



ISSN (E): 2277-7695  
ISSN (P): 2349-8242  
NAAS Rating: 5.23  
TPI 2022; 11(11): 1780-1787  
© 2022 TPI  
[www.thepharmajournal.com](http://www.thepharmajournal.com)  
Received: 13-09-2022  
Accepted: 18-10-2022

**Deshmukh AS**  
College of Agriculture, Parbhani  
VNMKV, Parbhani,  
Maharashtra, India

**Deosarkar DB**  
College of Agriculture, Parbhani  
VNMKV, Parbhani,  
Maharashtra, India

**Kalpande HV**  
College of Agriculture, Parbhani  
VNMKV, Parbhani,  
Maharashtra, India

**Shinde AV**  
College of Agriculture, Parbhani  
VNMKV, Parbhani,  
Maharashtra, India

**Thakur NR**  
College of Agriculture, Parbhani  
VNMKV, Parbhani,  
Maharashtra, India

**Corresponding Author:**  
**Deshmukh AS**  
College of Agriculture, Parbhani  
VNMKV, Parbhani,  
Maharashtra, India

## Combining ability studies for fibre quality traits in intra (*G. hirsutum* L. x *G. hirsutum* L.) and inter (*G. hirsutum* L. x *G. barbadense* L.) specific crosses of cotton

**Deshmukh AS, Deosarkar DB, Kalpande HV, Shinde AV and Thakur NR**

### Abstract

The present investigation was focused on studying combining ability for fibre quality traits designed among 15 parents and 56 crosses developed through line x tester method. The analysis of variance indicated substantial variability among the experimental material for fibre quality traits. All the characters were predominantly controlled by non-additive gene action except uniformity ratio. Line NH-615 recorded high significant GCA effects for most of the traits viz., ginning outturn, upper half mean length, micronaire value, fibre strength and uniformity ratio. The line NH-635 considered as a good combiner for upper half mean length and fibre strength as it had significant positive value. Among the testers, *barbadense* tester, RHC-011 and RHC-1014 obtained high GCA effect for fibre characters while *hirsutum* tester, PH-1009 and AC-738 observed significant GCA effects for ginning outturn. The *barbadense* cross NH-545 x RHC-1014 recorded highest SCA effects for the traits viz., ginning outturn, micronaire value and fibre strength and were turned out to be best specific combiner while *hirsutum* cross NH-615 x AKH-8828 showed high SCA effects for the traits viz., ginning outturn, upper half mean length and fibre strength NH-545 x RHC-1014, NH-545 x RHC-011 and NH-615 x AKH-8828 were identified as the best hybrids well suited for exploitation through heterosis breeding with regard to *per se* and SCA effects of studied characters.

**Keywords:** ANOVA, GCA, gene action, SCA and UHML

### Introduction

Cotton (*Gossypium* spp.) is the world's versatile natural plant fibre crop with unique properties rendering its highly spinnable into yarn for textile use, is considered as "White Gold," has long been produced in India. Cotton belongs to the genus *Gossypium* under tribe *Gossypiene* of family *Malvaceae*. It comprises 50 species, four of which are cultivated, 44 are wild diploids and two are wild tetraploids. The place of origin of the genus *Gossypium* is not known, however the primary centers of diversity are west-central and southern Mexico (18 species), north-east Africa and Arabia (14 species) and Australia (17 species).

Different methods have been applied to improve the selection of genes controlling the useful agronomic traits. The most used breeding designs are bi-parental, multiple crosses, test crosses, line x tester and diallel designs (Nduwumuremyi *et al.*, 2013) [20]. The major purpose of these designs is to determine the combining abilities of experimental crosses and parental lines besides understanding the heredity of the evaluated traits (Sharma, 2006) [7].

Line x tester mating design is an extension of top cross method in which several testers are used. The line x tester analysis is a common approach for assessing the expression of genetic aspects of traits (Kempthorne, 1957) [1], which provides information about GCA effects of parents and at the same time it is helpful in identifying best heterotic crosses on the basis of SCA effects. Also, line x tester analysis provides information about regarding genetic mechanism controlling yield and yield components.

### Material and Methods

The experimental material used in the present investigation comprised of 56 new crosses (42 *hirsutum* and 14 *barbadense*) obtained through 7 *hirsutum* lines x 8 testers (six *hirsutum* and two *barbadense*) design. These lines, testers, crosses along with four checks were evaluated in Randomized Block Design with two replications during *kharif* 2021-22 at three locations viz., Cotton Research Station, Mahboob Baugh Farm, VNMKV., Parbhani (E<sub>1</sub>), Cotton Research Station, Nanded (E<sub>2</sub>) and National Agriculture Research Project, Aurangabad (E<sub>3</sub>).

