



## Genetic Studies for Morphological and Fiber Quality Traits in Upland Cotton (*Gossypium hirsutum* L.)

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**Abstract:** Different morphological and fiber traits of upland cotton (*Gossypium hirsutum* L.) were studied for the presence of genetic variability and effects due to GCA and SCA. The objective was to determine the genetic variability and the effects due to GCA and SCA. In this experiment, a set of twelve genotypes, i.e., FH-119, MNH-888, CRSM-38, Bt-23, Bt-222, Bt-2333, FH-161 and FH-174, were selected as male parents and four genotypes, i.e., SB-149, FH-153, VH-144 and NIAB-111, as female parents. The genotypes were crossed, using North Carolina Mating design-II (NCM-II), to develop thirty two crosses. The seeds of 12 parents and their 32 F<sub>0</sub> hybrids were sown in the university research area, using randomized complete block design (RCBD) under three replications. The data of quality parameters and morphological parameters, i.e., plant height, number of monopodia, number of sympodia, number of bolls per plant, seed index, fiber length, fiber strength, fiber fineness and fiber uniformity, were collected. The analysis of variance demonstrated that all the parents and their F<sub>1</sub> hybrids differed significantly from each other for all the parameters studied except fiber fineness.

**Key words:** Genetic variability, Morphological characters, NCM-II, Heritability.

### INTRODUCTION

Pakistan is an ideal country for agriculture, having fertile lands and the world's best canal irrigation system that are necessary for good agricultural produce. Agriculture sector shares 21% of total GDP, 43.7% of the country's work force and 62% income of population living in rural areas (Anonymous, 2014-15). Therefore, all over the world, it is recognized as an agricultural country. During 2014-15, cotton production remained 13,983 (000 bales) as compared to 12,769 (000 bales) in 2013-14 and registered an increase of 9.5 percent (Anonymous, 2014-15).

Cotton is recognized as silver fiber in cotton producing countries of the world. It acts as a concrete pillar in holding Pakistan's economy. Its importance in earning foreign exchange cannot be overlooked as Pakistan generates a considerable amount of foreign exchange, by exporting cotton yarn and other value added products. The tropical and sub-tropical areas of Pakistan are suitable for cotton crop cultivation. Therefore, it is grown on a large area in Punjab and Sindh. Pakistan ranks at 4<sup>th</sup> position among the top cotton producing countries of the world. During 2014-

15, the crop was cultivated in an area of 2961 (000 ha), a 5.5% increase over last year's area of 2806 (000 ha) (Anonymous, 2014-15). The production stood at 13.9 million bales during the period 2014-15, an increase of 9.5% over the last year production of 12.7 million bales (Anonymous, 2014-15). The increasing trend in cotton production was due to suitable climatic conditions for crop (Anonymous, 2014-15).

The average per hectare yield of cotton in Pakistan is 802 kg/ha and it accounts for 1.5% of GDP and 7.1% of the value added in agriculture (Anonymous, 2014-15). Cotton cultivation engaged around 1.5 million farmer families and considered as a source of livelihood for several millions of labour in large cities and towns as well. In cotton producing areas, about 40% of cash income of rural household may depend on sale of cotton produced on their agricultural lands. The Ministry of Food, Agriculture and Livestock has set forth a target of 20.7 million bales production with an average yield of 1050 kg ha<sup>-1</sup> for the coming year 2016. This target will help in the sustainable production of quality raw cotton and yarn. The target of 2016, i.e., production of 20.7 million bales will include 20.1 million bales for local

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consumption and 0.6 million bales as exportable cotton surplus (Anonymous, 2014-2015). These targets will be achieved by improving the yarn recovery rate up to 92% from the current low recovery rate of 84%. Due to its vital share in the country's economy, several efforts have been placed on various aspects of increased cotton production. Increased attack of insect pests and diseases, like CLCuV, has reduced the area under this crop, so the production of high yielding and disease/insect pest resistant cultivars would be the only possible solution to the problem.

