



## Research Article

# COMBINING ABILITY ANALYSIS TO IDENTIFY SUITABLE PARENTS AND CROSSES FOR SEED COTTON YIELD, FIBRE QUALITY AND OIL CONTENT IN INTRA AND INTER SPECIFIC DIALLEL CROSSES OF DIPLOID COTTON

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**Abstract-** The 10 x 10 half diallel cross investigation was carried out in order to determine gene action as well as general and specific combining ability in the material studied. All the traits were predominantly controlled by non-additive type of gene action. The parents GBhv- 287 and 824 were found to be good general combiners for seed cotton yield and most of the fibre quality traits, respectively. Variety GAM-165 had maximum number of dominant genes for oil content while GBhv- 283 had maximum number of dominant genes for boll weight. Hybrid, GBhv-282 x G 27 had significant sca effects for seed cotton yield per plant with good fibre quality in aspect of many fibre quality traits such as fibre strength, fibre elongation percentage and fibre maturity coefficient. 824 x G 27 proves superiority proved superior for fibre length and fibre fineness for sca effects. 824 x GAM- 173 was useful for oil content improvement in future as it showed high sca effects.

**Keywords-** Combining ability, Cotton, Gene action, Diallel analysis.

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## Introduction

Cotton occupies prominent place among commercial crops as it leads the destiny of a large section of the farming community as well as that of a flourishing textile industry. Cotton is also a heavily traded agricultural commodity. Through the export of textiles, cotton contributes to broader national economic growth, as a result of the significant multiplier effects deriving from employment and earnings in the manufacturing sector. Cotton also plays a role in the feed and oil industries with its seed, rich in oil (18 – 24%) and protein (20 – 40%). In India, cotton is grown in 126.55 lakh ha with a productivity of 537 kg/ ha and total production of 400 lakh bales [1]. Cotton crop is mainly cultivated for fibre and oil. Fibre quality of a specific cotton genotype is a combination of various characteristics, including fibre length, fibre strength, fineness, and fibre elongation. These traits have their distinctive importance in spinning, weaving and dyeing units [2]. Fibre length and strength properties mainly influence textile processing [3]. In addition, fibre uniformity is also of tremendous value to the textile industry. It is greatly correlated with the efficient spinning and weaving processes, which convert the fibre into fabrics. However, these traits are highly affected by the environment with special reference to the fineness [4-5].

The developments in biotechnology have replaced our indigenous diploid cotton varieties with American Bt cotton. Cotton production has declined to 40 -50 percent in mainly two states viz. Punjab and Haryana, due to susceptibility of Bt hybrids to white fly and leaf curl virus. Our native diploid cotton varieties are robust and sturdy in nature that provides them resilience against biotic and abiotic stress and produce well even in rainfed conditions. If fibre quality and yielding capacity of diploid cotton varieties is improved, then they will be preferred by farmers under

abiotic, biotic stress and poor environment with low inputs and investment to fetch good income. Present scenario of cotton farming necessitates that cotton breeders to develop high yielding and better fibre quality native cotton varieties for rainfed farming to sustain under abiotic and biotic stresses. To combine yield, fibre quality and oil content we need to identify suitable genotypes and use them in a crossing programme. Information on gene action and combining ability is necessary for selection of desirable parents for exploitation of hybrid vigour and transgressive expression to develop potential hybrids with a reasonable level of stability. Diallel analysis is a mating design whereby the selected parents are crossed in a certain order to predict combining ability of the parents and elucidate the nature of gene action involved in the inheritance of traits. In combining ability analysis, the entire genetic variability of each trait can be partitioned into GCA and SCA as defined by Sprague and Tatum (1942) [6] and reciprocal effects as outlined by Griffing's (1956) [7]. They stated that GCA effects administer the additive type of gene action whereas SCA effects are shown due to genes which are non-additive (dominant or epistatic) in nature. The objectives of present study was to evaluate general combining ability of parents and specific combining ability of hybrids and estimate gene action in diploid cotton and selecting the superior parents that can be used in breeding program of cotton.

## Materials and Methods

The crossing block (F<sub>0</sub>) and F<sub>1</sub> field experiment was conducted at Main Cotton Research Station (MCRS), Surat of Navsari Agricultural University (NAU), Navsari, Gujarat (India). The present investigation was conducted during *kharif* 2011-12 (F<sub>0</sub> or crossing block) and *kharif* 2012-2013 (F<sub>1</sub>).

## Genetic material and Field procedures

Ten diverse diploid cotton genotypes were selected as parents based on their agronomic and technological performance out of which five cotton varieties belong to *Gossypium herbaceum* species (GShv- 273/07, GBhv- 282, GBhv- 283, GBhv- 286 and GBhv- 287) and five cotton varieties from *Gossypium arboreum* species (824, G 27, GAM-141, GAM-165 and GAM-173). Each parental genotype was planted in 4 meter long rows, adopting 120 cm and 40 cm space between and within rows, respectively, to ensure easy crossing and to handle breeding material properly. In a half diallel mating design (excluding reciprocals), crossing was operated in *kharif* 2011-12 to generate 45  $F_1$  hybrids using hand emasculation and pollination suggested by [8]. At crop maturity stage, the crossed bolls were picked and ginned separately cross wise. During *kharif* 2012-2013, 45  $F_1$ , their parents along with a check viz. G Cot DH- 7 were raised in randomized block design (RBD) with three replications, spaced 120 cm and 40 cm space between and within rows, respectively. Recommended cultural practices for cotton production for the location were carried out and crop was maintained under uniform field conditions to minimize environmental variations to a maximum possible extent.

## Sampling Trait Measurements and Statistical analysis

Five plants were randomly selected on maturity from each replication for each genotype and  $F_1$ , the average value per plot was computed for recording observations for eleven characters regarding seed cotton yield and its contributing traits, fibre quality parameters and oil quantity. Fibre quality parameters namely

2.5 % span length (mm), fibre strength (g tex<sup>-1</sup>), fibre fineness (mv), fibre elongation percentage (%), fibre maturity coefficient, short fibre index (SFI), fibre uniformity ratio (%) were analyzed using High Volume Instrument (HVI) (Premier Evolvics Pvt. Ltd., Coimbatore) in ideal condition (R.H. 65±2 % and temperature 27±2°C) at CIRCOT, Regional Station, Surat. The oil content in cotton seed was determined by Nuclear Magnetic Resonance (NMR) technique.

