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

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ABSTRACT

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 for yield and fiber attributes in first and second filial generation so as 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, strength & micronaire value. Additive gene effect was most promising for all the studied yield and fiber traits. Genotype FH-142 was found to be appropriate parents to create crossing blocks regarding enhancement of yield & fiber attributes. Hybrid FH-142 × AA-934 and CRIS-600 × CEMB-33 was 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.

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 5th major cotton producing country, 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 (Khan *et al.*, 2007). 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. One of most significant step in any breeding scheme is selection of parent genotypes. Effective selection of genotypes and their best hybrids enhances chance of attaining fruitful breeding scheme (Queiroz *et al.*, 2017). Diallel analysis fashion is the design established by Griffing, 1956 which provides most important evidence concerning parent's performance with one another. It provides the information of overall combining capability that is accredited to the genetic factors having additive possessions and specific combining capability accredited to the non-additive impacts of various arrangements.

Bechere *et al.* (2016) confirmed that additive gene action as pre-dominant in controlling most of morphological and qualitative parameters in cotton crop. In few of the states like China and India, positive heterosis developed and utilized for seed cotton yield and fiber quality improvement (Khan *et al.*, 2007). However, the F_1 crosses of these also has the highest inbreeding depression over the advanced generations that avert their utilization in breeding approaches intended at use of pure lines (Soomro and Kalhoro, 2000).

Inbreeding depression is the result of enhancement in homozygosity having 2 possible reasons that decrease the adaptability of increased homozygosity. It might be homozygosity enhancement of incomplete mutations of recessive genes or enhanced homozygosity of alleles in loci with advantage of heterozygotes. Hybrid vigor is opposite to the inbreeding depression and those attributes which depict maximum heterosis on account of dominant alleles, also show high inbreeding depression on account of allelic genes having increased homozygosity. Zhang *et al.* (2016) have revealed inbreeding depression for morphological and fiber quality attributes in cotton.

OBJECTIVE: Keeping these genetic behaviours 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 favourable 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 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 31º 49´ N latitude and 70º 55´ E longitude) during the crop season 2017-18. Crosses were performed at the flowering stage. Some of seed of F_1 was sown in the preceding year, 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 of F_1 seed and other of F_2 seed in 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 ANOVA was performed for F_1 and F_2 so as to split source of treatments, so as to confirm consequences of F_1 vs. F_2 compare to assess incidence or nonexistence of inbreeding depression. For the calculation of general (GCA) & specific combining ability (SCA) data was exposed to diallel analysis of both F_1 and F_2 separately as per Griffing's approach, method 4 (Griffing, 1956) along with quadratic components of 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 ≠ 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 it 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 ANOVA revealed highly noteworthy variances in treatments for all the studied attributes (table 1). This significant variation depicted existence of genetic variation among the treatments including parents and there is a possibility of selection of the superior genotypes with an advancement of segregating generations. F_1 vs. F_2 was also highly noteworthy for investigated traits except micronaire that depicted presence of variation in mean performance of F_1 and F_2 and hence existence 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).

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 ANOVA of yield and fiber attributes investigated in 6 cotton crosses in F_1 and F_2.

These findings are in close analogy with the previous findings of Khan *et al.* (2009) who also utilized the diallel crosses in cotton. The GCA for the studied attributes was found to be highly significant both in F_1 and F_2 (table 2) Similarly, the SCA was significant for all the studied traits except fiber length and 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 (table 2). 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. Quadratic component related to the additive gene (Φ_{gc}) was greater in comparison to non-additive in control of the studied attributes 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 attain segregating generations on account of reason that additive effects are directly fixable. Like finding were obtained in various studies which utilized the diallel in cotton (Khan *et al.*, 2009). Although quadratic component related to the non-additive effects (Φ_{sc}) for fiber strength in F_1 and number of bolls plant^{-1}and ginning out turn % in F_2 generations were high as compared to additive effects, most of the non-additive effects almost 0 except number of bolls plant^{-1} (Φ_{sc} = 17.76) and ginning out turn % (Φ_{sc} = 23.37) in F_2 generations. It reflects the presence of hybrid vigor on account of variances in genetic components of 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).

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 6 crosses in F_1 and F_2.

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 GCA between parents for yield and fiber attributes investigated in 4 genotypes in F_1 and F_2.

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 depict more produce and quality fiber and took target of concentrated selection and accordingly higher incidence of promising alleles. These findings suggest that such genotypes must be involved in breeding scheme when its aim is to enhance produce and fiber contributing attributes 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 involved in crossing program when aim is to enhance morphological yield related attributes in cotton. The estimates of SCA were found to be significant only for ginning out turn and fiber strength. In table 4 depicted cross FH-142 × AA-934 and CRIS-600 × CEMB-33 presented the highest SCA effects in F_1, which presented noteworthy estimate of ginning out turn, boll weight and strength of fiber. Though, in F_2, higher estimates attained by 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 reduction in average performance of crosses from F_1 to F_2 due to inbreeding depression and segregation. Similarly Khan *et al.* (2007) and Tigga *et al.* (2017) also reported that F_1 having more heterosis are associated with high inbreeding depression.

Means grouping between both generations: Mean values of F_1 and F_2 depicted significant variances among themselves for all studied traits indicating that one of cross depicted the inbreeding depression (table 5). These findings are similar with the previous findings of Khan *et al.* (2009) and Tigga *et al.* (2017)which also concluded distinct depression in various morphological attributes. The average performance of hybrid FH-142 × AA-934 and FH-142 × CRIS-600 was slightly different between the two (F_1 and F_2) for most of studied attributes. Khan *et al.* (2009) confirmed average performance of F_1 is not appropriate for estimation of enactment in subsequent generation. After analysis in combination with F_2, it was shown as virtuous indicator to find out auspicious segregating population. Based on these such crosses are suggested to choice genotypes both for morphological and qualitative 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.* (2007); 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 selection approaches can be utilized in such crosses on account of predominance of additive genetic effects for enhancing the agronomic and quality

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 SCA among parents for yield and fiber attributes investigated in 6 crosses in F_1 and F_2.

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 6 crosses in F_1 and F_2.

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 average inbreeding depression of yield and fiber traits investigated in 6 crosses in F_1 and F_2.

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 enhancement of yield and fiber attributes. Hybrid FH-142 × AA-934 and CRIS-600 × CEMB-33 was the most favorable to achieve segregating generations with the aim to choice the larger genotypes. Inbreeding depression was supplementary distinct in yield related attributes in comparison to fiber attributes..

CONFLICT OF INTEREST: Authors have no conflict of interest

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