

Original Research Article

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Combining Ability Analysis for Fibre Quality Traits in Desi Cotton (*Gossypium arboreum* L.) Across the Environments

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ABSTRACT

Cotton is one of the most important fiber and cash crop of India and plays a dominant role in the industrial and agricultural economy of the country. Fifty six crosses with fifteen parents and four checks viz., PKVDH 1, PKVSuvarna, NACH 12 and PA 255 were grown in Randomized Block Design with two replications during *kharif*, 2016 at three locations viz., Cotton Research Station, Mahboob Baugh Farm, Parbhani (L₁), Cotton Research Station, Nanded (L₂), and Agricultural Research Station, Badnapur (L₃). Pooled over the environments, the highest GCA effect for fibre quality traits was showed by line PA 812, PA 809 and testers CNA 449, DWDa 1402, JLA 794. Pooled over the environments, among the crosses highest SCA for fibre quality traits was reported in PA 740 X HD 514 exhibiting significant SCA for UHML (1.40), micronaire (-0.21), uniformity index (0.19) and fibre strength (2.60) pooled over the locations. Selection in further generations would be rewarding to get best transgressive segregants for fibre quality.

Keywords

Combining ability,
Fibre strength,
GCA, SCA, Upper
half mean length

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Introduction

Cotton, the 'white gold' enjoys a pre-eminent status among all cash crops in the country. It is grown commercially in the temperate and tropical regions of more than 70 countries. Genetic improvement in *desi* cotton could be gained either through selection or exploitation of specific hybrid. Therefore, more emphasis should be given to increase the seed cotton

yield per unit area by developing hybrids with longer staple length with sustained yield in multiple environments.

To achieve such desirable characteristics in a new cultivar, proper breeding strategies should be followed. There is an urgent need to promote those cottons that could come closer in quality to the most sought by modern textile mills.

Selection of parents on the basis of phenotypic performance alone is not a sound procedure, since phenotypically superior lines may yield poor recombinants in the segregating generations. It is, therefore essential that parents should be chosen on the basis of their combining ability. Combining ability analysis is the most widely used biometrical tool for identifying prospective parents and for formulating breeding procedures most likely to succeed. In heterosis breeding programme, the selection of parents or inbreds based on their morphological diversity with good combining ability is very important in producing superior hybrids. The analysis of general combining ability and specific combining ability helps in identifying potential parents or inbreds for the production of superior hybrids. The Line \times Tester analysis (Kempthorne, 1957) is one of the simplest and efficient methods of evaluating large number of inbreds/parents for their combining ability. Based on the information from Line \times Tester analysis production of commercially viable hybrids is possible. The combining ability studies provide information on the genetic architecture of the parents as well as crosses, which is useful in developing a specific breeding strategy.

Materials and Methods

The present study comprised of seven females (lines) and eight males (testers) with four standard checks thus making 56 F₁s using Line \times Tester mating design. These lines, testers and hybrids along with four checks were sown during *kharif*, 2016 at three locations *viz.*, Cotton Research Station, Nanded (L-1), Experimental farm of Department of Agricultural Botany, VNMKV, Parbhani (L-2) and Experimental farm, Agricultural Research Station, Badnapur (L-3). The observations were recorded on days to ginning percentage, upper

half mean length, micronaire value, uniformity index and fibre strength. Combining ability analysis was based on the procedure developed by Kempthorne (1957) related to design II of Comstock and Robinson (1952).

Results and Discussion

Environment wise analysis of variance for combining ability is tabulated in Table 1. The mean sum of squares due to parent vs. crosses, testers were found significant at all the locations while the variance due to lines and line \times tester was significant at E₁ only for ginning percentage. The variance due to parents was non-significant at all the locations. For upper half mean length the variances due to genotypes, parents, parent vs. crosses, crosses testers, line \times tester were found significant at all the locations whereas lines MSS was significant at E₂ and E₃ only. The variances showed by genotypes, parents, parent vs. crosses, crosses, testers and line \times testers were significant at all the locations. The variance due to lines were significant at E₁ and E₂ only for micronaire whereas for fibre strength, The variances due to genotypes, parents, parent vs. crosses, crosses, testers and line \times tester were significant at all the locations whereas, variances due to lines were non-significant at all the locations. Environmentwise combining ability effects were tabulated in Table 2.

Upper Half Mean Length (mm)

The highest positively significant GCA among lines for improving fibre UHML was observed in PA 812 (0.80). It imparted significantly higher GCA at all the locations (E₃=0.83, E₂=0.82, E₁=1.75). Next highest GCA for bestowing UHML was reported in PA 785 (0.53). It also exhibited relatively closer significantly higher GCA at E₃ (0.55) than E₂ (0.53) and E₁ (0.52). Amongst the

testers the tester *i.e.* DWDa 1402 (1.91) showed significantly positive GCA for contributing towards the progeny. It exhibited high GCA over the locations among the testers ($E_1 = 1.93$, $E_2 = 1.92$, $E_3 = 1.90$). The combination of this highest combiners *i.e.* PA 812 x DWDa 1402 (-1.35) possessed significant negative SCA.

