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Combining ability and gene action studies for yield and fibre traits in *Gossypium arboreum* using Griffings numerical and Haymans graphical approach

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Abstract

Background For the purpose of utilising hybrid vigour to produce possible hybrids with a suitable level of stability, the knowledge of gene activity and combining ability is a crucial prerequisite before choosing desirable parents. The present study was carried out with six parents crossed in full diallel fashion and generated 30 F_1 hybrids. These hybrids were evaluated in two replications in Randomized Block Design at Department of Cotton, TNAU for combining ability and gene action. Diallel analysis was carried out according to Griffing's method-I (parents + F_1 + reciprocals) and model-I and Hayman's graphical approach by using INDOSTAT software.

Results Analysis of variance for combining ability indicated that mean square values of GCA, SCA and reciprocals were highly significant for all the traits except for the uniformity index. RG763 and K12 showed highly positively significant GCA effects for most of the yield traits while PA838 and K12 for fibre quality traits, so they were found as best general combiners. PAIG379 × K12 and PDB29 × K12 for yield traits, and PDB29 × PA838, RG763 × PA838, and CNA1007 × RG763 cross combinations for fibre quality traits could be recommended for future breeding programms.

Conclusion The results of both Griffing's and Hayman's approaches showed that non-additive gene action predominates as SCA variance was bigger than GCA variance, so heterosis breeding is thought to be a more fruitful option for enhancing GCA of many traits.

Keywords Gene action, Combining ability, Diallel analysis, Hayman's approach, Griffing's approach, Vr-Wr graph, Desi cotton

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Background

The "White Gold" of textiles, cotton, has long been produced in India. Commercial cultivation of it is practised in more than 70 nations' temperate and tropical regions. Around 9% of India's total agricultural crop land is used for cotton farming. India's overall agricultural crop is made up of 14%–16% cotton. Tetraploid cotton cultivars are currently facing socioeconomic difficulties that are putting them into the hands of money lenders since growing tetraploid cotton varieties and hybrids is riskier and more unprofitable (Deshpande 2007). Because of the high cost of seeds, extra plant protection, and heavy fertiliser use, these cotton hybrids require more money to cultivate. Contrarily, low-cost seeds, minimal or no costs for plant nourishment and protection are associated with diploids. If this situation was taken into consideration, one would be extremely optimistic for the cultivation of desi cotton, assuming that it had yields comparable to those of tetraploid cotton varieties and hybrids and had fibre of a desirable quality.

The fact that some crossings are better than others at passing on advantageous parental features or genes to their progeny is a well-known phenomenon among cotton breeders. Exploiting the hybrid vigour that cotton possesses is crucial for the development of potential hybrids. The most crucial factor, which depends on both the ability to combine and the diversity of the parents, is the choice of parent for the hybridization. The most effective breeding approach for identifying and selecting superior genotypes as parents with desirable traits and imposing a promising rise in production per unit area is combining ability analysis with selection. For the purpose of utilising hybrid vigour to produce possible hybrids with a suitable level of stability, knowledge of gene activity and combining ability is a crucial prerequisite before choosing desirable parents. In contrast to special combining ability (SCA), which is the performance of parents in particular cross combinations judged by non-additive gene activity, general combining ability (GCA) is the average performance of strains in a series of crosses (Sprague and Tatum 1942). Diallel is one of the ways that is frequently used to evaluate the parents' additive and non-additive gene actions. The breeder can identify promising recombinants created by mixing the parental individuals and potential genotypes by diallel mating design.

Materials and methods

Thirty hybrids (F_1s) were produced in the current study's full diallel crossing of six parents, which was conducted during summer 2022 (Fig. 1). The parents used for this study includes PDB29, PAIG379, RG763, CNA1007, PA838, and K12. At the Department of Cotton, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University (TNAU), Coimbatore, these hybrids were raised in a Randomized Block Design (RBD) with two

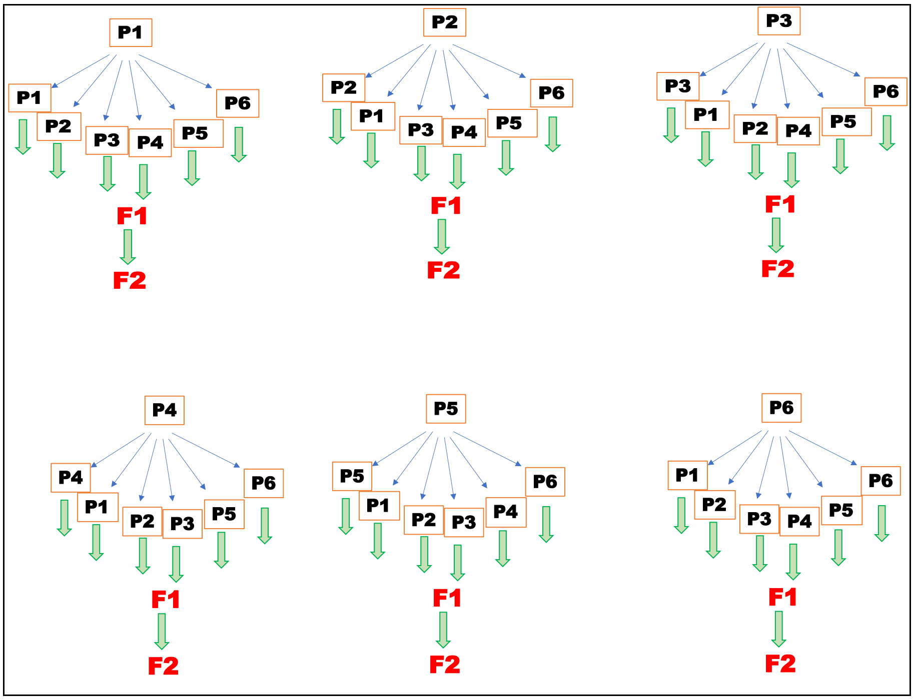


Fig. 1 Overview of a six-parent full diallel design (Each parent crossed to all different parents)

Table 1 Anova for combining ability

Source of Variation	d.f	DFF	PH	NMB/P	NSB/P	NB/P	NL/B	DBB	BW	NS/B	SCY/P	GOT	SI	LI	UHML	UI	Str	EL	Mic
GCA	5	14.29^{a}	947.538^{a}	0.62^{a}	27.333^{a}	35.374^{a}	0.082^{a}	36.689^{a}	0.028^{a}	15.659^{a}	154.646^{a}	52.962^{a}	2.123^{a}	0.338^{a}	7.702^{a}	2.922	13.615^{a}	0.196^{a}	0.914^{a}
SCA	15	20.262^{a}	732.27^{a}	0.659^{a}	12.342^{a}	29.3^{a}	0.086^{a}	18.977^{a}	0.236^{a}	34.469^{a}	174.699^{a}	55.403^{a}	2.572^{a}	0.28^{a}	2.6^{a}	1.03	3.275^{a}	0.078^{a}	0.41^{a}
Reciprocals	15	19.213^{a}	1150.14^{a}	0.662^{a}	18.258^{a}	24.203^{a}	0.104^{a}	30.718^{a}	0.195^{a}	27.227^{a}	195.709^{a}	83.336^{a}	2.653^{a}	0.185^{a}	4.243^{a}	2.294	5.052^{a}	0.057^{a}	0.537^{a}
Maternal effect	5	11.57	931.178	0.314	4.745	32.577	0.101	37.228	0.321	29.687	280.498	94.033	2.273	0.127	5.115	-	7.59	0.112	0.918
Maternal interaction	10	23.034^{a}	1259.62^{a}	0.837^{a}	25.015^{a}	20.016^{a}	0.105^{a}	27.462^{a}	0.132^{a}	25.996^{a}	153.314^{a}	77.987^{a}	2.843^{a}	0.213^{a}	3.807^{a}	-	3.783^{a}	0.03^{b}	0.346^{a}
Error	35	1.791 389	10.119	0.002	0.33	0.465	0.007	5.708	0.002	0.31	2.242	1.904	0.062	0.013	0.522	1.531	0.302	0.011	0.014