Breeding for new high yielding and disease-resistant varieties of upland cotton, genetic sequencing of different characters (quantitative and qualitative) of economic interest is a pre-requisite. This facility helps the cotton breeders in improving the genetic structure of plant in an exact direction for preserving and improving the suitable crop production level (Nadeem and Azhar, 2004; Abbas *et al.*, 2008). In order to achieve the targets, the utilization of already present genetic variability in the breeding material as well as, the formation or the introduction of new genetic variability along with its understanding is essential for a breeding program to be successful. The introduction of this genetic variability, through North Carolina Mating design II, has been frequently used by the cotton researchers (Iqbal *et al.*, 2003; Basal and Turgut, 2005; Abbas *et al.*, 2008; Ali *et al.*, 2008; Ali and Awan, 2009).

The presence of additive gene action and partial dominance for plant height, number of monopodia per plant, number of sympodia branches, staple length and fiber strength has already been reported (Ahmad *et al.*, 2003; Khan *et al.*, 2003; Basal and Turgut, 2005; Nadeem and Azhar, 2004; Ali and Khan, 2007; Ali and Awan, 2009). May and Green (1994), Iqbal *et al.* (2003) and, Haq and Azhar (2004) also reported the additive type of gene action for fiber length and fiber strength. However, some other groups of researchers stated that instead of showing the additive type of gene action, these characters expressed over dominance type of gene action in lint percentage and seed cotton yield (Ahmad *et al.* 2000; Basal and Turgut, 2005; Haq and Azhar, 2004). Khan *et al.* (2001) and Ahmad *et al.* (2003) studied non-additive type of gene action for staple length, number of bolls, seed cotton yield and seed index, while they described additive effects for fiber strength and fineness.

The objective of this experiment was to study the genetic variation and interaction effects of parents in different morphological and fiber traits of American cotton cultivars and their F<sub>1</sub> crosses. For this purpose, a North Carolina Mating design-II, developed by Comstock and Robinson (1952), has been pursued to create the variability in a cotton plant population. Current study may help the breeders to understand the actual genetic mechanism of variation involved in different plant traits.

## MATERIALS AND METHODS

Current study relates to the estimation of gene action involved in the inheritance of some morphological traits of upland cotton, and is conducted in the department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, during 2012-2014. The experimental material, used in this study, was developed by crossing twelve genotypes, viz. FH-119, MNH-888, CRSM-38, Bt-23, Bt-222, Bt-2333, FH-161, FH-174, SB-149, FH-153, VH-144 and NIAB-111, according to North Carolina Mating design-II method.

All the plant material was maintained in the gene pool of the department. The parents were grown in the earthen pots (12"×12") placed in the glasshouse, during November 2012. Temperature (25 to 30 °C) and light duration were possibly controlled in a way to provide favorable condition for germination and growth of the plants. Tinning was made twice after 15 and 30 days of germination when the plant height was 15 to 30 cm, respectively, to ensure single plant per hill. At flowering, all possible crosses were made among the genotypes, keeping in view the necessary precautionary measures to avoid any contamination of the genetic material. Maximum number of pollinations was done in order to produce adequate quantities of F<sub>1</sub> hybrid seeds.

The seed of the twelve parents and 32 F<sub>1</sub> crosses were hand sown in the field, during the month of May, 2013, with row-to-row and plant-to-plant distance of 75 cm and 30 cm, using Randomized Complete Block Design with 3 replications. All the recommended agronomic practices and plant protection measure were followed from sowing to picking of the crop. At maturity, the data were collected from the guarded plants on the following plant traits on an individual plant basis.

The cross classification of NCM-II Design analysis was carried out for determining the genetic variability and the effects due to combining ability, as described by Comstock and Robinson (1948) and adopted by Hallauer and Miranda (1986).

**Traits measurement:** The data was recorded on an individual plant basis for the following parameters. Plant height (PH cm), number of monopodials per plant (NOM), number of sympodials per plant (NOS), number of bolls per plant (BPP), seed cotton yield per plant (SCY/P), seed index (SI g), lint index (LI g), ginning out turn percentage (GOT %), fiber length (FL mm), fiber strength (FS g/tax), fiber fineness (FF µg/inch) and fiber uniformity ratio (FUR).