The data were subjected to ANOVA technique using INDOSTAT computer software package individually for all the traits, to assess statistical differences among  $F_1$  and their parental genotypes. The data were further subjected to combining ability analysis as outlined by [7] Method-II and Model-I (Fixed effect) as described by [9].

## Results and Discussion

### Mean performance

ANOVA revealed that variances due to parental lines were highly significant for all the characters. The mean squares due to  $F_1$  hybrids showed significant variation for all the characters except fibre maturity coefficient. In addition, the parents versus hybrids component showed significant variation for all the characters except fibre uniformity ratio and oil content. The analysis of variance [Table-1] indicated that the mean squares of genotypes for all characters investigated were significantly different that indicates the presence of variability among hybrids and their parents, hence later analysis for combining ability was possible. Ashok kumar and Ravikesavan (2013) [10] observed all the characters were significantly different with parents and hybrids in upland cotton, and it confirmed our results.

**Table-1** Analysis of variance for biometrical traits from Half diallel analysis of intra- and interspecific diploid cotton

Source of variations	d.f.	SCY/Plant	No. Of Bolls/ Plant	Boll Weight (g)	2.5% Span length (mm)	g tex <sup>-1</sup>	Micronaire Value	Fibre Elongation Percentage	Maturity Coefficient	Short Fibre Index	Fibre Uniformity Ratio	Oil %
Replications	2	1.059	10.68	0.02	0.72	0.08	0.09	0.23	0.10	0.07	0.38	0.20
Genotypes	54	4703.52**	1027.40**	0.25**	17.96**	17.15**	1.38**	0.66**	0.001**	21.95**	15.11**	0.83**
Parents	9	744.60**	196.50**	0.16**	28.28**	15.75**	1.65**	0.76**	0.002**	18.20**	39.87**	0.84**
Hybrids	44	5193.64**	1096.95**	0.26**	15.54**	15.00**	1.34**	0.50**	0.001	22.81**	10.23**	0.84**
Parents vs. Hybrids	1	18768.42**	5445.44**	0.42**	31.53**	124.43**	0.66**	6.87**	0.02**	17.83**	6.98	0.05
Error	108	149.02	27.60	0.02	0.68	0.70	0.09	0.12	0.0006	0.31	3.27	0.09
SE±		7.05	3.03	0.08	0.48	0.48	0.17	0.20	0.14	0.10	1.04	0.17

\*, \*\* significant at 5 per cent and 1 per cent levels of probability, respectively.

**Table-2** Genetic components of variance and genetic contribution of parents and hybrids in a 10 x 10  $F_1$  Halfdiallel cross of intra- and interspecific diploid cotton.

Characters	Seed cotton yield per plant (g)	No. of bolls per plant	Boll weight (g)	2.5% span length (mm)	Fibre strength (3.2 g tex <sup>-1</sup> )	Fibre fineness (mv)	Fibre elongation percentage (%)	Fibre maturity coefficient	Short Fibre Index	Fibre uniformity ratio	Oil content (%)
<i>gca</i> (9 d.f.)	1610.88**	405.40**	0.15**	10.37**	7.94**	1.14**	0.12**	0.02	6.71**	10.52**	0.68**
<i>sca</i> (45 d.f.)	1559.23**	329.88**	0.07**	5.11**	5.27**	0.32**	0.24**	0.04**	7.44**	3.94**	0.19**
Error (108 d.f.)	49.67	9.2	0.01	0.23	0.23	0.03	0.04	0.02	0.10	1.10	0.03
$\sigma^2 gca$	130.10	33.01	0.01	0.85	0.64	0.09	0.01	0.0002	0.55	0.79	0.05
$\sigma^2 sca$	1509.56	320.68	0.06	4.88	5.04	0.30	0.20	0.02	7.33	2.85	0.17
$\sigma^2 gca / \sigma^2 sca$	0.09	0.10	0.19	0.17	0.13	0.31	0.03	0.0001	0.08	0.28	0.33

\*, \*\* significant at 5 per cent and 1 per cent levels of probability, respectively

Mean performance of parents and hybrids are presented in [Table-3] and [Table-5], respectively. For yield and its contributing characters, G 27, GBhv- 286 and GAM- 165 recorded high mean performance for no. of bolls per plant (42.82), mean boll weight (2.62) and seed cotton yield per plant (97.70), respectively. In present study, hybrid GBhv- 282 x G- 27 recorded higher mean performance for no. of bolls per plant (97.40) and seed cotton yield per plant (223.15 g). GBhv- 283 x GAM-165 exhibited highest mean performance for mean boll weight (2.94 g).

For fibre quality traits, parental line 824 was prominent for most of fibre quality characters such as 2.5 % span length (30.1 mm), fibre strength (22.70 g tex<sup>-1</sup>), fibre fineness (4.20 mv), fibre elongation ratio (6.20 %) and fibre maturity coefficient (0.84 %). Genotype G 27, recorded highest mean performance for short fibre index (6.50) and fibre uniformity ratio (56.00) in desirable direction. Highest amount of oil was 17.48 percent was present in GAM- 141 genotype. Mean performance for fibre quality and oil content indicated that *arboreum* cultivars were superior in comparison to *herbaceum* cultivars.

Selection of hybrids can be done based on *per se* performance, although it is not only criteria for selection of hybrids, *sca* effects and hybrid vigour for crosses also considered when non-additive gene action is predominating. In present study, hybrid GBhv- 282 x G- 27 recorded higher *per se* performance for no. of bolls per plant (97.40) and seed cotton yield per plant (223.15 g) while highest mean value for mean boll weight (2.94 g) was exhibited by cross combination, GBhv- 283 x GAM-165.

