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Genetic variability and association study of yield attributing traits in F_2 populations of American cotton

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ABSTRACT

Cotton is one of the most important fiber crops, grown all over the world. Genetic variability is a crucial factor from an evolutionary point of view for crop species. It defines the adaptation of populations by allowing them to alter their genetic constitution in changing environment. Genetic variability in *Gossypium hirsutum* is declining due to selection pressure, hence causing low yield. The present study was conducted to evaluate ten parental genotypes with their F_2 generations to uncover their genetic potential for yield by accessing genetic variability, heritability, genetic advance, and the association between fiber, yield and yield linked traits. High values of phenotypic and genotypic coefficient of variance were observed for the node of the first fruiting branch, monopodia per plant, boll weight, fiber strength, and yield per plant. All morphological and fiber quality traits represented broad sense heritability ranging from 51% to 90%. The high value of genetic advance was shown by plant height and yield per plant. Positive association of yield per plant was recorded for traits such as plant height, a node of the first fruiting branch, monopodia per plant, number of bolls per plant, seeds per boll, and ginning outturn. Additionally, F_2 progeny of CIM-534×MNH-814 had a high yield per plant along with a maximum number of bolls per plant and seed per boll. So, such F_2 progeny can further be explored to improve yield and yield contributing traits.

Keywords: Correlation, genetic advance, gene action, *Gossypium hirsutum*, heritability, segregating generation.

INTRODUCTION: Cotton (*Gossypium hirsutum*) is the leading fiber-producing crop and is the backbone of the textile industry worth 600 billion dollars worldwide (Ashraf *et al.*, 2018). More than 70 countries are involved in cotton production worldwide, with a major share from India, China, the USA, Pakistan, and Brazil. During the last decade, the cotton yield has been reduced due to high insects pests attacks as well as climate change like low and uneven distribution of rainfall in cotton-producing countries. Another reason for low yield and poor fiber quality was low genetic variability caused by domestication and repeated cycles of selection, which lead toward a narrow genetic base of cultivated germplasm of *G. hirsutum* (Seyoum *et al.*, 2018). A successful breeding program for yield improvement relies upon the available genetic variability in genotypes for yield contributing traits. In addition to such genetic variability; knowledge about heritability, genetic advance, coefficient of phenotypic and genotypic variation help to achieve the objective of yield enhancement. In cotton heritability, broad sense and genetic advance were studied for yield and yield contributing traits. Traits such as plant height, boll per plant, and boll weight showed higher values of heritability broad sense along with genetic advance (Khan *et al.*, 2009). Similarly, genetic variability heritability broad sense and genetic advance were studied for yield and yield-related traits in F_2 population of upland cotton. Genetic variance values were observed slightly higher than the environmental variance for all traits. However, higher heritability broad sense values along with genetic advance were shown by traits like plant height, the number of bolls per plant, boll weight, and yield. Moreover, heritability broad sense and genetic advance were studied for yield and its related traits. High values of heritability broad sense and genetic advance were recorded for traits like yield per plant along with yield contributor traits like plant height, number of monopodia, number of bolls per plant, and boll weight (Baloch *et al.*, 2018). Aziz *et al.* (2014) observed a higher value of heritability broad sense and genetic advance for yield contributing traits in segregating the population of cotton. In upland cotton, genetic variability analysis for fiber traits showed that traits like staple length, fiber strength, and fiber fineness had high phenotypic variance as compared to genotypic variance. F_2 population of upland cotton was studied for yield improvement by utilizing yield contributing traits. Higher estimates of heritability along with genetic advance and genotypic coefficient of variation were observed for traits such as plant height, monopodial and sympodial branches per plant, number of bolls per plant, and boll weight. Therefore, such traits could be utilized as indirect selection criteria for yield improvement (Ahsan *et al.*, 2015). Adhikari *et al.* (2018) observed that the traits which had a high value of heritability broad sense and genetic advance were under the influence of the additive type of gene action. For such traits, improvement through simple selection could easily be made. Yield is a complex trait in cotton which is controlled by different traits which are much affected by environmental conditions. Therefore, for yield improvement knowledge about the correlation between the yield and various yield contributing traits is necessary for the selection of useful traits and breeding methods. A correlation study of yield along with contributing parameters might be helpful to improve the yield because correlation helps to determine the linkage between yield and its different yield contributing parameters.