DFF days to fifty percent flowering (days), *PH* plant height (cm), *NMB/P* the number of monopodia per plant, *NSB/P* the number of sympodia per plant, *NB/P* the number of bolls per plant, *NL/P* the number of locules per boll, *DBB* days to first boll bursting (days), *BW* boll weight (g), *NS/B* the number of seeds per boll, *SCY/P* seed cotton yield per plant (g), *SI* seed index (g), *LI* lint index (g), *GOT* ginning out turn (%), *UHML* upper half mean length (mm), *Str* fibre strength (cN·tex^{-1}), *UI* uniformity index, *EL* elongation percentage (%), *Mic* micronaire, *S.E (Gi)* standard error for GCA effect of ith parent, *S.E.(Gi-Gj)* standard error for GCA effect between ith and jth parents

[a] significant at 1%,

[b] significant at 5%

replications and a spacing of 90 cm (row to row) × 60 cm (plant to plant) in Kharif, 2022. Practices for crop management were carried out. Doak's method of hand emasculation and pollination was used to generate hybrids (Doak 1934). These hybrids and parents were evaluated for combining ability and gene action.

Thirteen quantitative parameters, *viz.*, days to 50% flowering (d), plant height (cm), the number of monopodia per plant, the number of sympodia per plant, the number of bolls per plant, the number of locules per boll, the number of seeds per boll, days to boll bursting (d), boll weight (g), seed cotton yield per plant (g), seed index (g), lint index(g), ginning out turn (%) and five fibre quality parameters such as upper half mean length (mm), fibre strength ($\mathrm{cN \cdot tex^{-1}}$), uniformity index, elongation per cent (%), and fibre micronaire using High volume instrument (HVI) were recorded by randomly selecting five plants from each replication of each cross. GCA and SCA effects in diallel analysis was carried out according to Griffing's method-I (parents + F_1 + reciprocals) and model-I and Hayman's graphical approach by using INDOSTAT software.

Results and discussion

Analysis of variance

Griffing's approach was carried out to evaluate the combining ability effects. Analysis of variance for combining ability was represented in Table 1 which indicated that mean square values of GCA were highly significant for all traits except for uniformity index. The mean square values of SCA and reciprocals were also significant for all traits except for uniformity index. Though the maternal effects are non-significant for all traits, the maternal interactions were significant for all traits under study.

Combining ability effects

General combining ability effects were presented in Table 2. Parents PA838 and CNA1007 showed negative significant GCA effects for days to 50% flowering whereas PAIG379 and PA838 for the number of monopodia per plant. PA838 was found highly significant for almost all traits except for the number of locules per boll and elongation percent. Parents such as PDB29 and PAIG379 were found negatively significant for plant height, the number of sympodia, the number of bolls, the number of seeds per boll, seed cotton yield per plant, ginning out turn, and lint index. In case of boll weight, seed cotton yield per plant, lint index, and fibre strength, RG763 and K12 were highly positively significant and can be found as the best general combiner for these traits and this high GCA effect in desirable selection indicated the presence of additive genes for those traits. In case of fibre quality traits, PA838 and K12 can be used as the best general combiners.

The SCA effects of 30 F_1 hybrids were presented in Table 3. The hybrids PAIG379 × K12 followed by RG763 × PA838 and RG763 × K12 showed highly positive significant SCA effects for seed cotton yield per plant, the number of sympodia per plant, and the number of bolls per plant. Even RG763 and K12 exhibited as the best general combiners for these traits, these hybrids also exhibited the highest SCA effects. The hybrids PDB29 × K12, PAIG379 × PDB29, PAIG379 × PA838, PAIG379 × K12, PA838 × RG763, and PA838 × CNA1007 showed positive significant SCA effects for boll weight and the number of seeds per boll. The hybrids PDB29 × K12, PAIG379 × K12, RG763 × PA838, and K12 × PDB29 showed positive significant SCA effects for ginning out turn. By these results, PAIG379 × K12 and PDB29 × K12 can be recommended as the best cross combinations for most of the traits under study. For fibre quality traits, PDB29 × PA838, RG763 × PA838, and CNA1007 × RG763 cross combinations can be recommended as they showed significant SCA effects.

Gene action studies

In our study, the magnitude of SCA variance was higher than GCA variance for all traits except for uniformity index (Table 4) indicating the preponderance of non-additive gene action, which could be exploited by heterosis studies and population improvement methods.

Hayman's graphical approach

For all of the relevant features, the estimates of the uniformity test, t^2, were not significant. Uniformity test provides insights into the consistency of the trait expression across the different genotypes. Genotypes with high uniformity are desirable as they exhibit consistent performance. Results of this uniformity test demonstrated the validity of the diallel analysis assumptions provided by Hayman (1954) for all relevant features. Moreover, it can be a sign that no epistatic interactions exist. All of the investigated features had substantial variations in the regression coefficients (b) of Vr-Wr. It showed that the parental materials' Vr (Variance of each array) and Wr (Covariance between parents and their offspring's) graphs were beneficial for the genetic analyses of the parents with regard to these qualities. These variance and covariance values were presented in Table 5. As a result, Vr-Wr can be plotted for all relevant features.

Among the components of variance, the values of dominance components (H_1, H_2) were greater than the additive (D) and average degree of dominance ($\sqrt{H_1/D}$) which denoted the overdominance type of gene action for

Table 2 General combining ability (GCA) effects for yield and fibre quality traits in *G. arboreum*

Parents	DFF	PH	NMB/P	NSB/P	NB/P	NL/B	DBB	BW	NS/B	SCY/P	GOT	SI	LI	UHML	UI	Str	EL	Mic
PDB29	0.310	-2.97^{a}	0.15^{a}	-1.00^{a}	-1.22^{a}	0.056^{a}	-1.02^{b}	-0.02^{a}	-0.71^{a}	-3.03^{a}	-1.20^{a}	-0.079	-0.105^{a}	-0.084	0.318	0.39^{a}	0.041^{b}	0.08^{a}
PAIG379	1.074^{a}	-9.61^{a}	-0.29^{a}	-1.09^{a}	-0.94^{a}	-0.080^{a}	1.87^{a}	-0.01	-0.26^{b}	-1.97^{a}	-1.46^{a}	0.006	-0.099^{a}	0.068	0.135	0.775^{a}	0.133^{a}	0.027
RG763	-0.243	0.53	0.078^{a}	0.020	1.939^{a}	-0.062^{a}	-1.38^{a}	0.05^{a}	1.44^{a}	4.011^{a}	1.93^{a}	0.073	0.122^{a}	0.074	0.114	0.13	0.005	0.260^{a}
CNA1007	-0.904^{a}	-1.55^{b}	-0.014	-0.100	-0.67^{a}	0.012	-0.370	-0.01^{b}	0.174	-0.004	-0.53^{b}	0.27^{a}	0.106^{a}	-0.251	0.106	-0.77^{a}	-0.105^{a}	-0.035
PA838	-0.761^{a}	6.19^{a}	-0.042^{a}	1.833^{a}	0.868^{a}	0.020	1.014^{b}	-0.02^{a}	-0.73^{a}	-0.61^{b}	1.776^{a}	-0.53^{a}	-0.118^{a}	0.964^{a}	-0.529^{b}	0.549^{a}	0.023	-0.31^{a}
K12	0.5254^{b}	7.41^{a}	0.118^{a}	0.344^{a}	0.038	0.053^{a}	-0.101	0.015^{b}	0.102	1.619^{a}	-0.505	0.261^{a}	0.094^{a}	-0.77^{a}	-0.145	-1.080^{a}	-0.098^{a}	-0.017
S.E (Gi)	0.249	0.593	0.008	0.107	0.127	0.015	0.445	0.007	0.104	0.279	0.257	0.046	0.021	0.135	0.231	0.102	0.019	0.022
S.E.(Gi-Gj)	0.546	1.299	0.017	0.235	0.278	0.034	0.975	0.016	0.227	0.611	0.563	0.101	0.046	0.295	0.505	0.224	0.042	0.048