The experiment was laid out as randomized block design with two replications. To reduce soil heterogeneity, each replication was divided into three tiers, each with 25 genotypes and the entries within the second replication were randomized. Each genotype was planted in a two rows plot of 6 m length following spacing of 90 cm between rows and 60 cm between plants within a row. The agronomic and plant protection measures were followed as and when required during the period of crop growth to raise the healthy crop.

A randomly bulk samples of lint were drawn from each entry produce weighing 100 g. The fibre quality viz., upper half mean length, uniformity ratio, micronaire value and fibre strength was determined using High Volume Instrument (HVI, USDA) mode facilities available at the CIRCOT, Wadi, Nagpur.

### Statistical Analysis

The mean data for different characters obtained from the experiments laid out in randomized block design was statistically analyzed for individual as well as pooled over the environments by the usual statistical procedure (Panse and Sukhatme, 1961) [2].

Combining ability analysis pooled over environments for the characters under study was carried out based on the procedure developed by Kempthorne (1957) [1] related to design II of Comstock and Robinson (1952) [9].

The general and specific combining ability effects of the  $ij^{\text{th}}$  observations were estimated by using following model.

$$Y_{ijk} = g + g_i + g_j + S_{ij} + E_1 + r_{ki} + (ge)_{ii} + (ge)_{ji} + (se)_j + e_{ijk}$$

Where,

i	=	1, 2,...l (female parent)
j	=	1, 2,...t (male parent)
k	=	1, 2,...r (replications)
i	=	1, 2,...l (environments)
$Y_{ijki}$	=	The values of $i^{\text{th}}$ environment in $k^{\text{th}}$ replication of progeny of the $i^{\text{th}}$ female and $j^{\text{th}}$ male parent
G	=	General mean
$g_i$	=	An effect common to $a_{ii}$ progenies of the $i^{\text{th}}$ female parent
$g_j$	=	An effect common to $a_{ji}$ progenies of the $j^{\text{th}}$ male parent
$S_{ij}$	=	An effect specific to the progenies of the $i^{\text{th}}$ female and $j^{\text{th}}$ male parent
$E_1$	=	The average effect of $i^{\text{th}}$ environment
$r_{ki}$	=	The effect of $k^{\text{th}}$ replication over $i^{\text{th}}$ environment
$(ge)_{ii}$	=	Interaction effect of $i^{\text{th}}$ female with $i^{\text{th}}$ environment
$(ge)_{ji}$	=	Interaction effect of $j^{\text{th}}$ male with $i^{\text{th}}$ environment
$(se)_{iji}$	=	Interaction effect of crosses of $i^{\text{th}}$ female and $j^{\text{th}}$ male parent with $i^{\text{th}}$ environment
$e_{ijk}$	=	Uncontrolled variation associated with the $i^{\text{th}}$ environment in the $k^{\text{th}}$ replication with progenies of the $i^{\text{th}}$ female and $j^{\text{th}}$ male parent and assumed to be homogenous for all cultivars and environment

The proportional contribution of lines, testers and their corresponding interaction in an individual environment as well as over the environments were determined by using following formulae.

$$1 \text{ Contribution of males} = \frac{S.S.(m)}{S.S.(crosses)} \times 100$$

$$2 \text{ Contribution of females} = \frac{S.S.(f)}{S.S.(crosses)} \times 100$$

$$3 \text{ Contribution of males x females} = \frac{(m \times f)}{S.S.(crosses)} \times 100$$

### Result and Discussion

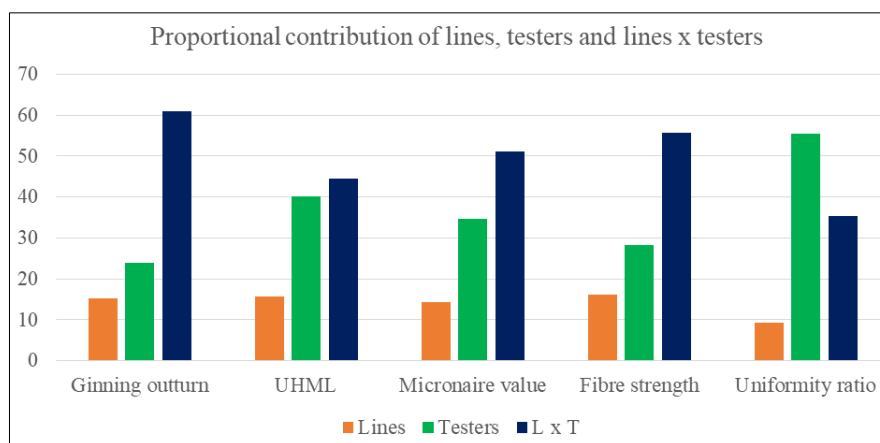
#### Analysis of variance for randomized block design

The mean values of observations recorded were subjected to analysis of variances for randomized block design in individual environments revealed that mean squares due to genotypes were found significant for all the characters in all environments (Table 1).