Correlation study of yield and yield contributing traits in upland cotton reveals a positive association of yield with traits like plant height, number of bolls per plant, boll weight, and seeds per boll (Méndez-Natera *et al.*, 2012). Association study for yield improvement in F_2 population of upland cotton revels that traits such plant height, sympodial and monopodial branches, number of bolls per plant, boll weight, ginning outturn were found to be positively correlated with yield; however, the negative interrelationship of yield and staple length was also reported (Yaqoob *et al.*, 2016). Similarly, a correlation study for yield improvement indicated a positive association of yield per plant with traits like plant height, bolls per plant, seeds per boll, and boll weight (Baloch *et al.*, 2018). While negative inter-linkage was recorded among yield per plant and fiber strength. Therefore, selection for fiber traits should be made carefully due to their negative association with yield per plant. In F_2 population of upland cotton, a correlation study explored positive and significant inter-relationship of yield with monopodial and sympodial branches, number of bolls per plant, boll weight, ginning outturn, and fiber fineness (Komala *et al.*, 2018). Genetic improvement and selection of exceptional genotypes from segregating populations of cotton crop rely upon the initial genetic variability estimation along with correlation studies of yield attributing parameters.

OBJECTIVES

The objective of the present study was to evaluate F_2 population of *G. hirsutum* based on genetic studies of various traits along with their parents for yield improvement. Best performing genotypes will be utilized in the future breeding program for yield improvement.

MATERIALS AND METHODS

Experimental materials and design: The experiment was based on ten parental genotypes as well as F_2 population of their crosses (table 1). All experimental genotypes were planted in a randomized complete block design (RCBD) with 3 replications. Each replication consisted of fifty plants of each parental and segregating (F_2) genotype. Plant to plant and row to row distance was maintained as 30 and 75 cm, respectively. During the experiment all agronomic practices were adopted.

Data collection and biometrical analysis: Data was recorded at maturity from all genotypes. Data were taken for different traits such as plant height (PH; cm), monopodia per plant (MB), a node of the first fruiting branch (NFB), number of bolls per plant (BP), boll weight (BW; g), seeds per boll (NSB), seed cotton yield per plant (YP; g), ginning outturn (GOT; %), staple length (SL; mm), fiber strength (FS; g/tax) and fiber fineness (FF; µg/inch). Fiber traits analysis was carried out by High volume instrument (HVI 900A). From the experimental data, analysis of variance (ANOVA) was computed with statistical software Statistics 8.1 using the technique given by Thomas and Maurice (2009). Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was estimated according to Steel and Torrie (1997). The range of PCV and GCV was described according to Sivasubramanian and Menon (1973) with values as < 10% = Low, 10 to 20% = Moderate, and > 20% = High. Heritability broad sense (H^2) was recorded by using the technique given by Hanson *et al.*, (1956). H^2 was explained based on recommendations are given by Johnson *et al.*, (1955). H^2 values ranges from 0-30% = Low, 31-61% = Medium, 61-100% = High. Genetic advance (GA) was estimated and explained according to Johnson *et al.*, (1955) with values < 10% = Low, 10 to 20% = Moderate, > 20% = High. The phenotypic correlation was determined by the technique of Kwon and Torrie (1964).