DFF days to fifty per cent flowering (days), *PH* plant height (cm), *NMB/P* the number of monopodia per plant, *NSB/P* the number of sympodia per plant, *NB/P* the number of bolls per plant, *NL/P* the number of locules per boll, *DBB* days to first boll bursting (days), *BW* boll weight (g), *NS/B* the number of seeds per boll, *SCY/P* seed cotton yield per plant (g), *SI* seed index (g), *LI* lint index (g), *GOT* ginning out turn (%), *UHML* upper half mean length (mm), *Str* fibre strength ($g \cdot tex^{-1}$), *UI* uniformity index, *EL* elongation percentage (%), *Mic* micronaire, *S.E (Gi)* standard error for GCA effect of ith parent, *S.E.(Gi-Gj)* standard error for gca effect between ith and jth parents

[a] significant at 1%,

[b] significant at 5%

Table 3 Specific combining ability (SCA) effects for yield and fibre quality traits in *G. arboreum*

Hybrids	DFF	PH	NMB/P	NSB/P	NB/P	NL/B	DBB
PDB29 × PAIG379	-4.0375 **	-2.1955	0.0690 **	-0.8713 **	0.0474	-0.0614	-0.3112
PDB29 × RG763	-1.7721 **	-2.8005 *	-0.3447 **	-1.1733 **	-2.1856 **	-0.1364 **	0.4142
PDB29 × CNA1007	-0.6367	-8.1947 **	0.0699 **	-1.1379 **	-1.3660 **	-0.1039 **	-1.3875
PDB29 × PA838	2.8808 **	15.2307 **	0.5907 **	1.5962 **	-1.7018 **	-0.0347	2.2475 *
PDB29 × K12	4.0963 **	-0.3155	0.1869 **	-0.3096	0.1724	0.2799 **	-1.9292
PAIG379 × RG763	2.2463 **	-10.2568 **	0.1561 **	-1.7879 **	0.2507	0.0507	4.2217 **
PAIG379 × CNA1007	0.1467	-23.6035 **	-0.6618 **	-2.4175 **	-2.8272 **	-0.0343	-0.6275
PAIG379 × PA838	-2.4583 **	2.4320	-0.3735 **	-0.4558	1.5519 **	0.0149	-2.0050
PAIG379 × K12	-0.1429	11.3957 **	0.0253	2.5508 **	4.1611 **	-0.0406	2.1908 *
RG763 × CNA1007	-0.8429	3.4690 *	-0.0906 **	0.4479	-2.4426 **	0.0082	0.4979
RG763 × PA838	-0.9829	7.7070 **	0.4153 **	0.7596 **	3.7090 **	-0.0576	0.4954
RG763 × K12	-0.4650	12.3432 **	-0.1685 **	2.1762 **	1.7182 **	-0.0256	-1.1312
CNA1007 × PA838	-0.0400	11.0628 **	0.4349 **	-0.3550	1.7611 **	-0.1376 **	-1.3412
CNA1007 × K12	0.0304	-7.7235 **	0.1711 **	0.1292	0.5853 *	-0.1981 **	-1.1454
PA838 × K12	-0.0221	-3.8830 **	-0.5056 **	-1.6167 **	-3.5431 **	0.0561	1.7246
Reciprocal effects							
PAIG379 × PDB29	-2.9825 **	-22.6425 **	0.0900 **	-3.4475 **	-1.6750 **	-0.0100	-2.4175 *
RG763 × PDB29	-2.3600 **	17.4900 **	1.0100 **	1.9375 **	-0.3425	-0.0375	3.8100 **
RG763 × PAIG379	4.5425 **	-10.6075 **	-0.2800 **	-0.7825 **	-6.1800 **	0.0025	0.1225
CNA1007 × PDB29	-0.9250	-8.9950 **	-0.1875 **	-1.3425 **	-0.3350	0.0850 *	-1.7900
CNA1007 × PAIG379	-1.0275	17.0350 **	0.0050	2.0525 **	-0.0500	-0.0025	0.9350
CNA1007 × RG763	-1.3750 *	6.2850 **	0.2400 **	0.2950	0.3650	0.0725	1.5075
PA838 × PDB29	4.9250 **	6.5650 **	0.3450 **	0.7550 *	-0.5800	-0.1425 **	-0.4850
PA838 × PAIG379	0.5250	2.8950	-0.2650 **	-1.1525 **	-3.3450 **	0.0700	1.5575
PA838 × RG763	-1.1925	9.7275 **	-0.2425 **	1.3600 **	-1.7175 **	-0.0250	-4.8600 **
PA838 × CNA1007	-0.1950	41.7525 **	0.6800 **	4.2000 **	-0.0975	-0.0150	1.2100
K12 × PDB29	0.7375	-17.4650 **	-0.5675 **	0.4500	2.1850 **	-0.5700 **	3.3675 **
K12 × PAIG379	-2.0925 **	-2.7450	-0.2200 **	-1.0100 **	-3.8200 **	-0.0425	-0.0525
K12 × RG763	-0.7725	-4.9400 **	-0.0100	0.5475	-1.3225 **	0.1450 **	2.8475 *
K12 × CNA1007	1.1825	-26.9475 **	-0.2475 **	-4.5850 **	-3.7125 **	0.0275	6.4050 **
K12 × PA838	0.4875	4.3375 **	0.3775 **	1.4775 **	0.1200	-0.0300	0.4950

Table 3 (Continued)

