and is greatly influenced by the environment.
Out of 32 crosses, four and three crosses showed significant heterobeltiosis and standard heterosis respectively for fiber length. The extent of heterobeltiosis ranged from -6.80 (GISV 319 × SIMA 5) to 11.31% (GSHV 191 × RAH 1071). The highest heterosis over better parent was recorded in the cross GSHV 191 × RAH 1071 (11.31%) followed by GSHV 191 ×

CPD 1602 (9.05%) and GSHV 191 × RHC 1217 (7.85%) (Table 3). The range of standard heterosis was from -9.3 (GISV 298 × RHC 1217) to 3.52% (GSHV 199 × SIMA 5). The highest value of standard heterosis was recorded in the cross GSHV 199 × SIMA 5 (3.52%) followed by GISV 191 × SIMA 5 (3.29%) and GSHV 199 × PBH 42 (3.05%) (Table 3). These results are in agreement with the results obtained by Kannan and Saravanan (2016) [10], Sharma et al. (2016) [27] and Lingaraja et al. (2017) [14].

3.2.2 Fiber strength (g/tex)
Fiber strength is one of the important properties of cotton fiber and controlled by several genes and is greatly influenced by the environment.

Among 32 crosses, significant heterobeltiosis and standard heterosis were recorded in 10 and 21 crosses, respectively for fiber strength. The heterobeltiosis for fiber strength from -19.1 (GISV 298 × SIMA 5) to 11.79% (GSHV 191 × F 2453). The highest heterobeltiosis was registered by the cross GSHV 191 × F 2453 (11.79%) followed by GSHV 199 × CPD 1602 (10.43%) and GSHV 191 × RAH 1071 (9.87%) (Table 3). The standard heterosis lied between - 8.94 (GISV 298 × CPD 1602) to 17.09% (GSHV 191 × F 2453). The highest value of standard heterosis was recorded in the cross GSHV 191 × F 2453 (17.09%) followed by GSHV 191 × BGDS 1033 (16.56%) and GISV 319 × BGDS 1033 (16.00%) (Table 3). Sharma et al. (2016) [27], Kannan and Saravanan (2016) [10] and Lingaraja et al. (2017) [14] reported similar results for fiber strength in cotton hybrids.

3.2.3 Maturity co-efficient
Although maturity of fiber is affected by cultural and environmental conditions, this character is hereditary. Fiber with practically immature cause production of neps in spinning.

Among all cross combinations, four and one crosses showed positive and significant heterosis over better parent and standard check, respectively for maturity co-efficient. The range of heterobeltiosis was from -1.98 (GISV 319 × SIMA 5) to 4.51% (GSHV 191 × RAH 1071). The highest heterobeltiosis was recorded by GSHV 191 × RAH 1071 (4.51%) followed by GSHV 191 × F 2453 (4.12%) and GSHV 199 × RHC 1217 (3.28%) (Table 3). Standard heterosis values for maturity co-efficient from -2.02 (GISV 298 × RAH 1071) to 2.82% (GSHV 191 × RAH 1071). GSHV 191 × RAH 1071 (2.82%) showed positive and significant standard heterosis (Table 3). Which is agreement with Kaliyperumal et al. [17] and Sharma et al. [23] for maturity co-efficient in cotton hybrids.

3.2.4 Fiber fineness (mv)
Fiber fineness is expressed as micronaire value means the air permeability of compressed cotton fibers. Cotton with a soft and silky feel is considered to be fine. Fiber fineness values in the range of 3.5 to 4.5 mv are more preferable than higher or lower value of fiber fineness. The heterosis over better parent varied from -8.89 (GISV 319 × CPD 1602) to 28.57% (GISV 298 × SIMA 5). Out of 32 crosses, which showed negative and significant heterosis over better parent, the highest value was observed for the cross GISV 319 × CPD 1602 (-8.89%) (Table 3). The heterosis over standard check range varied from -6.82 (GSHV 199 × SIMA 5) to 22.73% (GISV 298 × RAH 1071). None of the hybrids showed significant and

negative heterosis (Table 3). Similar results have been reported earlier by Kannan and Saravanan (2013), Sharma et al. (2016) [27] and Lingaraja et al. (2017) [14].

For majority of fiber quality parameters, low magnitude of heterosis was observed in the present study and this suggested that significant advancement for these characters can be made in segregating population using simple selection procedure which would increase the frequency of desirable genes. Hence, there is possibility of getting high yielding hybrids without loss in fiber quality.

3.2.5 Oil percentage
Now days, cotton seed oil is widely used for human consumption. Thus, cotton has become a fiber cum oil yielding crop. The range of heterobeltiosis was from -8.46 (GSHV 199 × HS 298) to 6.28% (GSHV 191 × PBH 42). Out of the 32 crosses none of the cross recorded positive and significant for heterobeltiosis (Table 3). Standard heterosis for oil percentage ranged from -4.30 (GISV 319 × SIMA 5) to 4.83% (GSHV 199 × PBH 42). Out of the 32 crosses none of the cross recorded positive and significant for standard heterosis (Table 3). The results are in parity with findings of Sewarkar et al. (2014) [26].

3.2.6 Gossypol content (%)
Gossypol is produced by pigment glands in cotton stems, leaves, seeds and flower buds. High concentration of free gossypol may be responsible for acute clinical signs of gossypol poisoning. So, selection has produced cotton variety devoid of gland producing gossypol but these varieties are less productive and are more vulnerable to attack by insects.

