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ANALYSIS OF GENETIC VARIABILITY AND PATH COEFFICIENT FOR YIELD CONTRIBUTING TRAITS IN ADVANCED LINES OF COTTON (*Gossypium hirsutum* L.)

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Cotton is industrial and one of the important cash crops in Pakistan. Warm environment is required for its cultivation. The present study aimed to assess genetic variation and path analysis for yield and yield contributing traits in advanced cotton lines under high temperature stress natural field conditions and to find out lines with desirable characteristics and high yield productivity. The experimental material consisted of six advanced lines of cotton along with the two standard varieties. The experiment was laid out in a randomized complete block design (RCBD) with three replications. Different yield and yield contributing traits and fiber quality parameters were studied. Analysis of data was carried out by using different statistical tools. Based on morphological results of advanced lines, NIAB-4-44-3 recorded high mean performance for yield and yield components and produced highest seed cotton yield per plant. NIAB-4-79-2 depicted the lowest number of gossypol glandes on different parts of cotton flower and boll i.e. thalamus, pedicle, calyx, boll surface. NIAB-4-100-5, NIAB-4-79-2 and NIAB-4-44-3 showed highest values for ginning out turn, micronaire, seed cotton yield and fiber strength. Sympodia per plant and 10th sympodial branch length were positively correlated with total number of bolls per plant. From these studies it is concluded that the morphological and fiber quality traits can be considered while making selection for genetic improvement of cotton.

Keywords: Cotton, lines, genetics, yield, quality, selections

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INTRODUCTION

Cotton is an important fibre crop in the world including Pakistan (Smith *et al.*, 2014). It has more than 50 species in which cultivated cotton species includes two diploids (*Gossypium herbaceum* and *Gossypium arboreum*) and two tetraploids (*Gossyium hirsutum* and *Gossypium barbadense*). Tetraploids are cultivated over 80% area of the world. However, Asia and the Middle East are famous for diploid cottons (Smith and Cothren, 1999). In Pakistan, among all the other crops, cotton (*G. hirsutum* L.) is the chief cash and textile crop in economic perception. Hence, it is the main source (roughly 62%) of our overseas exchange earnings. Cotton cultivation helps the textile industry and offers 40% employment to industrial labor. Besides its use in clothing industry, cotton seed is the major source of cooking oil (60-70% of total edible oil) (Anonymous 2017-18a) , cotton seed cake and proteins that are rich with the essential amino acids (Zhang *et al.*, 2008; Zhang and Oik, 2015). Cotton industry plays a vital role in the economy of Pakistan as cotton ~~ginning~~ has a 2.34 percent contribution in agriculture sector and in GDP its share is 0.46 percent as agriculture accounts for 19.53 percent of GDP and employed bulk of the total work force (Anonymous, 2017-18b). In Pakistan, cotton industry includes 1263 ginning factories, 517 textile mills, 13.41 million spindles, 9084 looms and 2622 oil expelling units. It also produces cotton seed which accounts 64% of the edible oil (Khan *et al.*, 2010; Anonymous, 2018).

At this time in Pakistan the cotton industry face problems in rising production costs and static return (Haidar *et al.*, 2007). In the present scenario we required development of high yielding genotypes with low cost of production to compete for land with other food crops, as well as with synthetic fibres. For this purpose, genetically diversity is required by using different quality traits and related characters to increase the crop productivity (Arshad *et al.*, 1993).

Genetic performance of different genotypes can be determined with the help of various parameters e.g genotypic and phenotypic correlations, genetic advance and path analysis of different commercial traits. Morphological/agronomical characters like 1st sympodial node number, 10th sympodial branch length, plant height, sympodial branches per plant, monopodial branches per plant, ~~and~~ cotton leaf curl virus (CLCuV) index and quality/fiber traits like ginning out turn, fiber strength, fiber length, fiber fineness etc. are important for any breeding program (Batool *et al.*, 2010). Fiber quality traits must be improved to maintain the economic viability. Gossypols contents are host plant resistance traits and have also have effect on oil quality. To determine the simple relation between the traits, correlation coefficient is an important biometrical tool but it may not give specific results about final selection criteria (Salahuddin *et al.*, 2010). Path analysis is a biometric tool that can be used to set a selection criteria for complex traits in agriculture (Azhar and Rana, 1993; Kumari and Subbaramamma. 2006; Abbas *et al.*, 2013).