Amongst the crosses highest SCA was found in cross PA 832 x Digvijay (1.79). It exhibited significantly positive SCA at all the three environments ($E_3 = 1.95$, $E_2 = 1.79$, $E_1 = 1.63$). Next highest positive significant SCA was observed in PAIG 346 x DWDa 1402 (1.65) ($E_1 = 1.72$, $E_2 = 1.63$, $E_3 = 1.60$). Among the interspecific group, cross PA 832 x Digvijay (1.79) exhibited significant and positive SCA effects. It possessed higher SCA at E_3 (1.95) than E_2 (1.79) and E_1 (1.63). This cross was followed by PA 785 x Digvijay (1.12) which exhibited high positive significant SCA at moderate yielding location ($E_2 = 1.25$) than low yielding ($E_3 = 1.13$) and high yielding environment ($E_1 = 0.99$).

Micronaire ($\mu\text{g}/\text{inch}$)

The highest significant GCA in desirable direction among lines was observed in PA 812 (-0.22). It recorded highest significant GCA in desirable direction at E_2 (-0.25) than E_1 (-0.22) and E_3 (-0.20). Among testers, highest negative significant GCA was observed in CNA 449 (-0.55). It showed highest significant GCA in desirable direction at E_2 (-0.57) than E_1 (-0.55) and E_3 (-0.52).

Among crosses, highest significant SCA in desirable direction was observed in PA 809 x DWDa 1402 (-0.72). It showed similar performance for SCA at all the locations ($E_2 = -0.75$, $E_3 = -0.73$, $E_1 = -0.70$). Cross PA 812 x AKA 8 (-0.30) also showed very close difference over the locations ($E_3 = -0.38$, $E_1 = -0.27$, $E_2 = -0.26$). Out of 14 interspecific crosses, four exhibited significant and

negative SCA effects. The maximum SCA effect was registered by PAIG 346 x G.Cot.23 (-0.42) ($E_1 = -0.39$, $E_2 = -0.36$, $E_3 = -0.51$) followed by PAIG 346 x Digvijay (-0.29) ($E_1 = -0.30$, $E_2 = -0.32$, $E_3 = -0.24$).

Uniformity index (%)

Among lines highest positively significant GCA for bestowing fibre uniformity was imparted by PA 812 (0.54). It showed high positive significant GCA at E_3 (0.57) than E_1 (0.55) and E_2 (0.50). PA 785 (0.44) was the second largest line with high GCA. It possessed high GCA at E_1 (0.63) than E_2 (0.43) and E_3 (0.27). Among the testers, highest positive significant GCA for fibre uniformity was reported in CNA 449 (0.77). It showed highest positive significant GCA at E_1 (0.82) than E_2 (0.77) and E_3 (0.72).

Tester DWDa 1402 showed second highest positive significant GCA (0.70) among testers. It also possessed higher GCA at E_1 (0.92) than E_2 (0.68) and E_3 (0.51).

Among crosses, highest positively significant SCA was reported in PAIG 346 x Phule Dhanwantary (1.44). It possessed comparatively higher SCA at E_2 (2.25) than E_3 (2.08) and E_1 (0.01). Next highest SCA was observed in PA 812 x HD 514 (1.41) and PA 785 x CNA 449 (1.37). Among the interspecific crosses, only one cross PA 832 x G.Cot 23 (1.27) exhibited significant and positive SCA effects in pooled analysis.

Fibre strength (g/ tex)

Among lines highest positive significant GCA for improving fibre strength was bestowed by PA 812 (0.30). It exhibited higher GCA at E_1 (0.33) than E_3 (0.29) and E_2 (0.28). It was accompanied by PA 785 (0.30). It also showed slightly higher GCA at E_1 (0.34) than E_3 (0.30) and E_2 (0.26).

Table.1 Analysis of variance of line x tester for fibre characters in different environments