Parents	Parents	F_2 Population	F_2 Population
BH-167	NIAB-111	BH-167×CIM-577	CIM-534×MNH-814
CIM-577	MNH-814	CIM-446×CRSM-38	CIM-577×MNH-814
CIM-446	CIM-534	CIM-577×CRSM-38	BH-36×MNH-814
CRSM-38	CIM-707	BH-36×CRSM-38	CIM-534×BH-18
BH-36	BH-118	NIAB-111×MNH-814	CIM-707×NIAB-111

Table 1: List of parent and their F_2 population

RESULTS: Analysis of variance and performance of parents and their F_2 population: Analysis of variance showed significant differences for yield and its related traits of upland cotton (table 2). It was observed that in parental lines, CIM-446 gave higher YP (113.6g) followed by CIM-534 (111.5 g) and MNH-814 (110.6 g). Whereas, F_2 progenies of CIM-534×MNH-814 had higher YP (121.7 g) followed by progenies from CIM-534×BH-118 (115.1g) as compared to their parental genotypes (table 3).

Traits	DF	MS
PH	19	125.5*
MB	19	7.35*
NFB	19	5.7*
NSB	19	24.49*
NBP	19	43.61*
BW	19	8.89*
YP	19	934.6*
GOT	19	2985*
SL	19	19.37*
FS	19	12.5*
FF	19	7.21*

Table 2: : Mean squares for yield and yield contributing traits of parent and F_2 genotypes.

DF: Degree of freedom, MS: Mean Squares, Significance at 5 % (*), PH= Plant height, NFB= Node of first fruiting branch, MB= Monopodial branches, BP= Numbers of boll per plant, BW= Boll weight, NSB= Seeds per boll, GOT= ginning out turn, SL= Staple length, FS= Fiber fineness, FF= Fiber fineness, and YP = Yield per plant

SL of parents ranged from 22.00 mm to 30.6 mm. The lowest value for SL was observed for genotype BH-167 and the highest SL was shown by NIAB 111. Whereas, among F_2 progenies SL ranged from 24.51 mm to 29.6 mm. The lowest SL was observed for the progeny of BH-36×CRSM-38 and the highest was shown by BH-167×CIM-577 progeny (table 3). FS of parents ranged from 29.5 g/tax to 36.4 g/tax. The lowest FS value was observed for genotype MNH-814 and the highest value was shown by genotype BH-36. However, FS values among F_2 progenies ranged from 27.8 g/tax to 34.3 g/tax. The lowest value for FS was shown by the progeny of BH-36×MNH-814 and the highest value was observed for CIM-534×BH-118 (table 3). Values of FF for parents ranged from 3.9 µg/inch to 4.8 µg/inch. The lowest value for FF was observed for genotype NIAB-111 and the highest value was observed for CRSM-38; while for F_2 progenies FF values ranged 3.5 µg/inch to 4.3 µg/inch. The lowest value for FF was shown by the progeny of N111×MNH-814 and the highest value was observed for CIM-577×CRSM-38 progeny (table 3).

Genetic variability: Maximum values of PCV were shown by traits like YP (53.18), FS (52.24), MB (38.81), and BW (29.49). Similarly, maximum values of (GCV) were shown by traits such as YP (50.71), FS (47.59), MB (32.15), and BW (24.00) as shown in (Figure1). High estimates of H^2 were observed for YP (90%), PH (85%), NSB (77%), BW (66%), SL (64%) and BP (62%; Figure 1). A high value for GA was shown by YP (60) and PH (20). However, low values of GA were observed for NFB (3.23), BP (1.02), BW (1.4), SL (4.82), and GOT (5.1) as shown in (figure 1).