Among the crosses, five and twenty-three crosses showed significant desirable heterosis over better parent and standard check, respectively for gossypol content. Heterobeltiosis for gossypol content ranged from -44.33 (GISV 319 × F 2453) to 277.78% (GISV 298 × PBH 42). The highest value for heterobeltiosis (desirable) was observed in GISV 319 × F 2453 (-44.33%) followed by GSHV 199 × SIMA 5 (-42.67) and GISV 298 × SIMA 5 (-42.67%) (Table 3). For standard heterosis, the range was observed from -71.33 (GSHV 199 × SIMA 5, GISV 298 × SIMA 5) to 36.00% (GISV 298 × PBH 42, GISV 298 × F 2453). The highest desirable heterosis was recorded by the cross GSHV 199 × SIMA 5, GISV 298 × SIMA 5 (-71.33%) followed by GISV 319 × F 2453 (-64.00%) and GSHV 199 × RAH 1071 (-62.67%) (Table 3). Similar results have been reported by Nishanth et al. (2014) [17] and Ramani et al. (2017) [24].

3.2.7 Phenol content (%)
Phenolic compounds play an important role in providing cotton plants with defense against herbivorous insects. Thirteen crosses were exhibited significant and positive heterosis over better parent with a range from -46.53 (GISV 319 × HS 298) to 66.72% (GISV 319 × F 2453) for phenol content. The cross GISV 319 × F 2453 (66.72%) showed highest heterobeltiosis followed by GISV 298 × BGDS 1033 (64.41%) and GISV 298 × CPD 1602 (57.78%) (Table 3). Total 10 crosses exhibited positive standard heterosis. The standard heterosis ranged from -39.15 (GSHV 191 × F 2453) to 60.71% (GISV 298 × BGDS 1033). The highest standard heterosis was recorded by the cross GISV 298 × BGDS 1033 (60.71%) followed by GISV 298 × CPD 1602 (54.23%) and GISV 319 × F 2453 (41.14%) (Table 3). Significant and

positive heterosis have been found by Balakrishnan (2006) [2]. Number of hybrids showing significant heterosis and range of heterosis presented in Table 2.

3.3 Combining ability and gene action
The analysis of variance of combining ability for all the traits presented in Table 4. Such studies not only provide necessary information regarding the choice of parents but, also illustrate the nature and magnitude of gene action involved in the inheritance of character which is useful in deciding breeding methodology aiming at exploitation of fixable (additive) and none fixable (non-additive) genetic variances. Griffing (1956) [8] and Carnahan *et al.* (1960) [5] suggested that GCA could include both additive effects as well as additive × additive interactions. The estimation of combining ability for female effect were significant for fiber length, fiber fineness, fiber strength, maturity co-efficient, fiber fineness and phenol content. Whereas, the mean squares due to male effect were non significant for all the traits which suggested female contribution was significant in favour of general combining ability (GCA) variance towards these traits and contributed towards additive genetic variance. The mean squares due to line × tester effect was found significant for all the characters except maturity co-efficient and oil percentage (Table 4) it suggested its significant contribution in favor of specific combining ability (SCA) variances and the result thus indicated that females behave differently with different males or *vice-versa.* This indicated that it contributed towards non-additive genetic variance. The estimated variances due to line $\sigma^2 l$ were non significant for all the trait except fiber strength, maturity co-efficient and phenol content. Whereas estimated variances due to line $\sigma^2 t$ were non-significant for all traits. The estimates of $\sigma^2 gca$ were significant for all the traits except phenol content (Table 4). The ratio of $\sigma^2 gca /\sigma^2 sca$ revealed that presence of additive or non- additive gene action. The estimates of *gca* effect of parents and *sca* effect of hybrids were estimated for seven traits, as presented in Table 5 and Table 6.

3.3.1 Fiber length (mm)
The general combining ability effects of parents for fiber length ranged from -0.86 (GISV 319) to 0.81 (GSHV 199). Two female GSHV 191 (0.77) and GSHV 199 (0.81) showed positive and significant GCA effects among the parents. Out of eight testers, two testers; SIMA 5 (0.74) and HS 298 (0.47) showed positive and significant GCA effects among the parents (Table 5). Specific combining ability effect ranged from -0.97 (GSHV 191 × PBH 42) to 1.03 (GSHV 199 × PBH 42). Two hybrids, GSHV 191 × RAH 1071 (1.02) and GSHV 199 × PBH 42 (1.03) showed positive and significant SCA effects for fiber length (Table 6). These specific crosses involved good × average general combiners.

3.3.2 Fiber strength (g/tex)
Three parents showed significant and positive GCA effect for fiber strength. These parents include two lines GSHV 191 (1.77) and GSHV 199 (0.59) as well as one tester BGDS 1033 (1.57) (Table 5). Specific combining ability effect ranged from -1.83 (GSHV 199 × RAH 1071) to 1.43 GSHV 199 × SIMA 5). Six hybrids *viz.*, GSHV 191 × F 2453 (1.12), GSHV 199 × CPD 1602 (1.38), GSHV 199 × SIMA 5 (1.43), GISV 298 × RAH 1071 (1.34), GISV 298 × RHC 1217 (1.07) and GISV 319 × BGDS 1033 (1.40) showed positive and

significant SCA effect for fiber strength (Table 6).