Cross GBhv- 286 x 824 recorded high mean performance (32.00 mm) for 2.5 percent span length while for fibre strength GBhv- 283 x 824 showed high value (24.10 g tex<sup>-1</sup>) for mean performance. In case of fibre fineness performance 824 x G 27 excelled and recorded 3.80 mv value. GBhv- 282 x G 27 noticed on top for fibre elongation percentage (6.60) as well as for fibre maturity ratio (0.88). For Short fibre index, cross GBhv- 286 x GBhv- 287 was superior with a mean value 6.80. Cross combinations, GShv- 273/07 x GBhv- 283 and GShv- 273/07 x GBhv- 287 ranked first for fibre uniformity ratio and exhibited a value of 53.00. For oil content, intraarboreum cross, 824 x GAM- 173 ranked first with 17.86 percent oil content.

### Effects of Gene Action

ANOVA for combining ability revealed mean squares of GCA for parental lines were found significant for all of investigated traits except fibre maturity coefficient

revealing important role of additive type gene effects while mean squares of SCA were observed significant for all of studied characters revealing role of non-additive gene action (dominant or epistatic). [Table-2]. The magnitude of *gca* and *sca* variances revealed that additive as well as non-additive gene action was important for inheritance of seed cotton yield, its contributing traits, fibre quality and oil content. Significance of both the variances had also been also suggested by [11-12].

The higher SCA than GCA of a character indicates the preponderance of non-additive gene action and *vice versa*. In the current study, analysis of combining ability revealed that the variances for the *sca* were larger than *gca* those for all the traits. The ratio of  $\sigma^2_{gca} / \sigma^2_{sca}$  showed that all the characters manifested less than unity values, which indicated preponderance of non-additive genetic variance for inheritance of these traits which could be exploited for the improvement of these traits by heterosis breeding. Similar findings were reported by [13-17] in cotton. Nimbalkar *et al.*, (2004) and Patel *et al.*, (2009) [11 and 18] also reported non additive type of gene action for seed cotton yield and its contributing traits in diploid cotton. Non-additive gene action for fibre quality traits: fibre length, fibre strength and micronaire value have been reported by [13,19-22]. Lukange *et al.* (2007) [23] revealed additive gene effects for fibre strength and microanire value and non-additive gene action for fibre length.

**Table-3** *Per se* performance of parents for yield and its yield attributing characters in a 10 x 10 F<sub>1</sub> Half diallel cross of intra- and interspecific diploid cotton

PARENTS	SCY /Plant	No. Of Bolls/plant	Boll Weight (g)	2.5% Span length (mm)	g tex <sup>-1</sup>	Micronaire Value	Fibre Elongation Percentage	Maturity Co efficient	Short Fibre Index	Fibre Uniformity Ratio	Oil (%)
<b>G. herbaceum</b>											
GShv-273/07	87.27	39.90	2.19	23.7	20.20	5.00	5.60	0.84	13.90	51.00	16.23
GBhv- 282	78.16	42.22	1.85	24.5	17.60	4.70	4.90	0.82	12.40	51.00	16.01
GBhv- 283	58.14	26.22	2.24	25.1	18.80	4.50	5.40	0.82	13.20	49.00	17.14
GBhv- 286	52.07	19.98	2.62	23.2	17.30	5.60	5.10	0.84	15.60	49.00	16.75
GBhv- 287	78.73	33.88	2.33	25.6	18.90	5.10	5.40	0.84	13.30	48.00	16.62
<b>G. arboreum</b>											
824	82.49	38.59	2.14	30.1	22.70	4.20	6.20	0.84	10.30	44.00	16.88
G 27	88.80	42.82	2.08	18.7	13.60	6.90	4.50	0.75	6.50	56.00	16.70
GAM- 141	81.33	33.48	2.44	25.9	18.70	5.30	6.00	0.84	12.10	49.00	17.48
GAM- 165	97.70	38.22	2.56	28.5	18.10	4.90	5.40	0.83	13.40	43.00	17.77
GAM- 173	53.68	23.37	2.29	25.6	18.20	4.90	5.70	0.83	13.00	48.00	16.89
<b>Check</b>											
G. Cot DH- 7	133.34	65.75	2.03	24.0	17.90	6.10	5.60	0.85	14.50	49.00	17.08

**Table-4** General combining ability effects of intra- and interspecific hybrids of diploid cotton for yield and yield contributing traits.

S. No.	Parents	SCY/Plant	No. Of Bolls/plant	Boll Weight (g)	2.5% Span length (mm)	g tex <sup>-1</sup>	Micronaire Value	Fibre Elongation Percentage	Maturity Coefficient	Short Fibre Index	Fibre Uniformity Ratio	Oil %
1	GShv- 273/07	0.01	-1.62	0.10**	-0.17	0.75**	-0.26**	-0.02	0.03	-0.60**	1.37**	-0.48**
2	GBhv- 282	11.19**	3.11**	0.07**	-0.04	0.23	-0.16**	-0.05	-0.05	-0.57**	0.78**	-0.24**
3	GBhv- 283	-12.87**	-7.83**	0.15**	0.35**	0.32*	-0.17**	-0.02	0.12	-0.63**	0.45	0.004
4	GBhv- 286	-9.97**	-4.59**	0.03	-0.24	-0.22	-0.06	-0.10	-0.13	0.41**	0.11	-0.10*
5	GBhv- 287	17.50**	7.52**	0.05**	0.86**	0.72**	-0.13**	0.15**	0.37	-1.02**	0.03	-0.03
6	824	6.88**	4.64**	-0.11**	1.44**	0.84**	-0.32**	0.14*	-0.22	-0.61**	-1.22**	0.04
7	G 27	12.35**	8.95**	-0.18**	-2.17**	-1.92**	0.75**	-0.17**	-1.05*	0.63**	1.12**	0.13**
8	GAM- 141	-0.98	-0.06	-0.03	-0.01	-0.22	0.16**	0.05	0.37	0.55**	0.63*	0.25**
9	GAM- 165	-8.89**	-5.25**	0.07**	0.14	-0.46**	0.06	-0.03	0.03	0.82**	-1.33**	0.16**
10	GAM- 173	-15.23**	-4.86**	-0.15**	-0.16	-0.03	0.15**	0.05	0.53	1.02**	-0.88**	0.33**
	<b>S.E. (g)</b>	1.93	0.83	0.02	0.13	0.13	0.05	0.05	0.40	0.09	0.29	0.05
	<b>S. E. (g) ±</b>	2.88	1.24	0.03	0.20	0.20	0.07	0.08	0.60	0.13	0.43	0.07

\*, \*\* significant at 5 per cent and 1 per cent levels of probability, respectively.