For seed index, after ginning, hundred cotton seeds free from lint, disease or any other insect pest, were weighed on electronic balance and hundred seed weight in gram (g) was treated as seed index. Lint index means the weight of lint obtained from one hundred seeds in grams, however, lint index of each plant was calculated by applying the following formula. For lint %, clean and dry seed cotton picked

from bolls of each plant was weighed and then ginned separately with 8-saw gins. The lint obtained from

each plant was weighed and the ginning out turn (G.O.T) was worked out by the formula given below:

$$\text{Lint index (g)} = \frac{\text{Seed index} \times \text{Lint \%}}{100 - \text{Lint \%}}; \quad \text{Lint \% (G.O.T.)} = \frac{\text{Weight of Lint in a sample}}{\text{Weight of seed cotton sample}} \times 100$$

$$\text{Genetic variance (Vg)} = \frac{\text{Genotypes mean squares (GMS)} - \text{Error mean squares (EMS)}}{\text{No. of replications (r)}}$$

$$\text{Environmental variance (Ve)} = \text{Error mean squares (EMS)}$$

$$\text{Phenotypic variance (Vp)} = \text{Vg} + (\text{Ve}/r)$$

Heritability broad sense ( $H^2$ ) on entry mean basis was calculated as:

$$H^2 = \frac{Vp}{Vg}$$

The expected response to selection ( $R_e$ ) for each trait was calculated as under:

$$R_e = k\sqrt{vpH^2}$$

where:

$k = 1.40$  at 20% selection intensity for a trait

$vp$  = Phenotypic variance for a trait

$H^2$  = Broad sense heritability for a trait

### Statistical analysis of data:

All the recorded data were subjected to analysis of variance (ANOVA) technique for a RCB design, as outlined by Steel and Torrie (1980), through Mstatc computer programme for all the traits to test the null hypothesis of no differences among the cotton genotypes. The genotype means for each parameter were further separated and compared, using the least significant difference (LSD) test, at 5% level of probability. For each trait, the genetic, environmental and phenotypic variances, broad sense heritability ( $H^2$ ) and expected response to selection ( $R_e$ ) were further estimated from the ANOVA mean squares according to Burton (1951). The simple correlation coefficient ( $r$ ) of seed cotton yield with other seed and fiber traits was also worked out through formulae. The collected data were subjected to analysis of variance (ANOVA) (Steel *et al.*, 1997), in order to determine the significance among genotype for plant character under study and the character showing significant genotypic differences among thirty two hybrids and their parents. Significantly varying genotypes were subjected to North Carolina Design II Mating scheme (Comstock and Robinson, 1948; Comstock and Robinson, 1952) to estimate their gene action.

### RESULTS AND DISCUSSION

The mean squares of male inbreds were significant for all the traits except ginning turnout percentage and fiber fineness, whereas, in case of female inbreds six characters [plant height (cm), number of monopodia, number of sympodia, seed cotton yield per plant, seed index, ginning turnout percentage] showed significant and five traits [number

of bolls per plant, fiber length, fiber strength, fiber fineness and fiber uniformity ratio] expressed non-significant mean squares. Male  $\times$  female interactions were significant for all the characters under study except fiber strength and fiber fineness (Table 1). Significant mean squares for both male and female inbreds designate GCA variances while male  $\times$  female interaction signify SCA variances employed that additive as well as non-additive genes were important in the expression of most of the characters studied. These results were in accordance with Baloch *et al.*, 2010, which confirmed the involvement of both types of gene action while they were contrary to those of Khan *et al.* (2009), which showed the contribution of only non-additive type of gene action for yield and its contributing traits.