3.3.3 Maturity co-efficient
The general combining ability effect of parent for maturity co-efficient ranged from -0.57 (HS 298) to 0.76 (SIMA 5). Out of four lines, only one line GSHV 191 (0.55) showed significant and positive GCA effect for maturity co-efficient and none of the testers showed significant and positive for GCA (Table 5). For examination of SCA estimates data ranged from -1.46 (GSIV 298 × RAH 1071) to GSHV 191 × RAH 1071 (1.44) (Table 6). None of the hybrid showed positive and significant SCA effect for maturity co-efficient.

3.3.4 Fiber fineness (mv)
An examination of GCA estimates revealed that data ranged from -0.29 (CPD 1602) to 0.23 (GISV 298). One line GSHV 199 (-0.15) and three tester *viz.*, CPD 1602 (-0.29), PBH 42 (-0.15) and SIMA 5 (-0.12) displayed significant and negative GCA effect for fiber fineness (Table 5). These parents thus, appeared to be worthy of use as donors in breeding programme for achieving segregants for fiber fineness. From examination of SCA estimation data ranged from -0.61 (GISV 298 × BGDS 1033) to 0.37 (GISV 298 × SIMA 5). Four hybrids *viz.*, GSHV 199 × SIMA 5 (-0.24), GISV 298 × HS 298 (-0.34), GISV 298 × BGDS 1033(-0.61) and GISV 319 × RAH 1071(-0.22) displayed significant and negative SCA effect for fiber fineness (Table 6). These specific crosses involved good × average, poor × average, poor × good, poor × average general combiners.

3.3.5 Oil percentage
Positive value for the combining ability effects is preferred for this trait. An examination of GCA estimates revealed that data ranged from -0.22 (SIMA 5) to PBH 42 (0.43). None of the parents showed positive and significant GCA effect for oil percentage (Table 5). The perusal of estimation of SCA effects revealed that range -0.52 (GISV 319 × SIMA 5) to 0.92 (GISV 319 × BGDS 1033) (Table 6). None of the hybrids showed positive and significant GCA effect for oil percentage.

3.3.6 Gossypol content (%)
Negative value for the combining ability effect is preferred for this trait. Two line *viz.*, GSHV 199 (-0.07) and GISV 319 (-0.04) showed significant and negative GCA for gossypol content. Whereas three testers *viz.*, SIMA 5 (-0.11), HS 298 (-0.02) and BGDS 1033 (-0.07) showed significant and negative GCA for gossypol content (Table 5). Out of 32 crosses, 15 hybrids *viz.*, GSHV 191 × PBH 42 (-0.10), GSHV 191 × HS 298 (-0.09), GSHV 191 × F 2453 (-0.14), GSHV 191 × BGDS 1033 (-0.10), GSHV 199 × CPD 1602 (-0.09), GSHV 199 × SIMA 5 (-0.04), GSHV 199 × RAH 1071 (-0.11), GSHV 199 × RHC 1217 (-0.03), GISV 298 × CPD 1602 (-0.06), GISV 298 × SIMA 5 (-0.17), GISV 298 × RAH 1071 (-0.14), GISV 298 × BGDS 1033 (-0.03), GISV 319 × PBH 42 (-0.09) and GISV 319 × F 2453 (-0.14) showed significant and negative SCA for gossypol content (Table 6).

3.3.7 Phenol content (%)
Out of four lines only one line GISV 298 (0.68) had significant and positive GCA effect for phenol content. In case of testers, two testers *viz.,* F 2453 (0.30) and BGDS 1033 (0.33) were identified as good general combiners for this trait

as they had significant and positive GCA effect for phenol content (Table 5). These parents thus, showed to be worthy of use as donors in breeding programme for achieving segregants with higher phenol content. Out of 32 crosses, 10 crosses reported highest positive SCA effect was exhibited by the cross GISV 319 × F 2453 (1.04) followed by GISV 298 × CPD 1602 (0.96), GISV 319 × RAH 1071 (0.70) and GISV 298 × BGDS 1033 (0.68) (Table 6).

The estimates of σ²gca were significant for all the traits except phenol content. While, the estimates of σ²sca were significant for fiber length, fiber strength, fiber fineness and gossypol content. For the gene action, ratio of σ²gca / σ²sca revealed that majority of the characters manifested less than unity *viz.,* fiber fineness, oil percentage, gossypol content and phenol content which indicated preponderance of non-additive genetic variance for inheritance of these traits. While fiber length, fiber strength and maturity co-efficient possess more than unity value of σ²gca/σ²sca which clearly indicated the preponderance of additive type of genetic variance in the inheritance of these characters (Table 4). Almost similar results have been reported by Patel *et al*. (2007) [20], Bhaskaren and Ravikesavan (2008) [4], Preetha and Raveendran (2008) [22], Patil *et al*. (2011) [21], Rajamani *et al*. (2014) [23], Usharani *et al*. (2016) [30] and Kumar *et al*. (2017) [13].

Table 1: Analysis of variance (mean sum of square) for experimental design for different traits in *G. hirsutum* L.

