



## Genetic Exploration of Yield and Quality Attributes in Upland Cotton

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**Abstract:** The present studies were carried out to find out the best combiner genotypes to improve lint yield and quality attributes. For this purpose, eight cotton genotypes were used to develop breeding population by crossing five lines (MNH-129, MNH-147, CIM-473, PB-899 and KZ-191) to tree testers (MNH-886, FH-142 and CIM-598), following line × tester crossing design in glass house during 2014-15. The fifteen hybrid genotypes thus obtained were grown in the field along with the parental genotypes during 2015. Field layout for sowing of the experiment was randomized complete block with three replications. Analysis of the data recorded for bolls number plant<sup>-1</sup>, weight boll<sup>-1</sup>, yield of seed cotton plant<sup>-1</sup>, lint percentage, seeds number boll<sup>-1</sup>, seed index, fiber span, fiber strength and micronaire revealed that magnitude of SCA variance was higher for all the recorded variables indicating a major role of non-additive genes in the inheritance of the traits. FH-142, CIM-473 and MNH-886 were considered good general combiners for various traits under consideration. MNH-129 × FH-142 seemed as the best cross for yield of seed cotton and lint percentage.

**Key words:** Genetics, combining ability, yield and quality attributes, cotton.

### INTRODUCTION

Upland cotton (*Gossypium hirsutum* L.) is grown in more than seventy countries of the world lying in both tropical and subtropical climate (Shakeel *et al.*, 2014). The crop dwells in the peak rank amongst all the crops with natural fibers in the world (Ali *et al.*, 2016). It is the chief source of fiber for textile industry and plays a key role in the agricultural economy of Pakistan (Anonymous, 2014-15). Cotton fiber is known as white gold owing to its universal significance (Dinakaran *et al.*, 2012). In addition, it has also a major share in local edible oil production (Qayyum *et al.*, 2009).

Pakistan ranks fourth in terms of production and consumption while third in relation to exports of cotton and its products worldwide (USDA, 2014). Cotton shares 7.1% in value added and >1.4% in GDP (Anonymous, 2013-14). Cotton-seed, in addition, contains substantial amount of edible oil and underwrites more than 70% of the total edible oil production in Pakistan (Ali and Awan, 2009; Amjad, 2014). In consequence of its massive role in the agricultural economy of the country, this crop is enjoying much focus of agricultural stake holders. Research efforts made in the realm of cotton breeding

resulted in the evolution of a galaxy of cultivars with high yield and improved quality.

The triumph of plant breeding program aiming the development of genotypes with high yield potential and better quality, fertilizer responsive and resilient to various biotic and abiotic stresses depends fundamentally on the choice of appropriate parents to be hybridized for manipulating genetic disparity to be imperiled to selection (Ali *et al.*, 2016a). These parents must be genetically loftier, physiologically proficient and possess good combining ability. However, before boarding any such breeding project, handiness of information about genetic control of imperative plant traits is indispensable (Ali *et al.*, 2016b).

General and specific combining ability effects for various plant variables help to apprehend the genetic basis of varietal differences for the concerned traits. Combining ability effects of the parents and crosses are considered very important before starting any breeding program. A number of academicians have reported importance of combining ability analysis for cotton improvement (Basal and Turgut, 2005; Ahuja and Dhayal, 2007; Shakeel *et al.*, 2014; Ali *et al.*, 2016a). Line × tester crossing method and its analysis

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developed by Kempthorne (1957) offers some superfluous benefits as it categorizes and ranks the parental genotypes rendering to their general as well as specific combining ability, and also delivers evidence on genetic regulator of the variables to be explored (Ali *et al.*, 2016a).