Hybrids	BW	NS/B	SCY/P	GOT	SI	LI
PDB29 × PAIG379	0.0521 **	-0.2686	1.6192 *	0.4460	-0.0201	-0.0115
PDB29 × RG763	-0.2912 **	-2.7224 **	-6.5567 **	-0.2382	0.2503 *	0.1710 **
PDB29 × CNA1007	-0.1433 **	-1.7174 **	-2.4887 **	1.3918 *	-0.7289 **	-0.1882 **
PDB29 × PA838	-0.1417 **	-1.4861 **	-3.5933 **	-3.2049 **	0.8765 **	0.0951
PDB29 × K12	0.3675 **	2.3914 **	4.7500 **	2.0022 **	-0.5926 **	-0.0578
PAIG379 × RG763	-0.0983 **	0.9035 **	0.0179	-2.5103 **	-0.0947	-0.1969 **
PAIG379 × CNA1007	-0.1379 **	-3.5390 **	-5.8517 **	0.7372	-0.8689 **	-0.2886 **
PAIG379 × PA838	0.1313 **	0.7797 **	3.5562 **	-1.3794 *	0.1340	0.0072
PAIG379 × K12	0.2404 **	3.9447 **	9.1646 **	3.1276 **	0.4149 **	0.4343 **
RG763 × CNA1007	-0.0837 **	-1.7603 **	-4.6000 **	-3.0644 **	0.5665 **	-0.0236
RG763 × PA838	0.2154 **	-0.3690	7.6104 **	11.4214 **	-2.1181 **	-0.2528 **
RG763 × K12	0.2071 **	3.2960 **	6.1712 **	-1.9640 **	0.4153 **	0.0518
CNA1007 × PA838	-0.0192	2.1960 **	-1.4517 *	-2.4061 **	0.0553	-0.1319 **
CNA1007 × K12	0.0725 **	-0.2365	-1.9308 **	-0.6990	-0.3464 **	-0.2649 **
PA838 × K12	-0.0808 **	-0.4403	-3.6654 **	-1.0532	0.3640 **	0.1285 **
Reciprocal effects						
PAIG379 × PDB29	0.1350 **	-1.3325 **	-3.8050 **	1.0700	-0.4200 **	-0.0425
RG763 × PDB29	-0.3675 **	-4.0600 **	-6.1800 **	0.1525	0.1075	0.0575
RG763 × PAIG379	-0.1150 **	-2.9850 **	-15.3600 **	-0.8575	0.3375 **	0.0350
CNA1007 × PDB29	-0.1200 **	-0.4925	-1.5475 *	-0.0150	0.6650 **	0.2475 **
CNA1007 × PAIG379	0.1000 **	0.3000	0.5500	-2.7375 **	-0.6900 **	-0.5075 **
CNA1007 × RG763	0.0000	-2.3900 **	0.1975	0.1475	-0.7575 **	-0.2600 **
PA838 × PDB29	-0.3225 **	-3.7650 **	-3.0650 **	0.2150	0.2950 *	0.1250 *
PA838 × PAIG379	-0.1200 **	-2.0000 **	-3.7250 **	-0.6475	0.3925 **	0.0775
PA838 × RG763	0.0550 **	2.8125 **	1.6450 *	-17.0850 **	2.7525 **	0.1550 **
PA838 × CNA1007	0.1100 **	0.7000 *	2.5825 **	-2.0250 **	-0.1925	-0.2750 **
K12 × PDB29	-0.1975 **	0.9150 **	2.7600 **	2.1350 **	0.4375 **	0.3750 **
K12 × PAIG379	-0.1250 **	-1.7725 **	-10.7150 **	1.0225	0.1050	0.1525 **
K12 × RG763	0.0975 **	-0.0450	0.0525	-0.8275	0.1725	-0.0275
K12 × CNA1007	-0.5675 **	-6.1900 **	-16.9300 **	0.5500	-0.0875	0.0250
K12 × PA838	0.0700 **	-0.1175	0.9325	-0.1875	-0.2425	-0.1125

Table 3 (Continued)

Hybrids	UHML	UI	Str	EL	Mic
PDB29 × PAIG379	0.7601 *	0.1750	-0.0811	0.0604	0.0188
PDB29 × RG763	-0.2732	0.0063	-0.0874	0.0567	0.1558 *
PDB29 × CNA1007	-0.7494 *	-0.1229	-0.5274 *	-0.1083 *	-0.0350
PDB29 × PA838	1.0572 **	-0.6071	1.3981 **	0.2983 **	0.1700 *
PDB29 × K12	-0.1253	0.4517	0.0051	-0.0175	-0.3333 **
PAIG379 × RG763	-0.7786 *	0.3917	-1.8086 **	-0.0508	0.3133 **
PAIG379 × CNA1007	0.6101	-0.5675	0.8714 **	0.2217 **	0.3875 **
PAIG379 × PA838	-0.8132 *	-0.1042	-0.2182	-0.0892 *	-0.1700 *
PAIG379 × K12	0.2018	0.0721	0.0414	-0.0675	0.1967 **
RG763 × CNA1007	0.4318	0.0538	0.5576 *	-0.0971 *	-0.2354 **
RG763 × PA838	0.8810 **	0.1121	1.3256 **	0.1221 **	-0.3479 **
RG763 × K12	0.0360	0.1708	0.8451 **	0.1013 *	0.2312 **
CNA1007 × PA838	1.1572 **	-0.3796	-0.3394	-0.0729	0.0562
CNA1007 × K12	-0.3353	-0.0958	-0.3199	0.0388	-0.0946
PA838 × K12	-0.1161	-0.2350	-0.5344 *	-0.0396	0.0254
Reciprocal effects					
PAIG379 × PDB29	-0.3675	0.5900	0.7850 **	0.1725 **	-0.1150
RG763 × PDB29	0.1750	0.0550	1.5925 **	0.2100 **	-0.0350
RG763 × PAIG379	-0.6525	0.5675	-0.5450	-0.0100	0.1675 *
CNA1007 × PDB29	0.4625	-0.5475	0.8225 **	0.1300 *	-0.1275
CNA1007 × PAIG379	0.5350	-0.7600	1.3600 **	0.1075 *	-0.1550
CNA1007 × RG763	-2.7475 **	1.8950 **	-2.5900 **	-0.2200 **	0.8800 **
PA838 × PDB29	-0.7050	0.5725	0.4475	0.1150 *	0.4400 **
PA838 × PAIG379	-0.5225	0.0325	-0.6600 *	0.0300	0.3550 **
PA838 × RG763	-0.5175	0.2325	-0.1825	-0.1125 *	0.3450 **
PA838 × CNA1007	-0.9675 *	-0.1175	-0.8125 **	-0.0975	0.3625 **
K12 × PDB29	-0.4125	0.0250	-0.2300	-0.0075	0.3025 **
K12 × PAIG379	-0.2575	0.6575	0.1200	0.0400	0.1775 *
K12 × RG763	-2.0825 **	1.4850 *	-1.4225 **	-0.0500	0.7900 **
K12 × CNA1007	0.6850	-0.7600	-1.6425 **	-0.1375 *	-0.0175
K12 × PA838	-0.5050	-0.1500	-0.3775	-0.0725	0.0450

DFF days to fifty per cent flowering (days), *PH* plant height (cm), *NMB/P* the number of monopodia per plant, *NSB/P* the number of sympodia per plant, *NB/P* the number of bolls per plant, *NL/P* the number of locules per boll, *DBB* days to first boll bursting (days), *BW* boll weight (g), *NS/B* number of seeds per boll, *SCY/P* seed cotton yield per plant (g), *SI* seed index (g), *LI* lint index (g), *GOT* ginning out turn (%), *UHML* upper half mean length (mm), *Str* fibre strength (g·tex^{-1}), *UI* uniformity index, *EL* elongation percentage (%), *Mic* micronaire

*significant at 5%,

**significant at 1%

Table 4 Estimation of gene action for various traits

	GCA Variance	SCA Variance	Ratio (GCA VAR/SCA VAR)	Gene Action
DFF	0.520 9	9.236	0.056 4	Non- additive
PH	39.057 7	361.086 5	0.108 2	Non- additive
NMB/P	0.025 8	0.328 8	0.078 4	Non- additive
NSB/P	1.125 1	6.006 3	0.187 3	Non- additive
NB/P	1.454 4	14.418 9	0.100 9	Non- additive
NL/B	0.003 1	0.039 9	0.078 4	Non- additive
DBB	1.289 6	6.641 4	0.194 2	Non- additive
BW	0.000 8	0.117 4	0.007 0	Non- additive
NS/B	0.639 6	17.080 1	0.037 4	Non- additive
SCY/P	6.350 3	86.227 6	0.073 6	Non- additive
GOT	2.127 4	26.749 1	0.079 5	Non- additive
SI	0.085 9	1.255 1	0.068 4	Non- additive
LI	0.013 6	0.133 6	0.101 6	Non- additive
UHML	0.299 2	1.038 4	0.288 2	Non- additive
UI	0.015 4	-0.474 7	-0.032 3	Non- additive
Str	0.554 8	1.486 3	0.373 3	Non- additive
EL	0.007 7	0.033 7	0.229 3	Non- additive
Mic	0.034 7	0.127 9	0.271 5	Non- additive

DFF days to fifty per cent flowering (days), *PH* plant height (cm), *NMB/P* the number of monopodia per plant, *NSB/P* the number of sympodia per plant, *NB/P* the number of bolls per plant, *NL/P* the number of locules per boll, *DBB* days to first boll bursting (days), *BW* boll weight (g), *NS/B* the number of seeds per boll, *SCY/P* seed cotton yield per plant (g), *SI* seed index (g), *LI* lint index (g), *GOT* ginning out turn (%), *UHML* upper half mean length (mm), *Str* fibre strength (g·tex^{-1}), *UI* uniformity index, *EL* elongation percentage (%), *Mic* micronaire

almost all traits. Average degree of dominance$(H_1/D)^{1/2}$ was more than unity for seed cotton yield per plant, ginning out turn, upper half mean length, and uniformity index which indicated the overdominance type of gene action, whereas the number of sympodia per plant, the number of bolls per plant, boll weight, the number of seeds per boll, fibre strength and elongation percent were slightly less than unity that indicated partial dominance (Table 6, Fig. 2(A-K)). Both additive and dominance type values are almost similar in fibre micronaire, it showed a slightly complete dominance (Table 6, Fig. 2(K)).