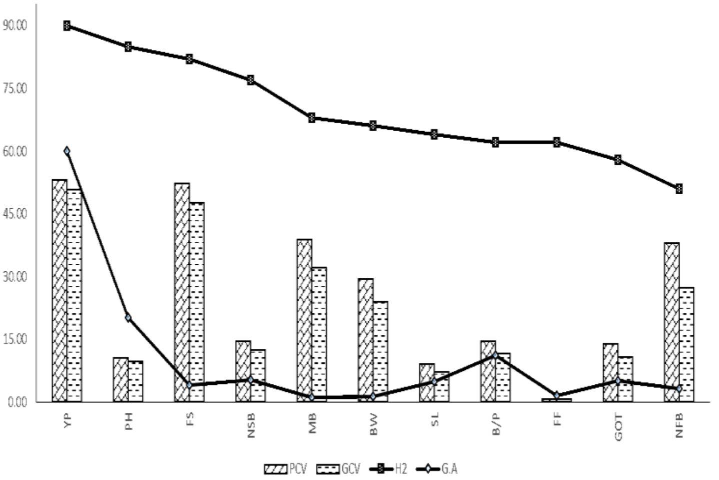

Figure 1: Phenotypic and Genotypic coefficient of variation, Heritability Broad sense and Genetic Advance of yield and yield contributing traits of parent genotypes and F_2 population.

Genotypes	PH	MB	NFB	NSB	BP	BW	GOT	SL	FS	FF	YP
BH-167	112.1	2.2	6.9	19.3	36.5	2.7	35.1	22.0	32.6	4.7	98.1
CIM-577	122.3	1.4	7.4	25.3	27.7	3.7	36.6	28.0	34.5	4.3	102.4
CIM-446	119.1	1.3	9.6	24.3	31.5	3.6	35.2	27.0	33.1	4.7	113.6
CRSM-38	123.0	2.1	9.1	18.7	22.9	2.8	33.5	29.7	32.3	4.8	64.1
BH-36	124.2	1.5	7.5	25.9	25.0	3.2	33.1	28.2	36.4	4.3	80.1
NIAB-111	106.4	2.9	8.7	18.3	29.1	2.9	36.2	30.6	35.1	3.9	84.3
MNH-814	112.3	2.1	6.9	26.7	31.6	3.5	34.9	27.9	29.5	4.1	110.6
CIM-534	117.0	1.8	8.7	27.4	33.8	3.3	34.6	29.7	33.3	4.5	111.5
CIM-707	101.4	2.2	8.3	24.3	30.1	2.8	33.1	30.2	30.2	3.9	72.4
BH-118	115.0	1.4	9.0	19.6	31.3	3.0	32.7	27.8	32.5	4.1	110.3
BH-167×CIM-577	110.2	2.0	6.9	21.2	32.0	3.1	36.1	29.6	33.4	4.2	99.2
CIM-446×CRSM38	118.8	1.5	9.8	21.6	29.0	3.2	34.2	27.2	31.5	3.9	92.9
CIM-577×CRSM-38	118.2	1.7	8.2	20.3	25.7	3.0	35.1	25.2	31.5	4.3	77.1
BH-36×CRSM-38	112.1	1.9	6.5	22.2	27.4	3.3	32.4	24.5	32.9	4.0	90.4
NIAB-111×MNH-814	101.0	2.1	5.9	21.3	29.8	3.1	32.7	27.1	30.6	3.5	92.3
CIM-534×MNH-814	109.1	1.7	7.4	25.4	35.8	3.4	33.2	26.1	31.4	4.2	121.7
CIM-577×MNH-814	116.1	1.2	7.5	24.2	31.5	3.6	32.2	27.4	33.4	3.9	113.4
BH-36×MNH-814	114.3	1.8	5.5	24.4	26.7	3.5	34.1	28.2	27.8	3.8	93.4
CIM-534×BH-118	105.4	1.6	9.2	21.4	31.2	3.4	35.1	26.5	34.3	4.2	115.1
CIM-707×NIAB-111	112.5	2.4	8.1	23.2	25.3	2.9	34.3	28.1	28.2	3.7	75.21

Table 3: Mean values of yield and yield contributing traits of parent genotypes and F_2 population.