Higher estimates of male  $\times$  female interaction variances along with lower value of male and female parent variances confirmed the prevalence of dominance gene action for all the traits (Iqbal and Nadeem, 2003). Similarly, the preponderance of lower additive effects and variances than dominant effects and the variances demonstrated the significant role of dominance in controlling majority of traits. Significant and higher value for phenotypic variance than genotypic variance confirmed the involvement of environmental effect in controlling the expression of the traits. A higher value of broad sense heritability (ranging from 0.42 to 0.98) and a lower estimate of narrow sense heritability (ranging from 0.10 to 0.32) strengthened the conclusion that both types of gene action were involved in controlling the traits and that the selection of these traits should be delayed for the next segregating generations. In case of male and

female parents, the involvement of dominance pointed towards the utilization of parents in the hybrid breeding program for these traits. Potence ratio (ranging from 2.22 to 12.32) was estimated in terms

of degree of dominance for all the traits. The value of potence ratio greater than unity ( $> 1$ ) revealed the presence of over dominance type of gene action in controlling the traits.

**Table 1: Mean squares from NCM Design-II analysis for various characters in F<sub>1</sub> hybrids of upland cotton (*Gossypium hirsutum* L.)**

SOV	DF	PH (cm)	NOM	NOS	BPP	SCY/P	SI (g)	LI (g)	GOT (%)	FL (mm)	FS (g/tax)	FF (µg/in)	FU (ratio)
Replications	2	11.01 <sup>NS</sup>	0.33 <sup>NS</sup>	9.28 <sup>NS</sup>	29.88 <sup>NS</sup>	9.367*	0.081 <sup>NS</sup>	0.113 <sup>NS</sup>	3.25 <sup>NS</sup>	0.926 <sup>NS</sup>	0.71 <sup>NS</sup>	0.12 <sup>NS</sup>	0.182 <sup>NS</sup>
Male (GCA)	7	123.16*	11.28*	20.29**	90.22**	2226.868**	0.172*	0.134*	3.36 <sup>NS</sup>	3.582*	4.87**	0.55 <sup>NS</sup>	22.95**
Female (GCA)	3	373.69**	30.47**	15.51*	16.76 <sup>NS</sup>	6612.482**	1.439**	0.648**	7.20*	0.606 <sup>NS</sup>	0.63 <sup>NS</sup>	0.64 <sup>NS</sup>	6.63 <sup>NS</sup>
M × F (SCA)	21	193.96*	7.96*	12.59*	142.43**	1186.343*	0.378*	0.137*	4.33*	3.429*	2.76 <sup>NS</sup>	0.49 <sup>NS</sup>	23.83**
Error	62	12.85	0.97	4.29	15.74	22.739	0.008	0.050	2.51	1.184	2.10	0.40	5.72

\*significant at 5% probability level; \*\*significant at 1% probability level; <sup>NS</sup>Non-significant

**Table 2: Estimation of components of variation and heritability.**

Genetic components	PH	NOM	NOS	BPP	SCY/P	SI	LI	GOT	FL	FS	FUR
Male variance ( $\sigma^2_m$ )	5.89	0.27	0.64	4.35	86.71	0.02	0.01	0.08	0.01	0.17	0.08
Female variance ( $\sigma^2_f$ )	7.48	0.93	0.12	5.23	226.08	0.05	0.02	0.11	0.11	0.08	2.18
Male × Female variance ( $\sigma^2_{fm}$ )	60.8	2.33	2.76	42.22	381.86	0.12	0.02	0.60	0.74	0.22	9.05
Additive effects ( $D_R$ )	6.35	4.85	3.05	38.34	1251.98	0.10	0.08	0.15	0.41	0.34	9.09
Additive variance ( $\sigma^2_A$ )	3.17	2.42	1.52	19.17	625.59	0.05	0.04	0.07	0.20	0.17	4.54
Dominance effects ( $H_R$ )	965.89	37.28	64.29	675.67	6205.88	1.96	0.46	9.71	11.97	3.53	144.91
Dominance variance ( $\sigma^2_D$ )	241.47	9.32	11.07	168.91	1551.47	0.49	0.11	2.42	2.99	0.68	36.22
Environmental variance ( $\sigma^2_E$ )	12.85	0.98	4.29	15.75	22.74	0.009	0.05	2.51	1.18	2.10	5.73
Phenotypic variance ( $\sigma^2_P$ )	230.73	11.40	17.93	167.26	1921.05	0.43	0.16	4.61	4.22	3.69	41.59
Genotypic variance ( $\sigma^2_G$ )	217.87	10.42	13.64	151.51	1898.31	0.42	0.11	2.10	3.04	1.58	35.87
Potence ratio ( $P_R$ )	12.32	2.77	3.82	3.47	2.22	4.26	2.33	7.89	5.34	3.18	3.99
Narrow sense heritability ( $h^2_{ns}$ )	0.31	0.21	0.14	0.11	0.32	0.12	0.25	0.16	0.30	0.19	0.10
Broad sense heritability ( $h^2_{bs}$ )	0.94	0.91	0.76	0.90	0.98	0.97	0.69	0.45	0.75	0.42	0.86