#### Analysis of variance for combining ability

The experimental data of parents and crosses (Table 2) were separately subjected to analysis of variance for combining ability. The total variances were partitioned in to three components viz., variance due to replication, crosses and error. The data on crosses were further analyzed to determine the lines, testers (GCA) and line x tester (SCA) variance components for all the traits in pooled environment.

Analysis of variance over pooled environment (Table 2) revealed mean squares due to lines were significant for micronaire value and fibre strength while mean squares due to testers were non significant for uniformity ratio. Mean squares due to L vs T were significant for all the characters except ginning outturn and upper half mean length. The values of parent's vs crosses were significant for all the studied traits except fibre strength. Mean sum squares due to crosses were significant for all the characters. Similar results were obtained by Ahuja *et al.*, (2007) [3], Basal *et al.*, (2011) [7], Alkudsi *et al.*, (2013) [4], Rangnatha *et al.*, (2013) [24], Rajmani *et al.*, (2014) [22], Usharani *et al.*, (2014) [30], Naik *et al.*, (2019) [19] and Hamed *et al.*, (2021) [12].



**Fig 1:** Proportional contribution of lines, testers and lines x testers pooled over environments

Proportional contribution of lines, testers and their interaction (lines x testers) pooled over environment to the variances for investigated characters were presented in Table 3. The results exhibited maximum per cent contribution of testers towards total variances than lines for studied characters while proportional contribution of lines x testers interaction was found to be greater than lines and testers for all studied characters except uniformity ratio (Heba *et al.*, 2021) [13]. Present study revealed that relatively line x tester contributions were greater as compared to lines and testers contributions for most of the trait depicting the importance of non-additive type of gene action for investigated traits (Khokhar *et al.*, 2018) [16].

#### GCA effects of parents studied over three environments

The general combining ability (GCA) of parents gives useful information on the choice of parents in terms of expected performance of their progenies as pointed out by Dhillon (1975) [10]. Singh and Hari Singh (1985) [28] suggested that parents with high GCA would produce transgressive segregants in  $F_2$  or later generations. Plant breeders use this method to critically analyze the parents for their ability to transmit performance to their progenies.

Based on the estimates of GCA effects, the line NH-615 recorded high significant gca effects for most of the traits *viz.*, ginning outturn (1.98), upper half mean length (1.25), micronaire value (-0.04), fibre strength (1.71) and uniformity ratio (0.66). The line NH-635 considered as a good combiner for upper half mean length (0.29) and fibre strength (0.60) as it had significant positive value. For fibre fines line BN-1 proved to be as good combiner.

Among the testers, *barbadense* tester RHC-011 and RHC-1014 obtained high GCA effect for fibre characters such as upper half mean length, micronaire value, fibre strength and uniformity ratio. While the tester PH-1009 and AC-738 observed significant GCA effects for ginning outturn 1.47 and 1.45 respectively. Similar results were reported by Ahuja *et al.*, (2007) [3], Karademir *et al.*, (2009) [15], Bolek *et al.*, (2010) [8], Patel *et al.*, (2012) [21], Kumar *et al.*, (2013) [17], Munir *et al.*, (2018) [18], Balcha *et al.*, (2019) [6] and Gopal *et al.*, (2020) [11].

#### SCA effects of crosses studied over three environments

The next major criterion for judging the hybrids is by studying their specific combining ability (SCA) effects. SCA is defined as the deviation from *per se* performance, predicted

based on the general combining ability (Allard, 1960). Sprague and Tatum (1942) reported that SCA effects are due to non-additive genetic interaction. Rojas and Sprague (1952) observed that specific combining ability not only involved dominance and epistasis, but also a considerable amount of genotype and environment ( $G \times E$ ) interaction. Jain and Virmani (1990) [14] reported that the SCA value of any cross is helpful in predicting the performance of the hybrids far better than the GCA of parents.

Among *barbadense* crosses, the cross NH-545 x RHC-1014 recorded highest SCA effects for the traits *viz.*, ginning outturn (2.04), micronaire value (-0.48) and fibre strength (2.80) and were turned out to be best specific combiner. While the cross NH-545 x RHC-011 showed significant positive SCA effect for ginning outturn (1.41), upper half mean length (1.74) and uniformity ratio (1.60).

