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Combining ability and inbreeding depression analysis for yield and fiber traits in cotton genotypes

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ABSTRACT

Review Proccess: Peer review

Cotton is the crop of great industrial relevance and provides 90% world textile fiber. The aim of the present study was to investigate the genetic control and inbreeding depression of the yield and fiber traits in F_1 and F_2 generations and to pin point the most promising hybrids to obtain the superior cotton genotypes. Four cotton genotypes were crossed in half diallel fashion and data was recorded on number of bolls plant^{-1}, boll weight, ginning out turn, fiber length, and fiber strength and micronaire value. The additive genetic effects were the most promising for all the studied yield and fiber traits. Genotype FH-142 was found to be the most appropriate parent to create crossing blocks for the enhancement of yield and fiber traits. The hybrids FH-142 × AA-934 and CRIS-600 × CEMB-33 were the most appropriate to obtain the segregating generations with the aim to select the most desirable genotypes. Inbreeding depression was recorded to be more prominent in the yield related traits in comparison to fiber traits.

Keywords: *Gossypium hirsutum*, combining ability, inbreeding depression, parent's selection, F1, F2 populations.

INTRODUCTION: Cotton produces approximately 90% of the natural fiber worldwide and is a crop of vital industrial importance. Worldwide it is cultivated in temperate, subtropical and tropical regions on an area of 30 million hectares (Panni *et al*., 2012). Pakistan is the 5th largest cotton producer, 3rd largest consumer of cotton, 3rd largest yarn producer, 2nd largest yarn exporter and 3rd largest cloth exporter in the world. Although it is cultivated on an area of more than 3 million hectares every year in the country, its production has been observed as erratic and considered as low due to various production constraints. Therefore the basic aim of the breeders is to develop cotton genotypes having maximum seed cotton yield and quality fiber to fulfill the needs of textile industry. The most important step in any breeding program is the choice and selection of parents. The effective selection of parents and their best hybrids enhances the chances of obtaining a successful breeding program (Queiroz *et al*., 2017). The diallel analysis fashion is the genetic design developed by Griffing (1956) which provides the most important information regarding the parent's behavior with one another. It provides the information of general combining ability that is attributed to the genes having additive effects and specific combining ability attributed to the non-additive effects of their hybrid combinations. Bechere *et al.* (2016) depicted that additive genetic action is predominant in controlling most of the agronomic and fiber quality parameters in cotton crop. However, in few of the countries like China and India, hybrid vigor has been developed and utilized for seed cotton yield and fiber quality improvement (Khan *et al.*, 2005). However the F_1 hybrids of these countries also has the highest inbreeding depression over the advanced generations, that averts their utilization in breeding approaches intended at using pure lines (Soomro *et al.*, 2000).

Inbreeding depression is the result of an increase in homozygosity in an individual. There are two possible reasons that decrease the adaptability of increased homozygosity. It might be an increase in homozygosity of partially recessive mutations or increase in homozygosity of alleles in loci where there is heterozygote advantage. Heterosis and inbreeding depression are opposite attributes and traits that have maximum Heterosis due to dominant alleles, proportionally depict high inbreeding depression on account of fixation of allelic genes with an increase in homozygosity. Different studies (Zhang *et al*., 2016) have revealed high inbreeding depression for morphological and fiber quality attributes in cotton.

OBJECTIVE: Keeping these genetic behaviors in view, the current study was designed with the objectives to estimate the inbreeding depression and gene action involved in controlling different morphological and fiber quality attributes in cotton breeding generations and to recognize the best favorable hybrids for finding superior genotypes.

MATERIAL AND METHODS: **Parent material:** Four upland cotton genotypes (FH-142, AA-934, CRIS-600 and CEMB-33) were crossed in half diallel fashion without reciprocal crosses and parental cross combinations. These genotypes were selected on the basis of their diversity for fiber traits.

Obtainment of F_1 and F_2 hybrids: The parents were sown at Cotton Research Station D.I.Khan (situated at 31°49´ N latitude and 70 °55´ E longitude) during the crop season 2017-18. Crosses were performed at the flowering stage. About 50% of the seeds of F_1 were sown next year in the same soil. They were self-pollinated at flowering stage so as to obtain the F_2 seeds. In the crop season 2019-20 the two experimental sets were carried out. One with the seeds of F_1 generation and other with F_2 generation in the same experimental soil.