Knowledge about relation of yield and its path is essential for selecting the yield and fiber quality traits. Heritability is an efficient key to understand the possibilities of transmitted attribute from parents to next progeny. It is also an effective statistical tool that facilitates the plant breeder to assess the environmental effect on all the traits in breeding program (Kazerani, 2012). Hence, breeders should have the maximum knowledge about heritability and genetic advance to develop the breeding plan according to their ~~purposes~~ objectives (Cheng *et al.*,2016;Guedes and Soto-Blanco. 2010)

Genotypes with their high genetic potential and desirable performance for various morphological parameters are desirable for achieving this purpose (Ahmad *et al*., 2008: Khan *et al*., 2014). Moreover, newly developed lines/germplasm needs screening before release. Hence, identification of various yield attributes is required for effective selection. The aim of these experiments was to determine genotype specific morphological plant measurements for field grown plant material. To understand the importance of these traits through the estimation of genetic parameters. And to identify suitable genotypes possessing high yield potential under natural field conditions and having combination of useful genetic traits.

MATERIAL AND METHODS

Field experiments were conducted to evaluate advanced cotton ~~breeding~~ lines for different yield and yield contributing traits and fiber quality. The simple approach of measurements of yield, yield contributing traits and whole plant fruit retention under natural field conditions was adopted to identify suitable genotypes.

***Experimental design and plant material*:** The research work was conducted at Nuclear Institute for Agriculture and Biology (NIAB), Faisalabad during 2016-2018. During 2016-17, the experimental material consisting of different entries were evaluated in preliminary yield trial (PYT) along with standard varieties. Whereas during 2017-18, six advanced lines of cotton compared with two standard/check varieties (FH-Lalazar and MNH-886) were evaluated in advanced yield trial (AYT) (Fig. 1) (Table 1). The experiment was planted in a Randomized Complete Block Design (RCBD)

Figure 1. Field view of six advanced cotton lines along with two standard varieties

with three replications. Row to row distance of 2.5 feet and plant to plant distance of 1 feet was maintained. Nitrogen was applied at a rate of 150 kg ha^{-1} as hydrous ammonia and phosphorous at a rate of 60 kg ha^{-1} as mono-ammonium phosphate prior to planting to ensure adequate nitrogen and phosphorous nutrition for the crop.

Table 1. Genotypes used in experiment and their pedigrees

Sr.	Genotypes	Pedigree
1	NIAB-4-100-5	NIAB-777 x (FH-1000 x Cocker-312)
2	NIAB-4-79-2	NIAB-777 x (FH-1000 x Cocker-312)
3	NIAB-4-54	NIAB-777 x (FH-1000 x Cocker-312)
4	NIAB-1-1	NIAB-846 x (FH-1000 x Cocker-312)
5	NIAB-14-43-19	NIAB-824 x (FH-1000 x Cocker-312)
6	NIAB-4-44-3	NIAB-777 x (FH-1000 x Cocker-312)
7	MNH-886 (check)	(FH-207 x MNH770) x Bollguard
8	FH-Lalazar (check)	FH-207 x Nucot-33B

***Evaluation of advanced lines*:** All these ~~generations~~ lines were raised and evaluated at NIAB. The soil at experiment site is clay loam having pH=7.2-7.5, EC value of 0.8-1.5 dS.m^{-1}/. Agronomic practices (hoeing, removal of weeds both by manually and use of weedicides, irrigations, application of fertilizers etc), were carried out. Plant protection measures by spray of insecticides/pesticides were carried out to control or minimize the sucking (thrips, jassid, whitefly, aphid) and bollworm (*Heliothious*, spotted, pink and army bollworms) insect pests.

***Recording of data for morphological parameters*:** Five plants were randomly selected from each replicate and data were recorded for plant height (cm), 1st sympodial branch node number, monopodial branches per plant, sympodial branches per plant, 10thsympodial branch length (cm), cotton leaf curl virus (CLCuV) incidence, total number of bolls per plant and seed cotton yield per plant. Plant height of all genotypes was measured at maturity from ground level to the apex with the help of metal rod and expressed in cm. First sympodial node is the lowest main stem node above the cotyledonary node from which a sympodial branch arises. Usually it occurs at 5 to 7 node at the main stem. It was also noted for all selected plants. Monopodial branch is a continuous, non-segmented, vegetative branch typically arising from lower nodes of the main stem (as opposed to the fruiting branch or sympodial). Sympodial branch is a segmented fruiting branch on cotton plant from which flowers and resulting bolls arise. This is in contrast to monopodial branch which are vegetative stems including the main stem that does not give rise the bolls directly. Total number of sympodial branches per plant was recorded. 10th sympodial branch length was also recorded which has significance to assess fruiting points, bolls formation/setting, earliness and ultimately yielding ability. No. of bolls both open and un-open were recorded. The CLCuV incidence was recorded by observing the symptoms and the abundance of the white fly or the thickening of the leaf veins by following the methodology of Akhtar *et al.*(2010).