Source of variation	d.f.	Mean sum of squares											
		Upper Half Mean Length (mm)			Micronaire (µg/ inch)			Uniformity index (%)			Fibre strength (g tex ⁻¹)		
		E ₁	E ₂	E ₃	E ₁	E ₂	E ₃	E ₁	E ₂	E ₃	E ₁	E ₂	E ₃
Replication	1	0.81	0.008	0.19	0.022	0.033	0.05	1.00	0.90	0.14	0.072	0.70	0.45
Genotype	70	7.09**	7.41**	7.27**	0.45**	0.45**	0.44**	3.41**	3.55**	3.24**	6.42**	6.46**	6.59**
Parents	14	10.51**	10.67**	10.40**	1.06**	1.00**	1.09**	7.53**	7.53**	6.97**	6.58**	6.63**	6.38**
Parent vs. Crosses	1	69.95**	69.78**	69.25**	0.64**	0.33**	0.44**	0.09	0.07	0.75	38.44**	40.91**	43.75**
Crosses	55	5.07**	5.44**	5.35**	0.29**	0.31**	0.27**	2.43**	2.61**	2.34*	5.80**	5.79**	5.97**
Lines	6	5.56	6.17*	6.25*	0.25**	0.32*	0.24	3.62*	3.78	3.67	1.79	1.88	1.93
Testers	7	20.16**	22.48**	22.07**	1.31**	1.35**	1.13**	8.12**	5.22*	3.75	17.81**	17.30**	17.17**
Line x Tester	42	2.49*	2.50*	2.43**	0.12**	0.14**	0.13**	1.31*	2.00*	1.92	4.37**	4.43**	4.67**
Error	70	0.43	0.60	0.51	0.014	0.012	0.01	0.78	1.07	1.50	0.73	0.54	0.72

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

Table 1 contd....

Source of variation	d.f.	Mean sum of squares		
		Ginning percentage (%)		
		E ₁	E ₂	E ₃
Replication	1	0.03	0.53	0.50
Genotype	70	4.05**	4.20**	4.46**
Parents	14	2.04	0.98	1.65
Parent vs. Crosses	1	38.61**	56.45**	60.40**
Crosses	55	3.94**	4.07**	4.15**
Lines	6	6.38*	3.92	2.45
Testers	7	10.61**	13.78**	12.92**
Line x Tester	42	2.48**	2.47	2.93
Error	70	1.32	1.30	1.52

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

Table.2 Pooled estimates of GCA effects of parents and SCA effects of crosses studied over three environments

Sr. No.	Genotype	Upper Half Mean Length (mm)				Micronaire (µg/inch)				Uniformity index (%)			
		E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
	GCA Lines												
1	PA 801	-0.60 **	-0.61**	-0.60**	-0.60**	0.04**	0.004*	0.013**	0.02	-0.70**	-0.76**	-0.76**	-0.74**
2	PA 740	-0.25 **	-0.31**	-0.34**	-0.30**	0.04**	0.05**	0.04**	0.05**	-0.19**	-0.29**	-0.18**	-0.22
3	PA 812	0.75**	0.82**	0.83**	0.80**	-0.22**	-0.25**	-0.20 **	-0.22**	0.55**	0.50**	0.57*	0.54**
4	PA 809	0.40**	0.39**	0.39**	0.39**	-0.05**	-0.07**	-0.07 **	-0.06**	0.05	0.08	0.09	0.08
5	PA 785	0.52**	0.53**	0.55**	0.53**	0.07**	0.08**	0.06**	0.07**	0.63**	0.43*	0.27	0.44**
6	PA 832	-0.81 **	-0.86**	-0.85 **	-0.84**	0.17**	0.21**	0.0**	0.19**	-0.34**	-0.36**	-0.41 **	-0.37*
7	PAIG 346	0.008	0.05	0.02	0.02	-0.05 **	-0.03**	-0.04 **	-0.04*	-0.002**	0.42*	0.43*	0.28
	GCA Testers												
1	AKA 8	-0.71**	-0.69**	-0.74**	-0.71 **	0.09**	0.09**	0.11**	0.10**	0.09	0.09	-0.006**	0.06
2	PhuleDhanwantary	-1.06**	-1.05**	-1.05**	-1.05**	0.39**	0.40**	0.37**	0.38**	-1.37**	-0.89**	-0.70**	-0.99**
3	CNA 449	1.25**	1.52**	1.43**	1.40**	-0.55 **	-0.57**	-0.52 **	-0.55 **	0.82**	0.77**	0.72*	0.77**
4	HD 514	-0.52 **	-0.54**	-0.51 **	-0.52**	0.25**	0.25**	0.20**	0.24**	-0.31**	-0.38**	-0.37**	-0.35*
5	DWDa 1402	1.93**	1.92**	1.90**	1.91**	-0.27 **	-0.24**	-0.24 **	-0.25 **	0.92**	0.68**	0.51*	0.70**
6	JLA 794	1.03**	1.00**	1.08**	1.03**	-0.15 **	-0.19**	-0.14 **	-0.16 **	0.53**	0.50*	0.49*	0.50**
7	Digvijay	-0.94**	-1.18**	-1.14**	-1.09**	0.13**	0.12**	0.11**	0.12 **	-0.47**	-0.56**	-0.41**	-0.48**
8	G.Cot 23	-0.97**	-0.98**	-0.97 **	-0.97**	0.12**	0.14**	0.11**	0.12 **	-0.21**	-0.19**	-0.23**	-0.21
	SCA Crosses												
1	PA 801 x AKA 8	0.48	0.48	0.60	0.52	-0.18*	-0.24**	-0.12	-0.18**	1.30*	1.29	1.06	1.21**
2	PA 801 x PhuleDhanwantary	-0.47	-0.45	-0.40	-0.46	0.03	0.07	0.13	0.08	-0.30	-0.67	-1.14	-0.70
3	PA 801 x CNA 449	0.02	-0.35	-0.30	-0.20	-0.02	0.02	-0.02	-0.009	-0.48	-0.54	-0.32	-0.44
4	PA 801 x HD 514	-1.09*	-1.03	-0.93	-1.02**	0.23**	0.15	0.14	0.17**	-0.28	-0.20	-0.04	-0.17
5	PA 801 x DWDa 1402	0.85	0.79	0.99	0.87**	-0.19*	-0.19*	-0.19 *	-0.192**	0.52	0.80	1.03	0.78
6	PA 801 x JLA 794	-0.45	-0.39	-0.56	-0.46	0.09	0.04	0.09	0.07	-0.16	-0.12	-0.06	-0.11
7	PA 801 x Digvijay	0.22	0.40	0.32	0.31	-0.08	0.01	-0.03	-0.03	-0.17	-0.08	-0.19	-0.14
8	PA 801 x G.Cot 23	0.45	0.55	0.35	0.45	0.12	0.15	-0.01	0.09	-0.44	-0.47	-0.33	-0.41
9	PA 740 x AKA 8	0.38	0.37	0.35	0.36	0.04	0.08	0.07	0.06	0.80	0.91	0.67	0.79
10	PA 740 x PhuleDhanwantary	-1.42 *	-1.31*	-1.37**	-1.36**	-0.06	-0.04	-0.04	-0.05	-0.80	-1.30	-1.39	-1.16**