Regarding the general combining ability estimates of female parents, SB-149 expressed maximum positive GCA value for a number of sympodia (0.74),

fiber strength (0.16) and fiber uniformity (0.68), whereas, FH-153 showed the highest value for bolls per plant (1.11) and seed cotton yield per plant

(22.65). Third female parent, VH-144, manifested maximum GCA effects for plant height (5.13), number of monopodia (1.43), seed index (0.33), lint index (0.25) and fiber length (0.22), while the last one, NIAB-111 exhibited the highest positive GCA for ginning turnout (0.61) (Table 3). Among male inbreds, maximum general combining ability

estimates for most of the traits were expressed by the parent FH-161, followed by Bt-2333 (Table 3). GCA estimates of male and female inbreds suggested that parents FH-161 and Bt-2333 from males and VH-144 and SB-149 from female inbreds may be selected and given preference for hybridization breeding.

**Table 3: General combining ability estimates for parents.**

Parent inbreds	PH	NOM	NOS	BPP	SCY/P	SI	LI	GOT	FL	FS	FUR
<b>Male inbred</b>											
FH-119	-2.79	-0.01	-0.51	-1.59	-16.52	-0.03	-0.18	-1.23	0.19	1.38	0.67
MNH-888	-1.46	-1.00	1.90	-4.51	-1.69	-0.02	0.02	0.14	-0.13	-0.58	-2.16
CRSM-38	0.96	-0.59	-0.73	1.49	5.44	0.06	0.02	-0.09	0.73	0.06	0.44
Bt-23	3.71	0.74	0.07	2.49	-2.45	-0.08	0.02	0.50	0.34	-0.27	-1.58
Bt-222	-0.29	-0.80	-1.10	-2.01	19.00	-0.23	-0.13	0.06	-0.77	0.16	1.30
Bt-2333	-1.21	-0.26	2.15	-0.09	7.01	0.06	0.05	0.07	-0.82	-0.69	1.61
FH-161	5.29	-0.09	-0.93	0.07	-21.51	0.17	0.13	0.16	0.11	0.14	-0.94
FH-174	-4.21	1.99	-0.85	4.16	10.72	0.06	0.09	0.38	0.34	0.11	0.65
<b>Female inbred</b>											
SB-149	-4.50	-1.26	0.74	0.03	-5.68	-0.03	-0.11	-0.59	-0.04	0.16	0.68
FH-153	-0.29	0.38	-1.14	1.11	22.65	-0.04	-0.07	-0.30	-0.02	-0.01	-0.26
VH-144	5.13	1.43	0.29	-0.89	-16.78	0.33	0.25	0.28	0.22	-0.22	0.09
NIAB-111	-0.33	0.20	0.11	0.26	-0.19	-0.26	-0.07	0.61	-0.16	0.07	-0.51

In consideration of hybrids performance, VH-144 × FH-161 observed maximum SCA values for plant height (112.46), seed Index (6.02) and lint index (3.73), followed by cross SB-149 × Bt-2333, which showed the highest SCA estimates for two characters [i.e., number of sympodia (8.99) and fiber uniformity ratio (48.99)]. The crosses, VH-144 × FH-174, FH-153 × FH-174, FH-153 × Bt-222, NIAB-111 × Bt-23, VH-144 × CRSM-38 and SB-149 × FH-119, exhibited maximum SCA values for number of monopodia, number of bolls per plant, seed cotton yield per plant, ginning turnout, fiber length and fiber strength, respectively.