***Recording of gossypol gland distribution*:** Gossypol glands at different parts of flower and bolls i.e. thalamus, pedicle, calyx, boll surface were recorded. The number of gossypol glandes (black spots) were observed on the different parts of the unopened bolls of cotton and quantified under magnifying glass. Ten bolls per genotype were taken for this purpose. Gossypol glands were counted on thalamus, pedicle, calyx and boll surface.

***Fiber quality parameters analysis*:** The fiber quality parameters like micronaire value (µg/inch), fiber length (mm), fiber strength (g/tax) were recorded using High Volume Instrument (HVI) as well as manually operated instruments at NIAB. Ginning out turn percentage was recorded by ginning the total seed cotton of the selected plants expressed in grams. Then weighing the cotton lint, dividing it with total weight of seed cotton and multiplying with 100 to calculate ginning outturn percentage.

***Statistical analysis*:** The data are presented as average of two years and consisting of three replicates along with standard deviation. Analysis of variance (ANOVA) was carried out following Steel *et al*. (1997). Genetic parameters (genotypic and phenotypic variance, heritability, genetic advance and principal component analysis), genotypic and phenotypic correlations and direct and indirect effects of different traits were studied according to Singh and Choudhry (1985); Dewey and Lu (1959). Heritability and genetic advance were calculated following the methodology of Kwon and Torrie (1964). In addition, data was analysed by using Fisher's least significant differences (LSD).

RESULTS

The advanced lines exhibited distinctive features like average stature, high number of bolls, well opening and yield potential as compared to parents and standards. Morphological differences were observed from seedling stage to maturity in advanced lines. Seed cotton yield along with other traits viz; plant heigh (cm), monopodial branches/plant, sympodial branches/plant, 1st sympodial branch node number, 10th sympodial branch length, total number of bolls/plant and seed cotton yield were recorded from selected single plants in all advanced lines and standards and were analyzed.

***Performance of advanced lines for morphological parameters*:** The cotton leaf curl virus (CLCuV) disease prevalence was non-significant among all the genotypes. The maximum grade 3 was observed in NIAB-1-1 which was non-significantly different with NIAB-4-54, MNH-886 and minimum value 1.53 was observed in FH-Lalazar which was non-significantly different with NIAB-4-100-5, NIAB-4-79-2, NIAB-14-43-19 and NIAB-4-44-3. Plant height was observed as significantly different. Maximum value of plant height was observed in genotype NIAB-4-100-5 which was

155.5 cm. Minimum value of plant height was observed in genotype FH-Lalazar which was 112.67 cm. The range of plant height was from 112.67 to 155.5 cm. Non-significant difference was observed for 1st sympodial node number among the genotypes. Highest value (5.67) was observed in NIAB-4-100-5 and lowest (4.73) in NIAB-14-43-19 and MNH-886. The genotypes showed highly significant differences in monopodial branches per plant. Maximum value (3.3) of monopodia per plant was observed in NIAB-4-54. Minimum value (1.6) of monopodial branches per plant was observed in NIAB-4-100-5. The range of monopodial branches per plant was from 1.6 to 3.3. Sympodial branches per plant were observed as statistically highly significant for all the genotypes. Range of sympodial branches per plant was from 26.9 to 18.27. Maximum value (26.9) was observed in NIAB-4-100-5 and minimum value (18.27) was observed in FH-Lalazar. 10th sympodial branch length (cm) was observed as statistically non-significant for all genotypes. Higher value of 10th sympodial branch length was (22.3) perceived in MNH-886 and lower value was (12.9) in FH-Lalazar. Range of total number of bolls per plant was from 47.47 to 72.9. Maximum value (72.9) was observed in NIAB-4-100-5 and minimum value (47.47) was in FH-Lalazar**.** Total number of bolls per plant was statistically significant ($p<0.05$) for all genotypes. The genotypes showed non-significant differences for seed cotton yield per plant. The range of yield per plant was from 190.58 g to 257.4 g. Maximum yield (257.4 g) was recorded in NIAB-4-44-3 and minimum (190.58 g) was in NIAB-4-54. Mean values and analysis of variance of mean square of eight genotypes of cotton are given in Table 2 and Table 3, respectively.

