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Combining ability analysis for fibre quality traits in desi cotton (*Gossypium arboreum* L.) across the environment

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Abstract

Cotton is one of the most important fibre and cash crop of India and plays a dominant role in the industrial and agricultural economy of the country. In present investigation total forty eight crosses with fourteen parents and three checks viz., PKV Suvarna, PKV DH 1 and NACH 12 were grown in Randomized Block Design with two replications during *kharif*, 2022 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 PAIG 411, PA 810 and testers AKA 7, PA 402. Pooled over the environments, among the crosses highest significant SCA for fibre quality traits was recorded in PAIG 411 x AKA 7 exhibiting significant SCA for GOT (2.79), UHML (1.18) and micronaire (-0.47) pooled over the locations. Next highest significant SCA recorded by PA 810 x PA 402 exhibiting significant SCA for GOT (1.39), UHML (1.64), micronaire (-0.26) and uniformity index (1.84) pooled over the locations. Selection in further generations would be rewarding to get best transgressive segregants for fibre quality.

Keywords: Comining ability, fibre strength, GCA, SCA, upper half mean length, Micronaire, Fibre strength and Unifomity ratio

Introduction

Among all the cash crops in the nation, cotton, also known as the "white gold," holds the top spot. More than 70 nations have temperate and tropical zones where it is grown for economic purposes. Over 32,636,000 hectares of land are used to produce over 25.5 million tonnes of cotton worldwide. China (5,730,000 tonnes), India (5,366,000 tonnes), and the United States (3,815,000 tonnes) are the top three producers of cotton. Turkey produces 833,000 tonnes of cotton fibre annually from 480,000 hectares of cotton production. Particularly in semi-arid areas, cotton farming has substantial economic importance and provides a substantial source of revenue for both large and small-scale farmers. Cotton (*Gossypium arboreum* L.) meet the textile industry's demand for natural fibre for surgical cotton, high quality denim etc. Therefore desi cotton could benefit genetically from specific hybrids being used or from selection. Therefore, more effort should be put into creating hybrids with longer staple lengths that can produce consistently in a variety of settings in order to maximise the yield of seed cotton per unit area. It is important to use appropriate breeding techniques while creating new cultivars in order to produce these desired traits. Promoting cottons that are closer in quality to the most sought-after varieties by contemporary textile mills is imperative.

It is not a good practice to select parents only based on phenotypic performance because phenotypically superior lines may produce subpar recombinants in the segregating generations. Therefore, it is imperative that parents be selected based on their capacity for combination. The most popular biometric method for selecting potential parents and creating breeding protocols that have the best chance of success is combining ability analysis. In a heterosis breeding project, it is crucial to choose parents or inbreds based on their good combining ability and physical diversity in producing superior hybrids.

Finding suitable parents or inbreds for the creation of superior hybrids is aided by the analysis of general and specific combining abilities. The Line x Tester study (Kempthorne, 1957) [6] is a straightforward and effective technique for assessing the combining ability of numerous inbreds or parents. The data from the Line x Tester analysis suggests that it is possible to produce hybrids that are profitable. The genetic architecture of the parents and crossings is revealed by the combining ability research, which is helpful in formulating a particular breeding plan.

Materials and Methods

Fourty eight hybrids (F₁s) were produced in the current study's by using line x tester mating design crossing of fourteen parents, which was conducted during *kharif* 2021. The parents used for this study includes eight female lines *viz.*, PA 810, PA 785, PA 837, PA 873, PA 904, PA 906, PAIG 384, and PAIG 411 and male testers *viz.*, AKA 7, JLA 794, PA 740, PA 08, PA 402 and CNA 1054 at the Cotton, Research Centre, Mahboob Baugh Farm, Parbhani, Vasantao Nike Marathwada Krishi Vidyapeeth, Parbhani. Doak's method of hand emasculation and pollination was used to generate hybrids. Evaluation of these fourty hybrids along with its fourteen parents and three check were raised in a Randomized Block Design (RBD) with two replications at a spacing of 60 cm (row to row) × 30 cm (plant to plant) in *Kharif*, 2022 at three location *viz.*, Cotton Research Station, Mahboob Baugh Farm, Parbhani (E₁), Cotton Research Station, Nanded (E₂), and ARS, Badnapur (E₃). Practices for crop management were carried out. These hybrids and parents were evaluated for specific combining ability and general combining ability respectively.

Results and Discussion

Environment wise analysis of variance for combining ability is tabulated in Table 1. The mean sum of squares due to genotype and parent vs. crosses was found significant at all the locations while the variance due to lines and testers found non-significant at all location for all parameters except for micronaire at E₂ and E₃ and fibre strength. The line x tester was significant at all location for all parameters except for UHML at E₂ and E₃. The variance due to parents was non-significant at all the locations except for GOT, UHML and fibre strength at E₁ and micronaire at E₃. The variance due to crosses was significant at all the locations for all parameters except for UHML at E₂ and E₃. For fibre strength the variances due to genotypes, parents, parent vs. crosses, crosses, lines, testers, line x tester were found significant at E₁ whereas parents MSS was non-significant at E₂ and E₃ only and line x tester effect at E₃. Environment wise combining ability effects were tabulated in Table 2.