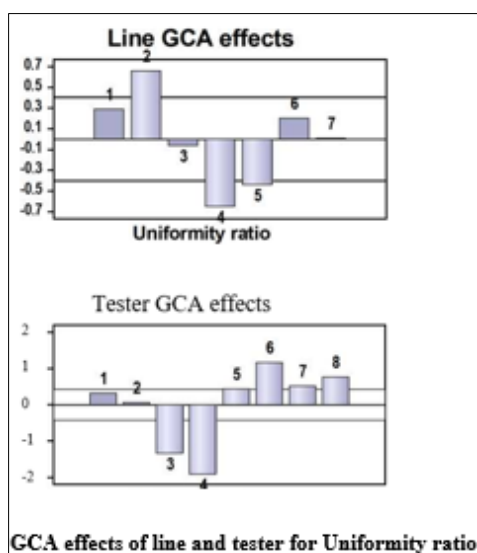
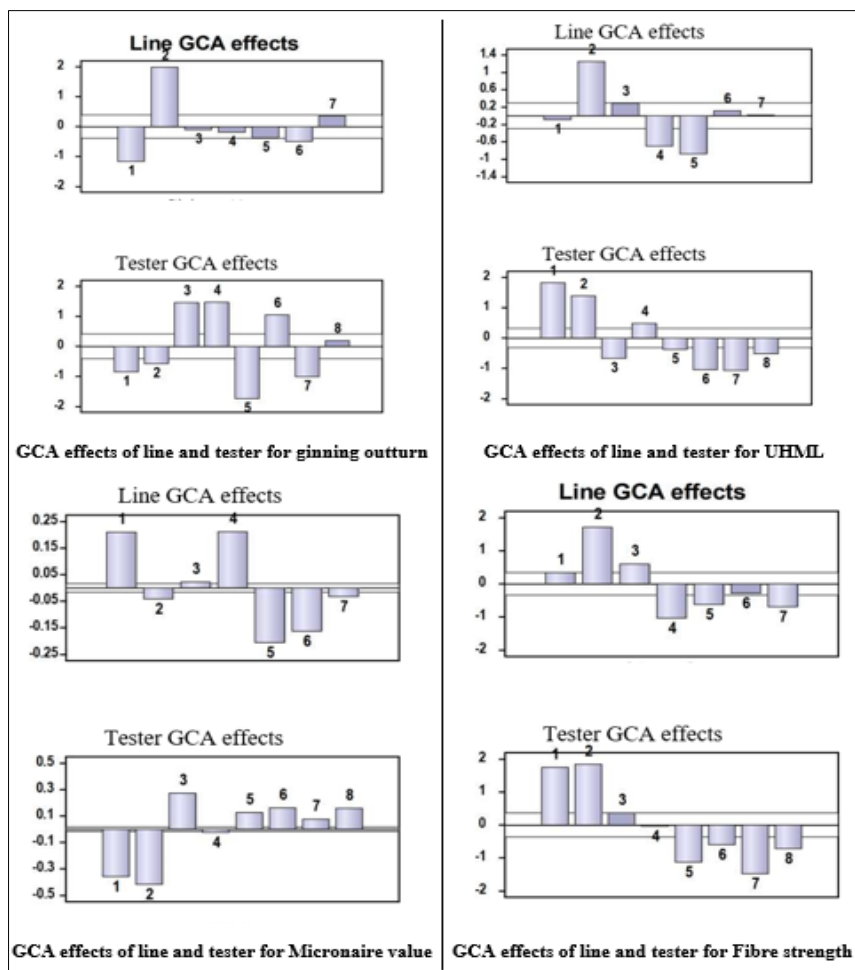
Among *hirsutum* crosses, the cross NH-615 x AKH-8828 showed high SCA effects for the traits *viz.*, ginning outturn (2.57), upper half mean length (2.41), fibre strength (4.73) and recorded desirable SCA effect for the trait uniformity ratio (1.11). On the basis of *per se* performance the cross NH-545 x AKH-1301 showed highest SCA effects for the trait fibre fineness (-0.43) while cross RCH-688 x AKH-09-01 showed highest SCA effects for the trait uniformity ratio (1.38). Similar results were reported by Ahuja *et al.*, (2007) [3], Karademir *et al.*, (2009) [15], Basal *et al.*, (2011) [7], Patel *et al.*, (2012) [21], Kumar *et al.*, (2013) [17], Gopal *et al.*, (2020) [11], Naik *et al.*, (2019) [19] and Ramdan *et al.*, (2021) [23].

#### Gene Action

The estimate of variance components revealed that, the magnitude of SCA variance was greater than corresponding GCA variance for all studied trait except uniformity ratio. GCA/SCA ratio less than unity indicated non additive gene action for governing these traits and can be exploited through heterosis breeding. In the traits where non- fixable component is predominant, heterosis breeding and recombination breeding with postponement of selection at later generations would be feasible with Kardemire *et al.*, (2009) [15], Basal *et al.*, (2011) [7], Rajmani *et al.*, (2014) [22], Khokhare *et al.*, (2018) [16] and Munir *et al.*, (2018) [18]. As predictability ratio for uniformity ratio was greater than unity indicating the importance of additive gene action. Therefore, while applying selection in the further generations, the gene action controlling the characters should be taken into considerations were fixable component i.e., additive gene action is evident,

the selection in the further generations would be rewarding after judging the positive correlation of the traits under investigation with the yield. Similar results were reported by

Bolek *et al.*, (2010) [8], Basal *et al.*, (2011) [7] and Usharani *et al.*, (2014) [30].