In general, it is considered that hybrid *per se* performance is revealed in GCA estimates and for confirmation in SCA estimates. Researchers observed that the crosses (HS-88 × TH-46 and H-777 × G-17) exhibited maximum *per se* performance for seed cotton yield and its yield contributing traits, while they did not show high SCA effects for those characters. In contrary, Kaushik and Kapoor (2006) noticed that the cross LH-1836 × H-113 exhibited the

highest SCA value along with maximum *per se* performance for bolls per plant and seed cotton yield per plant. These results pointed out that such exemptions did not completely hold true in all cases.

SCA value showed that maximum positive SCA effect were expressed by the hybrids FH-153 × Bt-23 for seed cotton yield per plant (37.87) and ginning turnout (1.84), FH-153 × Bt-222 for plant height (13.21) and fiber strength (1.47), VH-144 × Bt-222 for monopodia per plant (2.86), VH-144 × FH-119 for sympodia per plant (4.12), NIAB-111 × Bt-23 for bolls per plant (16.76), NIAB-111 × FH-161 for seed index (0.51), NIAB-111 × Bt-2333 for lint index (0.40), NIAB-111 × CRSM-38 for fiber length (2.17) and FH-153 × Bt-2333 for fiber uniformity ratio (5.79) (Table 5). These hybrids may be considered to improve various yield contributing and fiber traits. It was noticed during this experiment that some parents who exhibited high GCA also showed high SCA for the same character in cross combination same results presented by Ashokkumar *et al.* (2010). These parents can be identified to improve the majority of the traits.

**Table 4: Performance of 32 crosses for various characters.**

F <sub>1</sub> hybrids	PH	NOM	NOS	BPP	SCY/P	SI	LI	GOT	FL	FS	FUR
SB-149 × FH-119	94.75	2.08	6.32	26.45	21.57	5.45	3.07	36.04	24.17	24.56	48.05
SB-149 × MNH-888	96.08	1.09	8.74	23.53	36.40	5.46	3.27	37.41	23.86	22.61	45.22
SB-149 × CRSM-38	98.50	1.49	6.10	29.53	43.53	5.54	3.28	37.17	24.72	23.25	47.82
SB-149 × Bt-23	101.25	2.83	6.90	30.53	35.64	5.40	3.27	37.76	24.32	22.91	45.80
SB-149 × Bt-222	97.25	1.29	5.74	26.03	57.09	5.25	3.12	37.33	23.22	23.02	48.68
SB-149 × Bt-2333	96.33	1.83	8.99	27.95	45.10	5.54	3.31	37.34	23.17	22.50	48.99
SB-149 × FH-161	102.83	1.99	5.90	28.11	16.58	5.65	3.38	37.43	24.09	23.32	46.44
SB-149 × FH-174	93.33	4.08	5.99	32.20	48.81	5.54	3.34	37.65	24.32	23.29	48.03
FH-153 × FH-119	98.96	2.96	4.44	27.53	49.90	5.47	3.11	36.33	24.20	24.40	47.11
FH-153 × MNH-888	100.29	1.96	6.86	24.61	64.72	5.56	3.31	37.70	23.88	22.44	44.28
FH-153 × CRSM-38	102.71	2.37	4.23	30.61	71.85	5.53	3.32	37.46	24.74	23.09	46.88
FH-153 × Bt-23	105.46	3.71	5.03	31.61	63.97	5.40	3.31	38.06	24.35	22.75	44.86
FH-153 × Bt-222	101.46	2.16	3.86	27.11	85.41	5.25	3.16	37.62	23.24	22.86	47.74
FH-153 × Bt-2333	100.54	2.71	7.11	29.03	73.43	5.53	3.34	37.63	23.19	22.34	48.05
FH-153 × FH-161	107.04	2.87	4.03	29.20	44.90	5.55	3.42	37.72	24.12	23.16	45.50
FH-153 × FH-174	97.54	4.96	4.11	33.28	77.13	5.45	3.38	37.94	24.35	23.13	47.09
VH-144 × FH-119	104.38	4.76	5.88	25.53	10.47	5.81	3.42	36.91	24.44	24.19	47.45
VH-144 × MNH-888	105.71	3.77	8.29	22.61	25.30	5.82	3.62	38.28	24.12	22.23	44.63
VH-144 × CRSM-38	108.13	4.18	5.66	28.61	32.43	5.90	3.63	38.05	24.98	22.87	47.23
VH-144 × Bt-23	110.88	5.51	6.46	29.61	24.54	5.77	3.62	38.64	24.59	22.54	45.20
VH-144 × Bt-222	106.88	3.97	5.29	25.11	45.99	5.61	3.47	38.21	23.48	22.64	48.09
VH-144 × Bt-2333	105.96	4.51	8.54	27.03	34.00	5.90	3.66	38.21	23.43	22.12	48.39
VH-144 × FH-161	112.46	4.68	5.46	27.20	5.48	6.02	3.73	38.31	24.35	22.94	45.84
VH-144 × FH-174	102.96	6.76	5.54	31.28	37.71	5.90	3.69	38.52	24.59	22.91	47.44
NIAB-111 × FH-119	98.92	3.54	5.69	26.16	27.06	5.22	3.10	37.25	24.06	24.48	46.86
NIAB-111 × MNH-888	100.25	2.54	8.11	23.24	41.89	5.23	3.30	38.61	23.74	22.52	44.04
NIAB-111 × CRSM-38	102.67	2.95	5.48	29.24	49.01	5.31	3.31	38.38	24.60	23.16	46.64
NIAB-111 × Bt-23	105.42	4.29	6.28	30.24	41.13	5.17	3.30	38.97	24.21	22.83	44.61
NIAB-111 × Bt-222	101.42	2.74	5.11	25.74	62.57	5.02	3.16	38.54	23.10	22.94	47.49
NIAB-111 × Bt-2333	100.50	3.29	8.36	27.66	50.59	5.31	3.34	38.55	23.05	22.41	47.80
NIAB-111 × FH-161	107.00	3.45	5.28	27.82	22.06	5.42	3.42	38.64	23.97	23.24	45.25
NIAB-111 × FH-174	97.50	5.54	5.36	31.91	54.29	5.31	3.37	38.86	24.21	23.21	46.84