Ginning percentage (%)

Among lines highest positive GCA for increasing ginning percentage was observed in PAIG 411 (0.51), which also imparted highest positive non-significant GCA at E₂ (0.81) than E₃ (0.39) and E₁ (0.33). This was followed by the line PA 785 (0.19) which also exhibited positive non-significant GCA at E₂ (0.28) than E₃ (0.26) and E₁ (0.04). Among the testers highest positive significant GCA was imparted by AKA 7 (0.81). It was also detected highest positive significant GCA at E₂ (1.05) than E₃ (1.01) and E₁ (0.36). This was followed by PA 402 (0.78) which was also

detected highest positive significant GCA at E₁ (0.60) than E₃ (0.88) and E₂ (0.85).

The combination of the two best general combiners *i.e.* PAIG 411 x AKA 7 (2.79) possessed positive significant SCA for ginning percentage. It was also reported highest positive significant SCA at E₃ (3.22) and E₁ (2.83) than E₂ (2.30).

The best combination for significantly positive highest SCA was recorded by the cross PA 906 x AKA 7 (2.91), which was also exhibited highest positive significant SCA at all location *i.e.* E₃ (3.17) than E₂ (2.93) and E₁ (2.61). This was followed by the cross PAIG 411 x AKA 7 (2.79). It was also ascertained highest positive significant SCA at E₃ (3.22) and E₁ (2.83) than E₂ (2.30). After that PAIG 411 x CNA 1054 (2.55) which was imparted highest significant SCA at E₃ (3.49) and E₂ (2.48) than E₁ (1.66). This was followed by PA 785 x PA 402 (2.44) as it was located highest significant SCA at E₁ (2.20) than E₃ (2.79) and E₂ (2.33). PAIG 384 x CNA 1054 (1.92) which was resulted in highest significant SCA at E₂ (2.56) than E₁ (1.60) and E₃ (1.60).

The predictability ratio for this character was 0.08 indicating the importance of non-additive gene action for the improvement of the trait.

Upper Half Mean Length (mm)

The highest positively significant GCA among lines for improving fibre UHML was observed in PAIG 411 (0.70). It was recorded positive GCA at all location (E₃=0.50, E₂=0.81, E₁=0.79). Next highest GCA for bestowing UHML was reported in PA 810 (0.51). It was also exhibited positively significant higher GCA at E₁ (0.68) than E₂ (0.58) and E₃ (0.26).

Amongst the testers, AKA 7 (0.73) showed significantly positive GCA for contributing towards the progeny. It also exhibited positively significant higher GCA at E₂ (0.90) than E₂ (0.84) and E₃ (0.44). The combination of this highest combiners *i.e.* PAIG 411 x AKA 7 (1.18) possessed significant positive SCA. It imparted highest significant positive SCA at E₁ (1.25) than E₃ (1.18) and E₂ (1.11).

Amongst the crosses highest SCA was found in cross PA 810 x CNA 1054 (2.20). It also detected positively significant higher SCA at E₃ (2.48) and E₁ (1.91) than E₂ (2.20). Next highest positive significant SCA was observed in PA 873 x PA 402 (2.04), it also exhibited positively significant SCA at E₂ (2.37) and E₁ (2.06) than E₃ (1.67). This followed by crosses PA 904 x PA 08 (1.83) (E₁ = 2.13, E₂ = 1.94, E₃ = 1.42), PAIG 384 x JLA 794 (1.65) (E₁ = 2.11, E₂ = 2.07, E₃ = 0.76) and PA 785 x PA 402 (1.43) (E₁ = 1.18, E₂ = 1.44, E₃ = 1.68).

The predictability ratio for this character was 0.18 indicating the importance of non-additive gene action for the improvement of the trait.

Micronaire (µg/inch)

The highest significant GCA in desirable direction among lines was observed in PA 810 (-0.47). It also recorded negatively significant higher GCA at all the locations (E₃=-0.46, E₂=-0.46, E₁=-0.49). Followed by PA 785 (-0.17) which was exhibited negatively significant higher GCA at E₃ (-0.18) than E₁ and E₂ (-0.16). Among testers, highest negative significant GCA was observed in PA 402 (-0.18), which also imparted negatively significant SCA at all location (E₃=-0.22, E₂=-0.21, E₁=-0.10).

This followed by CNA 1054 (-0.13), which recorded negatively significant higher GCA at E₃ (-0.14) than E₂ (-0.13) and E₁ (-0.11).

The combination of this highest combiners *i.e.* PA 785 x CNA 1054 (-0.28). It also imparted significant negative SCA at location E₃ (-0.25) than E₁ (-0.31) and E₂ (-0.27). Followed by cross PA 810 x PA 402 (-0.26) possessed significant negative SCA. It also reported significant negative SCA at E₃ (-0.33) than E₂ (-0.23) and E₁ (-0.20).