**Table 1:** Analysis of variance for randomized block design for different characters in an individual environment

S.N.	Characters	Location	Source of variation		
			Replication	Genotypes	Error
			d.f. (1)	d.f. (74)	d.f. (74)
1.	Ginning outturn (%)	E-1	0.33	14.13**	1.31
		E-2	0.54	18.28**	1.05
		E-3	0.76	18.43**	2.36

		Pool	0.02	9.56**	0.68
2.	UHML (mm)	E-1	3.38	7.56**	0.75
		E-2	0.15	5.79**	0.82
		E-3	0.80	7.58**	1.03
		Pool	0.03	6.67**	0.33
3.	Micronaire value ( $\mu$ g/ inch)	E-1	0.02	0.34**	0.01
		E-2	0.01	0.40**	0.01
		E-3	0.004	0.35**	0.01
		Pool	0.002	0.32**	0.001
4.	Fibre strength (g/ tex)	E-1	2.61	10.87**	0.66
		E-2	0.70	76.63**	0.92
		E-3	1.76	10.65**	0.93
		Pool	0.79	10.20**	0.44
5.	Uniformity ratio (%)	E-1	4.18	5.73**	2.01
		E-2	3.02	3.64**	4.10
		E-3	2.36	4.44**	2.28
		Pool	3.67	3.78**	0.60

\*,\*\*.- Significant at 5 per cent and 1 per cent level, respectively

**Table 2:** Pooled analysis of variance for combining ability

Source of Variations	df	Ginning outturn		UHML		Micronaire value		Fibre strength		Uniformity ratio	
Replication	1	0.033		0.04		0.001		1.10		3.32	
Genotypes	70	9.93	**	5.61	**	0.32	**	9.88	**	3.75	**
Parents	14	1.10		6.09	**	0.26	**	10.64	**	2.93	**
Line	6	0.65		0.60		0.20	**	5.98	**	0.05	
Testers	7	1.54	*	11.64	**	0.34	**	13.81	**	1.33	
L vs T	1	0.66		0.27		0.06	**	16.44	**	31.36	**
Parents vs Crosses	1	65.63	**	7.17	**	0.45	**	1.07		19.95	**
Crosses	55	11.17	**	5.46	**	0.33	**	9.84	**	3.66	**
Error	70	0.70		0.35		0.001		0.42		0.62	

**Table 3:** Proportional contribution of lines, testers and lines x testers pooled over environments

Source of variation	Ginning outturn	UHML	Micronaire value	Fibre strength	Uniformity ratio
Lines	15.26	15.57	14.19	16.14	9.32
Testers	23.88	40.04	34.71	28.21	55.41
L x T	60.85	44.39	51.10	55.65	35.27

**Table 4:** Pooled estimates of GCA effects of parents studied over three environments

Sr. No.	Genotypes	Ginning percentage (%)		UHML		Micronaire value		Fibre strength		Uniformity ratio	
<b>GCA of Lines</b>											
1	NH-545	-1.17	**	-0.09		0.21	**	0.34	**	0.28	**
2	NH-615	1.98	**	1.25	**	-0.04	**	1.71	**	0.66	**
3	NH-635	-0.11		0.29	*	0.02	**	0.60	**	-0.06	*
4	PH-348	-0.19		-0.70	**	0.21	**	-1.04	**	-0.65	**
5	BN-1	-0.38	**	-0.88	*	-0.21	**	-0.63	**	-0.44	**
6	RCH-688	-0.50	**	0.12		-0.16	**	-0.29	**	0.2	
7	AKH-09-01	0.36	**	0.02		-0.03	**	-0.70	**	0.009	
<b>GCA of tester</b>											
1	RHCB-011	-0.84	**	1.83	**	-0.36	**	1.75	**	0.32	
2	RHCB-1014	-0.58	**	1.38	**	-0.42	**	1.84	**	0.06	
3	AC-738	1.45	**	-0.68	**	0.27	**	0.36	*	-1.34	**
4	PH-1009	1.47	**	0.48	**	-0.03	**	-0.03	**	-1.92	**
5	AKH-1301	-1.74	**	-0.38	*	0.13	**	-1.13	**	0.43	*
6	AKH-9916	1.05	**	-1.04	**	0.16	**	-0.60	**	1.17	**
7	AKH-8828	-1.01	**	-1.07	**	0.08	**	-1.48	**	0.51	*
8	NH-452	0.20		-0.52	**	0.16	**	-0.72	**	0.76	**
	Gi (L)	0.19		0.15		0.01		0.17		0.19	
	Gi (T)	0.21		0.16		0.01		0.18		0.21	
	Gi-Gj (L)	0.27		0.21		0.01		0.24		0.28	
	Gi-Gj (T)	0.29		0.23		0.01		0.26		0.30	
	Var GCA	1.18		0.81		0.04		1.18		0.59	
	Var SCA	4.15		1.41		0.11		3.36		0.52	
	Var GCA/SCA	0.28		0.58		0.36		0.35		1.14	
Types of gene action		Non additive gene action		Non additive gene action		Non additive gene action		Non additive gene action		Additive gene action	