In our study, there were differences between H_1 and H_2 values which indicated dissimilar distribution of positive and negative genes as authenticated by $H_2/4H_1$ value (not equal to 0.25).

In Vr-Wr graph, the numbers along the regression line indicated six parents used in the study (1- PDB29; 2- PAIG379; 3-RG763; 4- CNA1007: 5- PA838; 6- K12) (Fig. 2). Parents close to the origin indicated presence of more dominant genes and above regression line indicated presence of duplicate gene action whereas below regression line indicated complementary gene action.

Fr values of each parent for all traits were presented in the Table 7. Parents which had positive Fr values indicated the presence of more dominant genes whereas the parents with negative values indicated the presence of more recessive genes for a particular trait.

Discussion

GCA

The results of the study indicate that different parents showed varying effects on different traits related to cotton plant growth and fibre quality. For example, PA838 was found to have a highly significant positive effect on most traits, except for the number of locules per boll and elongation percent. On the other hand, parents like PDB29 and PAIG379 had negative significant effects on traits such as plant height, the number of sympodia, the number of bolls, the number of seeds per boll, seed cotton yield per plant, ginning out turn, and lint index. Interestingly, RG763 and K12 were identified as best general combiners for traits like boll weight, seed cotton yield per plant, lint index, and fibre strength, as they showed highly significant positive effects. This suggests that these parents may carry additive genes that contribute to favourable traits related to cotton fibre quality. Similar findings were reported in previous studies by Reddy et al. (2017), Bilwal et al. (2018), Deshmukh et al. (2021), Çetin and Çopur (2022) indicating consistency in the results.

It's worth noting that the study focused on general combining ability (GCA) effects, which represent the additive genetic effects of a parent on the performance of its progeny. GCA effects are important in plant breeding as they reflect the potential of a parent to pass on desirable traits to its offspring. However, it's also important to consider specific combining ability (SCA) effects, which represent the non-additive genetic effects resulting from interactions between specific parental combinations. Both GCA and SCA effects play a role in determining the performance of progeny in a breeding program.

In conclusion, the study's findings suggest that different parents have varying effects on cotton plant traits, and some parents may be better general combiners for specific traits than others. PA838 and K12 were identified as the best general combiners for fibre quality traits, while RG763 and K12 showed high GCA effects for traits related to boll weight, seed cotton yield per plant, lint index, and fibre strength. These results provide valuable information for cotton breeding programs and highlight the importance of selecting appropriate parental lines to achieve desired traits in cotton progeny. Further researches considering SCA effects and field performance are warranted to fully understand the potential of these parental lines in cotton breeding programs.

Table 5 Variances and covariances for yield and fibre quality traits in *G. arboreum*

S.No	Parents	DFF		PH		NMB/P		NSB/P		NB/P		NL/B		DBB		BW		NS/B		SCY/P	
		Wr	**Vr**	**Wr**	**Vr**	**Wr**	**Vr**	**Wr**	**Vr**	**Wr**	**Vr**	**Wr**	**Vr**	**Wr**	**Vr**	**Wr**	**Vr**	**Wr**	**Vr**	**Wr**	**Vr**
1	**PDB29**	2.038	6.337	38.232	280.985	-0.136	0.142	1.186	6.533	0.955	13.52	-0.003	0.013	-5.493	4.381	0.035	0.049	2.708	9.078	8.547	66.587
2	**PAIG379**	0.968	4.074	217.445	210.419	-0.069	0.057	1.05	2.531	-3.392	8.62	-0.011	0.002	7.426	4.713	0.021	0.009	-0.15	5.106	-1.767	29.973
3	**RG763**	0.834	7.434	144.843	308.932	0.29	0.333	1.786	8.435	0.018	4.245	-0.012	0.021	5.505	12.07	0.04	0.065	-0.336	3.87	-2.733	39.272
4	**CNA1007**	0.835	0.547	-26.611	412.156	-0.013	0.175	0.595	10.752	-0.973	5.05	0.003	0.019	-5.072	4.283	-0.005	0.017	0.16	3.891	-0.595	40.205
5	**PA838**	0.568	3.085	32.002	46.949	0.082	0.039	0.6	3.154	2.138	6.11	0.016	0.013	6.923	5.933	-0.036	0.039	-0.104	6.679	2.993	17.365
6	**K12**	3.455	6.926	43.378	170.868	0.134	0.241	-1.995	5.405	6.052	11.914	0.159	0.171	10.925	14.767	0.042	0.135	4.076	18.501	19.719	100.217
	Total	8.698	28.403	449.288	1430.309	0.289	0.987	3.221	36.811	4.796	49.459	0.151	0.24	20.215	46.146	0.098	0.314	6.355	47.126	26.164	293.621
	Mean	1.45	4.734	74.881	238.385	0.048	0.165	0.537	6.135	0.799	8.243	0.025	0.04	3.369	7.691	0.016	0.052	1.059	7.854	4.361	48.937

Table 5 (Continued)

S.No	Parents	GOT		SI		LI		UHML		UI		Str		EL		Mic	
		Wr	Vr	Wr	Vr	Wr	Vr	Wr	Vr	Wr	Vr	Wr	Vr	Wr	Vr	Wr	Vr
1	**PDB29**	1.573	2.589	-0.063	0.021	-0.019	0.043	0.941	0.488	0.369	0.153	1.127	1.649	0.025	0.041	0.072	0.098
2	**PAIG379**	-3.197	50.561	-0.144	1.631	0	0.078	0.135	0.855	0.627	1.233	0.119	1.674	-0.005	0.014	0.129	0.195
3	**RG763**	0.947	0.946	-0.161	0.17	-0.013	0.037	1.959	2.614	0.372	0.576	1.349	1.61	0.009	0.027	0.14	0.145
4	**CNA1007**	1.294	1.871	0.293	0.543	0.052	0.117	1.37	2.063	0.099	1.289	0.913	3.071	0.008	0.041	0.058	0.059
5	**PA838**	-4.356	47.329	-0.249	1.145	0.011	0.014	1.191	1.536	0.309	0.125	1.218	2.692	0.023	0.047	0.034	0.031
6	**K12**	-1.254	2.043	0.208	0.303	0.027	0.093	0.127	0.88	0.282	0.54	0.193	1.032	-0.001	0.008	0.095	0.084
	Total	-4.993	105.339	-0.117	3.813	0.058	0.381	5.722	8.437	2.057	3.916	4.92	11.728	0.059	0.177	0.527	0.612
	Mean	-0.832	17.556	-0.019	0.636	0.01	0.064	0.954	1.406	0.343	0.653	0.82	1.955	0.01	0.03	0.088	0.102