Among crosses, highest significant SCA in desirable direction was observed in PAIG 411 x AKA 7 (-0.47) which also reported negatively significant SCA at all location E₃ (-0.47), E₂ (-0.47) and E₁ (-0.45). Followed by PAIG 411 x CAN 1054 (-0.46), which also imparted negatively significant SCA at all location E₃ (-0.49), E₂ (-0.45) and E₁ (-0.45). PA 810 x JLA 794 (-0.46), which also recorded negatively significant SCA at all location E₃ (-0.48), E₂ (-0.44) and E₁ (-0.43). PA 873 x PA 402 (-0.34), which also exhibited negatively significant SCA at all location E₁ (-0.60), E₂ (-0.58) and E₃ (-0.14). PA 785 x CNA 1054 (-0.28) which was also the combination of best combiner, followed by cross PA 810 x PA 402 (-0.26).

Predictability ratio for this trait was 0.38 which was indicating the importance non-additive gene action for this trait.

Fibre strength (g/ tex)

Among lines highest positive significant GCA for improving fibre strength was bestowed by PAIG 411 (1.02).

It also exhibited positively significant GCA at all location E₂ (1.11), E₁ (0.98) and E₃ (0.97). It was accompanied by PA 873 (0.77), which also reported positively significant GCA at E₃ (1.00) and E₁ (0.80) than E₂ (0.49). This followed by PA 810 (0.60), which also recorded significantly positive GCA at E₁ (0.90) than E₂ (0.52) and E₃ (0.38).

Among testers, highest positive significant GCA was observed in AKA 7 (1.39). It also ascertained significantly positive GCA at all location E₁ (1.49), E₂ (1.35) and E₃ (1.33). It was followed by PA 402 (1.32), which also detected negatively significant GCA at all location E₁ (1.46), E₂ (1.34) and E₃ (1.15).

Among the crosses, highest positive significant SCA was reported in PAIG 384 x PA 402 (2.35) It also imparted significantly positive SCA at all location E₂ (2.51), E₁ (2.38) and E₃ (2.16). Next highest SCA was observed in PA 810 x CNA 1054 (2.16), which also reported positively significant SCA at E₁ (2.15) and E₃ (2.06) than E₂ (2.26). Another cross with significantly positive SCA was reported by PA 837 x CNA 1054 (1.82), which also recorded positively significant SCA at E₃ (2.12) and E₁ (1.81) than E₂ (2.53). This followed by PA 904 x PA 08 (1.39). It was also exhibited positive SCA at all location E₂ (1.87), E₁ (1.16) and E₃ (1.13) and PA 906 x AKA 7 (1.35), which also imparted positively significant SCA at E₁ (1.30) than E₂ (1.44) and E₃ (0.31).

The predictability ratio for this trait was 0.98 which was very close to unity indicate the importance of additive gene action in the improvement of this trait.

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

Source of variation	D.F.	Mean sum of squares											
		Ginning percentage (%)			Upper Half Mean Length (mm)			Micronaire (µg/ inch)			Fibre strength (g tex ⁻¹)		
		E1	E2	E3	E1	E2	E3	E1	E2	E3	E1	E2	E3
Replication	1	0.0261	2.7303	0.3241	0.2712	4.4007	0.3040	0.0020	0.0112	0.0025	0.3512	3.2971	1.0777
Genotype	61	5.7871**	8.5650**	9.5296**	4.1250**	4.3598*	4.5972*	0.2410**	0.2333**	0.2238**	5.7104**	5.1183**	4.9480**
Parents	13	2.6763**	4.8749	4.8720	2.7879**	2.9908	2.9220	0.0672	0.0373	0.0463*	2.6566**	2.5454	2.3168
Parent vs. Crosses	1	86.5291**	83.8358**	55.3786**	53.2687**	60.0603**	62.1289**	0.7450**	0.7032**	0.5804**	56.6354**	50.6657**	57.2713**
Crosses	47	4.9296**	7.9842**	9.8424**	3.4492**	3.5533	3.8364	0.2784**	0.2775**	0.2653**	5.4715**	4.8609**	4.4446**
Lines	7	0.3689	2.8821	0.9575	3.4684	3.6316	6.5112	0.6163**	0.6057**	0.6925**	7.8095*	5.8930*	6.4368*
Testers	5	4.4058	11.2083	15.4734	4.3464	4.9598	2.0531	0.4274	0.4660*	0.2986	22.2870**	19.6012**	16.5500**
Line x Tester	35	5.9166**	11.2083**	10.8149**	3.3173**	3.3367	3.5562	0.1895**	0.1850**	0.1751**	2.6017**	2.5487**	2.3168
Error	61	0.8156	3.2145	4.5699	0.8116	2.5993	2.7088	0.0803	0.0881	0.0218	0.8103	2.6308	1.6167

*, ** - Significant at 5% and 1% level, respectively.

Table 1 Contd...