PH= Plant height, NFB= Node of first fruiting branch, MB= Monopodial branches, BP= Number of boll per plant, BW= Boll weight, NSB= Seeds per boll, GOT= ginning out turn, SL= Staple length, FS= Fiber fineness, FF= Fiber fineness and YP = Yield per plant.

Correlation: In correlation studies, a significant and positive association was observed between YP and traits like PH (0.63**), NSB (0.58**), BP (0.49*), and GOT (0.53**). While, positive but non-significant correlation of YP with BW (0.21), FS (0.29), and FF (0.19) was also observed. However, a negative but non-significant correlation of SL was observed for yield contributing traits and with YP (table 4).

DISCUSSION: PCV and GCV are the fundamentals for the estimation of genetic variability in crop species (Ahmad *et al.*, 2011). PCV and GCV estimates of plant traits are required to access heritable genetic variation in crop species. Both heritable and non-heritable variations exist in crop species (Sami *et al.*, 2013). Heritable variations are estimated in terms of GCV; while, non-heritable variations were estimated in terms of PCV. Small differences between values of PCV and GCV indicated that traits under study were less affected by the environment and variation which was shown by traits was due to the inheritance of genotypes (Joshi and Patil, 2018). In the present study, PCV was somewhat higher than GCV in all traits. This is the indication of the slight impact of the environment on the expression of all traits. However, traits like YP, FS, MB, BW, and node of NFB showed higher estimates of PCV and GCV, from which it can be concluded that the selection of genotypes based on the phenotypic performance of such traits would be fruitful for genetic improvement (Ahsan *et al.*, 2015).

Similarly, H^2 is another tool for the study of genetic variability; its estimates the presence of genetic variations and is helpful in the determination of variation flow from one generation to the next generation. But, estimates of H^2 are also affected by environmental factors which cause fluctuation in these values. So, dependence only on H^2 is not significant for the selection of desired traits. The selection of superior genotypes could be made more precise by utilizing H^2 along with GA (Abebe *et al.*, 2017). Therefore, H^2 along with GA were calculated for all traits under study. High values of H^2 and GA were observed for YP and PH; while, BP showed a high value of $H^{2,}$ and the value for GA was moderate, which indicates that these traits were under the influence of the additive type of gene action that was fixable. So, phenotypic selection for such traits will be effective in early breeding populations.

	PH										
PH	1	**NFB**									
NFB	0.19	1	**MB**								
MB	0.44*	0.30	1	**BP**							
BP	0.63**	0.25	0.32	1	**BW**						
BW	0.57**	-0.09	0.49*	-0.55**	1	**NSB**					
NSB	0.54**	0.31	-0.25	0.14	0.32	1	**GOT**				
GOT	0.43*	-0.20	0.51*	-0.15	-0.62**	0.21	1	**SL**			
SL	-0.05	0.44*	0.28	0.13	-0.12	-0.04	0.16	1	**FS**		
FS	-0.16	0.26	0.10	0.24	-0.08	-0.20	0.19	0.18	1	**FF**	
FF	0.24	0.14	0.31	0.22	0.19	-0.32	-0.11	-0.14	0.23	1	**YP**
YP	0.63**	0.49*	0.36	0.46*	0.21	0.58**	0.53**	-0.07	0.29	0.19	1

Table 4: : Phenotypic correlation of yield and yield contributing traits of parent and F_2 population.

Significance at 5 % (*) significance at 1 % (**), A positive and highly significant correlation for YP was observed for traits such as PH (0.63**), NSB (0.58**) and GOT (0.53**). Similarly, traits like BP (0.49*) and NFB (0.49*) were positively and significantly associated with YP. However, positive but non-significant inter-linkage of YP with traits such as BW (0.21), FS (0.29), and FF (0.19) was also observed. Moreover, a non-significant and negative interrelationship of SL was observed for YP and some of the yield contributing traits.