## MATERIALS AND METHODS

Present studies on the combining ability analysis for various plant traits contributing towards the final yield of seed cotton and the quality of fiber in upland cotton were conducted in the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, during the year 2014 through 2015. Eight cotton genotypes were grown in 15" × 15" clay pots during October, 2014, in greenhouse under controlled conditions. Temperature was maintained between 60°F and 100°F, using electric heaters. As flowering was initiated, each of the five lines, i.e., MNH-129, MNH-147, CIM-473, KZ-191 and PB-899, was crossed to three testers, i.e., MNH-886, FH-142 and CIM-598. The proposed female parents were manually emasculated in the evening and pollinated the following morning. A plenty of flower buds were crossed in this way to produce enough F<sub>1</sub> hybrid seeds. Rigorous preventive measures were taken to evade pollen contamination during selfing and crossing operations.

The seeds of the crosses and their respective parents were sown in the field, during first week of May in 2014, following randomized block design with three replications. The seeds were planted in single row plot 75 cm, apart from the other and having ten holes spaced 30 cm. Standard agronomic practices and plant protection procedures were implemented during whole crop duration. Data were taken on five consecutive middle plants.

The recorded data for various parameters were subjected to statistical analysis (Steel *et al.*, 1997) to test whether the differences among genotypes for concerned traits were genotypic or environmental. Combining ability analysis was carried out following the basic line × tester analysis (Kempthorne, 1957) to classify the parents on the basis of general and specific combining ability effects and draw inference about the genetic control of traits under considerations.

## RESULTS AND DISCUSSION

The basic line × tester analysis revealed remarkable differences ( $P \geq 0.01$ ) among genotypes for all the traits under consideration (Table 1). Genotypic mean squares were partitioned into parents and crosses, which also presented significant differences for all traits. Parental variability was further divided into variability through lines, testers and their mutual interaction. The lines presented significant variability for all variables, except seeds number boll<sup>-1</sup> and seed index, while testers exhibited insignificant mean squares for lint percentage and seeds number boll<sup>-1</sup>.

Line × tester interaction was found to be non-significant for seed index. Total genetic variability was dissected into various components like additive and dominance variances (Table 2). It is evident from the results that estimates of SCA variance ( $\delta^2_{SCA}$ ) were greater than GCA variance ( $\delta^2_{GCA}$ ) for the all characters. Variance due to dominant factors ( $\delta^2_D$ ) was higher than variance due to additive ones ( $\delta^2_A$ ) for the all characters, which confirmed the earlier findings. Degree of dominance ( $\delta^2_{GCA}/\delta^2_{SCA}$ ) was more than one which indicated the pervasiveness of genes exhibiting non-additive effects for all characters.

Analysis of combining ability showed that the female parent MNH-886 exhibited the superlative general combining ability effects for seed cotton yield, seeds number boll<sup>-1</sup>, fiber span and fiber fineness (Table 3). FH-142 showed the highest GCA effects for weight boll<sup>-1</sup>, lint percentage, seed index and fiber strength, while for bolls number plant<sup>-1</sup> CIM-598 was considered the desirable genotype. Among male parents, CIM-473 produced the peak GCA effects for weight boll<sup>-1</sup>, lint percentage, seeds number boll<sup>-1</sup>, seed index and fiber strength. MNH-147 was favorable genotype for bolls number plant<sup>-1</sup> and seed cotton yield owing to its highest GCA effects while for fiber span and fiber fineness, PB-899 was the most desirable parent.

The highest specific combining ability values for the yield of seed cotton, lint percentage and seeds number boll<sup>-1</sup> were presented by the cross MNH-129 × FH-142 (Table 4). MNH-129 was considered the best specific combiner to MNH-886 for weight boll<sup>-1</sup> and seed index as it exhibited the highest SCA effects towards the traits. KZ-191 × MNH-886, PB-899 × CIM-598 and MNH-129 × CIM-598 exhibited good SCA effects for bolls number per plant<sup>-1</sup>, fiber strength and fiber fineness, respectively. For fiber span two crosses, CIM-473 × FH-142 and PB-899 × MNH-886 presented equal value of SCA effects.