**Table 5:** Pooled estimates of SCA effects of parents studied over three environments

Sr. No.	Genotypes	Ginning outturn (%)	UHML	Micronaire value	Fibre strength	Uniformity ratio				
<i>Barbadense crosses</i>										
1	NH-545 x RHC-011	1.41	*	1.74	**	-0.01	0.53	1.60	**	
2	NH-615 x RHC-011	-1.69	**	-1.33	**	-0.42	**	1.07	*	-1.12
3	NH-635 x RHC-011	0.53		2.82	**	-0.28	**	1.70	**	-0.57
4	PH-348 x RHC-011	1.05		-0.98	*	-0.48	**	-0.86		-0.37
5	BN-1 x RHC-011	-0.46		-0.52		0.29	**	-1.96	**	0.63
6	RCH-688 x RHC-011	-1.84	**	-0.90	*	0.47	**	-0.06		0.26
7	AKH-09-01 x RHC-011	1.00		-0.83		0.44	**	-0.42		-0.42
8	NH-545 x RHC-1014	2.04	**	0.39		-0.48	**	2.80	**	-1.52
9	NH-615 x RHC-1014	-1.49	**	1.59	**	0.66	**	0.29		0.11
10	NH-635 x RHC-1014	0.325		1.00	*	-0.20	**	0.47		0.87
11	PH-348 x RHC-1014	0.15		0.26		0.67	**	-0.05		0.99
12	BN-1 x RHC-1014	0.30		0.59		-0.05	**	-0.35		1.65
13	RCH-688 x RHC-1014	-1.14	*	-0.90	*	-0.24	**	-0.66		-1.25
14	AKH-09-01 x RHC-1014	-0.19		-2.92	**	-0.35	**	-2.50	**	-0.84
<i>Hirsutum crosses</i>										
15	NH-545 x AC-738	1.73	**	-0.86	*	0.41	**	-1.74	**	1.01
16	NH-615 x AC-738	-1.92	**	-1.51	**	0.03		-1.85	**	-0.33
17	NH-635 x AC-738	0.02		-1.64	**	0.39	**	-1.54	**	0.26
18	PH-348 x AC-738	0.48		0.79		-0.32	**	-1.35	**	0.16
19	BN-1 x AC-738	-1.06		1.68	**	0.23	**	3.53	**	0.58
20	RCH-688 x AC-738	1.44	*	0.55		-0.39	**	0.93		-1.48
21	AKH-09-01 x AC-738	-0.69		1.00	*	-0.36	**	2.03	**	-0.20
22	NH-545 x PH-1009	2.23	**	0.33		0.23	**	0.94		-0.64
23	NH-615 x PH-1009	0.15		-0.82		0.01		0.23		-0.15
24	NH-635 x PH-1009	-0.56		0.75		-0.11	**	0.32		-0.34
25	PH-348 x PH-1009	1.01		0.18		-0.28	**	0.79		0.35
26	BN-1 x PH-1009	-3.35	**	-0.16		0.004		1.39	**	0.62
27	RCH-688 x PH-1009	1.47	**	0.08		0.17	**	-1.88	**	0.10
28	AKH-09-01 x PH-1009	-0.95		-0.36		-0.02		-1.79	**	0.06
29	NH-545 x AKH-1301	-3.36	**	-0.48		-0.43	**	-0.52		0.07
30	NH-615 x AKH-1301	0.28		-0.23		-0.24	**	-2.52	**	0.47
31	NH-635 x AKH-1301	-1.38	*	-1.20	**	0.31	**	-1.15	*	-0.58
32	PH-348 x AKH-1301	2.21	**	1.15	**	-0.04		2.86	**	-0.17
33	BN-1 x AKH-1301	1.93	**	-0.01		-0.12	**	1.80	**	0.09
34	RCH-688 x AKH-1301	-1.34	*	-0.57		0.63	**	-0.09		-0.29
35	AKH-09-01 x AKH-1301	1.65	**	1.33	**	-0.11	**	-0.38		0.41
36	NH-545 x AKH-9916	3.67	**	-0.03		0.03		-0.004		-0.45
37	NH-615 x AKH-9916	0.71		0.03		-0.24	**	-0.42		-0.13
38	NH-635 x AKH-9916	-0.49		-0.67		-0.12	**	0.36		-0.65
39	PH-348 x AKH-9916	-5.15	**	-0.39		0.17	**	0.51		-0.37
40	BN-1 x AKH-9916	2.54	**	0.50		-0.15	**	0.75		-0.39
41	RCH-688 x AKH-9916	0.97		0.89	*	-0.16	**	-0.21		1.38
42	AKH-09-01 x AKH-9916	-2.24	**	-0.33		0.47	**	-0.98	*	0.61
43	NH-545 x AKH-8828	-3.82	**	-0.13		0.16	**	-0.47		-0.02
44	NH-615 x AKH-8828	2.57	**	2.41	**	0.15	**	4.73	**	1.11
45	NH-635 x AKH-8828	-0.08		-0.56		0.06	*	-0.82		0.53
46	PH-348 x AKH-8828	-0.15		-0.745		0.06	**	-0.89		-1.13
47	BN-1 x AKH-8828	-1.28	*	-2.15	**	-0.06	*	-5.01	**	-2.55
48	RCH-688 x AKH-8828	2.57	**	-0.67		-0.25	**	1.20	*	1.13
49	AKH-09-01 x AKH-8828	0.18		1.84	**	-0.12	**	1.27	*	0.92
50	NH-545 x NH-452	-3.90	**	-0.97		0.10	**	-1.54	**	-0.05
51	NH-615 x NH-452	1.39	*	-0.13		0.05	*	-1.52	**	0.05
52	NH-635 x NH-452	1.64	**	-0.49		-0.04		0.66		0.48
53	PH-348 x NH-452	0.39		-0.27		0.22	**	-1.00	*	0.54
54	BN-1 x NH-452	1.38	*	0.07		-0.14	**	-0.14		-0.61
55	RCH-688 x NH-452	-2.13	**	1.52	**	-0.23	**	0.77		0.16
56	AKH-09-01 x NH-452	1.23	*	0.27		0.05	*	2.78	**	-0.55
	Sij	0.55		0.43		0.02		0.48		0.57
	Sij-Skl	0.77		0.60		0.03		0.68		0.80