Ahsan *et al.* (2015) observed higher H^2 estimates for PH and YP. Likewise, Raza *et al.* (2016) also observed higher values of H^2 for YP, plant height, and boll per plant. However, higher GA for YP and PH as well as moderate GA for BP was reported by Ahsan *et al.* (2015). While rest of the traits represented high to moderate values of H^2 along with a low value of GA indicating that these traits were heritable but variation is non-fixable. Therefore, selection for such traits should be delayed to later generations. In-plant breeding, correlation analysis has a significant role in the determination of genetic linkage between different traits. Therefore, correlation studies help make an indirect selection for traits improvement. So, it is preferred to make an indirect selection of yield contributing traits with higher H^2 values. In the present study, YP was seen to be positively and significantly inter-linked with PH, BP, NSB, and GOT. While, a positive and non-significant association of YP was recorded with MB, NFB, BW, FS, and FF. So, to improve YP, selection criteria should be based on above-mentioned traits. Therefore, to improve YP fruitful selection can be made based on PH, BP, and NSB as PH is positively correlated with yield contributing traits like NFB, BP, BW, and NSB. Similarly, BP is also a major yield contributor and has a positive association with PH and NSB (Komala *et al.*, 2018). Moreover, a positive correlation of BP with PH was also reported by (Rehman *et al.*, 2020). However, NSB also had a pivotal role in yield improvement as it was positively interlinked with yield as well as with PH and BP. So, selection based on NSB would be fruitful in yield enhancement. Similarly, a Positive correlation of NSB with YP was also observed by Rai and Sangwan (2020). The node of first fruiting branch also positively correlated with PH, BP, NSB and YP which suggested that in early breeding generation fruitful selection can be made based on NFB to improve YP and earliness. Positive inter-relationship of NFB branch with YP and BP was reported by Iqbal *et al.* (2006). Similarly, a positive association of NFB with PH and YP was also reported by Singh and Narkhede (2010).

GOT was significantly and positively interlinked with YP but the correlation with traits like NFB, BP, BW and FF were negative. So, selection based on ginning out turn in an early breeding generation will not be fruitful. Yaqoob *et al.* (2016) reported a positive association of GOT with YP. Iqbal *et al.* (2006) recorded a negative association of GOT with NFB, BP, BW, and FF. A positive association of MB with YP was observed which suggested that selection for yield improvement based on MB is also possible but higher MB is not preferable due to high insect pest infestation on such branches (Munir *et al.*, 2018). Therefore, to improve yield, selection criteria for traits should be based on PH and NSB as these traits are significantly and positively associated with YP and its contributing traits like NFB, BW, and BP. A positive correlation of FS and FF was observed for BP and YP, which indicated that YP can be improved without compromising fiber quality. However, the negative association of SL with PH, BW, NSB, and YP suggested that care should be followed in the selection of SL for YP improvement as SL is negatively associated with yield and its contributing traits. A negative association of YP with staple length was observed by Karademir *et al.* (2010). Moreover, Yaqoob *et al.* (2016) also reported similar findings of fiber traits with YP. However, this negative inter-linkage of SL with other traits could be minimized by making further crosses in segregating populations by using a specific matting design.

CONCLUSION: From the results it can be concluded that all parental genotypes and their F_2 progenies showed significant differences for all traits. The magnitude of variability can be accessed by PCV and GCV values. Direct selection could be made for the traits which showed higher PCV and GCV values. However, traits with low PCV and GCV values indicate that scientists have to explore more sources of variation to make improvements to such traits. All traits showed moderate to high H^2, which suggested that all traits are heritable. Moderate to high GA values of traits indicated further improvement of such traits. Traits like PH, NSB, BP, and GOT showed significant association with YP. Parent genotypes such as CIM-446 and CIM-534 along with F_2 progeny CIM-534×MNH-814 showed maximum YP; therefore, these genotypes and F_2 progeny could be explored for yield improvement in future crop breeding programs.

CONFLICT OF INTEREST: All authors have no conflict of interest.

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