Estimation of general combining ability effects for all the ten parents and specific combining ability effects for 45 half diallel crosses for eleven characters with their corresponding standard error are presented in [Table-4 and 5], respectively. The results of GCA&SCA effects are presented as under;

The combining ability analysis gives useful information regarding selection of parents based on the performance of their hybrids and further it helps for the exploitation of heterosis. The estimate of *gca* effects showed that none of the parental lines excelled as a good general combiner for all the characters, so it was

difficult to pick good combiners for all the characters together because the combining ability effects were not consistent for all the yield components, possibly because of negative association among some of the characters. This shows that genes for different desirable characters would have to be combined from different sources. In current investigation, combining effects were estimated in which parental line GBhv- 287 recorded high GCA effects for seed cotton yield per plant. Apart from this GBhv- 287 also showed high GCA effects for fibre quality traits viz. fibre elongation percentage and short fibre index and proves its worthiness for

**Table-5** *Per se performance and Specific combining ability effects of intra- and interspecific hybrids of diploid cotton for yield and yield contributing traits.*

S. No.	Crosses	Seed cotton yield per plant (g)		No. of bolls per plant		Boll weight (g)		2.5 per cent span length (mm)	
		Mean	SCA	Mean	SCA	Mean	SCA	Mean	SCA
1	GShv- 273/07 x GBhv- 282	90.62	-19.04**	39.11	-8.44**	2.31	-0.023	25.9	0.11
2	GShv- 273/07 x GBhv- 283	66.83	-18.78**	29.69	-6.91*	2.29	-0.13	25.1	-1.13*
3	GShv- 273/07 x GBhv- 286	69.81	-18.70**	30.82	-9.02**	2.26	-0.04	25.2	-0.42
4	GShv- 273/07 x GBhv- 287	74.88	-41.09**	26.73	-25.23**	2.81	0.50**	25.7	-1.02*
5	GShv- 273/07 x 824	151.28	45.93**	68.60	19.53**	2.20	0.05	27.3	0.04
6	GShv- 273/07 x G 27	136.76	25.94**	71.70	18.32**	1.91	-0.18	25.1	1.38**
7	GShv- 273/07 x GAM- 141	123.67	26.17**	56.85	12.48**	2.17	-0.06	26.6	0.75
8	GShv- 273/07 x GAM- 165	96.00	6.41	39.78	0.60	2.42	0.09	28.2	2.20**
9	GShv- 273/07 x GAM- 173	98.84	15.60*	44.05	4.47	2.25	0.14*	27.7	2.00**
10	GBhv- 282 x GBhv- 283	59.46	-37.33**	22.66	-18.68**	2.65	0.26**	26.6	0.26
11	GBhv- 282 x GBhv- 286	76.78	-22.91**	34.60	-9.97**	2.23	-0.04	25.3	-0.45
12	GBhv- 282 x GBhv- 287	85.87	-41.28**	38.97	-17.71**	2.20	-0.09	24.8	-2.01**
13	GBhv- 282 x 824	75.66	-40.87**	36.15	-17.66**	2.09	-0.04	24.8	-2.62**
14	GBhv- 282 x G 27	223.15	101.15**	97.40	39.29**	2.29	0.23**	25.6	1.79**
15	GBhv- 282 x GAM- 141	152.33	43.66**	62.00	12.90**	2.47	0.27**	27.6	1.62**
16	GBhv- 282 x GAM- 165	117.18	16.42*	44.73	0.82	2.62	0.31**	28.5	2.38**
17	GBhv- 282 x GAM- 173	180.00	85.58**	83.86	39.55**	2.14	0.05	27.6	1.81**
18	GBhv- 283 x GBhv- 286	95.00	19.37**	39.08	5.45	2.42	-0.07	26.7	0.56
19	GBhv- 283 x GBhv- 287	92.33	-10.76	42.68	-3.07	2.17	-0.20**	28.8	1.56**
20	GBhv- 283 x 824	158.33	65.86**	76.56	33.70**	2.07	-0.14*	30.3	2.48**
21	GBhv- 283 x G 27	105.57	7.63	54.56	7.39**	1.94	-0.20**	23.8	-0.41
22	GBhv- 283 x GAM- 141	95.01	10.39	34.29	-3.87	2.76	0.48**	26.5	0.10
23	GBhv- 283 x GAM- 165	65.86	-10.85	22.41	-10.56**	2.94	0.55**	24.8	-1.72**
24	GBhv- 283 x GAM- 173	73.99	3.63	38.27	4.90	1.95	-0.22**	27.7	1.48**
25	GBhv- 286 x GBhv- 287	111.00	5.01	50.94	1.95	2.18	-0.07	30.1	3.45**
26	GBhv- 286 x 824	122.22	26.85**	61.70	15.60**	1.98	-0.11	32.0	4.78**
27	GBhv- 286 x G 27	160.67	59.83**	79.59	29.19**	2.02	0.004	23.3	-0.32
28	GBhv- 286 x GAM- 141	89.60	2.08	48.35	6.95*	1.86	-0.30**	25.9	0.12
29	GBhv- 286 x GAM- 165	54.93	-24.68**	29.09	-7.11*	1.89	-0.38**	24.3	-1.59**
30	GBhv- 286 x GAM- 173	79.33	6.07	37.36	0.76	2.13	0.08	24.2	-1.43**
31	GBhv- 287 x 824	210.86	88.02**	93.09	34.88**	2.30	0.19**	29.1	0.78
32	GBhv- 287 x G 27	146.73	18.42**	72.29	9.77**	2.02	-0.02	24.7	-0.02
33	GBhv- 287 x GAM- 141	150.57	35.58**	72.73	19.22**	2.07	-0.11	27.4	0.52
34	GBhv- 287 x GAM- 165	128.74	21.69**	62.83	14.51**	2.05	-0.23**	26.8	-0.23
35	GBhv- 287 x GAM- 173	134.63	33.91**	68.84	20.12**	1.96	-0.11	28.0	1.27**
36	824 x G 27	73.16	-44.53**	35.85	-23.79**	2.10	0.22**	30.4	5.14**
37	824 x GAM- 141	73.00	-31.37**	38.23	-12.40**	1.90	-0.12	22.3	-5.16**
38	824 x GAM- 165	81.64	-14.81*	42.37	-3.07	1.93	-0.19**	21.8	-5.80**
39	824 x GAM- 173	54.50	-35.61**	32.53	-13.31**	1.68	-0.23**	25.2	-2.10**
40	G 27 x GAM- 141	70.10	-39.73**	39.52	-15.42**	1.77	-0.19**	24.8	0.95*
41	G 27 x GAM- 165	86.33	-15.59*	45.90	-3.84	1.88	0.18*	24.0	0.04
42	G 27 x GAM- 173	51.16	-44.42**	31.50	-18.64**	1.62	-0.22**	21.1	-2.59**
43	GAM- 141 x GAM- 165	92.14	3.54	50.87	-10.13**	1.81	-0.39**	27.1	0.94*
44	GAM- 141 x GAM- 173	62.28	-19.97**	36.06	-5.08	1.73	-0.25**	26.2	0.38
45	GAM- 165 x GAM- 173	58.20	0.12	29.11	-6.83*	1.99	-0.10	25.4	-0.61
	<b>S.E.<sub>(sij)</sub> ±</b>		6.49		2.79		0.07		0.44
	<b>S.E.<sub>(sij - sik)</sub> ±</b>		9.54		4.11		0.10		0.65
	<b>S.E.<sub>(-sij - sik)</sub> ±</b>		9.10		3.92		0.10		0.62