Distribution of gossypol glands on different parts of the cotton flower and boll**:** Significant variations were observed for the number of gossypols in thalamus, pedicel and boll surface. No significant variations existed for the number of gossypol glands on calyx. The number of gossypol glands was highest in thalamus and pedicel of NIAB-4-100-5 while lowest in NIAB-4-79-2. The boll of cotton plant shows highly significant differences in response to gossypol with the maximum spots on the bolls of MNH-886 and the minimum spots on the boll of NIAB-4-79-2. Distribution of gossypol glands on different parts of the cotton flower of advanced lines of cotton and standard checks are given in Figure 2.

Fiber quality analysis of advanced lines**:** Ginning out turn (GOT %), fiber fineness (Micronaire), fiber length and fiber strength were recorded for all the candidate lines. Higher ginning out turn (39.90) was observed for NIAB-4-100-5 and minimum GOT (37.62) was observed for NIAB-4-54. Least significant difference was observed in micronaire. Maximum value (4.9) was observed in NIAB-4-79-2 and NIAB-4-44-3 and lowest value (4.0) was observed for NIAB-14-43-19. Maximum fiber length (29.4) was observed in standard variety FH-Lalazar and minimum fiber length (26.00) was in second standard variety MNH-886. Fiber strength was observed less variant in all the genotypes. Maximum fiber strength was observed in NIAB-4-100-5 and minimum was in NIAB-4-79-2. Seed cotton yield (4792 kg ha^{-1}) was highest in NIAB-4-79-2. The lowest (2706 kg ha^{-1}) yield was observed

Table 2. Mean values for different morphological traits of cotton

Genotypes	**PH (cm)**	**1st SB NN (No)**	**MB (No.)**	**SB (No.)**	**10th SBL (cm)**	**CLCuV (score)**	**Total Bolls (No.)**	**Y/Plant (kg.ha^{-1})**
NIAB-4-100-5	155.50 **a**	5.67 **ns**	1.60 **c**	26.93 **a**	20.20 **ns**	2.00 **ns**	72.93 **a**	201.30 **b**
NIAB-4-79-2	137.20 **b**	4.93	2.87 **ab**	23.33 **b**	15.47	1.80	65.67 **a**	204.70 **b**
NIAB-4-54	129.40 **bc**	5.27	3.33 **a**	22.07 **b**	17.93	2.07	62.67 **a**	190.58 **b**
NIAB-1-1	134.07 **bc**	5.13	2.93 **ab**	23.87 **b**	16.13	3.00	68.40 **a**	254.48 **a**
NIAB-14-43-19	124.67 **c**	4.73	2.00 **bc**	23.00 **b**	16.73	2.07	60.47 **a**	199.93 **b**
NIAB-4-44-3	124.00 **c**	5.07	1.80 **c**	23.27 **b**	17.20	1.73	61.80 **a**	257.40 **a**
MNH-886	133.40 **bc**	4.73	3.07 **a**	22.67 **b**	22.33	2.13	72.40 **a**	206.60 **b**
FH-Lalazar	112.67 **d**	4.93	2.93 **ab**	18.27 **c**	12.93	1.53	47.47 **b**	239.10 **a**
St. Deviation	13.16	0.41	0.79	2.55	4.64	0.61	10.21	26.85

PH=Plant height,1st SB NN=1st sympodial branch node number, ns= non-significant, MB= Monopodial branches, SB=Sympodial branches, 10thSBL= 10thSympodial branch length, CLCuV score =cotton leaf curl virus disease score, TB= Total bolls,

Table 3. Significance of different morphologica traits in cotton

Source of Variation	**PH**	**1st Sp NN (No.)**	**MB (No.)**	**SB (No.)**	**10th SB L (cm)**	**CLCuV score**	**Total Bolls (No.)**	**Y/Plant (kg.ha^{-1})**
Replication	113.202	0.012	0.622	1.085	44.127	0.782	159.740	108.323
Genotypes	463.798**	0.284ns	1.303**	17.034**	24.956ns	0.575ns	199.265*	2134.107**
Error	36.242	0.128	0.298	2.024	16.519	0.212	48.641	101.495