**Table 5: Specific combining ability of 32 crosses for various characters.**

F <sub>1</sub> hybrids	PH	NOM	NOS	BPP	SCY/P	SI	LI	GOT	FL	FS	FUR
SB-149 × FH-119	-5.75	1.59	-1.32	6.22	5.21	0.46	0.16	-0.71	0.19	0.67	0.95
SB-149 × MNH-888	-4.08	0.25	2.60	-1.20	37.85	-0.11	-0.15	-0.61	0.51	0.16	0.44
SB-149 × CRSM-38	-0.83	1.17	-0.10	0.47	4.66	0.02	-0.03	-0.31	-1.05	-0.11	0.58
SB-149 × Bt-23	9.42	-1.49	0.76	-3.53	-16.98	0.50	0.23	-0.56	0.44	0.25	3.97
SB-149 × Bt-222	6.75	0.71	-1.40	-0.70	-24.24	-0.12	0.05	0.87	-0.95	-1.66	-2.95
SB-149 × Bt-2333	-2.67	0.17	1.01	-0.61	-7.28	-0.40	-0.29	-0.34	-1.20	-0.46	-3.19
SB-149 × FH-161	-2.17	-0.33	-1.57	4.22	5.09	-0.57	-0.12	1.67	1.81	0.11	-1.77
SB-149 × FH-174	-0.67	-2.08	0.01	-4.86	-4.31	0.23	0.14	-0.01	0.24	1.04	1.97
FH-153 × FH-119	-3.96	-0.96	-1.78	-2.86	-28.23	-0.40	-0.10	0.94	-0.37	-1.54	0.73
FH-153 × MNH-888	0.04	-0.26	1.81	0.39	-16.62	0.35	0.16	-0.26	-0.75	-1.41	3.68

Contd....

Concl...