\*, \*\* - Significant at 5 per cent and 1 per cent level, respectively

## Conclusion

Based on the estimates of GCA effects, the line NH-615 recorded high significant GCA effects for most of the traits. For fibre fineness line BN-1 proved to be as good general combiner. Among the testers, *barbadense* tester RHCB-011 and RHCB-1014 obtained high GCA effect for fibre characters while *hirsutum* tester PH-1009 and AC-738 observed significance GCA effects for ginning outturn. Among *barbadense* crosses, the cross NH-545 x RHCB-1014 and NH-545 x RHCB-011 recorded highest SCA effects for most of the traits. Among *hirsutum* crosses, the cross NH-615 x AKH-8828 showed high SCA effects for the traits viz., ginning outturn, upper half mean length and fibre strength. The magnitude of GCA variance to SCA variances remarks the importance of both additive and non-additive gene action.

## Acknowledgement

We express our hearty thanks to Cotton Research Station, Nanded, Dr. PDKV., Akola, MPKV., Rahuri and University of Agricultural Sciences, Dharwad for providing parental material for this research work. Also, we express deep sense of gratitude to Chhatrapati Shahu Maharaj Research, Training and Human Development Institute (SARTHI) Pune (M.S.) for providing financial assistance in the form "CSMNR-2020" for the completion of this research work without which we could not have come out with this manuscript.