\*, \*\* significant at 5 per cent and 1 per cent levels of probability, respectively.

Table-5 continued..

S. No.	Crosses	Fibre strength (3.2 g tex <sup>-1</sup> )		Fibre fineness (mv)		Fibre elongation percentage (%)		Fibre maturity coefficient	
		Mean	SCA	Mean	SCA	Mean	SCA	Mean	SCA
1	GShv- 273/07 x GBhv- 282	21.80	0.59	4.60	-0.22	5.70	-0.09	0.84	-0.58
2	GShv- 273/07 x GBhv- 283	20.30	-1.01*	4.80	0.02	5.50	-0.31	0.84	-0.75
3	GShv- 273/07 x GBhv- 286	22.90	2.14**	4.40	-0.52**	5.60	-0.14	0.84	-0.50
4	GShv- 273/07 x GBhv- 287	20.40	-1.31**	4.80	-0.05	5.50	-0.49**	0.84	-1.00
5	GShv- 273/07 x 824	23.40	1.57**	4.50	-0.13	6.20	0.23	0.85	0.58
6	GShv- 273/07 x G 27	18.60	-0.47	6.20	0.47**	5.90	0.24	0.86	2.417
7	GShv- 273/07 x GAM- 141	20.80	0.03	5.00	-0.14	5.90	0.01	0.85	0.00
8	GShv- 273/07 x GAM- 165	21.90	1.37**	5.10	0.05	6.50	0.69**	0.86	1.33
9	GShv- 273/07 x GAM- 173	21.20	0.24	5.10	-0.03	6.20	0.31	0.85	-0.17
10	GBhv- 282 x GBhv- 283	21.00	0.18	4.60	-0.34*	5.90	0.12	0.84	-0.67
11	GBhv- 282 x GBhv- 286	18.30	-1.97**	5.10	0.11	5.60	-0.11	0.83	-1.42
12	GBhv- 282 x GBhv- 287	20.50	-0.71	4.90	-0.05	5.60	-0.36*	0.84	-0.92
13	GBhv- 282 x 824	20.90	-0.41	4.90	0.17	5.80	-0.14	0.85	0.67
14	GBhv- 282 x G 27	22.10	3.56**	6.40	0.57**	6.60	0.97**	0.88	4.50**
15	GBhv- 282 x GAM- 141	22.50	2.19**	5.60	0.36*	6.40	0.54**	0.87	2.08
16	GBhv- 282 x GAM- 165	21.20	1.20**	5.10	-0.08	6.30	0.53**	0.85	0.42
17	GBhv- 282 x GAM- 173	22.00	1.56**	5.10	-0.09	6.10	0.24	0.86	0.92
18	GBhv- 283 x GBhv- 286	19.80	-0.57	5.20	0.19	5.60	-0.13	0.85	0.42
19	GBhv- 283 x GBhv- 287	21.80	0.52	5.50	0.56**	6.40	0.42*	0.87	1.92
20	GBhv- 283 x 824	24.10	2.67**	4.60	-0.15	6.50	0.54**	0.86	1.50
21	GBhv- 283 x G 27	19.20	0.53	6.50	0.68**	6.10	0.44*	0.87	3.33*
22	GBhv- 283 x GAM- 141	20.30	-0.08	5.20	-0.03	5.60	-0.28	0.85	-0.08
23	GBhv- 283 x GAM- 165	19.60	-0.53	5.00	-0.13	5.30	-0.50**	0.84	-0.75
24	GBhv- 283 x GAM- 173	23.00	2.44**	5.20	-0.02	6.40	0.52**	0.86	0.75
25	GBhv- 286 x GBhv- 287	20.80	0.04	5.50	0.45**	6.20	0.29	0.86	1.17
26	GBhv- 286 x 824	23.70	2.81**	4.30	-0.56**	6.20	0.31	0.84	-0.25
27	GBhv- 286 x G 27	19.60	1.51**	6.00	0.07	6.30	0.72**	0.86	2.58
28	GBhv- 286 x GAM- 141	20.60	0.77	4.80	-0.54**	5.90	0.09	0.84	-0.83
29	GBhv- 286 x GAM- 165	21.40	1.85**	4.30	-0.94**	5.50	-0.22	0.83	-1.50
30	GBhv- 286 x GAM- 173	18.50	-1.52**	6.10	0.77**	6.10	0.30	0.86	1.00
31	GBhv- 287 x 824	22.50	0.67	4.90	0.08	6.50	0.36*	0.85	0.25
32	GBhv- 287 x G 27	21.40	2.34**	5.50	-0.36*	6.30	0.47**	0.86	2.08
33	GBhv- 287 x GAM- 141	21.60	0.83	4.50	-0.73**	6.20	0.14	0.84	-1.33
34	GBhv- 287 x GAM- 165	21.60	1.11*	5.50	0.30	6.30	0.33	0.86	1.00
35	GBhv- 287 x GAM- 173	23.00	2.07**	4.80	-0.46**	6.40	0.34	0.85	-0.50
36	824 x G 27	22.00	2.84**	3.80	-1.87**	6.10	0.29	0.82	-1.33
37	824 x GAM- 141	15.90	-4.97**	6.40	1.32**	5.30	-0.74**	0.84	-0.75
38	824 x GAM- 165	14.70	-5.92**	6.30	1.31**	5.30	-0.66**	0.83	-1.42
39	824 x GAM- 173	20.30	-0.75	5.70	0.63**	5.70	-0.34	0.86	1.08
40	G 27 x GAM- 141	17.50	-0.60	6.10	-0.01	5.40	-0.33	0.85	1.08
41	G 27 x GAM- 165	18.90	1.05*	5.80	-0.25	5.70	0.05	0.85	1.42
42	G 27 x GAM- 173	13.20	-5.12**	6.50	0.36*	4.90	-0.83**	0.83	-1.08
43	GAM- 141 x GAM- 165	20.20	0.64	5.90	0.44**	6.40	0.53**	0.86	1.00
44	GAM- 141 x GAM- 173	23.40	3.41**	5.40	-0.15	5.90	-0.06	0.87	1.50
45	GAM- 165 x GAM- 173	21.40	1.65**	5.70	0.25	5.90	0.03	0.87	1.83
	<b>S.E.(sij) ±</b>		0.44		0.16		0.18		0.18
	<b>S.E.(sij - sik) ±</b>		0.65		0.23		0.27		0.27
	<b>S.E.(sij - skl) ±</b>		0.62		0.22		0.26		0.26