Source of variation	D.F.	Mean sum of squares		
		Uniformity index (%)		
		E1	E2	E3
Replication	1	0.5964	0.7385	0.1589
Genotype	61	4.2325**	3.3836**	3.2861**
Parents	13	1.6286	2.2668	2.0738
Parent vs. Crosses	1	14.1933**	12.4557**	7.8620*
Crosses	47	4.7408**	3.4912**	3.5241**
Lines	7	6.0492	3.8014	3.7547
Testers	5	0.6097	2.1983	2.2970
Line x Tester	35	5.0693**	3.6113**	3.6533**
Error	61	1.1403	1.4765	1.4048

*, ** - Significant at 5% and 1% level, respectively.

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

Sr. No.	Genotype	Ginning percentage				UHML				Micronaire			
		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 810	-0.06	-0.149	0.302	0.03	0.688 *	0.585	0.256	0.51*	-0.469 **	-0.462 **	-0.492 **	-0.47**
2.	PA 785	0.049	0.281	0.265	0.19	0.225	-0.02	-0.281	-0.02	-0.163	-0.163	-0.185 **	-0.17**
3.	PA 837	-0.076	0.451	-0.027	0.11	-0.049	-0.205	-0.468	-0.24	0.204 *	0.199 *	0.181 **	0.19**
4.	PA 873	-0.206	-0.709	-0.185	-0.36	0.098	0.215	0.279	0.19	0.036	0.041	0.208 **	0.09**
5.	PA 904	-0.005	-0.096	-0.122	-0.07	-0.755 **	-0.655	-0.789	-0.73**	0.199 *	0.193 *	0.180 **	0.19**
6.	PA 906	-0.176	-0.417	-0.287	-0.29	-0.810 **	-0.773	-0.914	-0.83**	0.049	0.051	0.026	0.04
7.	PAIG 384	0.144	-0.174	-0.337	-0.12	0.103	0.042	1.131 *	0.42	0.166 *	0.176 *	0.128 **	0.15**
8.	PAIG 411	0.330	0.813	0.39	0.51	0.5	0.812	0.787	0.70**	-0.021	-0.034	-0.045	-0.03
GCA Testers													
1.	AKA 7	0.365	1.058 *	1.014	0.81**	0.848 **	0.905 *	0.442	0.73**	-0.032	-0.042	-0.071	-0.05
2.	JLA 794	0.106	-0.784	-0.907	-0.53*	-0.623 **	-0.559	-0.429	-0.54*	0.036	0.051	0.025	0.04
3.	PA 740	-0.693 **	-0.871	-1.127 *	-0.89**	-0.216	-0.015	0.034	-0.07	0.059	0.077	0.069	0.07*
4.	PA 08	-0.589 *	0.229	0.742	0.13	-0.178	-0.327	0.033	-0.16	0.263 **	0.266 **	0.225 **	0.25**
5.	PA 402	0.601 *	0.851	0.889	0.78**	0.366	0.393	0.318	0.36	-0.216 **	-0.213 **	-0.102 **	-0.18**
6.	CNA 1054	0.211	-0.484	-0.611	-0.29	-0.197	-0.397	-0.398	-0.33	-0.11	-0.139	-0.147 **	-0.13**
SCA Crosses													
1.	PA 810 X AKA 7	-2.098 **	-1.296	-2.614	-2.00**	0.377	0.494	-0.957	-0.03	-0.289	-0.275	-0.239 *	-0.27**
2.	PA 810 X JLA 794	-0.349	-1.365	-2.033	-1.25	-0.512	-0.462	0.414	-0.19	-0.438 *	-0.448 *	-0.485 **	-0.46**
3.	PA 810 X PA 740	1.940 **	1.623	1.717	1.76*	-1.369 *	-1.816	-1.799	-1.66**	0.319	0.326	0.381 **	0.34**
4.	PA 810 X PA 08	-0.294	0.103	1.098	0.30	-1.907 **	-1.905	-2.068	-1.96**	0.526 *	0.508 *	0.525 **	0.512**
5.	PA 810 X PA 402	1.076	1.59	1.501	1.39*	1.499 *	1.485	1.927	1.64**	-0.206	-0.234	-0.338 **	-0.26**
6.	PA 810 X CNA 1054	-0.274	-0.655	0.331	-0.19	1.912 **	2.205	2.483 *	2.20**	0.088	0.122	0.157	0.12
7.	PA 785 X AKA 7	0.094	-0.636	-0.178	-0.24	-1.22	-1.071	-0.36	-0.88	-0.146	-0.145	-0.116	-0.14
8.	PA 785 X JLA 794	0.863	0.065	0.184	0.37	-0.849	-0.788	-0.789	-0.81	0.385	0.393	0.468 **	0.41**
9.	PA 785 X PA 740	-1.329 *	-0.747	-0.056	-0.71	0.304	0.289	-0.413	0.06	-0.117	-0.044	-0.076	-0.08
10.	PA 785 X PA 08	-0.012	2.083	0.015	0.69	-1.194	-0.98	-1.261	-1.14	-0.091	-0.162	-0.172	-0.14
11.	PA 785 X PA 402	2.208 **	2.33	2.798	2.44**	1.183	1.440	1.684	1.43*	0.288	0.236	0.145	0.22*
12.	PA 785 X CNA 1054	-1.823 **	-3.095 *	-2.762	-2.56**	1.775 **	1.110	1.140	1.34*	-0.319	-0.278	-0.250 *	-0.28**
13.	PA 837 X AKA 7	-2.211 **	-2.756 *	-1.826	-2.26**	-0.496	-0.436	-0.654	-0.53	0.187	0.203	0.237 *	0.20*