Experimental layout and crop management: Each experimental unit was conducted in a 2 row plot of 5 m long a spacing of 0.75 m between and 0.30 m within the hills. The plot size was 20 m^2. Seeds were planted in hills and each hill received 3 seeds which were irrigated immediately. In these experiments, 60 kg ha^{-1} of P_2O_5 as single super phosphate and 50 kg ha^{-1} of nitrogen as urea were applied prior to sowing and 50 kg ha^{-1} nitrogen as urea used at the flowering and 50 kg ha^{-1} at boll formation stage. After 3 weeks of planting seedlings were thinned to single plant per hill. Picking was performed after 150 days of planting. All the remaining cultural practices were performed as per the recommendations.

Recording of observations and Statistical analysis: Data were recorded for number of bolls plant^{-1}, boll weight (g), ginning out turn %, fiber length (mm), fiber strength (g tex^{-1}) and micronaire (µg inch^{-1}). The data recorded were subjected to statistical analysis. Homogeneity of variance was pointed out each within F_1 and F_2 experiments, and then analysis of variance was performed for both the generations so as to split the treatments source, so as to confirm the significance of F_1 vs. F_2 contrast to assess the incidence or nonexistence of inbreeding depression. These mean performance values were clustered through Scott and Knott test at 5% level of probability. For the calculation of general combining ability (GCA) and specific combining ability (SCA) the data was subjected to diallel analysis of each generation separately according to Griffing's approach, method 4 (Griffing, 1956) along with the quadratic components of these traits using equation given below.

$$Y_{ij} = \mu + g_i + g_j + s_{ij} + e_{ij}$$

Where

Y_{ij} is the average performance of hybrid combination ($i \neq j$), μ is the general mean, g_i and g_j are the effects of general combining ability of ith and jth genotypes respectively; s_{ij} is the effect of specific combining ability for the crosses between parents i and j; and e_{ij} is the effect of mean error associated with ij observation.

Inbreeding depression was estimated as percent decrease (d) of the traits in F_2 in relation to F_1, using the following equation.

$$D = [(F_2 - F_1)/F_1] \times 100$$

Where, F_1 is the mean of hybrid in diallel fashion; F_2 is the mean of F_2 generation after selfing. The significance of GCA, SCA and inbreeding depression estimates was verified by t-test at 5% level of probability. All the analysis was performed using the Genes software (Cruz, 2013).

RESULTS AND DISCUSSIONS: **Diallel analysis and joint analysis of variance:** The analysis of variance revealed highly significant differences among the treatments for all the studied traits (table 1).

This significant variation depicted the presence of genetic variability among the treatments including parents and thus there is a possibility of selection of the superior genotypes with an advancement of segregating generations. The F_1 vs. F_2 was also highly significant for all the investigated traits except micronaire, which depicted the presence of variation in the mean performance of F_1 and F_2 generations and hence the presence of inbreeding depression. The coefficient of variation of the experiment ranged from 2.64% (seed cotton yield) to 16.64% (fiber strength) which revealed a good experimental precision as suggested by Pimentel-Gomes and Garcia (2002). These results are in close analogy with the previous findings of Khan *et al.* (2009) and Hague *et al.* (2008) who also utilized the diallel crosses in cotton. The general combining ability for all the studied traits was found to be highly significant both in F_1 and F_2 generations (table 2). Similarly the specific combining ability was significant for all the studied traits except fiber length and

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micronaire in F1 generations which was non-significant. While in F_2 it was non-significant for boll weight and fiber length while significant for the remaining studied traits. These results of combining ability revealed the involvement of additive genetic effects for all the studied traits except fiber length, boll weight and micronaire which have non-additive genetic effects regardless of the generation. The quadratic components related with the additive effects (Φ_{gc}) were superior in comparison to non-additive effects in genetic control of the studied traits except fiber strength in F_1 generation and number of bolls plant^{-1}and ginning out turn % in F_2 generations. These findings encourage the utilization of genotypes with high GCA so as to obtain the segregating generations for selection on account of the reason that additive effects are directly fixable. Similar finding were obtained in other various studies which utilized the diallel crosses in cotton (Hague *et al*., 2008).