\*, \*\* significant at 5 per cent and 1 per cent levels of probability, respectively.



Table-5 continued..

S. No.	Crosses	Short Fibre Index		Fibre uniformity ratio		Oil content (%)	
		Mean	SCA	Mean	SCA	Mean	SCA
1	GShv- 273/07 x GBhv- 282	10.40	-0.11	51.00	-0.39	16.58	0.49**
2	GShv- 273/07 x GBhv- 283	10.60	0.15	53.00	1.95*	16.58	0.24
3	GShv- 273/07 x GBhv- 286	12.30	0.82**	50.00	-0.72	15.44	-0.80**
4	GShv- 273/07 x GBhv- 287	9.50	-0.56	53.00	2.36*	16.28	-0.03
5	GShv- 273/07 x 824	9.40	-1.06**	50.00	0.61	15.93	-0.37*
6	GShv- 273/07 x G 27	11.70	0.002	51.00	-0.72	16.40	-0.07
7	GShv- 273/07 x GAM- 141	11.60	-0.02	48.00	-1.97*	16.97	0.38*
8	GShv- 273/07 x GAM- 165	8.00	-3.89**	51.00	1.53	16.37	-0.12
9	GShv- 273/07 x GAM- 173	9.90	-2.19**	49.00	-0.72	16.17	-0.49**
10	GBhv- 282 x GBhv- 283	10.60	0.12	50.00	-0.47	16.42	-0.16
11	GBhv- 282 x GBhv- 286	11.00	-0.51	51.00	0.86	16.84	0.36*
12	GBhv- 282 x GBhv- 287	14.00	3.91**	48.00	-2.05*	15.92	-0.63**
13	GBhv- 282 x 824	12.50	2.00**	50.00	1.20	16.36	-0.18
14	GBhv- 282 x G 27	12.00	0.27	49.00	-2.14*	17.29	0.59**
15	GBhv- 282 x GAM- 141	8.30	-3.36**	51.00	1.61	16.80	-0.03
16	GBhv- 282 x GAM- 165	8.80	-3.12**	49.00	0.11	16.30	-0.43**
17	GBhv- 282 x GAM- 173	9.20	-2.92**	50.00	0.86	17.52	0.62**
18	GBhv- 283 x GBhv- 286	10.20	-1.26**	50.00	0.20	17.05	0.33*
19	GBhv- 283 x GBhv- 287	8.90	-1.13**	48.00	-1.72	17.05	0.26
20	GBhv- 283 x 824	7.00	-3.44**	49.00	0.53	15.99	-0.79**
21	GBhv- 283 x G 27	13.00	1.33**	52.00	1.20	16.49	-0.46**
22	GBhv- 283 x GAM- 141	11.10	-0.50	49.00	-0.05	16.69	-0.38*
23	GBhv- 283 x GAM- 165	12.70	0.84**	50.00	1.45	17.12	0.15
24	GBhv- 283 x GAM- 173	10.40	-1.66**	48.00	-0.80	17.29	0.15
25	GBhv- 286 x GBhv- 287	6.80	-4.26**	50.00	0.61	16.74	0.05
26	GBhv- 286 x 824	7.20	-4.27**	46.00	-2.14*	16.84	0.16
27	GBhv- 286 x G 27	13.60	0.89**	52.00	1.53	17.22	0.37*
28	GBhv- 286 x GAM- 141	12.90	0.27	48.00	-0.72	17.39	0.42**
29	GBhv- 286 x GAM- 165	13.90	1.00**	49.00	0.78	16.11	-0.76**
30	GBhv- 286 x GAM- 173	14.20	1.10**	49.00	0.53	16.63	-0.41**
31	GBhv- 287 x 824	7.00	-3.05**	51.00	2.95**	16.45	-0.30
32	GBhv- 287 x G 27	13.20	1.92**	49.00	-1.39	17.47	0.55**
33	GBhv- 287 x GAM- 141	10.90	-0.31	48.00	-0.64	16.76	-0.28**
34	GBhv- 287 x GAM- 165	10.00	-1.47**	50.00	1.86	17.18	0.24
35	GBhv- 287 x GAM- 173	9.30	-2.37**	49.00	0.61	17.52	0.41
36	824 x G 27	10.30	-1.39**	44.00	-5.14**	16.79	-0.12
37	824 x GAM- 141	15.90	4.29**	51.00	3.61**	16.93	-0.10
38	824 x GAM- 165	16.70	4.82**	51.00	4.11**	17.56	0.63**
39	824 x GAM- 173	14.50	2.42**	47.00	-0.14	17.86	0.76**
40	G 27 x GAM- 141	14.30	1.45**	48.00	-1.72	17.25	-0.05
41	G 27 x GAM- 165	15.60	2.49**	48.00	-1.22	16.86	-0.24
42	G 27 x GAM- 173	19.20	5.89**	50.00	0.53	17.34	0.07
43	GAM- 141 x GAM- 165	11.80	-1.24**	47.00	-0.47	16.63	-0.60**
44	GAM- 141 x GAM- 173	14.00	0.76*	46.00	-1.72	17.58	0.19
45	GAM- 165 x GAM- 173	13.90	0.39	47.00	-0.22	17.14	-0.16
	S.E. <sub>(sij)</sub> ±		0.30		0.96		0.15
	S.E. <sub>(sij - sik)</sub> ±		0.43		1.41		0.23
	S.E. <sub>(sij - skl)</sub> ±		0.41		1.35		0.22