14.	PA 837 X JLA 794	-0.592	1.765	-0.325	0.28	-0.675	-0.462	-0.792	-0.64	0.019	-0.009	-0.009	0.00
15.	PA 837 X PA 740	0.726	-0.477	-1.215	-0.32	0.607	0.384	0.634	0.54	-0.024	-0.075	-0.093	-0.06
16.	PA 837 X PA 08	1.063	0.343	0.717	0.70	1.880 **	1.105	0.935	1.31 *	-0.168	-0.154	-0.099	-0.14
17.	PA 837 X PA 402	-1.258	0.600	2.469	0.60	-0.864	-0.355	-0.64	-0.62	0.031	0.035	-0.061	0.00
18.	PA 837 X CNA 1054	2.273 **	0.525	0.179	0.99	-0.451	-0.235	0.516	-0.06	-0.045	0.001	0.024	-0.01
19.	PA 873 X AKA 7	0.899	1.314	1.262	1.15	0.447	0.614	1.00	0.69	0.456 *	0.442 *	0.271 *	0.39**
20.	PA 873 X JLA 794	-0.362	-0.415	-1.216	-0.66	-0.522	-0.793	0.151	-0.39	-0.013	-0.041	-0.185	-0.08
21.	PA 873 X PA 740	-1.294 *	-1.817	-1.766	-1.62*	0.321	0.094	-0.023	0.13	-0.086	-0.097	-0.229 *	-0.14
22.	PA 873 X PA 08	0.573	-0.617	2.775	0.91	-1.167	-1.255	-1.761	-1.39*	-0.139	-0.126	-0.255 *	-0.17
23.	PA 873 X PA 402	2.413 **	1.92	-0.693	1.21	2.069**	2.375 *	1.674	2.04**	-0.601**	-0.587 **	0.142	-0.34**
24.	PA 873 X CNA 1054	-2.228 **	-0.385	-0.363	-0.99	-1.148	-1.035	-1.04	-1.07	0.383	0.409	0.257 *	0.35**
25.	PA 904 X AKA 7	-0.253	1.931	1.609	1.09	-0.29	0.064	0.518	0.09	0.182	0.160	0.149	0.16
26.	PA 904 X JLA 794	1.626 *	0.322	0.33	0.75	0.331	0.007	-0.101	0.08	-0.226	-0.203	-0.147	-0.19*
27.	PA 904 X PA 740	1.905 **	-0.031	2.39	1.42*	0.774	0.964	0.956	0.89	-0.149	-0.129	-0.111	-0.13
28.	PA 904 X PA 08	-0.379	-2.031	-3.018	-1.80**	2.136 **	1.945	1.427	1.83**	-0.303	-0.218	-0.237 *	-0.25**
29.	PA 904 X PA 402	-2.659 **	0.147	-0.036	-0.84	-1.807 **	-2.025	-1.828	-1.88**	0.026	0.061	-0.02	0.02
30.	PA 904 X CNA 1054	-0.239	-0.338	-1.276	-0.62	-1.145	-0.955	-0.972	-1.02	0.470 *	0.327	0.365 **	0.39**
31.	PA 906 X AKA 7	2.619 **	2.932 *	3.174 *	2.91**	0.565	0.402	1.103	0.69	-0.158	-0.198	-0.198	-0.18*
32.	PA 906 X JLA 794	0.338	-0.796	0.935	0.16	0.636	0.436	0.384	0.49	0.124	0.159	0.156	0.15
33.	PA 906 X PA 740	-1.224	-1.809	-1.675	-1.57*	-0.121	0.412	-0.029	0.09	-0.199	-0.247	-0.237 *	-0.23*
34.	PA 906 X PA 08	-0.988	2.321	0.887	0.74	1.311 *	1.353	1.162	1.276 *	-0.073	-0.066	0.006	-0.04
35.	PA 906 X PA 402	0.232	-1.551	-2.111	-1.14	-1.702 *	-1.907	-1.923	-1.84**	0.186	0.223	0.134	0.18
36.	PA 906 X CNA 1054	-0.978	-1.096	-1.211	-1.09	-0.69	-0.697	-0.697	-0.69	0.12	0.129	0.139	0.13
37.	PAIG 384 X AKA 7	-1.881 **	-3.791 **	-4.656 **	-3.44**	-0.638	-1.183	-1.832	-1.22*	0.226	0.287	0.371 **	0.29**
38.	PAIG 384 X JLA 794	-1.212	1.39	3.015	1.06	2.113 **	2.071	0.769	1.65**	0.057	0.024	0.025	0.03
39.	PAIG 384 X PA 740	1.116	1.908	2.225	1.75*	-0.534	0.197	1.236	0.29	0.084	0.088	0.131	0.10
40.	PAIG 384 X PA 08	-0.398	-1.992	-2.633	-1.67*	-1.072	-0.982	1.187	-0.29	0.081	0.079	0.055	0.07
41.	PAIG 384 X PA 402	0.772	-0.075	0.439	0.38	0.434	0.208	0.062	0.23	-0.201	-0.222	-0.378 **	-0.27**
42.	PAIG 384 X CNA 1054	1.603 *	2.560 *	1.609	1.92**	-0.303	-0.312	-1.422	-0.68	-0.247	-0.256	-0.203	-0.23*
43.	PAIG 411 X AKA 7	2.832 **	2.302	3.228 *	2.79**	1.255	1.117	1.181	1.18*	-0.458 *	-0.473 *	-0.476 **	-0.47**
44.	PAIG 411 X JLA 794	-0.309	-0.966	-0.891	-0.72	-0.524	-0.009	-0.037	-0.19	0.094	0.124	0.178	0.13
45.	PAIG 411 X PA 740	-1.840 **	1.351	-1.621	-0.70	0.019	-0.523	-0.561	-0.35	0.171	0.178	0.234 *	0.19*
46.	PAIG 411 X PA 08	0.436	-0.209	0.16	0.13	0.011	0.718	0.38	0.37	0.167	0.139	0.178	0.16