Comparative impact of lines, testers and line × tester interaction to the over-all variance exposed that the contribution of lines was the highest for variability in lint percentage only. For bolls number plant<sup>-1</sup>, seed cotton yield and seed index, contribution of testers was the greatest, while line × tester interaction contributed the major proportion of total variability for traits like weight boll<sup>-1</sup>, seeds number boll<sup>-1</sup>, fiber span, fiber strength and fiber fineness (Table 5).

Handiness of evidences on the relative influence of various genetic factors in the ultimate development of a trait is indispensable before imperiling the targeted population to selection (Ali and Khan, 2007; Shakeel *et al.*, 2014; Ali *et al.*, 2016a). Basic statistical analysis of the data showed that disparity among genotypes for bolls number plant<sup>-1</sup>, weight boll<sup>-1</sup>, seed cotton yield, lint percentage, seeds number boll<sup>-1</sup>, seed index, fiber span, fiber strength and micronaire were genetically demonstrated (Abbas *et al.*, 2008; Imran *et al.*, 2012). This genetic erraticism

in each character was further apportioned into different components, i.e., additive factor due to general combining ability and non-additive factor due to specific combining ability as described by Kempthorne (1957).

**Table 1: Analysis of variance showing mean squares for various plant traits in *G. hirsutum* L.**

SOV	d.f	Bolls/plant	Boll weight	Seed cotton yield	Lint percentage	Seeds/boll	Seed index	Fiber span	Fiber strength	Fiber fineness
Reps	2	5.4	0.32	42.2	3.80	18.5	0.46	0.26	0.06	0.07
Genotypes	22	96.7 **	0.96 **	862.2 **	25.8 **	45.2 **	0.68 **	1.19 **	4.30 **	0.22 **
Parents	7	26.0 *	0.67 *	282.0 **	28.5 **	39.1 *	1.15 **	1.61 **	3.2 **	0.36 **
Crosses	14	102.2 **	0.94 **	556.6 **	25.7 **	35.4 *	0.49 *	1.0 **	3.7 **	0.13 **
P vs C	1	515.8 **	3.25 **	9202.7 **	9.48 *	224.8 **	0.08	0.90 *	19.4 **	0.58 **
Lines	4	184.7 **	0.73 *	1475.7 **	45.8 **	26.6	0.19	0.74 *	5.2 **	0.13 **
Testers	2	201.9 **	1.53 **	497.8 **	1.55	7.5	1.74 **	0.93 *	0.8 **	0.23 **
L×T	8	36.0 **	0.89 **	111.8 **	21.6 **	46.8 *	0.33	1.15 **	3.7 **	0.10 *
Error	44	10.2	0.22	37.4	2.58	16.8	0.21	0.21	0.061	0.034

**Table 2: Estimates of variances due to GCA and SCA for various plant traits in *G. hirsutum* L.**

Genetic components	Bolls/plant	Boll weight	Seed cotton yield	Lint percentage	Seeds/boll	Seed index	Fiber span	Fiber strength	Fiber fineness
Cov H.S (lines)	11.059	0.043	25.730	-1.342	-2.621	0.094	-0.015	-0.191	0.009
Cov H.S (tester)	18.591	-0.020	170.400	3.018	-2.535	-0.017	-0.051	0.194	0.004
Cov H.S (Aveg)	2.238	0.002	15.040	0.136	-0.386	0.006	-0.005	0.001	0.001
Cov F.S	48.994	0.311	246.600	7.663	3.832	0.202	0.276	1.210	0.046
$\delta^2_{GCA}$	2.238	0.002	15.040	0.136	-0.386	0.006	-0.005	0.001	0.001
$\delta^2_A$	8.953	0.006	60.170	0.544	-1.544	0.022	-0.020	0.005	0.004
$\delta^2_{SCA}$	8.591	0.223	24.800	6.366	10.028	0.038	0.315	1.222	0.022
$\delta^2_D$	34.360	0.893	99.190	25.464	40.114	0.152	1.261	4.887	0.089
$\delta^2_{GCA}/\delta^2_{SCA}$	0.260	0.006	0.600	0.021	-0.038	0.135	-0.015	0.0009	0.045