Vr variance, *Wr* covariance, *DFF* days to fifty per cent flowering (days), *PH* plant height (cm), *NMB/P* the number of monopodia per plant, *NSB/P* the number of sympodia per plant, *NB/P* the number of bolls per plant, *NL/P* the number of locules per boll, *DBB* days to first boll bursting (days), *BW* boll weight (g), *NS/B* the number of seeds per boll, *SCY/P* seed cotton yield per plant (g), *SI* seed index (g), *LI* lint index (g), *GOT* ginning out turn (%), *UHML* upper half mean length (mm), *Str* fibre strength (g·tex^{-1}), *UI* uniformity index, *EL* elongation percentage (%), *Mic* micronaire

Table 6 Genetic components of variance for yield and fibre quality traits in *G. arboreum*

Components	DFF	PH	NMB/P	NSB/P	NB/P	NL/B	DBB	BW	NS/B	SCY/P	GOT	SI	LI	UHML	UI	Str	EL	Mic
D (Additive effect)	3.781	244.916	0.537	3.724	4.146	0.165	13.389	0.056	2.084	4.310	1.287	0.346	0.038	2.108	0.346	1.433	0.033	0.144
F (Mean Fr over arrays)	2.368	193.682	0.881	5.409	5.246	0.232	15.154	0.046	0.032	-8.041	6.521	0.790	0.042	0.573	-0.184	-0.301	0.030	-0.059
H_1 (Dominance effect)	15.404	890.493	1.001	25.848	33.541	0.219	26.040	0.198	29.012	180.663	73.297	2.916	0.244	3.487	0.343	5.691	0.103	0.190
H_2	13.988	734.382	0.578	21.147	27.437	0.132	21.739	0.172	24.846	160.971	64.829	2.089	0.197	3.083	0.367	4.386	0.067	0.167
h_2	0.171	2.965	0.004	2.052	4.738	0.113	6.735	0.050	2.118	3.862	12.357	0.253	0.212	-0.130	0.432	0.032	0.012	0.023
E (Environ. comp.)	0.908	5.063	0.001	0.162	0.228	0.004	2.781	0.001	0.151	1.171	0.927	0.030	0.006	0.258	0.745	0.169	0.006	0.006
vH_1/D	2.018	1.907	1.365	0.934	0.844	1.151	1.395	1.890	0.731	6.474	7.546	2.903	2.527	1.286	1.997	0.993	0.766	1.149
$H_2/4H_1$	0.227	0.206	0.144	0.205	0.205	0.150	0.209	0.217	0.214	0.223	0.221	0.179	0.202	0.221	0.268	0.193	0.163	0.220
$V4dh_1 + F/v4DH_1$-F	1.367	1.523	4.015	1.761	1.572	4.142	2.366	1.567	1.004	0.748	2.011	2.296	1.557	1.236	0.578	0.900	1.710	0.697
h_2/H_2	0.012	0.004	0.008	0.097	0.173	0.856	0.310	0.290	0.085	0.024	0.191	0.121	1.079	-0.042	1.176	0.007	0.185	0.138
h^2 (ns)	0.375	0.626	0.153	0.458	0.383	0.140	0.571	0.653	0.210	0.074	0.064	0.432	0.372	0.566	0.099	0.389	0.503	0.583
t^2 values	5.600	0.502	0.832	3.949	0.150	0.079	1.296	0.791	4.240	4.725	4.450	7.312	1.269	0.193	6.925	0.672	1.067	3.070
a (intercept)	0.376	98.760	-0.109	0.136	-1.933	-0.015	-4.234	-0.002	-1.365	-8.047	0.799	0.062	-0.022	-0.067	0.333	0.222	-0.010	0.024
b (slope)	0.227	-0.100	0.955	0.065	0.339	1.009	0.989	0.354	0.309	0.254	-0.093	-0.129	0.499	0.726	0.015	0.306	0.655	0.629
standard error	0.175	0.351	0.500	0.207	0.383	0.091	0.579	0.296	0.065	0.067	0.023	0.162	0.235	0.251	0.168	0.313	0.199	0.148
(b-0)/SE	0.227*	-0.1*	0.955*	0.065*	0.339*	1.009*	0.989*	0.354*	0.309*	0.254*	-0.093*	-0.129*	0.499*	0.726*	0.015*	0.306*	0.655*	0.629*

D Component of variation due to additive effect of gene, H_1 Component of variation due to dominant effect of gene, H_2 Proportion of dominance variance due to positive and negative effect of gene

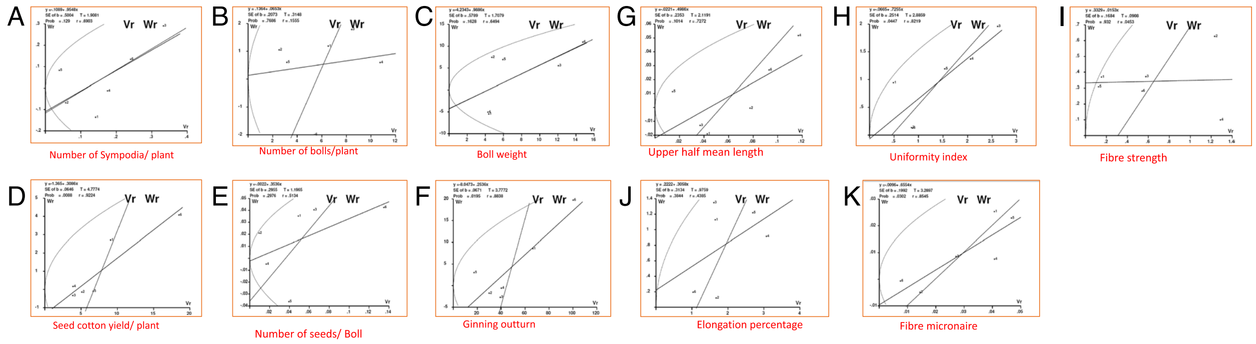
h^2 Dominance effect expressed as the algebraic sum over all loci in heterozygous phase in all crosses, *F* Mean of Fr over arrays, Fr Covariance of additive and non-additive effect in the r^{th} array

Average degree of dominance = $(H_1/D)^{1/2}$; Proportion of genes with positive and negative effect in the parents = $H_2/4h_1$; V4dh1 + F/V4dh1-F -Proportion of dominance and recessive egnes in the parents

h^2 *(ns)* Heritability in narrow-sense

*significant at 5%,

**significant at 1%



Number of Sympodia/ plant
Number of bolls/plant
Boll weight
Upper half mean length
Uniformity index
Fibre strength
Seed cotton yield/ plant
Number of seeds/ Boll
Ginning outturn
Elongation percentage
Fibre micronaire

Fig. 2 Vr-Wr graph for different traits. Note: 1- PDB29; 2- PAIG379; 3-RG763; 4- CNA1007: 5- PA838; 6- K12. **A** the number of sympodia per plant, **B** the number of bolls, **C** Boll weight, **D** Seed cotton yield per plant, **E** the number of seeds per boll, **F** Ginning out turn, **G** Upper half mean length (UHML), **H** Uniformity index, **I** Fibre strength, **J** Elongation percent, **K** Fibre micronaire

SCA

The results of the study indicate that specific combining ability (SCA) effects also play a significant role in determining the performance of cotton hybrids for various traits. The hybrids PAIG379 × K12, RG763 × PA838, and RG763 × K12 showed highly positive and significant SCA effects for traits such as seed cotton yield per plant, the number of sympodia per plant, and the number of bolls per plant, despite the fact that RG763 and K12 were identified as the best general combiners for these traits. Similar results for these traits are consistent with previous studies by Nidagundi et al. (2011), Kumar et al. (2014), Bilwal et al. (2018), Lokesh et al. (2018), Thombre et al. (2018), Chinchane et al. (2020), and Deshmukh et al. (2021).