47.	PAIG 411 X PA 402	-2.784**	-4.961**	-4.367**	-4.04**	-0.812	-1.222	-0.955	-0.99	0.476 *	0.488 *	0.375**	0.45**
48.	PAIG 411 X CNA 1054	1.666*	2.484	3.493*	2.55**	0.05	-0.082	-0.009	-0.01	-0.450 *	-0.456 *	-0.490**	-0.46**
	S.E. \pm												
	Lines	0.368	0.732	0.872	0.39	0.367	0.065	0.671	0.34	0.115	0.121	0.060	0.05
	Tester	0.319	0.633	0.755	0.34	0.318	0.569	0.581	0.29	0.100	0.104	0.052	0.04
	Crosses	0.903	1.179	2.138	1.19	0.900	1.610	1.645	1.03	0.283	0.296	0.148	0.16

*, ** - Significant at 5% and 1% level, respectively.

Table 2 contd....

Sr. No.	Genotype	Fibre Strength				Uniformity index			
		E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
GCA Lines									
1.	PA 810	0.900 **	0.520	0.383	0.60*	0.246	0.539	0.166	0.32
2.	PA 785	-0.475	-0.252	-0.219	-0.31	-1.336 **	-1.055 **	-1.011 **	-1.13**
3.	PA 837	-0.459	-0.35	-0.360	-0.39	0.291	0.436	0.529	0.42*
4.	PA 873	0.808 **	0.497	1.005 **	0.77**	0.843 *	0.567	0.707 *	0.71**
5.	PA 904	-0.217	-0.013	-0.265	-0.16	-0.387	-0.365	-0.264	-0.34
6.	PA 906	-1.242 **	-1.180 *	-1.109 **	-1.17**	-0.451	-0.315	-0.254	-0.34
7.	PAIG 384	-0.302	-0.332	-0.41	-0.34	0.729 *	-0.066	-0.266	0.13
8.	PAIG 411	0.988 **	1.110 *	0.976 *	1.02**	0.066	0.259	0.394	0.24
GCA Testers									
1.	AKA 7	1.495 **	1.356 **	1.332 **	1.39**	0.145	0.413	0.127	0.22
2.	JLA 794	-1.011 **	-0.923 **	-1.062 **	-0.99**	-0.263	0.144	0.238	0.04
3.	PA 740	-1.061 **	-1.153 **	-0.884 **	-1.03**	-0.237	-0.634 *	-0.496	-0.45**
4.	PA 08	-0.288	-0.09	-0.239	-0.27	0.113	-0.221	-0.461	-0.19
5.	PA 402	1.463 **	1.346 **	1.157 **	1.32**	0.086	0.161	0.217	0.15
6.	CNA 1054	-0.598 *	-0.535	-0.304	-0.47*	0.156	0.136	0.374	0.22
SCA Crosses									
1.	PA 810 X AKA 7	-0.237	-0.728	-0.805	-0.59	-0.575	0.865	-1.307	-0.34
2.	PA 810 X JLA 794	-0.331	-0.079	0.008	-0.13	-1.167	-1.686	-1.298	-1.38**
3.	PA 810 X PA 740	-1.181	-0.779	-1.019	-0.99	0.557	-2.007 *	0.266	-0.39
4.	PA 810 X PA 08	-1.303 *	-1.101	-0.954	-1.12*	-2.543 **	-0.551	-1.759 *	-1.62**
5.	PA 810 X PA 402	0.895	0.423	0.71	0.67	1.834 *	1.638	2.053 *	1.84**
6.	PA 810 X CNA 1054	2.157 **	2.264	2.061 *	2.16**	1.894 *	1.742 *	2.046 *	1.89**
7.	PA 785 X AKA 7	-0.012	-0.036	-0.134	-0.06	-0.993	-1.352	-0.99	-1.11*