PH=Plant height,1st SB NN=1st sympodial branch node number, MB= Monopodial branches, SB=Sympodial branches, 10thSBL= 10thSympodial branch length, CLCuV=cotton leaf curl virus disease score, TB= Total boll

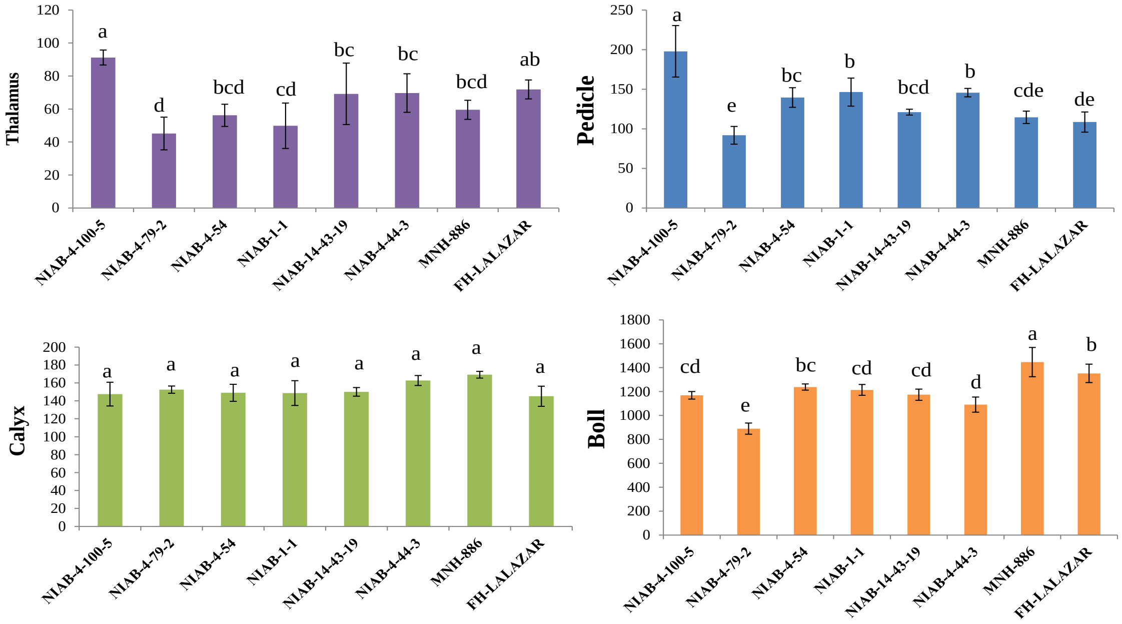

Figure 2. Distribution of gossypol glands on different parts of the cotton flower and boll of advanced lines of cotton developed at NIAB with two standard varieties

in FH-Lalazar. Mean values of fiber analysis are given in Table 4.

***Genotypic and phenotypic correlations of morphological parameters*:** Genotypic and phenotypic correlations were calculated for all possible combinations among all morphological traits. Mostly genotypic correlations were higher than the phenotypic correlations which indicate that the genetic factors have dominant effects on morphological parameters than the environmental ones (Haidar and Khan, 1998.a). Sympodial branches per plant and 10th sympodial branch length were positively and highly significantly correlated with total number of bolls per plant and ultimately correlated with seed cotton yield at genetic level. The total quantity of bolls on each plant was also indicated positive and noteworthy genotypic association with seed cotton yield per plant. These correlations matrixes are given in Table 5.

***Direct indirect effect of different parameters*:** Positive direct effect of 1st sympodial node number (0.5238) and total number of bolls per plant (0.7735) was observed on seed cotton yield. The data displayed in the Table 6 indicates that the direct effects of the monopodial branches per plant, sympodia per plant and 10th sympodial branch length on seed cotton yield per plant was negative.