Table.2 (Contd...)

Sr. No.	Genotype	Upper Half Mean Length (mm)				Micronaire (µg/inch)				Uniformity index (%)			
		E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
11	PA 740 x CNA 449	0.22	0.09	0.08	0.13	-0.22*	-0.23**	-0.25**	-0.23**	-0.88	-0.86	-0.74	-0.83
12	PA 740 x HD 514	1.35**	1.48**	1.37**	1.40**	-0.23**	-0.24**	-0.17*	-0.21**	0.30	0.18	0.09	0.19
13	PA 740 x DWDa 1402	-1.40 **	-1.41*	-1.17*	-1.32**	0.19*	0.15	0.16*	0.16**	0.83	1.33	1.37	1.17**
14	PA 740 x JLA 794	0.19	0.25	0.24	0.22	-0.02	0.01	-0.08	-0.03	0.31	0.50	0.45	0.42
15	PA 740 x Digvijay	0.38	0.20	0.14	0.24	0.01	-0.07	-0.007	-0.02	0.41	0.04	0.38	0.27
16	PA 740 x G.Cot 23	0.30	0.33	0.34	0.32	0.29**	0.33**	0.32**	0.31**	-0.97	-0.80	-0.84	-0.86
17	PA 812 x AKA 8	0.33	0.36	0.20	0.29	-0.27**	-0.26**	-0.38**	-0.30**	-1.01	-1.16	-1.05	-1.07*
18	PA 812 x PhuleDhanwantary	0.58	0.55	0.63	0.58	-0.09	-0.19*	-0.14	-0.14**	-1.58 *	-1.92 *	-0.66	-1.38**
19	PA 812 x CNA 449	-0.69	0.47	0.47	0.083	0.15	0.21**	0.15*	0.17**	-0.61	-0.55	-0.57	-0.57
20	PA 812 x HD 514	0.94*	0.94	0.76	0.88**	-0.03	0.001	0.04	0.00	1.46*	1.57*	1.21	1.41**
21	PA 812 x DWDa 1402	-1.31**	-1.35*	-1.42**	-1.35**	-0.03	-0.009	-0.02	-0.02	0.16	0.33	0.17	0.22
22	PA 812 x JLA 794	-0.81	-0.99	-0.79	-0.86**	0.41**	0.35**	0.35**	0.37**	-0.44	-0.37	-0.63	-0.47
23	PA 812 x Digvijay	0.36	-0.56	-0.41	-0.20	0.04	0.01	0.09	0.05	0.64	0.70	0.46	0.59
24	PA 812 x G.Cot 23	0.59	0.58	0.57	0.58	-0.16	-0.11	-0.08	-0.11**	1.37*	1.39	1.07	1.27**
25	PA 809 x AKA 8	-1.02*	-1.10*	-1.06*	-1.05**	0.14	0.20*	0.11	0.15**	-0.51	-0.38	-0.30	-0.39
26	PA 809 x PhuleDhanwantary	1.23*	1.16*	1.27*	1.22**	0.15	0.23**	0.20**	0.19**	0.95	0.50	0.41	0.62
27	PA 809 x CNA 449	-0.18	-0.35	-0.41	-0.31	-0.22*	-0.33**	-0.23**	-0.26**	0.81	0.91	0.69	0.80
28	PA 809 x HD 514	-0.40	-0.43	-0.35	-0.39	0.27**	0.29**	0.25**	0.26**	-1.12	-1.06	-0.92	-1.03 *
29	PA 809 x DWDa 1402	1.45**	1.39*	1.29*	1.37**	-0.70**	-0.75**	-0.73**	-0.72**	0.59	0.87	1.15	0.87
30	PA 809 x JLA 794	1.25**	1.36*	1.37**	1.32**	-0.12	-0.15	-0.17*	-0.14**	0.26	0.23	0.18	0.22
31	PA 809 x Digvijay	-2.28**	-2.06**	-1.97**	-2.10**	0.10	0.09	0.05	0.08	-0.85	-0.82	-0.89	-0.85
32	PA 809 x G.Cot 23	-0.05	0.04	-0.15	-0.053	0.39**	0.41**	0.51**	0.44**	-0.13	-0.25	-0.31	-0.23
33	PA 785 x AKA 8	-0.94*	-0.93	-0.83	-0.90**	-0.08	-0.01	-0.07	-0.09	-0.07	0.18	0.41	0.17
34	PA 785 x PhuleDhanwantary	-0.59	-0.55	-0.65	-0.59	-0.31**	-0.30**	-0.31**	-0.30**	0.36	0.20	-0.19	0.12
35	PA 785 x CNA 449	1.29**	1.07	1.20*	1.18**	0.37**	0.37**	0.28**	0.33**	1.13	1.51*	1.46	1.37**
36	PA 785 x HD 514	-0.22	-0.32	-0.40	-0.31	-0.05	-0.02	-0.12	-0.07	0.36	0.54	0.79	0.56
37	PA 785 x DWDa 1402	-0.48	-0.42	-0.51	-0.46	0.38**	0.41**	0.42**	0.40**	-0.97	-2.38**	-3.09**	-2.14**
38	PA 785 x JLA 794	-0.68	-0.75	-0.65	-0.69*	-0.05	-0.02	0.03	-0.01	0.45	0.82	1.01	0.76
39	PA 785 x Digvijay	0.99*	1.25*	1.13*	1.12**	-0.03	0.006	-0.10	-0.04	-0.49	-0.32	-0.21	-0.34
40	PA 785 x G.Cot 23	0.62	0.65	0.71	0.66*	-0.22*	-0.34**	-0.11	-0.22**	-0.77	-0.56	-0.20	-0.50