\*, \*\* significant at 5 per cent and 1 per cent levels of probability, respectively.

yield and quality improvement in future breeding programme. For no. of bolls per plant and mean boll weight, G- 27 and GBhv- 283 exhibited high GCA, respectively. *Aroboreum* line 824 observed good general combiner for 2.5 percent span length, fibre strength and fibre fineness. Therefore, line 824 was identified as good source of favourable genes in improving fibre quality. Among the parents, none of the parent showed positive significant GCA effects for fibre maturity coefficient while GShv- 273/07 was good general combiner for fibre uniformity ratio. For oil content most of *aroboreum* cultivars showed significant GCA value among them GAM- 173 was on top. However, an overall appraisal of general combining ability effects revealed that, GBhv- 287 and 824 were good general combiners for most of yield and fibre quality traits under study.

The specific combining ability value of any cross was helpful in predicting the performance of the better parents. Out of 45 crosses 16 crosses exhibited highly significant and positive *sca* effects for no. of bolls per plant. Among them, GBhv- 282 x GAM-173 and GBhv-282 x G 27 showed high *sca* effects for no. of bolls per plant and have good x poor and good x good GCA effect parents, respectively. In case of  $F_1$ SCA effects for seed cotton yield per plant, 17 specific crosses showed positive SCA effects ranging from -44.53 to 101.15, while maximum SCA effects were gained by the hybrids GBhv-282 x G 27 (101.15) and GBhv-287 x 824 (88.02) and have good x good *gca* effects parents. Hybrids, GBhv-283 x GAM-165 and GShv-273/07 x GBhv-287 possessed highest and significant *sca* effects for mean boll weight.

Fibre length is the most important cotton fibre character, which determines the amount by which fibres can overlap with one another. The greater overlapping, the easier it is for the fibres to be bound together and result in better yarn strength [24]. Fibre fineness is another important fibre character affecting yarn strength. It contributes to the number of fibres in the cross-section of yarn. For 2.5 percent span length and fibre fineness, cross 824 x G 27 (5.14) produced maximum *sca* effects in desirable direction to respective traits. 824 was good general combiner for both the characters while G 27 was poor general combiner for both the characters. Highest significant *sca* effects for fibre strength ( $g\ tex^{-1}$ ) (3.56), fibre elongation percentage (0.97) and fibre maturity coefficient (4.50) was recorded by the cross combination, GBhv- 282 x G 27. Hybrids, GBhv- 286 x 824 and 824 x GAM- 165 exhibited significant *sca* effects in desired direction for short fibre index (-4.27) fibre uniformity ratio (4.11), respectively.

For oil content, eleven hybrids depicted significant positive *sca* effects. Among them intra *aroboreum* cross, 824 x GAM- 173 (0.76) recorded highest *sca* effect for oil percent followed by cross, 824 x GAM- 165 (0.63). 824 was average general combiner while, GAM- 173 and GAM- 165 were good general combiners for oil content. Specific combining ability effects of these crosses were related with general combining ability effects of their parents as they involved at least one parent with high or average GCA effects for particular traits. Poor x good and good x poor combinations produce high performing cross due to dominance effects. In such situations recombination breeding is useful and could be exploited for practical breeding which is expected to throw stable performing transgressive segregants carrying fixable genes. Similar results have been reported by [13, 25-27].