Based on these results, PAIG379 × K12 and PDB29 × K12 can be recommended as the best cross combinations for most of the traits studied. These findings are in line with previous studies for similar traits by Giri et al. (2006), Preetha and Raveendran (2008), Khan et al. (2015), Saravanan et al. (2010), Ranganatha et al. (2013), Kumar et al. (2013), Kumar et al. (2014), and Lokesh et al. (2018). For fiber quality traits, hybrids such as PDB29 × PA838, RG763 × PA838, and CNA1007 × RG763 showed significant SCA effects, indicating their potential for improving fibre quality. These findings for similar traits are consistent with previous studies by Reddy et al. (2016), Solanke et al. (2015), Patel et al. (2018), Thombre et al. (2018) and Shinde et al. (2022).

Gene action

The results of the study indicate that for all the traits studied, except for uniformity index, the magnitude of specific combining ability (SCA) variance was higher than general combining ability (GCA) variance. This suggests that non-additive gene action plays a predominant role in determining the performance of these traits, indicating the potential for exploiting heterosis through hybrid breeding and other population improvement methods. These findings are consistent with previous reports by Laxman et al. (2010), Patil et al. (2012), Pushpam et al. (2015), Choudhary et al. (2017), Anil et al. (2017), Vekariya et al. (2017), and Gunjiganvi and Patil (2018).

Non-additive gene action refers to the interaction between genes from different parental lines, resulting in progeny that exhibit traits that are not simply the average of the parental lines. This non-additive gene action can lead to the expression of superior traits in hybrids, known as heterosis or hybrid vigour. By exploiting non-additive gene action through hybrid breeding and other population improvement methods, breeders can develop improved cotton varieties with desirable traits.

The higher magnitude of SCA variance compared with GCA variance for most of the traits studied suggests that specific parental combinations play a crucial role in determining the performance of cotton hybrids for these traits. This highlights the importance of evaluating hybrids and their specific combining ability effects in cotton breeding programs, as it can lead to the identification of superior cross combinations that exhibit high heterosis and improved performance for target traits.

Hayman's graphical analysis

The results of the study showed that for all the relevant traits investigated, the estimates of the uniformity test, t^2, were not significant, indicating that the assumptions of the diallel analysis proposed by Hayman (1954) were valid for these traits. This suggests that there may be no significant epistatic interactions among the genes governing these traits.

The regression coefficients (b) of Vr-Wr, which represent the variance of each array and the covariance among parents and their offspring's, showed substantial variation for all the investigated traits. This indicates that the Vr-Wr graphs of the parental materials are

Table 7 Fr values for yield and fibre quality traits in G. *arboreum*

Parents	DFF	PH	NMB/P	NSB/P	NB/P	NL/B	DBB	BW	NS/B	SCY/P	GOT	SI	LI	UHML	UI	Str	EL	Mic
PDB29	-2.016	181.781	1.296	3.315	-5.618	0.343	39.499	0.015	-5.713	-51.715	31.644	2.106	0.141	2.434	0.764	-0.305	-0.023	-0.017
PAIG379	4.652	-35.513	1.329	11.591	12.876	0.381	12.997	0.123	7.946	42.141	-54.759	-0.952	0.034	3.312	-1.913	1.661	0.09	-0.326
RG763	-1.801	-87.336	0.06	-1.688	14.806	0.344	2.125	-0.027	10.791	25.476	36.184	2.005	0.141	-3.853	-0.088	-0.67	0.038	-0.249
CNA1007	11.972	49.126	0.982	-3.941	15.178	0.319	38.853	0.16	9.755	19.333	33.639	0.35	-0.149	-1.573	-0.969	-2.72	0.013	0.086
PA838	7.43	662.313	1.064	11.247	6.835	0.305	11.563	0.178	4.71	57.836	-45.976	0.231	0.137	-0.162	0.939	-2.572	-0.03	0.191
K12	-6.026	391.722	0.557	11.933	-12.601	-0.298	-14.11	-0.171	-27.296	-141.318	38.392	0.999	-0.051	3.277	0.163	2.797	0.095	-0.038

Fr Covariance of additive and non-additive effect in the r^{th} Array, *DFF* days to fifty per cent flowering (days), *PH* plant height (cm), *NMB/P* the number of monopodia per plant, *NSB/P* the number of sympodia per plant, *NB/P* the number of bolls per plant, *NL/P* the number of locules per boll, *DBB* days to first boll bursting (days), *BW* boll weight (g), *NS/B* number of seeds per boll, *SCY/P* seed cotton yield per plant (g), *SI* seed index (g), *LI* lint index (g), *GOT* ginning out turn (%), *UHML* upper half mean length (mm), *Str* fibre strength ($g\cdot tex^{-1}$), *UI* uniformity index, *EL* elongation percentage (%), *Mic* micronaire useful for genetic analysis of the parents with respect to these traits.

The dominance components (H_1, H_2) were greater than the additive component (D) for most of the traits studied. This indicates that overdominance, where the heterozygotes (having two different alleles) exhibit superior performance compared with either homozygote (having two identical alleles), is prevalent for these traits. Specifically, for traits such as seed cotton yield per plant, ginning out turn, upper half mean length, and uniformity index, the average degree of dominance $(H_1/D)^{(1/2)}$ was greater than unity, indicating complete overdominance. This means that individuals with two different alleles at these loci have an advantage in terms of performance compared with individuals with two identical alleles.

For other traits like the number of sympodia per plant, the number of bolls per plant, boll weight, the number of seeds per boll, fibre strength, and elongation percent, the average degree of dominance $(H_1/D)^{(1/2)}$ was slightly less than unity, indicating partial dominance. In partial dominance, the heterozygotes still have an advantage, but it is not as pronounced as in complete overdominance. Regarding the trait of fibre micronaire, both the additive and dominance components were found to be almost similar, suggesting slightly complete dominance. This means that both the heterozygotes and one of the homozygotes have comparable performance, with the other homozygote showing inferior performance.

These findings suggest that for the traits studied, overdominance plays a significant role in determining the phenotypic variation. It indicates that the presence of different alleles at these loci leads to superior performance, emphasizing the importance of heterozygosity in these traits.

The H_1 and H_2 values showed differences, indicating dissimilar distribution of positive and negative genes, as authenticated by $H_2/4H_1$ value not being equal to 0.25. In the Vr-Wr graph, the position of parents along the regression line indicates the presence of more dominant genes for parents closer to the origin, and the presence of duplicate gene action for parents above the regression line, whereas parents below the regression line indicate complementary gene action. The Fr values of each parent for all the traits, as presented in Table 7, showed that parents with positive Fr values have more dominant genes, while parents with negative Fr values have more recessive genes for a particular trait. This suggests that parents with more dominant genes can be effectively utilized in the development of cotton hybrids.

Overall, the results of the study provide insights into the genetic architecture and gene action of the traits investigated, highlighting the importance of dominance and overdominance effects in determining the performance of cotton hybrids. These findings can have implications for cotton breeding programs aiming to develop improved varieties with desirable traits through exploiting gene action and utilizing parents with favourable gene combinations. However, further researches and validation in different genetic backgrounds and environments are needed to fully understand the underlying genetic mechanisms and potential for cotton improvement.

Conclusion

In breeding programs, it is crucial to identify cross combinations with high mean performance and favourable SCA (Specific combining ability) effects that exhibit stability across different environments. Among the parents evaluated, RG763 and K12 showed highly significant positive GCA effects for most of the yield traits, while PA838 and K12 showed favourable effects for fibre quality traits, making them the best general combiners. Cross combinations such as PAIG379 × K12 and PDB29 × K12 for yield traits, and PDB29 × PA838, RG763 × PA838, and CNA1007 × RG763 for fibre quality traits, were identified as promising options for future breeding programs.