Table.2 (Contd...)

Sr. No.	Genotype	Upper Half Mean Length (mm)				Micronaire (µg/inch)				Uniformity index (%)			
		E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
41	PA 832 x AKA 8	-0.20	-0.15	-0.20	-0.18	0.02	-0.002	0.02	0.014	-0.09	-0.03	-0.14	-0.08
42	PA 832 x PhuleDhanwantary	0.94*	0.81	0.92	0.89**	0.04	0.008	0.03	0.027	1.36*	0.94	0.88	1.06*
43	PA 832 x CNA 449	-1.57*	-1.70**	-1.72**	-1.66**	-0.13	-0.14	-0.14	-0.13**	0.23	0.02	0.26	0.17
44	PA 832 x HD 514	0.32	0.28	0.32	0.30	-0.16	-0.16*	-0.001	-0.10*	-0.73	-0.60	-0.59	-0.64
45	PA 832 x DWDa 1402	-0.74	-0.72	-0.78	-0.74*	0.16	0.23**	0.09	0.16**	-0.85	-0.59	-0.43	-0.62
46	PA 832 x JLA 794	-0.84	-0.71	-0.97	-0.83*	-0.19*	-0.13	-0.10	-0.13**	-0.46	-0.58	-0.64	-0.56
47	PA 832 x Digvijay	1.63**	1.79**	1.95**	1.79**	0.26**	0.27**	0.23**	0.25**	0.44	0.62	0.55	0.53
48	PA 832 x G.Cot 23	0.46	0.39	0.48	0.44	-0.02	-0.07	-0.13	-0.07	0.09	0.23	0.11	0.14
49	PAIG 346 x AKA 8	0.97*	0.98	0.94	0.96**	0.34**	0.32**	0.38**	0.34**	-0.42	-0.80	-0.65	-0.62
50	PAIG 346 xPhuleDhanwantary	-0.28	-0.21	-0.32	-0.26	0.25**	0.21*	0.13	0.19**	0.01	2.25**	2.08*	1.44**
51	PAIG 346 x CNA 449	0.91	0.77	0.66	0.78*	0.07	0.11	0.21**	0.13**	-0.21	-0.49	-0.78	-0.49
52	PAIG 346 x HD 514	-0.91	-0.92	-0.77	-0.86**	-0.03	-0.02	-0.13	-0.05	0.002	-0.43	-0.55	-0.32
53	PAIG 346 x DWDa 1402	1.63**	1.72**	1.60**	1.65**	0.19*	0.16	0.28**	0.21**	-0.29	-0.37	-0.20	-0.28
54	PAIG 346 x JLA 794	1.33**	1.23*	1.36**	1.30**	-0.12	-0.10	-0.12	-0.11*	0.04	-0.48	-0.31	-0.25
55	PAIG 346 x Digvijay	-1.29**	-1.02	-1.17*	-1.16**	-0.30**	-0.32**	-0.24**	-0.29**	0.03	-0.14	-0.10	-0.07
56	PAIG 346 x G.Cot 23	-2.36**	-2.55**	-2.31**	-2.40**	-0.39**	-0.36**	-0.51**	-0.42**	0.84	0.46	0.50	0.60
	S.E. ±												
	Lines	0.164	0.193	0.179	0.11	0.029	0.027	0.026	0.016	0.221	0.259	0.306	0.16
	Tester	0.176	0.206	0.191	0.12	0.031	0.029	0.028	0.017	0.237	0.277	0.327	0.17
	Crosses	0.465	0.546	0.507	0.32	0.084	0.078	0.074	0.045	0.627	0.732	0.866	0.45