## References

- Kempthorne O. An Introduction to Genetic Statistics John Wiley and Sons Inc., New York; c1957. p. 453-471.
- Panse VG, Sukhatme PV. Statistical methods for agricultural workers. Indian council of agricultural research, New Delhi; c1961. p. 381.
- Ahuja SL, Dhayal LS. Combining ability estimates for yield and fibre quality traits in 4 x 13 line x tester crosses of *Gossypium hirsutum*. Euphytica. 2007;153:87-98
- Alkuddsi YA, Gururaja MR, Patil SS, Gowda TH, Joshi M. Combining ability analysis for seed cotton yield (Kapas Yield) and its components in intra *hirsutum* hybrids and forming heterotic boxes for exploitation in cotton. Genomics and app. bio. 2013;4(5):35-49.
- Allard RW. Principles of Plant Breeding. John Wiley and Sons, Inc., New York; c1960 .p. 485.
- Balcha M, Mohammedand W, Desalegn Z. Combining ability and heritability for yield, yield related and fiber quality traits in cotton (*Gossypium* spp.) at Werer, Ethiopia. Int. J of plant breed and genet. 2019;6(8):001-014
- Basal H, Canavar O, Khan NU, Cerit CS. Combining ability and heterotic studies through Line x Tester in local and exotic upland cotton genotypes. Pak. J of Bot. 2011;43(3):1699-1706.
- Bolek Y, Cokkizgin H, Bardak A. Combining ability and heterosis for fibre quality traits in cotton. Plant breed. and seed Sci. 2010;62:1-16.
- Comstock RE, Robinson HF. Estimation of average dominance of genes in heterosis Ed. G. W. Gowen. Iowa state college press, Ames, Iowa; c1952. p. 494-516
- Dhillon BS. Application of partial diallel crosses in plant breeding: A review. Crop Improv. 1975;2:1-7.
- Gopal GR, Deosarkar DB, Churchane VN. Combining ability studies in CMS based and conventional hybrids of cotton (*Gossypium hirsutum* L.). J Cott. Res. Dev. 2020;34(1):27-36.
- Hamed HHE, Said SRN. Estimation of heterosis and combining ability for yield and fiber quality traits by using line x tester analysis in cotton (*Gossypium barbadense* L.). Menoufia J of plant production. 2021;6(3):35-51.
- Heba HE, Hamed, Said SRN. Estimation of heterosis and combining ability for yield and fibre quality traits by using line x tester analysis in cotton (*Gossypium barbadense* L.) Menoufia J Plant Prod. 2021;6:35-51.
- Jain YP, Virmani SS. Combining ability for yield and four related traits in selection to breeding in rice. Oryza. 1990;27:1-10.
- Karademir C, Karademir E, Ekinci R, Gencer O. Combining ability estimates and heterosis for yield and fiber quality of cotton in line x tester design. Notulae botnicae horti agrobotanici. 2009;37(2):228-233.
- Khokhar ES, Shakeel A, Maqbool MA, Abuzar MK, Zareen S, Aamir SS, et al. Studying combining ability and heterosis in different cotton (*Gossypium hirsutum* L.) genotypes for yield and yield contributing traits. Pak. J of Agric. Res. 2018;31(1):55-68.
- Kumar M, Nirania KS, Sangwan RS, Yadav NK. Combining ability studies for yield and quality traits in upland cotton (*Gossypium hirsutum* L.). J Cott. Res. Dev. 2013;27(2):171-174.
- Munir S, Qureshi MK, Shahzad AN, Manzoor H, Shahzad MA, Aslam K, et al. Assessment of gene action and combining ability for fibre and yield contributing traits in interspecific and intraspecific hybrids of cotton. Czech J of genet and plant breed. 2018;54(2):71-77.
- Naik KS, Satish Y, Babu JDP. Combining ability analysis and gene action for seed cotton yield and fibre quality traits in cotton (*Gossypium hirsutum* L.). J of cotton Res. Dev. 2019;33(1):57-63.
- Nduwumuremyi A, Tongoona P, Habimana S. Mating design: Helpful tool for quantitative plant breeding analysis. J of Plant Breed and Genet. 2013;1(3):117-129.
- Patel NA, Patel BN, Bhatt JP, Patel JA. Heterosis and combining ability for seed cotton yield and component traits in inter specific cotton hybrids (*Gossypium hirsutum* L. x *Gossypium barbadense* L.). Madras Agri. J. 2012;99(10-12):649-656.
- Rajamani S, Gopinath M, Reddy KHP. Combining ability for seed cotton yield and fibre characters in upland cotton (*Gossypium hirsutum* L.). J Cott. Res. Dev. 2014;28(2):207-210.
- Ramdan BM. Combining ability and genetic divergence in cotton (*G. barbadense* L.). Menoufia J. of plant production. 2021;6(2):151-164.
- Ranganatha HM, Patil SS, Manjula SM, Arvindkumar BN, Swathi P. Combining ability studies for fibre quality traits in upland cotton (*Gossypium hirsutum* L.). Int. J of plant Sci. 2013;8(2):312-315.
- Reddy KB, Reddy VC, Ahmed ML, Naidu TCM, Srinivasrao V. Combining ability study for yield and its component traits through diallele mating design in upland cotton (*Gossypium hirsutum* L.). J Cott. Res. Dev. 2016;30(2):180-184.
- Rojas BA, Sprague GF. A comparison of variance components in corn yield trials III. General and specific combining ability and their interaction with locations and years. Agron. J. 1952;46:10-15.

27. Sharma JR. Statistical and biometrical techniques in plant breeding. New Age International, New Delhi, Delhi, India; c2006.
28. Singh A, Hari Singh. Combining ability and heterosis for seed yield and its component characters in Indian mustard sown early and late. Indian J Agric. Sci. 1985;55:309-315.
29. Sparague GF, Tautum LA. General versus specific combining ability in single crosses of corn. J American Soc. Agron. 1942;34:923-932.
30. Usharani KS, Vindhiyavarman P, Amala BP. Combining ability analysis in intraspecific F<sub>1</sub> diallele cross of upland cotton (*Gossypium hirsutum* L.). Electronic J of plant breed. 2014;5(3):467-474.
31. Zhang J, Wu Man, Yu J, Li X, Pei W. Breeding potential of introgression lines developed from interspecific crossing between (*Gossypium hirsutum*) and (*Gossypium barbadense*): heterosis, combining ability and genetic effects. PLoS ONE. 2016;11(1):e0143646. DOI: 10.1371/j.pone.0143646