***Heritability and genetic advance*:** Estimates of broads sense heritability of eight morphological characters were measured that showed significance at 5% possibility level for plant elevation, monopodial branches on each plant, sympodial branches on each plant, sum of bolls on each plant and seed cotton yield of each plant as the values of heritability are higher than their standard errors. Genetic advance at specific selection intensity is also considered valuable in trait selection. Highest value of genetic advance was perceived for

Table 4. Yield (kg.ha^{-1}) and mean values of fiber analysis for advanced lines of cotton

Genotypes	GOT (%)	Mic. (µg/inch)	Length (mm)	Strength (g/tax)	Yield (kg.ha^{-1})
NIAB-4-100-5	39.90 **ns**	4.60 **ns**	28.20 ns	30.40 **ns**	4200 **ab**
NIAB-4-79-2	37.96	4.90	27.73	24.30	4792 **a**
NIAB-4-54	37.62	4.60	28.32	26.10	3801 **b**
NIAB-1-1	38.68	4.70	26.20	24.70	4043 **ab**
NIAB-14-43-19	38.17	4.00	27.00	25.80	3601 **b**
NIAB-4-44-3	39.60	4.90	27.51	27.00	3595 **b**
MNH-886 (St)	38.11	4.50	26.00	25.40	3881 **b**
FH-Lalazar (St)	38.53	4.80	29.40	25.50	2706 **c**
SD Total	3.38	0.74	2.96	3.73	692.50
Within	3.95	0.83	3.31	3.90	473.26

GOT= ginning out turn, ns= non-significant, SD= standard deviation

Table 5. Genotypic (rg) and phenotypic correlation (rp) matrix of different morphological parameters in cotton

Variable	Cor.	PH (cm)	1st SB NN (No.)	MB (No.)	SB (No.)	10th SB L (cm)	CLCuV score	T. Bolls (No.)	Yield (kg.ha^{-1})
PH	**rg**	1.0000	0.9414^{+}	-0.3152	0.9403^{+}	0.9457^{+}	0.5150	0.9740^{++}	-0.4158
	rp	1.0000	0.6553**	-0.3230**	0.9019**	0.6032**	0.3130**	0.8547**	-0.3945**
1st SB NN	**rg**		1.0000	-0.4569	0.8923^{+}	0.2343	0.2116	0.5168	-0.0813
	rp		1.0000	-0.3303**	0.5695**	0.1820**	0.1114**	0.3271**	-0.0732**
MB	**rg**			1.0000	-0.5249	-0.1904	0.3250	-0.2578	-0.1303
	rp			1.0000	-0.5649**	-0.1490**	0.2081**	-0.1521**	-0.1091**
SB	**rg**				1.0000	1.0379^{++}	0.5512	1.0295^{++}	-0.2317
	rp				1.0000	0.5861**	0.3913**	0.8504**	-0.2197**
10th SB L	**rg**					1.0000	0.5471	1.0880^{++}	-0.6960
	rp					1.0000	0.2171**	0.8119**	-0.4232**
CLCuV score	**rg**						1.0000	0.8417^{+}	0.1881
	rp						1.0000	0.5277**	0.1691**
Total Bolls	**rg**							1.0000	0.9767^{++}
	rp							1.0000	-0.2902**
Yield	**rg**								1.0000
	rp								1.0000

Table 6. Direct and Indirect effect of different morphological parameters in cotton

Variables	PH (cm)	1st SB NN (No.)	MB (No.)	SB (No.)	10th SB L (cm)	CLCuV score	T.Bolls (No.)	rg
PH	**(-0.2625)**	0.2212	0.0960	-0.3414	-0.2062	-0.0013	0.5670	-0.4158
1st SB NN	-0.1109	**(0.5238)**	0.0708	-0.1257	-0.0744	-0.0063	0.1521	-0.0813
MB	0.0878	-0.1292	**(-0.2871)**	0.2469	0.0834	-0.0133	-0.0618	-0.1303
SB	-0.2209	0.1622	0.1746	**(-0.4059)**	-0.1588	-0.0360	0.4913	-0.2317
10th SB L	-0.1305	0.0939	0.0577	-0.1553	**(-0.4149)**	0.0096	0.5820	-0.6960
CLCuV	-0.0017	0.0167	-0.0194	-0.0743	0.0202	**(-0.1969)**	0.0712	0.1881
Total Bolls	-0.1925	0.1030	0.0229	-0.2578	-0.3122	-0.0181	**(0.7735)**	0.9767

plant stature, sympodial branches per plant, 10th sympodial branch length, total bolls on each plant and yield of each plant. Monopodial branches per plant, 1st sympodial node number and CLCuV incidence showed very low values of genetic advance ~~are~~ (Table 7).