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

Table.2 (Contd...)

Sr. No.	Genotype	Fibre strength (g/tex)				Ginning percentage (%)			
		E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
	GCA Lines								
1	PA 801	-0.04*	0.10	0.04	0.03	-0.06**	-0.22	-0.64*	-0.31
2	PA 740	0.09	0.03	0.07	0.07	0.60**	0.57	0.13	0.43**
3	PA 812	0.33**	0.28**	0.29*	0.30*	-0.62**	-0.35	-0.25	-0.40**
4	PA 809	-0.34**	-0.36**	-0.28**	-0.32**	0.76**	0.54	0.36	0.55**
5	PA 785	0.34**	0.26**	0.30*	0.30**	-0.43**	-0.07	0.23	-0.09
6	PA 832	-0.54**	-0.58**	-0.64**	-0.59**	-0.77**	-0.76**	-0.26	-0.60**
7	PAIG 346	0.17	0.28**	0.21*	0.22	0.53*	0.29	0.43	0.42*
	GCA Testers								
1	AKA 8	-0.22**	-0.23**	-0.22**	-0.22	0.80**	0.99**	1.22**	1.00**
2	PhuleDhanwantary	-0.99	-1.00**	-1.06**	-1.01**	-0.28**	0.10	0.25	0.02
3	CNA 449	0.99**	0.99**	0.96**	0.98**	-0.31**	-0.69*	-0.56	-0.52**
4	HD 514	-1.06**	-1.03**	-0.95**	-1.01**	1.77**	1.74**	1.50**	1.67**
5	DWDa 1402	1.93**	1.93**	1.92**	1.92**	-0.91**	-1.16**	-1.12**	-1.06**
6	JLA 794	0.88**	0.83**	0.84**	0.85**	-0.28**	-0.28	-0.65	-0.40*
7	Digvijay	-0.96*	-0.89**	-0.91**	-0.92**	-0.66**	-0.96**	-0.80*	-0.81**
8	G.Cot 23	-0.57*	-0.59**	-0.59**	-0.58**	-0.13**	0.26	0.16	0.09
	SCA Crosses								
1	PA 801 x AKA 8	0.61	0.36	0.28	0.41	0.57	0.056	0.21	0.27
2	PA 801 x PhuleDhanwantary	-2.42*	-2.30	-2.33**	-2.35**	-0.23	-0.19	0.10	0.19
3	PA 801 x CNA 449	1.29*	1.26*	1.40*	1.31**	1.07	0.63	-0.07	0.54
4	PA 801 x HD 514	-0.65	-0.94	-1.03	-0.87*	-0.56	-0.76	-0.68	-0.66
5	PA 801 x DWDa 1402	0.88	1.02	0.81	0.90*	0.37	0.36	1.20	0.64
6	PA 801 x JLA 794	0.01	0.01	0.14	0.05	-1.58	-1.07	-1.46	-1.37**
7	PA 801 x Digvijay	0.58	0.69	0.94	0.73*	0.28	0.29	-0.13	0.14
8	PA 801 x G.Cot 23	-0.30	-0.11	-0.21	-0.20	0.08	0.70	-0.06	0.24
9	PA 740 x AKA 8	0.89	0.74	0.94	0.85*	0.40	0.80	1.46	0.88
10	PA 740 x PhuleDhanwantary	-0.03	0.21	0.08	0.08	0.32	0.027	-0.67	-0.10

Table.2 (Contd...)