8.	PA 785 X JLA 794	-0.606	0.093	0.03	-0.16	-0.585	-0.423	-0.571	-0.53
9.	PA 785 X PA 740	-0.106	-0.307	-0.807	-0.41	2.478**	2.666**	2.512**	2.55**
10.	PA 785 X PA 08	-0.428	-0.52	0.647	-0.10	-0.962	-0.908	-0.633	-0.83
11.	PA 785 X PA 402	1.17	0.954	0.891	1.00	1.066	0.951	0.95	0.98*
12.	PA 785 X CNA 1054	-0.018	-0.185	-0.627	-0.28	-1.004	-0.935	-1.268	-1.07*
13.	PA 837 X AKA 7	-0.929	-0.487	-0.742	-0.72	-2.120 *	-2.302 *	-1.820 *	-2.08**
14.	PA 837 X JLA 794	0.678	0.461	0.462	0.53	1.858 *	1.486	1.399	1.58**
15.	PA 837 X PA 740	-0.473	-0.409	-0.756	-0.55	-1.238	-0.815	-1.078	-1.04*
16.	PA 837 X PA 08	-0.395	-0.421	-0.491	-0.44	0.452	0.651	0.847	0.65
17.	PA 837 X PA 402	-0.696	-0.678	-0.597	-0.66	-0.561	-0.57	-0.61	-0.58
18.	PA 837 X CNA 1054	1.815**	1.534	2.124*	1.82**	1.609	1.549	1.262	1.47**
19.	PA 873 X AKA 7	-0.845	-1.044	-0.607	-0.83	1.259	1.437	1.681	1.46**
20.	PA 873 X JLA 794	0.561	0.715	0.247	0.51	-0.264	-0.244	-0.48	-0.33
21.	PA 873 X PA 740	0.761	0.165	1.219	0.71	-0.09	0.604	0.574	0.36
22.	PA 873 X PA 08	0.088	-0.088	0.084	0.03	-0.14	-0.389	-0.481	-0.34
23.	PA 873 X PA 402	-0.313	0.076	-0.412	-0.22	0.417	0.559	0.321	0.43
24.	PA 873 X CNA 1054	-0.252	0.177	-0.531	-0.20	-1.183	-1.966 *	-1.616	-1.59**
25.	PA 904 X AKA 7	-0.42	-0.354	-0.007	-0.26	2.059 *	1.798 *	1.873 *	1.91**
26.	PA 904 X JLA 794	0.486	-0.145	0.067	0.14	0.466	0.017	-0.278	0.07
27.	PA 904 X PA 740	1.036	1.155	1.019	1.07	-0.56	-0.164	-0.544	-0.42
28.	PA 904 X PA 08	1.163	1.872	1.134	1.39*	-1.41	-0.798	-0.599	-0.94
29.	PA 904 X PA 402	-1.988 **	-2.024	-1.662	-1.89**	-0.602	-0.819	-0.947	-0.79
30.	PA 904 X CNA 1054	-0.277	-0.503	-0.551	-0.44	0.047	-0.035	0.496	0.17
31.	PA 906 X AKA 7	1.305 *	1.443	1.316	1.35*	1.332	0.468	0.783	0.86
32.	PA 906 X JLA 794	0.661	0.531	0.48	0.56	1.880 *	1.837 *	2.002 *	1.91**
33.	PA 906 X PA 740	0.911	1.001	0.742	0.88	-1.497	-1.054	-1.154	-1.23*
34.	PA 906 X PA 08	0.488	0.259	0.238	0.33	-1.007	-0.418	-0.549	-0.66
35.	PA 906 X PA 402	-1.963 **	-1.878	-1.889 *	-1.91**	-0.819	-0.999	-1.057	-0.96
36.	PA 906 X CNA 1054	-1.402 *	-1.356	-0.888	-1.21*	0.111	0.165	-0.024	0.08
37.	PAIG 384 X AKA 7	0.965	0.864	0.578	0.80	-1.568	-1.300	-0.855	-1.24*
38.	PAIG 384 X JLA 794	-0.879	-0.797	-0.678	-0.78	-0.7	0.659	0.684	0.21