## Conclusion

Cotton textile industry demands high amount of cotton with high quality cotton to clothe ever increasing population, for this reason improvement of yield and fiber quality is one of the important objectives of all cotton breeders. In this study, non-additive gene effects were prominent for no. of bolls per plant, mean boll weight, seed cotton yield per plant, 2.5 % span length, fibre strength, fibre fineness, fibre elongation percentage, fibre maturity coefficient, short fibre index and fibre uniformity ratio. Heterosis breeding will be worthy enough to improve above traits. *Aroboreum* cultivars were good general combiner for major fibre quality traits (line 824) and oil content (GAM- 165). For seed cotton yield per plant, herbaceous parental line GBhv- 287 was superior for GCA. Specific combining ability was significant for seed cotton yield per plant and no. of bolls per plant with acceptable fibre quality for fibre strength, fibre elongation percentage and fibre maturity coefficient in GBhv- 282 x G 27. 824 x G 27 was superior for fibre length and fibre fineness for *sca* effects. 824 x GAM- 173 would be useful for oil content

improvement in future as it showed high *sca* effects. Seed cotton yield was negatively correlated with fibre quality and oil content. Several workers found that hybrids superior with fibre quality traits were not good in seed cotton yield and vice-versa [21, 28-30].

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## Author Contributions

Rakesh Choudhary- research outcome of my M.Sc. (Agri) Genetics and Plant Breeding thesis

Study conception and Design-Dr. B. G. Solanki and Rakesh Choudhary

Data recording, Analysis and interpretation of data- Navin Chander Gahtyari, Tapas Paul and Ramesh Choudhary

## Abbreviations

MCRS- Main Cotton Research Station, NAU- Navsari Agricultural University, GCA- General Combining Ability, SCA- Specific Combining Ability, HVI- High Volume Instrument, SFI- Short Fibre Index, CIRCOT- Central Institute For Research On Cotton Technology, RBD- Randomized Block Design, NMR- Nuclear Magnetic Resonance, ANOVA- Analysis Of Variance

## Ethical approval

This article does not contain any studies with human participants or animals performed by any of the authors.

Conflict of Interest: None declared

## References

- [1] Anonymous (2014-15) All India Coordinated Cotton Improvement Project. Annual Report, CICR Regional Station, Coimbatore.
- [2] Munro J.M. (1987) Cotton: Tropical Agriculture series, 2nd edition. Longman Scientific and technical John Wiley Sons Inc, New York, USA, P. 161.
- [3] Kohel R.J. (1999) Cotton germplasm resources and the potential for improved fibre production and quality. Cotton Fibres, The Haworth Press, Inc., NY, USA. pp. 167-182.
- [4] Yuan Y.L., Zhang T.Z., Guo W.Z., Pan J.J. and Kohel R.J. (2005) *Acta Gene. Sinica*. 32(1), 79-85.
- [5] Percy R.G., Cantrell R.G. and Zhang J. (2006) *Crop Sci.*, 46(3), 1311-1317.
- [6] Sprague G.F. and Tatum L.A. (1942) *Journal of Amer. Soc. Agron.*, 34, 923-32.
- [7] Griffing B. (1956) *Heredity*, 10, 31-50.
- [8] Dock J. W. and Moll R. H. (1934) *J. Heridity*, 25, 201-204.
- [9] Singh R.K., and Choudhry B.D., eds., (1979) Biometrical methods in quantitative genetic analysis, Kalyani Publisher, New Delhi, pp.191-200.
- [10] Ashok kumar K. and Ravikesavan R. (2013) *Afr. J. Biotechnol*, 12(33), 5183-5191.
- [11] Nimbalkar R.D., Jadhav A.C. and Mehete S.S. (2004) *J. Cotton Res. Dev.*, 18, 50-55.
- [12] Laxman S. (2010) *J. Cotton Res. Dev.*, 24(1), 26-28.
- [13] Ahuja S.L. and Dhayal L.S. (2007). *Euphytica*, 153, 87-98.
- [14] Ilyas M., Naveed T.M. and Khani I.A. (2007) *Journal of Agricultural and Social Sciences*, 3, 39-42.
- [15] Karademir C., Karademir E., Ekinici R. and Gencer O. (2009) *Not. Bot. Hort. Agrobot. Cluj.*, 37(2), 228-233.
- [16] Linga swamy M., Gopinath M. and Murthy K.G.K. (2013) *Helix*, 5, 378-382.
- [17] Deosarkar D.B., Deshmukh J.D. and Deshmukh V.D. (2014) *Journal of Cotton Research and Development*, 28(1), 18-23.
- [18] Patel K.G., Patel R.B., Patel M.I. and Kumar V. (2009) *J. Cotton Res. Dev.*, 23, 23-26.

- [19] Baloch M.J., Butto H.U., Lakho A.R. (1997) *Pakistan Journal of Science and Industrial Research*, 40, 95-98.
- [20] Hassan G., Mahood G., Khan N.U., Razzaq A. (1999) *Sarhad Journal of Agriculture*, 15, 563-568.
- [21] Hassan G., Mahood G., Razzaq A. and Hayatullah (2000) *Sarhad Journal of Agriculture*, 16, 407-410.
- [22] Preetha S. and Raveendran T.S. (2008) *International Journal of Plant Breeding and Genetics*, 2(2), 64-74.
- [23] Lukange E.P., Labuschagne M.T. and Herselman L. (2007) *Euphytica*, 161, 383-389.
- [24] Ahmad I., Nawaz M. and Tayyab M. (2003) *Int. J. Agric. Biol.*, 5(4), 642-644.
- [25] Kumaresan D., Senthilkumar P. and Ganesan J. (1999) *Madras Agricultural Journal*, 18, 430-432.
- [26] Shakeel A., Khan I.A. and Azhar F.M. (2001) *Journal of Biological Science*, 1, 67-70.
- [27] Usharani K.S., Vindhiyavarman P. and Balu P.A. (2014) *Electronic Journal of Plant Breeding*, 5(3), 467-474.
- [28] Tuteja O.P., Senapati B.K. and Singh A.K. (1995) *Journal of Indian Society for Cotton Improvement*, 20(2), 129-132.
- [29] Jagtap D.R. (1994) *Annals of Agricultural Research*, 15(1), 54-59.
- [30] Neelam Dheva, Satange I.V. and Patdukhe N.R. (2002) *Journal of Cotton Research and Development*, 16(2), 161-164.