Although the quadratic components related with the non-additive effects (Φ_{sc}) for fiber strength in F_1 generation and number of bolls plant^{-1}and ginning out turn % in F_2 generations were higher than the additive effects, most of the non-additive effects were close to zero except number of bolls plant^{-1} ($\Phi_{sc} = 17.76$) and ginning out turn % ($\Phi_{sc} = 23.37$) in F_2 generations. It reflects the presence of hybrid vigor on account of differences in genetic components of the parents utilized in the study which can be explored to enhance these traits. Similar results of non-additive effects for these traits were also previously found by Khan *et al.* (2009).

Combining ability: The genotype FH-142 depicted higher GCA for number of bolls plant^{-1}, boll weight, ginning out turn and fiber strength both in F_1 and F_2 generations (table 3). Similarly the genotype AA-934 also depicted significant GCA effects for boll weight, ginning out turn and fiber length in both the generations. Similar results were expected from these genotypes on account of the reason that these genotypes have high yield and good quality fiber and had been the target of intense selection and consequently have high frequency of favorable alleles. These findings suggest that these genotypes must be included in breeding scheme when the breeding aim is to enhance the yield and fiber quality contributing traits in cotton. On the other hand, the genotypes CRIS-600 and CEMB-33 although presented significantly higher GCA for the yield contributing traits, however they depicted negative or non-significant GCA for fiber quality parameters both in F_1 and F_2 generations. These results suggested that these genotypes must be included in crossing blocks when the aim of breeding scheme is to enhance the main morphological yield related attributes in cotton.

The estimates of SCA were found to be significant only for ginning out turn and fiber strength. Table 4 depicted that cross FH-142 × AA-934 and CRIS-600 × CEMB-33 presented the highest SCA effects in F_1 generation, both presenting significant estimates for ginning out turn, boll weight and fiber strength. However, in F_2 generation, the higher estimates were obtained by the crosses FH-142 × CRIS-600 and AA-934 × CEMB-33. These results are in close analogy with the previous findings of Khan *et al.* (2009) who also reported decrease in the mean performance of best crosses from the F_1 generation to F_2 generation due to inbreeding depression and segregation. Similarly Khan *et al.* (2005) and Tigga *et al.* (2017) also reported that F_1 hybrids with high Heterosis were also those associated with high inbreeding depression.

Source of variation	Degree of freedom	No. of bolls plant^{-1}	Boll weight (g)	Ginning out turn (%)	Fiber length (mm)	Fiber strength (g tex^{-1})	Micronaire (µg inch^{-1})
Blocks	2	0.112	0.014	10.23	0.12	3.68	0.16
Treatments	11	8.82**	2.58**	39.37**	2.63**	69.63**	0.48**
F_1	5	4.53**	2.17**	15.43**	2.69**	8.95ns	0.11ns
F_2	5	5.87**	3.18**	41.17**	1.33ns	114.58**	0.73**
F_1 vs F_2	1	11.21**	6.48**	154.7**	7.86**	147.64**	0.11ns
Residue	22	2.899	0.53	2.59	0.76	5.67	0.11
CV%		6.69	7.24	5.63	3.21	16.64	3.87

Table 1: Joint analysis of variance of yield and fiber traits investigated in six cotton crosses in F_1 and F_2 generations.

Source of variation	Degree of freedom	No. of bolls plant^{-1}	Boll weight (g)	Ginning out turn (%)	Fiber length (mm)	Fiber strength (g tex^{-1})	Micronaire (µg inch^{-1})
				F_1			
GCA	3	17.85**	3.87**	21.89**	3.83**	14.57**	0.22*
SCA	2	3.25**	0.47**	2.97**	0.09ns	5.74**	0.08ns
Φ_{gc}	--	3.59	0.67	4.36	0.71	1.65	0.04
Φ_{sc}	--	0.85	0.07	0.73	0.00	1.83	0.00
				F_2			
GCA	3	27.65**	7.88**	32.84**	2.23**	138.44**	0.73**
SCA	2	63.36**	0.07ns	71.17**	0.32ns	31.73**	0.82**
Φ_{gc}	--	3.29	1.16	4.78	0.37	19.86	0.16
Φ_{sc}	--	17.76	0.00	23.37	0.00	5.82	0.23

Table 2: Diallel analysis of variance of yield and fiber traits investigated in six cotton crosses in F_1 and F_2 generations.