Sr. No.	Genotype	Fibre strength (g/tex)				Ginning percentage (%)			
		E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
11	PA 740 x CNA 449	-0.057	-0.01	0.12	0.07	0.07	0.15	-0.13	0.033
12	PA 740 x HD 514	2.55**	2.61	2.64**	2.60**	0.41	0.43	0.56	0.46
13	PA 740 x DWDa 1402	-2.08**	-2.09**	-2.13**	-2.10**	0.007	-0.11	-0.56	-0.22
14	PA 740 x JLA 794	-0.83	-0.83	-0.91	-0.85*	-1.10	-1.16	-1.28	-1.18 *
15	PA 740 x Digvijay	0.12	-0.01	-0.05	0.022	0.028	1.25	1.28	0.85
16	PA 740 x G.Cot 23	-0.55	-0.62	-0.69	-0.62	-0.15	-1.39	-0.64	-0.72
17	PA 812 x AKA 8	0.84	0.95	1.01	0.93*	0.13	0.54	0.34	0.33
18	PA 812 x PhuleDhanwantary	0.31	0.28	0.23	0.27	0.33	0.36	0.73	0.47
19	PA 812 x CNA 449	1.93**	2.07**	2.13**	2.04**	-0.21	-0.28	-0.59	-0.36
20	PA 812 x HD 514	0.18	0.09	-0.03	0.08	-1.49	-1.15	-1.07	-1.23 *
21	PA 812 x DWDa 1402	-1.50*	-1.56**	-1.58*	-1.55**	-0.28	-0.68	-0.82	-0.59
22	PA 812 x JLA 794	-0.53	-0.52	-0.61	-0.55	0.73	0.91	0.70	0.78
23	PA 812 x Digvijay	-0.82	-0.90	-0.88	-0.86*	0.71	0.60	0.79	0.70
24	PA 812 x G.Cot 23	-0.41	-0.41	-0.28	-0.36	0.08	-0.32	-0.08	-0.10
25	PA 809 x AKA 8	1.22*	1.22*	1.09	1.17**	-0.81	-0.56	0.11	-0.42
26	PA 809 x PhuleDhanwantary	3.27**	3.38	3.53**	3.39**	-1.05	-0.27	-0.01	-0.43
27	PA 809 x CNA 449	-1.57*	-1.71**	-1.77**	-1.68**	0.14	-0.75	-0.55	-0.38
28	PA 809 x HD 514	-0.83	-0.70	-0.86	-0.79*	-0.54	-0.98	-0.30	-0.60
29	PA 809 x DWDa 1402	0.67	0.69	0.73	0.69	0.43	1.66*	-0.06	0.67
30	PA 809 x JLA 794	1.13	0.94	1.28*	1.11**	1.86*	1.45	1.59	1.63**
31	PA 809 x Digvijay	-1.96**	-1.77**	-1.91**	-1.88**	-0.23	-0.18	-1.01	-0.47
32	PA 809 x G.Cot 23	-1.94**	-2.05	-2.08**	-2.02**	0.20	-0.36	0.24	0.025
33	PA 785 x AKA 8	-0.48	-0.47	-0.50	-0.48	1.47	1.55	0.87	1.29**
34	PA 785 x PhuleDhanwantary	-0.32	-0.86	-0.76	-0.64	0.29	-0.37	-0.60	-0.22
35	PA 785 x CNA 449	0.41	0.30	0.18	0.29	1.04	1.30	3.01**	1.78**
36	PA 785 x HD 514	-0.79	-0.59	-0.26	-0.55	-0.85	0.46	-0.23	-0.20
37	PA 785 x DWDa 1402	-0.41	-0.43	-0.45	-0.43	-2.01 *	-2.41 **	-2.29*	-2.23**
38	PA 785 x JLA 794	-1.55*	-1.44	-1.59*	-1.52**	-0.48	-0.24	-1.04	-0.58
39	PA 785 x Digvijay	1.87**	2.09**	1.94**	1.96**	-0.39	-1.08	0.13	-0.44
40	PA 785 x G.Cot 23	1.27*	1.39	1.45*	1.37**	0.92	0.78	0.14	0.61

Table.2 (Contd...)