Table 7. Heritability (h^2_{BS}) and Genetic advance of different parameters at 10% selection intensity

Traits	h^2_{BS}	ΔG (10%)	REGA (%)
PH	0.9219±0.4698	20.11	15.31
1st Sp N	0.5503±0.4950	0.30	6.03
Mp	0.7714±0.4759	0.89	0.68
Sp	0.8812±0.4709	3.68	72.85
10th Sp L	0.3381±0.5237	1.71	66.67
CLCV	0.6306±0.4867	0.48	2.11
Total Bolls	0.7559±0.4768	10.81	62.26
Yield	0.9524±0.4693	44.58	2183.62

DISCUSSION

The existing research was conceded to study heritability, genetic association, genetic advance, direct indirect effect and genetic variability for seed cotton yield and yield contributing traits among all the genotypes (Khokhar *et al.*, 2017). It has been shown in the present work that there were noteworthy variances in plant elevation, monopodial branches per plant, sympodial branches per plant, CLCuV incidence and seed cotton yield per plant and non-significant for other traits. Earlier it is reported that when we increase the quantity of bolls per plant, the yield of seed cotton of the plant is also improved (Hussain *et al.*, 2010). Sympodial branch on each plant has the straight influenced on the yield of the plant. Hence, this trait should be keeps in view while selection, so better genotypes with highest yield can be developed (Rahman *et al.*, 2013). Some important fiber quality traits were analyzed and it was seen that GOT, fiber length, fiber strength, fiber fineness and seed cotton yield (kg.ha^{-1}) are characters that should kept in mind while developing breeding program to increase seed cotton yield ~~per~~ (Khan *et al.*, 2014). Significant and positive correlation of seed cotton yield with some morphological traits and quality was earlier reported (Haidar and Khan, 1998ab; Haidar *et al.*, 1999).

Highly significant positive genetic and phenotypic correlation, high heritability and direct positive effect of sympodial branches per plant, 10th sympodial branch length and total number of bolls per plant were correlated with seed cotton yield. Earlier it is reported that seed cotton yield can be improved by using these traits (Farooq *et al.*, 2014). In our study monopodial branches on each plant indicated negative relationship with the yield and same results have been reported previously (Ekinci *et al.*, 2010; Rauf *et al.*, 2014). While sympodial branches on each plant displayed negative direct effect which has been also reported earlier (Ahuja *et al.*, 2006). Total bolls on each plant showed positive direct effect on yield (Asad *et al*., 2002) which also confirmed our results. It was reported that total number of bolls per plant showed positive correlation while plant height, sympodia per plant and monopodia per plant showed negative correlation with seed cotton yield which is accordance with the findings of our results (Salahuddin *et al.*, 2013). It was also reported that plant height showed positive correlation with seed cotton yield which are opposing with our findings (Arshad *et al.*, 1993). It was also reported by many researchers that number of bolls per plant showed positive and significant results towards seed cotton yield (Tyagi, 1987; Kumari and Subbaramamma 2006). These results are matched with our finding. Broad-sense heritability measures proportion of phenotypic variance among individuals in a population that results from genetic differences. Earlier, modest to high heritability evaluate for yield and yield paying traits were reported by many researchers. Previously high heritability joined with higher genetic advance for yield was reported (Abbas, *et al* 2013) which is according to our findings as plant height, sympodial branches per plant and total number of bolls per plant. Selection is effective when high heritability is combined with high genetic advance and this is due to additive gene action. Similarly, modest to high heritability for fiber length, fiber strength, cotton yield, boll weight, number of bolls and lint percentage was reported by other researchers (Srinivas *et al.*, 2014; Aziz *et al.*, 2014; Ahsan *et al.*, 2015)

***Conclusion*:** Based on morphological results advanced line NIAB-4-44-3 recorded high mean performance for yield and yield components and produced highest seed cotton yield per plant. NIAB-4-79-2 showed good performance and depict the lowest number of gossypol glandes on different parts of cotton flower and boll i.e. thalamus, pedicle, calyx, boll surface. NIAB-4-100-5, NIAB-4-79-2 and NIAB-4-44-3 showed highest values for ginning out turn, micronaire and seed cotton yield and fiber strength. The identified lines both for higher yield, better fibre quality and gossypol contents can be utilized as germplasm for cotton improvement.

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