GCA	No. of bolls plant^{-1}	Boll weight (g)	Ginning out turn (%)	Fiber length (mm)	Fiber strength (g tex^{-1})	Micronaire (µg inch^{-1})
			F_1			
FH-142	0.92*	0.52*	0.58*	-0.07	0.73*	-0.17
AA-934	-0.13	0.483*	-1.78*	1.13*	-0.09	-0.06
CRIS-600	0.89*	0.14	2.39*	-0.15	-0.47	-0.09
CEMB-33	-0.21	-1.35*	-0.96*	-0.88*	-0.11	0.32
			F_2			
FH-142	0.98*	0.84*	2.62*	0.12	1.82*	0.32
AA-934	-0.25	0.531*	-0.69	0.78*	0.75*	-0.18
CRIS-600	1.76*	0.17	0.62	-0.72*	-1.56*	0.37
CEMB-33	-0.23	-1.51*	-2.41*	-0.18	-0.79*	-0.41

Table 3. Estimates of general combining ability between parents for yield and fiber traits investigated in 4 cotton genotypes in F_1 and F_2 generations.

SCA	No. of bolls plant^{-1}	Boll weight (g)	Ginning out turn (%)	Fiber length (mm)	Fiber strength (g tex^{-1})	Micronaire (µg inch^{-1})
			F_1			
FH-142 × AA-934	-0.13	0.25*	0.83*	-0.11	3.27*	0.11
FH-142 × CRIS-600	0.04	-0.17	-0.63*	0.07	2.53*	-0.13
FH-142 × CEMB-33	0.06	-0.13	-0.13	0.05	-1.06	0.00
AA-934 × CRIS-600	0.07	-0.15	-0.12	0.05	-1.11	0.01
AA-934 × CEMB	0.05	0.14	-0.79*	0.04	2.63*	-0.12
CRIS-600 × CEMB-33	-0.13	0.31*	0.93*	-0.14	2.58*	0.11
			F_2			
FH-142 × AA-934	0.12	0.04	-2.53*	0.11	-7.14*	0.29
FH-142 × CRIS-600	0.15	-0.02	3.27*	0.13	3.57*	-0.47
FH-142 × CEMB-33	-0.26	-0.03	-0.73*	-0.23	3.59*	0.13
AA-934 × CRIS-600	-0.22	-0.02	-0.77*	-0.19	3.64*	0.15
AA-934 × CEMB-33	0.14	0.00	3.43*	0.11	3.85*	-0.43
CRIS-600 × CEMB-33	0.11	-0.02	-2.47*	0.08	-6.85*	0.23

Table 4. Estimates of specific combining ability among parents for yield and fiber traits investigated in six cotton crosses in F_1 and F_2 generations.

Means grouping between both generations: The mean values of the F_1 and F_2 generations depicted significant differences among themselves for all the studied traits indicating that at least one of the cross depicted the inbreeding depression. These results are in close analogy with the previous findings of Khan *et al.* (2009) and Tigga *et al.* (2017) who reported more pronounced inbreeding depression in different agronomic traits of cotton plants. The mean performance of the hybrid FH-142 × AA-934 and FH-142 × CRIS-600 were slightly different between the two (F_1 and F_2) generations for most of the studied traits. Khan *et al.* (2009) stated that the mean of F_1 hybrids are not appropriate for the estimation of the performance in the next generations; however, when analyzed in conjunction with F_2 generation, it becomes a good indicator to find out the most promising segregating populations. Based on these considerations, it is evident that these crosses are recommended to select cotton genotypes for both agronomic and fiber traits.