Source of variation	Df	Fiber length (mm)	Fiber strength (g/tex)	Maturity co-efficient	Fiber fineness (mv)	Oil percentage	Gossypol content (%)	Phenol content (%)
Replication	2	0.01	0.73	0.39	0.03	0.16	0.01	0.32**
Treatments	43	3.91**	13.43**	3.55**	0.37**	0.59	0.05**	1.14**
Parents	11	4.13**	19.11**	3.76*	0.49**	1.09	0.03**	0.59**
Lines	3	3.99**	1.93*	0.97	1.09**	2.15*	0.01**	0.52**
Testers	7	4.69**	27.61**	5.47**	0.29**	0.48	0.03**	0.55**
Lines *vs* Testers	1	0.63	11.12**	0.12	0.06	2.16	0.06**	1.04**
Parents *vs* Crosses	1	23.21**	61.02**	30.14**	1.39**	0.73	0.08**	0.83**
Crosses	31	3.21**	9.88**	2.62	0.29**	0.41	0.06**	1.35**
Line Effect	3	20.35**	58.73**	8.37*	0.65*	0.35	0.12	6.41**
Tester Effect	7	2.27	7.74	1.89	0.39	0.53	0.05	0.49
Line × Tester effect	21	1.07**	3.62**	2.04	0.19**	0.38	0.05**	0.91**
Error	86	0.45	0.65	1.83	0.03	0.68	0.01	0.01

* and ** indicates significance at 5% and 1% levels of probability, respectively

Table 2: Number of hybrids showing significant heterosis and range of heterosis in *G. hirsutum* L.

Sr. No.	Characters	Range of heterosis (%)				Number of crosses with significant heterosis			
		Heterobeltiosis (%)		Standard heterosis (%)		H₁ (%)		H₂ (%)	
						+Ve	-Ve	+Ve	-Ve
1.	Fiber length (mm)	-6.80 to	11.31	-9.31 to	3.52	4	3	3	12
2.	Fiber strength (g/tex)	-19.16 to	11.79	-8.94 to	17.09	10	8	21	2
3.	Maturity co-efficient	-1.98 to	4.51	-2.02 to	2.82	4	0	1	0
4.	Fiber fineness (mv)	-8.89 to	28.57	-6.82 to	22.73	24	1	11	0
5.	Oil percentage	-8.46 to	6.28	-4.30 to	4.83	0	4	0	0
6.	Gossypol content (%)	-44.33 to	277.78	-71.33 to	36.00	23	5	4	23
7.	Phenol content (%)	-46.53 to	66.72	-39.15 to	60.71	13	14	10	16

Table 3: Per cent heterobeltiosis (H₁) and standard heterosis (H₂) for various characters in *G. hirsutum* L.

Crosses	Fiber length (mm)		Fiber strength (g/tex)		Maturity co-efficient		Fiber fineness (mv)		Oil percentage		Gossypol content (%)		Phenol content (%)	
	H₁ (%)	H₂ (%)	H₁ (%)	H₂ (%)	H₁ (%)	H₂ (%)	H₁ (%)	H₂ (%)	H₁ (%)	H₂ (%)	H₁ (%)	H₂ (%)	H₁ (%)	H₂ (%)
GSHV 191 × CPD 1602	9.05**	0.42	8.44**	12.59**	1.23	-0.81	8.55*	-3.79	2.33	1.69	200.00**	8.00*	34.07**	-37.04**
GSHV 191 × SIMA 5	1.19	3.29*	-0.79	12.89**	-0.40	1.61	9.40*	-3.03	-1.76	-0.46	183.33**	2.00	-8.22*	-26.19**
GSHV 191 × RAH 1071	11.31**	2.27	9.87**	14.07**	4.51**	2.82*	17.09**	3.79	2.63	1.63	264.81**	31.33**	-17.97**	-30.56**
GSHV 191 × RHC 1217	7.85**	-0.91	9.27**	13.46**	1.23	-0.81	17.95**	4.55	-1.23	1.30	177.78**	0.00	-23.80**	-30.56**
GSHV 191 × PBH 42	3.72	-4.33*	5.20*	9.22**	2.47	0.40	12.82**	0.00	6.28	5.25	140.74**	-13.33**	-2.80	-21.83**
GSHV 191 × HS 298	3.52	-0.19	6.03*	10.09**	0.00	-0.81	25.64**	11.36**	1.54	0.55	79.63**	-35.33**	-32.77**	-15.34**
GSHV 191 × F 2453	2.32	-1.69	11.79**	17.09**	4.12**	2.02	17.95**	4.55	2.17	1.17	62.96**	-41.33**	-28.13**	-39.15**
GSHV 191 × BGDS 1033	4.82*	1.13	0.41	16.56**	1.20	1.61	23.08**	9.09*	-0.28	-1.25	40.74**	-49.33**	-31.12**	-32.67**
GSHV 199 ×	-0.72	-1.40	10.43**	10.70**	2.46	0.81	8.77*	-6.06	-6.93*	0.51	0.00	-50.00**	-22.71**	-26.19**