**Table 3: General combining ability (GCA) effects of lines and testers for various plant traits in *G. hirsutum* L.**

	Bolls/plant	Boll weight	Seed cotton yield	Lint percentage	Seeds/boll	Seed index	Fiber span	Fiber strength	Fiber fineness
<b>Lines</b>									
MNH-129	-2.34	-0.28	-11.7	-2.75	-2.24	-0.15	-0.39	-1.05	0.18
MNH-147	7.88	-0.25	19.04	0.29	0.18	-0.14	0.25	-0.13	-0.02
CIM-473	-0.25	0.42	6.92	3.04	1.74	0.15	-0.11	0.81	-0.06
PB-899	-2.20	0.06	-5.33	-1.56	-1.18	0.14	0.32	-0.31	-0.14
KZ-191	-3.09	0.05	-8.88	0.98	1.51	0.005	-0.06	0.68	0.05
<b>Testers</b>									
MNH-886	2.03	-0.04	3.83	-0.20	0.59	-0.25	0.18	-0.08	-0.14
FH-142	-4.23	0.34	-6.62	0.37	0.18	0.39	0.09	0.27	0.06
CIM-598	2.20	-0.30	2.78	-0.17	-0.78	-0.14	-0.28	-0.19	0.09

**Table 4: Specific combining ability (SCA) effects of crosses for various plant traits in *G. hirsutum* L.**

Crosses	Bolls/plant	Boll weight	Seed cotton yield	Lint percentage	Seeds/boll	Seed index	Fiber span	Fiber strength	Fiber fineness
MNH-129×MNH-886	-7.00	1.29	1.40	4.07	0.90	0.98	-0.01	-1.25	-0.06
MNH-129×FH-142	5.39	0.88	32.10	4.49	7.65	-0.81	-0.65	-0.06	0.11
MNH-129×CIM-598	-0.58	-0.17	-6.60	2.52	-2.40	-0.14	0.78	1.32	-0.45
MNH-147×MNH-886	-11.16	-0.03	-31.00	-1.55	-0.23	0.32	0.21	0.42	-0.18
MNH-147×FH-142	-7.76	-0.25	-28.70	-2.37	1.26	-0.21	0.16	1.03	-0.30
MNH-147×CIM598	-12.33	0.59	-23.20	-5.51	4.33	0.04	-0.33	1.13	0.11
CIM-473×MNH-886	7.30	-0.62	14.90	-4.84	-0.39	-0.12	0.78	-1.25	-0.31
CIM-473×FH-142	-1.29	0.03	-3.80	1.17	1.54	0.19	1.25	1.10	0.10
CIM-473×CIM-598	-4.80	-0.11	-21.40	1.21	-0.90	0.24	-0.07	-0.74	-0.08
PB-899×MNH-886	2.12	-0.47	0.12	-2.60	-2.78	0.02	1.25	1.10	0.10
PB-899×FH-142	4.12	-0.08	13.30	1.76	3.87	-0.80	0.16	0.31	0.14
PB-899×CIM-598	0.08	0.46	14.00	2.05	3.58	0.40	-0.99	1.44	0.37
KZ-191×MNH-886	15.54	-0.75	25.00	1.79	-5.12	-0.36	-0.32	-1.25	0.30
KZ-191×FH-142	13.54	-0.86	26.00	1.08	-5.54	-0.09	-0.08	-2.26	0.06
KZ-191×CIM-598	-3.16	0.10	-12.10	-3.27	-5.77	0.34	-0.78	0.62	0.03

**Table 5: Proportional contribution of lines, testers and line × tester interaction in overall genetic variation for various plant traits in *G. hirsutum* L.**

Character	Bolls/plant	Boll weight	Seed cotton yield/plant	Lint percentage	Seeds/boll	Seed index	Fiber span	Fiber strength	Fiber fineness
Lines	28.2	23.3	12.7	50.9	3.0	11.1	13.6	3.2	26.2
Testers	51.6	22.2	75.7	0.8	21.4	50.4	21.2	40.1	29.0
L×T interaction	20.1	54.4	11.4	48.2	75.5	38.3	65.5	56.6	44.6