Inbreeding depression: It was observed that the yield and yield related attributes depicted more inbreeding depression verifying the previous results of Khan *et al.* (2009) and Tigga *et al.* (2017). The crosses FH-142 × AA-934 and FH-142 × CRIS-600 had the minimum inbreeding depression for most of the studied attributes. Based on these results, the conventional selection methods can be utilized in these crosses on account of predominance of additive genetic effects for enhancing the agronomic and fiber quality parameters. The crosses AA-934 × CRIS-600 and CRIS-600 × CEMB-33 which consist of genotype CRIS-600 presented more inbreeding depression.

CONCLUSIONS: The additive genetic effects were found to be most promising in the studied yield and fiber traits. Genotype FH-142 was the most appropriate parental genotype to create crossing blocks for the enhancement of yield and fiber traits. The hybrid FH-142 × AA-934 and CRIS-600 × CEMB-33 were the most favorable to achieve segregating generations with the aim to choice the superior genotypes. Inbreeding depression was more distinct in the yield related traits in comparison to fiber traits.

CONFLICT OF INTEREST: Authors have no conflict of interest

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Generations	No. of bolls plant^{-1}	Boll weight (g)	Ginning out turn (%)	Fiber length (mm)	Fiber strength (g tex^{-1})	Micronaire (µg inch^{-1})
FH-142 × AA-934	26.67 bc	3.17 a	37.12 cd	28.33 cd	28.97 cd	4.48 d
FH-142 × CRIS-600	31.33 a	2.95 b	37.35 c	28.93 b	29.76 ab	4.49 d
FH-142 × CEMB-33	28.67 ab	2.72 c	38.74 b	29.55 a	30.02 a	4.70 abc
AA-934 × CRIS-600	24.67 cd	2.64 cd	36.87 de	28.08 de	29.48 abc	4.80 a
AA-934 × CEMB	26.67 bc	3.17 a	39.35 a	29.64 a	29.94 ab	4.47 d
CRIS-600 × CEMB-33	25.00 cd	2.71 c	36.56 e	28.10 de	29.45 abc	4.43 d
FH-142 × AA-934	23.33 d	2.55 d	35.78 f	27.85 e	28.58 de	4.70 abc
FH-142 × CRIS-600	25.00 cd	2.55 d	38.78 b	28.56 c	29.39 bc	4.75 ab
FH-142 × CEMB-33	23.33 d	2.26 f	34.35 i	27.88 e	28.15 ef	4.72 abc
AA-934 × CRIS-600	23.33 d	2.38 ef	35.42 g	28.40 cd	29.06 cd	4.50 d
AA-934 × CEMB	24.00 cd	2.40 e	34.89 h	27.33 f	27.96 f	4.62 c
CRIS-600 × CEMB-33	23.33 d	2.55 d	33.55 j	27.93 e	28.56 de	4.63 bc
$LSD_{0.05}$	2.88	0.123	0.36	0.36	0.59	0.12
Mean F_1	27.16	2.89	37.66	28.77	29.60	4.56
Mean F_2	23.72	2.45	35.46	27.99	28.62	4.65

Table 5: Mean performance of yield and fiber traits investigated in six cotton crosses in F_1 and F_2 generations.

Generations	No. of bolls plant^{-1}	Boll weight (g)	Ginning out turn (%)	Fiber length (mm)	Fiber strength (g tex^{-1})	Micronaire (µg inch^{-1})
FH-142 × AA-934	-4.87*	-10.21*	-7.26*	-2.15	-7.79	+3.49
FH-142 × CRIS-600	-7.34*	-3.83*	-2.87*	-2.87	-12.15	+7.23
FH-142 × CEMB-33	-6.23*	-13.27*	-10.21*	-1.03	-3.26	-3.82
AA-934 × CRIS-600	-7.62*	-23.29*	-15.67*	-1.39	-107.5*	-3.29
AA-934 × CEMB	-7.69*	-7.87*	-6.83*	-5.68*	-15.48	+6.51
CRIS-600 × CEMB-33	-6.61*	-17.69*	-17.65*	-1.47	-19.85	-22.19
Mean	-6.73	-12.69	-10.08	-2.43	-27.67	-2.01

Table 6: Estimates of mean inbreeding depression of yield and fiber traits investigated in six cotton crosses in F_1 and F_2 generations.

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