Crosses														
CPD 1602														
GSHV 199 × SIMA 5	1.42	3.52*	-0.43	13.30**	0.00	2.02	7.89	-6.82	-7.72*	0.33	-42.67**	-71.33**	25.74**	-15.34**
GSHV 199 × RAH 1071	-1.24	-1.92	2.65	2.90	2.87*	1.21	26.32**	9.09*	-6.20	1.30	-12.50	-62.67**	-25.63**	-37.04**
GSHV 199 × RHC 1217	-0.76	-1.44	7.61**	7.88**	3.28*	1.61	23.68**	6.82	-5.47	2.09	29.33**	-35.33**	31.06**	19.44**
GSHV 199 × PBH 42	3.76	3.05*	7.77**	8.04**	2.05	0.40	8.77*	-6.06	-2.94	4.83	138.89**	-14.00**	26.81**	1.98
GSHV 199 × HS 298	1.28	0.59	9.48**	9.75**	1.22	0.40	21.05**	4.55	-8.46*	-1.14	88.00	-6.00	-17.23**	4.23
GSHV 199 × F 2453	-2.40	-3.07	0.60	5.37*	1.23	-0.40	16.67**	0.76	-4.88	2.73	25.33**	-37.33**	28.44**	8.73**
GSHV 199 × BGDS 1033	2.55	1.85	-2.39	13.30**	-1.20	-0.81	26.32**	9.09*	-7.53*	-0.13	-1.33	-50.67**	0.00	-2.25
GISV 298 × CPD 1602	1.52	-6.51**	-12.60**	-8.94**	0.82	-0.40	5.88	9.09*	1.61	0.97	64.00**	-18.00**	57.78**	54.23**
GISV 298 × SIMA 5	-4.38*	-2.40	-19.16**	-8.01**	-1.58	0.40	28.57**	15.91**	1.01	2.35	-42.67**	-71.33**	13.26**	10.71**

* and ** indicates significance at 5% and 1% levels of probability, respectively

Table 3: Continue….

Crosses	Fiber length (mm)		Fiber strength (g/tex)		Maturity co-efficient		Fiber fineness (mv)		Oil percentage		Gossypol content (%)		Phenol content (%)	
	H1 (%)	H2 (%)	H1 (%)	H2 (%)	H1 (%)	H2 (%)	H1 (%)	H2 (%)	H1 (%)	H2 (%)	H1 (%)	H2 (%)	H1 (%)	H2 (%)
GISV 298 × RAH 1071	0.44	-8.79**	1.17	5.41*	-0.82	-2.02	11.72**	22.73**	0.04	-1.65	34.38**	-42.67**	13.26**	10.71**
GISV 298 × RHC 1217	-0.13	-9.31**	0.85	5.07*	0.41	-0.81	13.64**	13.64**	-3.02	-0.53	98.67**	-0.67	4.33	1.98
GISV 298 × PBH 42	2.35	-5.59**	-6.55**	-2.64	1.63	0.40	17.65**	6.06	4.05	1.36	277.78**	36.00**	11.23**	8.73**
GISV 298 × HS 298	1.28	-2.35	-1.92	2.19	0.00	-0.81	-1.43	4.55	2.19	-0.46	56.00**	-22.00**	17.23**	4.23
GISV 298 × F 2453	-0.74	-4.63*	-4.76*	-0.25	0.41	-0.81	10.77**	9.09*	2.88	0.33	172.00**	36.00**	13.26**	10.71**
GISV 298 × BGDS 1033	-0.15	-3.67	-10.23**	4.20	-0.80	-0.40	-4.35	0.00	1.27	-0.70	28.00**	-36.00**	64.41**	60.71**
GISV 319 × CPD 1602	2.92	-5.23*	-7.83**	-0.90	0.00	-0.40	-8.89*	-6.82	-4.31	-2.28	53.61**	-0.67	-31.86**	-34.92**
GISV 319 × SIMA 5	-6.80*	-4.87*	-7.84**	4.86	-1.98	0.00	13.45**	2.27	-6.29	-4.30	-13.79*	-50.00**	3.43	-28.17**
GISV 319 × RAH 1071	1.19	-8.35**	0.08	7.60**	0.00	-0.40	2.22	4.55	-3.43	-1.38	68.75**	-28.00**	30.78**	10.71**
GISV 319 × RHC 1217	2.52	-7.15**	-1.22	6.21*	-0.40	-0.81	5.30	5.30	-1.22	1.32	28.87**	-16.67**	-14.22**	-21.83**
GISV 319 × PBH 42	0.14	-7.63**	-9.20**	-2.37	-0.40	-0.81	16.81**	5.30	-1.37	0.73	79.63**	-35.33**	-16.28**	-32.67**
GISV 319 × HS 298	1.28	-2.35	-2.18	5.17*	-0.81	-1.21	5.19	7.58*	-2.28	-0.20	-34.02**	-57.33**	-46.53**	-32.67**
GISV 319 × F 2453	0.26	-3.67	-4.03	3.19	-0.40	-0.81	3.08	1.52	-1.51	0.59	-44.33**	-64.00**	66.72**	41.14**
GISV 319 × BGDS 1033	-4.63*	-7.99**	-0.06	16.00**	0.00	0.40	14.07**	16.67**	2.97	5.16	11.34*	-28.00**	2.30	0.00
S.E ±	0.54	0.54	0.66	0.66	1.10	1.10	0.13	0.13	0.67	0.67	0.016	0.016	0.08	0.08
CD @ 5%	1.09	1.09	1.32	1.32	2.20	2.20	0.30	0.30	1.34	1.34	0.03	0.03	0.16	0.16
CD @ 1%	1.46	1.46	1.75	1.75	2.93	2.93	0.40	0.40	1.79	1.79	0.04	0.04	0.21	0.21
Range	-6.80 to 11.31	-9.31 to 3.52	-19.16 to 11.79	-8.94 to 17.09	-1.98 to 4.51	-2.02 to 2.82	-8.89 to 28.57	-6.82 to 22.73	-88.46 to 6.28	-4.30 to 4.83	-44.33 to 277.78	-71.33 to 36.00	-46.53 to 66.72	-39.15 to 60.71