The relative involvement of general and specific combining ability delivered some insight on the genomic mechanism of inheritance of the traits under question. It was shown that the all traits seemed to be controlled by non-additive genes as were supported by Khan *et al.* (2001); Azhar and Khan (2005); Preetha and Raveendran (2008); Shaukat *et al.* (2013). Proportional contribution of female and male parental interaction in the phenotype of concerned traits was higher than female and male individual impact for the characters like weight boll<sup>-1</sup>, seeds number boll<sup>-1</sup>, fiber span, fiber strength and micronaire, which also reinforced the prevalence of non-additive genes in inheritance of most of the characters (Azhar and Khan, 2005; Shakeel *et al.*, 2014; Ali *et al.*, 2016a,b). Such basic insight, like the findings resulting from current study, about the type of genetic control of various plant traits in question may deliver a guideline to a breeder while subjecting the population to selection. It has been well established that the plant traits under a major influence of non-additive genetic components possess low heritability (Falconer and Mackay, 1996), signifying that early segregating populations, like F<sub>2</sub> are not docile to selection pressure. In this case, the selection procedure may be

started when the genes have been stabilized in the population (Subhan *et al.* 2000; Neelima *et al.*, 2004).

Combining ability analysis is expedient in categorizing parental genotypes in terms of their hybrid performance. Evaluation of the performance of parental genotypes for general combining ability revealed that the genotype FH-142 can be the most effective donor parent for the favorable genes controlling weight boll<sup>-1</sup>, lint percentage, seed index and fiber strength. While CIM-473 was proved to be superior general combiner for weight boll<sup>-1</sup>, lint percentage, seed index, seeds number boll<sup>-1</sup> and fiber strength. The genotype PB-899 may be a good source of desirable genes for fiber span and fiber strength.

Bolls number plant<sup>-1</sup> pay directly to the ultimate yield of seed cotton (Ali *et al.*, 2016a, b). On this criterion, two genotypes CIM-598 and MNH-147 may be suggested for their use in future breeding program aiming improvement in boll size. Heavier bolls contain more seeds resulting in an increase in seed surface area and in due course the lint yield. CIM-473 also displayed superior GCA effects for weight boll<sup>-1</sup>. For the yield of seed cotton MNH-147, CIM-473, MNH-886 and CIM-598 revealed better general

combining ability which can be exploited in future breeding program.

On the basis of the results obtained from the current study, it may be clinched that the parental genotypes CIM-473, FH-142, PB-899 may be much fruitful for a researcher manipulating variability in the characters like these. The parental genotypes with good general combining ability for a certain character are likely to produce better hybrids (Irfanullah *et al.*, 1994; Shakeel *et al.*, 2014). And this comportment of the parents used in this study seems to be valid, for example CIM-473, FH-142 and PB-899 being descent general combiners regarding the yield of seed cotton produced fruitful crosses for the trait.

For bolls number plant<sup>-1</sup> KZ-191 × MNH-886 and KZ-191 × FH-142 seemed the unsurpassed crosses due to their maximum positive SCA values for the character. Although, both the crosses originated from the poor performer parental genotypes for the trait. For the ultimate yield of seed cotton, the cross MNH-129 × FH-142 seemed to be superior although the both parents involved in this cross showed poor GCA values for a particular trait. The reason is that occasionally the parents showing low GCA may notch well in producing potential hybrids (Imran *et al.*, 2012; Ali *et al.*, 2016a,b) as has been observed in case of cross PB-899 × CIM-598 for fiber span and fiber strength. For fiber fineness negative value for micronaire is preferred, due to which MNH-129 × FH-142 may be recommended for improvement in fiber fineness.

### CONCLUSION

It can be concluded that all the traits under consideration are governed by non-additive type of genes which necessitates selection in later generations for improvement. The cross MNH-129 × FH-142 may be considered for improvement in seed cotton yield and the contributing traits.

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