Sr. No.	Genotype	Fibre strength (g/tex)				Ginning percentage (%)			
		E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
41	PA 832 x AKA 8	-1.68**	-1.43**	-1.54**	-1.54**	-0.07	-0.89	-0.98	-0.65
42	PA 832 x PhuleDhanwantary	-0.72	-0.70	-0.68	-0.68	-0.10	-0.05	-0.78	-0.31
43	PA 832 x CNA 449	-1.30*	-1.33*	-1.33**	-1.33**	-1.12	-1.11	-1.02	-1.08*
44	PA 832 x HD 514	1.05	0.96	0.96**	0.96**	0.49	-0.10	0.34	0.24
45	PA 832 x DWDa 1402	-0.30	-0.29	-0.30	-0.30	0.18	-0.07	0.39	0.16
46	PA 832 x JLA 794	0.32	0.28	0.31	0.31	-1.32	-0.59	-0.28	-0.72
47	PA 832 x Digvijay	1.76**	1.68**	1.72**	1.72**	1.38	1.14	1.01	1.17*
48	PA 832 x G.Cot 23	0.87	0.83	0.85*	0.85*	0.56	1.69*	1.33	1.19*
49	PAIG 346 x AKA 8	-1.40*	-1.38*	-1.36**	-1.36**	-1.69*	-1.49	-1.99 *	-1.72**
50	PAIG 346 xPhuleDhanwantary	-0.09	-0.01	-0.07	-0.07	0.44	0.49	0.34	0.42
51	PAIG 346 x CNA 449	-0.70	-0.58	-0.65	-0.65	-1.01	0.05	-0.66	-0.53
52	PAIG 346 x HD 514	-1.51*	-1.44	-1.43**	-1.43**	2.52**	2.10*	1.40	2.00**
53	PAIG 346 x DWDa 1402	2.75**	2.66**	2.78**	2.78**	1.31	1.25	2.14*	1.56**
54	PAIG 346 x JLA 794	1.46*	1.56	1.45**	1.45**	1.89*	0.71	1.76*	1.45**
55	PAIG 346 x Digvijay	-1.56*	-1.78**	-1.70**	-1.70**	-1.78*	-2.01 *	-2.07 *	-1.95**
56	PAIG 346 x G.Cot 23	1.06	0.97	0.99**	0.99**	-1.69*	-1.10	-0.92	-1.23*
	S.E. ±								
	Lines	0.213	0.184	0.13	0.13	0.287	0.285	0.309	0.17
	Tester	0.228	0.197	0.14	0.14	0.307	0.305	0.330	0.18
	Crosses	0.604	0.521	0.32	0.32	0.813	0.807	0.874	0.48

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

Among testers, highest positive significant GCA was observed in DWDa 1402 (1.92). It showed relatively closer GCA across the environments ($E_1=1.93$, $E_2=1.93$, $E_3=1.92$). It was followed by CNA 449 (0.98) and JLA 794 (0.85).

Among the crosses, highest positive significant SCA was reported in PA 809 x PhuleDhanwantary (3.39). It showed high positive significant SCA at E_3 (3.53) than E_2 (3.38) and E_1 (3.27). Next highest SCA was observed in PAIG 346 x DWDa 1402 (2.78) which also exhibited higher SCA at E_3 (2.94) than E_1 (2.75) and E_2 (2.66). Another cross with significantly positive SCA was PA 740 x HD 514 (2.60). It showed higher SCA at E_3 (2.64) than E_2 (2.61) and E_1 (2.55). Among the interspecific group, out of 14 crosses, six crosses recorded significantly positive SCA in pooled analysis. Cross PA 785 x Digvijay (1.96), PA 832 x Digvijay (1.72) and PA 785 x G.Cot 23 (1.37) exhibited highly significant and positive SCA effects for this trait in all the locations as well as in pooled analysis.

Ginning percentage (%)

Among lines highest positively significant GCA for increasing ginning percentage was observed in PA 809 (0.55). It exhibited highest GCA at E_1 (0.76) than E_2 (0.54) and E_3 (0.36). Second highest GCA among lines was observed in PA 740 (0.43). It showed significantly higher GCA at E_1 (0.60) and E_2 (0.57) than E_3 (0.13). Among the testers highest positive significant GCA was imparted by HD 514 (1.67). It showed relatively closer GCA across the environments ($E_1 = 1.77$, $E_2 = 1.74$, $E_3 = 1.50$). The combination of the two best general combiners *i.e.* PA 809 x HD 514 possessed negative non-significant SCA for ginning percentage.

The best combination for significantly positive highest SCA was PAIG 346 x HD

514 (2.00). It showed significantly highest SCA at E_3 (2.14) than E_1 (1.31) and E_2 (1.25). Next significantly highest SCA was observed in PA 785 x CNA 449 (1.78). It possessed significantly higher SCA at E_3 (3.01) than E_2 (1.30) and E_1 (1.04). Among the interspecific crosses, only two crosses *viz.*, PA 832 x G.Cot 23 (1.19) and PA 832 x Digvijay (1.17) recorded significant and positive SCA effects in pooled analysis.

For fibre quality parameters, PA 740 X HD 514 was found to be the best combination exhibiting significant SCA for UHML (1.40), micronaire (-0.21), uniformity index (0.19) and fibre strength (2.60) pooled over the locations. Selection in further generations would be rewarding to get best transgressive segregants for fibre quality.

The estimates of GCA effect further revealed that the parental lines exhibited high to average GCA effect for one or more fibre quality characters. Selection of the most encouraging cross combination needs high SCA along with high GCA effects of respective parents. Almost identical results have been reported by Tomar and Singh (1996), Saxena *et al.*, (1998), Kajjidoni *et al.*, (2002), Deshpande *et al.*, (2003), Maisuria *et al.*, (2006), Preetha and Ravindran (2008), Laxman (2010), Kumar *et al.*, (2014), Madhuri *et al.*, (2014), Patel and Choudhari (2015) and Shakeel *et al.*, (2016). Parents possessing good gca for yield and yield contributing characters need to be widely used in breeding programme for combining desirable characters.

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