* and ** indicates significance at 5% and 1% levels of probability, respectively

Table 4: Mean sum of square for combining ability and variance components for different characters in *G. hirsutum* L

Source	Df	Fiber length (mm)	Fiber strength (g/tex)	Maturity co-efficient	Fiber fineness (mv)	Oil percentage	Gossypol content (%)	Phenol content (%)
Replications	2	0.065	1.48	4.13	0.01	0.15	0.01*	0.19**
Crosses	31	3.21**	9.88**	2.61	0.28*	0.41	0.06**	1.35**
Line effect	3	20.35**	58.72**	8.37*	0.65*	0.35	0.12	6.41**

Tester effect	7	2.27	7.73	1.89	0.39	0.53	0.05	0.44
Line × Tester effect	21	1.07**	3.61**	2.03	0.19**	0.38	0.05**	0.91**
Error	62	0.32	0.74	1.82	0.01	0.81	0.01	0.01
Variance components								
$\sigma^2 l$		0.82	2.41**	0.27*	0.02	-0.01	0.01	0.26**
$\sigma^2 m$		0.15	0.59	0.01	0.03	-0.01	0.01	0.04
$\sigma^2 gca$		0.60**	1.80**	0.18**	0.02**	-0.01*	0.01*	0.19
$\sigma^2 sca$		0.20**	0.98**	0.07	0.05**	-0.10	0.01**	0.30
$\sigma^2 gca/\sigma^2 sca$		2.91	1.83	2.62	0.5	0.12	0.41	0.63

* and ** indicates significance at 5% and 1% levels of probability, respectively

Table 5: General combining ability effect of parents for different characters in *G. hirsutum* L

Sr. No.	Parents	Fiber length (mm)	Fiber strength (g/tex)	Maturity co-efficient	Fiber fineness (mv)	Oil percentage	Gossypol content (%)	Phenol content (%)
				Lines				
1	GSHV 191	0.77**	1.77**	0.55*	-0.06	0.10	0.06**	-0.56**
2	GSHV 199	0.81**	0.59**	0.46	-0.15**	0.10	-0.07**	0.02
3	GISV 298	-0.72**	-1.90**	-0.53	0.23**	-0.08	0.05**	0.68**
4	GISV 319	-0.86**	-0.46**	-0.49	-0.01	-0.12	-0.04**	-0.14**
	S.E (g$_i$)	0.13	0.16	0.27	0.03	0.16	0.001	0.02
				Testers				
1	CPD 1602	-0.10	-0.89**	-0.24	-0.29**	-0.07	0.05**	-0.10**
2	SIMA 5	0.74**	-0.25	0.76	-0.12*	-0.24	-0.11**	-0.20**
3	RAH 1071	-0.39*	0.21	0.26	0.22**	-0.12	0.01	-0.12**
4	RHC 1217	-0.53**	0.39	-0.24	0.12*	0.07	0.06**	-0.02
5	PBH 42	-0.23	-0.97**	0.01	-0.15**	0.43	0.09**	-0.10**
6	HS 298	0.47*	0.03	-0.57	0.09	-0.17	-0.02**	-0.07**
7	F 2453	-0.13	-0.09	-0.07	-0.03	0.09	-0.01	0.30**
8	BGDS 1033	0.17	1.57**	0.09	0.17**	0.02	-0.07**	0.33**
	S.E(g$_j$)	0.19	0.23	0.39	0.05	0.23	0.01	0.02

* and ** indicates significance at 5% and 1% levels of probability, respectively

Table 6: Specific combining ability effect of crosses for different characters in *G. hirsutum* L

Sr. No.	Crosses	Fiber length (mm)	Fiber strength (g/tex)	Maturity co-efficient	Fiber fineness (mv)	Oil percentage	Gossypol content (%)	Phenol content (%)
1	GSHV 191 × CPD 1602	0.22	0.72	-1.05	-0.01	0.16	0.04**	-0.09
2	GSHV 191 × SIMA 5	0.17	0.15	-0.05	-0.15	-0.06	0.18**	0.27**
3	GSHV 191 × RAH 1071	1.02*	0.01	1.44	-0.20	0.19	0.21**	0.08
4	GSHV 191 × RHC 1217	0.27	-0.33	-1.05	-0.06	-0.05	-0.01	-0.01
5	GSHV 191 × PBH 42	-0.97*	-0.10	-0.30	0.01	0.29	-0.10**	0.29**
6	GSHV 191 × HS 298	-0.52	-0.88	-0.71	0.25*	0.05	-0.09**	0.42**
7	GSHV 191 × F 2453	-0.33	1.12*	1.11	0.09	-0.11	-0.14**	-0.55**
8	GSHV 191 × BGDS 1033	0.14	-0.67	0.61	0.08	-0.47	-0.10**	-0.42**
9	GSHV 199 × CPD 1602	-0.32	1.38**	0.36	-0.03	-0.05	-0.09**	-0.40**
10	GSHV 199 × SIMA 5	0.19	1.43**	0.36	-0.24*	-0.04	-0.04**	-0.03
11	GSHV 199 × RAH 1071	-0.18	-1.83**	0.19	0.10	0.13	-0.11**	-0.66**
12	GSHV 199 × RHC 1217	0.09	-0.67	1.03	0.11	0.08	-0.03**	0.66**
13	GSHV 199 × PBH 42	1.03*	0.74	-0.21	-0.17	0.22	0.03**	0.30**
14	GSHV 199 × HS 298	-0.35	0.19	0.36	0.04	-0.25	0.19**	0.33**
15	GSHV 199 × F 2453	-0.76	-0.86	-0.80	0.01	0.17	0.02	0.06
16	GSHV 199 × BGDS 1033	0.30	-0.38	-1.30	0.16	-0.26	0.02*	-0.24**
17	GISV 298 × CPD 1602	-0.19	-1.41**	0.36	0.25*	0.21	-0.06**	0.96**
18	GISV 298 × SIMA 5	0.09	-1.81**	0.03	0.37**	0.63	-0.17**	-0.03

* and ** indicates significance at 5% and 1% levels of probability, respectively

Table 6: Continue…….