39.	PAIG 384 X PA 740	-0.629	-0.617	0.024	-0.41	0.363	0.568	-0.473	0.15
40.	PAIG 384 X PA 08	-0.202	-0.32	-1.181	-0.57	4.473 **	0.934	1.482	2.29**
41.	PAIG 384 X PA 402	2.387**	2.514*	2.163*	2.35**	-0.999	-0.177	0.005	-0.39
42.	PAIG 384 X CNA 1054	-1.642 *	-1.645	-0.906	-1.39*	-1.569	-0.683	-0.843	-1.03*
43.	PAIG 411 X AKA 7	0.175	0.343	0.401	0.30	0.605	0.385	0.635	0.54
44.	PAIG 411 X JLA 794	-0.569	-0.779	-0.615	-0.65	-1.487	-1.646	-1.456	-1.53**
45.	PAIG 411 X PA 740	-0.319	-0.209	-0.422	-0.32	-0.013	0.203	-0.103	0.03
46.	PAIG 411 X PA 08	0.588	0.319	0.523	0.48	1.137	1.479	1.692 *	1.44**
47.	PAIG 411 X PA 402	0.507	0.613	0.796	0.64	-0.336	-0.582	-0.715	-0.54
48.	PAIG 411 X CNA 1054	-0.382	-0.286	-0.682	-0.45	0.094	0.162	-0.053	0.07
	S.E. \pm								
	Lines	0.367	0.662	0.519	0.31	0.483	0.496	0.483	0.28
	Tester	0.318	0.573	0.449	0.27	0.418	0.429	0.419	0.24
	Crosses	0.900	1.622	1.271	0.93	1.184	1.215	1.182	0.84

*, ** - Significant at 5% and 1% level, respectively

Uniformity index (%)

Among lines highest positively significant GCA for bestowing fibre uniformity was imparted by PA 873 (0.71) It also imparted positively significant GCA at all location E₁ (0.84) and E₃ (0.70) than E₂ (0.56). PA 837 (0.42) was the second largest line with high GCA, which imparted positive GCA at E₃ (0.52), E₂ (0.43) and E₁ (0.29).

Among the testers, highest positive GCA for fibre uniformity was reported in AKA 7 (0.22), It also imparted positive GCA at all location E₂ (0.41), E₁ (0.14) and E₃ (0.12). This followed by CNA 1054 (0.22). It also imparted positive GCA at E₃ (0.37), E₁ (0.15) and E₂ (0.13). No tester found significant for uniformity index.

The combination of two highest combiners *i.e.* PA 873 x AKA 7 (1.46) showed significant positive SCA effect. It also imparted positive SCA at E₃ (1.68), E₂ (1.43) and E₁ (1.25).

Among crosses, highest positively significant SCA was reported in PA 785 x PA 740 (2.55). It also imparted positively significant SCA at all locations E₂ (2.66), E₃ (2.51) and E₁ (2.47). Next highest SCA was observed in PAIG 384 x PA 08 (2.29). It also imparted positively significant SCA at E₁ (4.47) than E₃ (1.48) and E₂ (0.93). This followed by PA 904 x AKA 7 (1.91). It also imparted positively significant SCA at all location *i.e.* E₁ (2.05), E₃ (1.87) and E₂ (1.79). PA 906 x JLA 794 (1.91), E₃ (2.00), E₁ (1.88) and E₂ (1.83). PA 810 x CNA 1054 (1.89), E₃ (2.04), E₁ (1.89) and E₂ (1.74) for uniformity index.

The predictability ratio for this trait was 0.09 which indicate the importance of non-additive gene action for the improvement of this character.

These findings were in agreement with Chinchane *et al.*, (2018a) [2], Shinde *et al.*, (2018) [10] and Naik *et al.*, (2019) [8].

Lines and testers showing high general combining ability in desirable direction for different characters showed in the table 4.5. None of the line and tester showed best combiner for all the characters studied results were accordance with the previously by Alkudsi *et al.*, (2013).

For fibre quality traits was recorded in PAIG 411 x AKA 7 exhibiting significant SCA for GOT (2.79), UHML (1.18) and micronaire (-0.47) pooled over the locations. Next highest significant SCA recorded by PA 810 x PA 402 exhibiting significant SCA for GOT (1.39), UHML (1.64), micronaire (-0.26) and uniformity index (1.84) pooled over the locations. Selection in further generations would be rewarding to get best transgressive segregants for fibre quality.

In the present study both GCA and SCA variances were significant for majority of the character studied. This suggested that non-additive variances were important in the expression of these characters except for fibre strength. Significance of both the variances have been reported by Karademir *et al.*, (2009) [5], Laxman (2010) [7], Patil *et al.*, (2014) [9], Chinchane *et al.*, (2018b) [2], Shinde *et al.*, (2018) [10], Naik *et al.*, (2019) [8], Bankar *et al.*, (2020) [11], Deshmukh *et al.*, (2022) [3] and Vadodariya *et al.*, (2022) [11] for seed cotton yield and other characters.

Parents possessing good GCA for yield and yield contributing characters need to be widely used in breeding programme for combining desirable characters.

Conclusion

It is a scientific study on the combining ability analysis for fibre quality traits in desi cotton (*Gossypium arboreum* L.) across different environments. The study extensively discusses the methodology, results, and significance of the genetic traits in cotton breeding, focusing on specific and general combining abilities (SCA and GCA) of various cotton genotypes. It presents detailed statistical analyses of traits like ginning percentage, fibre strength, and micronaire values across different environmental conditions, highlighting the potential for genetic improvement in cotton cultivation. The study found significant GCA effects in certain lines and testers, and notable SCA effects in specific crosses, suggesting that selection in further generations could yield transgressive segregants for improved fiber quality.

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