The results obtained from both Griffing's and Hayman's approaches indicated that non-additive gene action, as evidenced by larger SCA variance compared with GCA variance, plays a predominant role in the inheritance of the investigated traits. This suggests that heterosis breeding, which exploits non-additive gene action, could be a more effective approach for improving the studied traits. These findings provide important insights for designing and implementing breeding programs to enhance various traits in cotton through heterosis breeding strategies.

Abbreviations

DFF	Days to fifty percent flowering (the number of days)
PH	Plant height (cm)
NMB/P	The number of monopodia per plant
NSB/P	The number of sympodia per plant
NB/P	The number of bolls per plant
NL/B	The number of locules per boll
DBB	Days to first boll bursting (the number of days)
BW	Boll weight (g)
NS/B	The number of seeds per boll
SCY/P	Seed cotton yield per plant (g)
SI	Seed index (g)
LI	Lint index (g)
GOT	Ginning out turn (%)
UHML	Upper half mean length (mm)
Str	Fibre strength ($cN\cdot tex^{-1}$)
UI	Uniformity index
EL	Elongation percentage (%)
Mic	Micronaire
GCA	General combining ability
SCA	Specific combining ability

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Declarations

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References

Anil K, Kalpande HV, Chinchane VN, Chandrawat KS. Combining ability estimation for morphological and yield contributing characters in Desi cotton (*Gossipium arboreum*). J Plant Dev Sci. 2017;9(1):1–9.

Bilwal BB, Vodadariya KV, Rajkumar BK, et al. Combining ability analysis for seed cotton yield and its component traits in cotton (*Gossypium hirsutum* L.). Int J Curr Microbiol Appl Sci. 2018;7(7):3005–10.

Çetin B, Çopur O. Combining ability and heterosis for fiber color and quality in cotton (*Gossypium hirsutum* L.). Notulae Botanicae Horti Agrobotanici Cluj-Napoca. 2022;50(2):12782.

Chinchane VN, Deosarkar DB, Baig KS, Kalpande HV. Combining ability analysis for fibre quality traits in desi cotton (*Gossypium arboreum* L) across the environments. Int J Curr Microbiol App Sci. 2020;9(1):1885–96.

Choudhary R, Solanki BG, Gahtyari NC, et al. Genetic effects of combining ability studies for quantitative traits in intra- and interspecific crosses of diploid cotton (*G. arboreum* and *G. herbaceum*). Electron J Plant Breed. 2017;8(1):10–9.

Deshmukh KH, Chinchane VN, HV KA. Combining ability studies for yield and yield contributing traits in desi cotton (*Gossypium arboreum* L). Pharma Innov J. 2021; 10(8): 39–41.

Deshpande. Model training course on cultivation of long staple cotton (ELS). CICR- Central Institute of Cotton Research 2007;15–22. https://krishi.icar.gov.in/jspui/bitstream/123456789/3868/1/general5.pdf. Accessed 15 Jan 2023.

Doak CC. A new technique in cotton hybridizing: Suggested changes in existing methods of emasculating and bagging cotton flowers. J Hered. 1934;25(5):201–4.

Giri RK, Nirania KS, Yagya D, Sangwan RS. Combining ability studies for yield and quality traits in upland cotton (*Gossypium hirsutum* L.). J Cotton Res Dev. 2006;20(2):178–80.

Gunjiganvi SM, Patil BR. Heterosis and combining ability studies for yield and its components in desi cotton (G*ossypium arboreum* L.). J Farm Sci. 2018;31(1):12–6.

Hayman BI. The analysis of variance of diallel tables. Biometrics. 1954;10:235–44.

Khan SA, Khan NU, Gul R, et al. Combining ability studies for yield and fibre traits in upland cotton. J Animal Plant Sci. 2015;25(3):698–707.

Kumar M, Shukla AK, Singh H, et al. A genotype-independent *Agrobacterium* mediated transformation of germinated embryo of cotton (*Gossypium hirsutum* L.). Int J Biotechnol Res. 2013;3:81–90.

Kumar KS, Ashokkumar K, Ravikesavan R. Genetic effects of combining ability studies for yield and fibre quality traits in diallel crosses of upland cotton (*Gossypium hirsutum* L.). Afr J Biotechnol. 2014;13(1):119.

Laxman S. Diallel analysis for combining ability for seed cotton yield and its components in desi cotton (*Gossypium arboreum* L.). J Cotton Res Dev. 2010;24(1):26–8.

Lokesh KM, Borgaonkar SB, Deosarkar DB, Chinchane VN. Study of combining ability analysis for seed cotton yield, yield contributing and fibre quality traits in desi cotton (*Gossypium arboreum* L.). Int J Plant Sci (Muzaffarnagar). 2018;13(1):1–6.

Nidagundi JM, Deshpande SK, Patil BR, Mane RS. Combining ability and heterosis for yield and fibre quality traits in American cotton. Crop Improv. 2011;38(2):179–85.

Patel HR, Baraiya VK, Upadhyay SN. Combining ability studies of GMS based hybrids in cotton (*Gossypium hirsutum* L.). J Pharmacogn Phytochem. 2018;7(4):1349–52.

Patil BR, Deshpande SK, Patil M, et al. Combining ability studies in GMS based diploid cotton with special reference to fibre quality traits. Crop Res. 2012;44(3):437–46.

Preetha S, Raveendran TS. Combining ability and heterosis for yield and fibre quality traits in line x tester crosses of Upland cotton (*G. hirsutum* L). Int J Plant Breed Genet. 2008;2(2):64–74.

Pushpam R, Thangaraj K, Raveendran TS. Heterosis and combining ability studies in upland cotton for yield characters. EJPB. 2015;6(2):459–63.

Ranganatha HM, Patil SS, Rajeev S, Swathi P. Combining ability studies for seed cotton yields and its component traits in upland cotton (*Gossypium hirsutum* L.). Bioinfolet-A Quarterly J Life Sci. 2013;10(4c):1549–53.

Reddy KB, Reddy VC, Ahmed ML, et al. Combining ability study for yield and Its component traits through diallele mating design in Upland cotton (*Gossypium hirsutum* L.). J Cotton Res Dev. 2016;30(2):180–4.

Reddy KB, Reddy VC, Ahmed ML, et al. Combining ability analysis for seed cotton yield and quality traits in upland cotton (*Gossypium hirsutum* L). Electron Plant Breed. 2017;8(1):142–52.

Saravanan NA, Ravikesavan R, Raveendran TS. Combining ability analysis for yield and fibre quality parameters in intraspecific hybrids of *G. hirsutum* L. EJPB. 2010;1(4):856–63.

Shinde AV, Deosarkar DB, Kalpande HV, et al. Combining ability studies for fibre quality traits in intra (*G. arboreum* x *G. arboreum*) and interspecific (*G. herbaceum* x *G. arboreum*) crosses of desi cotton. Pharm Innov J. 2022;11(1):307–10.

Sprague GF, Tatum LA. General vs. specific combining ability in single crosses of corn. J Am Soc Agron. 1942;34(10):923–32.

Solanke A, Deshmukh SB, Mhasal GS, Marawar MW. Heterosis and combining ability in genetic male sterility based diploid cotton hybrids for yield, yield component, fibre quality characters and oil content. Electronic Journal of Plant Breeding. 2015;6(1):150–6.

Thombre KS, Deosarkar DB, Chinchane VN, Borgaonkar SB. Study of combining ability analysis for seed cotton yield, yield contributing and fibre quality traits in desi cotton (*Gossypium arboreum* L). Int J Plant Sci (Muzaffarnagar). 2018;13(1):35–41.

Vekariya RD, Nimbal S, Batheja A, et al. Combining ability and gene action study for seed cotton yield and its related traits in diploid cotton (*Gossypium arboreum* L.). EJPB. 2017;8(4):1159–68.