Sr. No.	Crosses	Fiber length (mm)	Fiber strength (g/tex)	Maturity co-efficient	Fiber fineness (mv)	Oil percentage	Gossypol content (%)	Phenol content (%)
19	GISV 298 × RAH 1071	-0.55	1.34**	-1.46	0.32**	-0.21	-0.14**	-0.12*
20	GISV 298 × RHC 1217	-0.55	1.07*	0.03	0.03	-0.20	0.01	-0.43**
21	GISV 298 × PBH 42	0.18	0.36	0.78	-0.02	-0.22	0.15**	-0.18**
22	GISV 298 × HS 298	0.37	0.66	0.36	-0.34**	0.05	-0.01	-0.32**
23	GISV 298 × F 2453	0.34	0.12	-0.13	-0.007	-0.07	0.25**	-0.54**

24	GISV 298 × BGDS 1033	0.31	-0.33	0.03	-0.61**	-0.18	-0.03*	0.68**
25	GISV 319 × CPD 1602	0.29	-0.68	0.32	-0.20	-0.32	0.11**	-0.46**
26	GISV 319 × SIMA 5	-0.45	0.22	-0.34	0.02	-0.52	0.03**	-0.19**
27	GISV 319 × RAH 1071	-0.28	0.49	-0.17	-0.22*	-0.11	0.03**	0.70**
28	GISV 319 × RHC 1217	0.18	-0.06	-0.01	-0.08	0.17	0.02*	-0.21**
29	GISV 319 × PBH 42	-0.24	-1.00*	-0.26	0.18	-0.29	-0.09**	-0.40**
30	GISV 319 × HS 298	0.51	0.02	-0.01	0.03	0.14	-0.09**	-0.43**
31	GISV 319 × F 2453	0.75	-0.39	-0.17	-0.09	0.01	-0.14**	1.04**
32	GISV 319 × BGDS 1033	-0.75	1.40**	0.65	0.36**	0.92	0.11**	-0.02
	SE(S$_{ij}$)	0.38	0.46	0.78	0.10	0.47	0.012	0.05

* and ** indicates significance at 5% and 1% levels of probability, respectively

4. Conclusion
In case of fiber quality parameters, the maximum value of standard heterosis in desired direction was 3.52% (GSHV 199 × SIMA 5) for fiber length and -6.82% (GSHV 199 × SIMA 5, GISV 319 × CPD 1602) for fiber fineness. Whereas, biochemical parameters, the maximum value of standard heterosis in desired direction for oil content was 4.83% (GSHV 199 × PBH 42), for gossypol content -71.33% (GSHV 199 × SIMA 5 and GISV 298 × SIMA 5) and for phenol content 60.71% (GISV 298 × BGDS 1033).

Among parents, line GSHV 199 was good general combiner for characters *viz.,* fiber length, fiber strength, fiber fineness and gossypol content, whereas tester CPD 1602 was good general combiner for fiber fineness. GSHV 199 registered good general combining ability for fiber length, fiber strength, fiber fineness and gossypol content, while CPD 1602 registered good general combining ability for fiber fineness. Among the hybrids, GSIV 298 × RAH 1071 (1.34) and GSIV 298 × RHC 1217 (1.07) for fiber strength, three for gossypol content *viz.,* GISV 298 × RAH 1071 (-0.14), GSHV 199 × RHC 1217 (-0.04) and GISV 319 × PBH 42 (-0.09) and for phenol content only one cross GSHV 199 × RHC 1217 (0.66) showed positive and significant SCA effect. The ratio of σ^2gca / σ^2sca revealed that for fiber fineness, oil percentage, gossypol content and phenol content presence of preponderance of non-additive. While, fiber length, fiber strength and maturity co-efficient possess additive type of gene action in the inheritance of these characters.

The most of the crosses exhibiting high SCA effect involved either good × poor, poor × poor or good × good general combiners, in that order, for majority of the characters studied. The results suggested the presence of additive × dominance, dominance × dominance and additive × additive type of gene interactions. The presence of additive or additive × additive interaction effects would enhance the chances of making improvement through simple selection. The prevalence of both additive and non-additive genetic effects suggested the simultaneous exploitation of these gene actions by adopting selective intermating and recurrent selection, which would accumulate more of additive genetic variability. The non-additive gene effect can be exploited by the breeding procedures involving heterosis breeding or biparental mating followed by few cycles of recurrent selection. When epistasis is present, the recurrent selection followed by pedigree or biparental mating or diallel selective mating systems may prove to be effective in improvement of seed cotton yield and its attributes in cotton.

Declaration of competing interest
The authors declare no conflict of interest.

Appendix A. Supplementary data

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Supplementary Table: Mean values of 45 genotypes for fiber quality and biochemical parameters characters in *G. hirsutum* L.