FH-153 × CRSM-38	10.63	-0.37	-0.56	9.39	-1.81	0.40	0.38	0.87	-0.11	0.75	0.75
FH-153 × Bt-23	-15.46	-0.71	-0.69	-11.61	37.87	-0.37	0.03	1.84	-0.35	-0.28	-3.86
FH-153 × Bt-222	13.21	-0.16	0.81	6.55	25.04	-0.22	-0.24	-0.86	-0.04	1.47	3.99
FH-153 × Bt-2333	4.12	-0.71	-1.11	-2.36	13.41	-0.11	-0.02	0.37	1.11	0.16	5.79
FH-153 × FH-161	-5.38	0.79	0.64	4.14	-28.10	0.26	-0.12	-1.86	-0.22	0.87	-2.00
FH-153 × FH-174	-3.21	2.38	0.89	-3.61	1.45	0.09	-0.09	-1.04	0.72	-0.59	-1.72
VH-144 × FH-119	9.96	0.90	4.12	-2.53	15.53	0.06	0.18	1.05	1.26	1.21	-0.49
VH-144 × MNH-888	5.62	0.89	-1.29	4.05	-9.97	-0.14	0.12	1.39	0.58	0.24	-0.46
VH-144 × CRSM-38	-7.79	-1.51	0.15	1.39	-2.59	-0.19	-0.22	-0.71	-1.01	-0.57	0.14
VH-144 × Bt-23	2.10	-0.51	-1.79	-1.61	-9.14	0.08	-0.02	-0.54	-0.39	0.06	1.73
VH-144 × Bt-222	-15.88	2.86	-1.63	-1.78	-20.14	0.37	0.10	-0.84	1.16	0.32	-1.65
VH-144 × Bt-2333	-2.96	-2.18	-1.88	4.97	-0.09	0.05	-0.09	-0.75	-0.73	-0.55	-1.03
VH-144 × FH-161	3.21	-0.01	2.87	-5.20	17.40	-0.19	0.07	1.16	-0.25	-1.08	-1.79
VH-144 × FH-174	5.71	1.57	-0.54	0.72	9.00	0.04	-0.13	-0.76	-0.62	0.36	-0.04
NIAB-111 × FH-119	-0.25	-1.54	-1.03	0.82	7.49	-0.12	-0.24	-1.28	-1.09	-0.35	-1.19
NIAB-111 × MNH-888	-1.58	-0.88	-3.11	-3.24	-11.25	-0.10	-0.14	-0.51	-0.34	1.01	3.70
NIAB-111 × CRSM-38	-2.00	0.71	0.52	-11.24	-0.26	-0.22	-0.12	0.15	2.17	-0.06	-1.47
NIAB-111 × Bt-23	3.92	2.71	1.72	16.76	-8.74	-0.21	-0.23	-0.74	0.29	-0.60	-1.84
NIAB-111 × Bt-222	-4.08	-1.41	2.22	-4.07	19.34	-0.04	0.09	0.83	-0.17	0.14	0.61
NIAB-111 × Bt-2333	1.50	2.71	1.97	1.99	-6.04	0.47	0.40	0.72	0.82	-0.85	-1.57
NIAB-111 × FH-161	4.33	-0.45	-1.94	-3.16	5.60	0.51	0.17	-0.97	-1.34	0.09	1.98
NIAB-111 × FH-174	-1.83	-1.87	-0.36	7.76	-6.14	-0.28	0.07	1.81	-0.34	-0.81	-0.21

### CONCLUSION

The parents and their hybrids manifested significant differences in mean performance for all characters studied expect fiber fineness. The significance of GCA and SCA mean squares expressed the importance of both additive and dominant variances for all characters. Higher GCA effects of female parents and male parents were, however, demonstrated by FH-153, VH-144, FH-161 and FH-119, for majority of the characters as good general combiners. It suggested that these parents may be preferred for hybridization and selection programmes. SCA effects indicated that for hybrids crop development, cross FH-153 × Bt-222 may be utilized for improving plant height and fiber length and FH-153 × Bt-23 for seed cotton yield per plant and GOT %.

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