Sr. No	Genotype	Fiber length (mm)	Fiber strength (g/tex)	Maturity co-efficient	Fiber fineness (mv)	Oil percentage (%)	Gossypol content (%)	Phenol content (%)
				Hybrid				
1	GSHV 191 × CPD 1602	27.90	30.40	0.82	4.23	18.47	0.54	1.59
2	GSHV 191 × SIMA 5	28.70	30.48	0.84	4.27	18.08	0.51	1.86
3	GSHV 191 × RAH 1071	28.42	30.80	0.85	4.57	18.46	0.66	1.75
4	GSHV 191 × RHC 1217	27.53	30.63	0.82	4.60	18.40	0.50	1.75
5	GSHV 191 × PBH 42	26.58	29.49	0.83	4.40	19.11	0.43	1.97
6	GSHV 191 × HS 298	27.73	29.72	0.82	4.90	18.26	0.32	2.13
7	GSHV 191 × F 2453	27.32	31.61	0.84	4.60	18.37	0.29	1.53
8	GSHV 191 × BGDS 1033	28.10	31.47	0.84	4.80	17.93	0.25	1.70
9	GSHV 199 × CPD 1602	27.40	29.89	0.83	4.13	18.25	0.25	1.86
10	GSHV 199 × SIMA 5	28.77	30.59	0.84	4.10	18.10	0.14	2.13
11	GSHV 199 × RAH 1071	27.25	27.78	0.83	4.80	18.40	0.19	1.59
12	GSHV 199 × RHC 1217	27.39	29.13	0.84	4.70	18.54	0.32	3.01
13	GSHV 199 × PBH 42	28.63	29.17	0.83	4.13	19.04	0.43	2.57
14	GSHV 199 × HS 298	27.95	29.63	0.83	4.60	17.95	0.47	2.63
15	GSHV 199 × F 2453	26.93	28.45	0.82	4.43	18.66	0.32	2.74
16	GSHV 199 × BGDS 1033	28.30	30.59	0.82	4.80	18.14	0.25	2.46
17	GISV 298 × CPD 1602	25.98	24.59	0.82	4.80	18.34	0.41	3.89
18	GISV 298 × SIMA 5	27.12	24.84	0.83	5.10	18.59	0.14	2.79
19	GISV 298 × RAH 1071	25.34	28.46	0.81	5.40	17.86	0.29	2.79
20	GISV 298 × RHC 1217	25.20	28.37	0.82	5.00	18.07	0.50	2.57
21	GISV 298 × PBH 42	26.23	26.29	0.83	4.67	18.41	0.68	2.74
22	GISV 298 × HS 298	27.13	27.59	0.82	4.60	18.08	0.39	2.63
23	GISV 298 × F 2453	26.50	26.93	0.82	4.80	18.22	0.68	2.79
24	GISV 298 × BGDS 1033	26.77	28.13	0.82	4.40	18.03	0.32	4.05
25	GISV 319 × CPD 1602	26.33	26.76	0.82	4.10	17.75	0.50	1.64
26	GISV 319 × SIMA 5	26.43	28.31	0.82	4.50	17.38	0.25	1.81
27	GISV 319 × RAH 1071	25.47	29.05	0.82	4.60	17.91	0.36	2.79
28	GISV 319 × RHC 1217	25.80	28.68	0.82	4.63	18.40	0.42	1.97
29	GISV 319 × PBH 42	25.67	26.36	0.82	4.63	18.29	0.32	1.70

30	GISV 319 × HS 298	27.13	28.40	0.81	4.73	18.12	0.21	1.70
31	GISV 319 × F 2453	26.77	27.86	0.82	4.47	18.27	0.18	3.56
32	GISV 319 × BGDS 1033	25.57	31.32	0.83	5.13	19.10	0.36	2.52
Female								
33	GSHV 191	25.53	28.03	0.81	3.90	17.98	0.18	2.02
34	GSHV 199	27.60	27.07	0.81	3.80	19.28	0.25	1.48
35	GISV 298	25.23	28.13	0.81	5.10	17.69	0.25	2.46
36	GISV 319	25.17	29.03	0.82	4.50	18.55	0.32	1.75
Male								
37	CPD 1602	25.59	26.33	0.80	4.53	18.05	0.43	2.41
38	SIMA 5	28.36	30.72	0.84	3.97	18.40	0.29	1.70
39	RAH 1071	25.03	23.42	0.81	4.83	17.85	0.21	2.13
40	RHC 1217	24.40	23.57	0.80	4.40	18.63	0.37	2.30
41	PBH 42	25.63	26.67	0.81	3.97	17.43	0.18	2.02
42	HS 298	26.79	24.75	0.82	4.67	17.64	0.36	3.17
43	F 2453	26.70	28.28	0.81	4.33	17.71	0.52	2.13
44	BGDS 1033	26.81	31.34	0.83	4.60	17.81	0.39	2.46
Check								
45	GN. Cot. Hy- 14 (C)	27.79	27.00	0.82	4.40	18.16	0.50	2.52
	Mean	26.78	28.36	0.82	4.55	18.22	0.36	2.31
	C. V.%	2.56	2.84	1.65	4.37	4.55	5.77	4.29
	S. Em.±	1.03	0.46	0.01	0.11	0.48	0.01	0.06
	C. D. at 5%	2.90	1.31	0.02	0.32	1.35	0.03	0.16