



# New Potential Cotton (*Gossypium hirsutum* L.) Varieties for Farmers in Rain-Fed Agro-Ecologies of North Western Ethiopia

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## ABSTRACT

Seed cotton yield and fiber quality traits are controlled by many genes and also greatly affected by biotic and abiotic environmental factors. Hence, selection based on only yield would not be effective. In order to improve the yield potential of the cotton cultivars, an understanding of the relationship among various traits is of more importance. The current research was aimed to determine and record phenotypic and genotypic variation of elite cotton lines for utilization of the information in the breeding program to enhance cotton crop productivity and production in Ethiopia. Thus, 14 genotypes, five rows each, were evaluated in three replications at Homosha district of Benishangul-Gumuz. The results depicted significant differences ( $P \leq 0.05$ ) among the varieties for all the studied traits, exhibiting the availability of substantial genetic variability among the cultivars for studied traits. Hence, these promising cultivars can further be exploited in various breeding programs to improve various characters of the cotton genotypes. Furthermore, correlation analysis showed that sympodial branches plant<sup>-1</sup>, boll weight and bolls plant<sup>-1</sup> made significant and positive associations with seed cotton yield plant<sup>-1</sup>. Thus, selection for these traits will ultimately enhance the chances of increasing seed cotton yield plant<sup>-1</sup>. High heritability estimates were found for all studied traits with the exception of monopodial branches plant<sup>-1</sup>, indicating that these traits were inherited together and direct selection may be proved to be useful for these traits.

## INTRODUCTION

Cotton, the king of fiber crops, is one of the momentous and an important cash crop exercising profound influence on economics and social affairs of the world. Any other fiber crop cannot compete with cotton for its fiber quality. It is also known as "White Gold". Apart from world's leading natural fiber, cotton is world's second most important oilseed crop (Kohel, 1987). Primarily it is industrial raw material in textile manufacturing which provides employment to millions of people all over the world for various activities such as cultivation, seed production, marketing, industrial utilization and research.

Cotton is most widely cultivated crop in the world and has attained main focus of research of which upland cotton (*Gossypium hirsutum* L.) species meet 90% of the bulk world's cotton demand. Upland cotton belongs to the genus *Gossypium*, which consists of 45 diploid and five Allotetraploid species which are distributed mostly in tropical and subtropical areas of the world. Historically, natural hybridization has played an important role in the evolution of modern cultivated cottons (Wendel and Crown, 2003).

The genetic variability of a trait within a population is the proportion of observable differences in a trait between individuals within a population that is due to genetic differences. Factors including genetics, environment and random chance can all contribute to the variation between individuals in their observable characteristics. Heritability measures the fraction of phenotype variability that can be attributed to genetic variation (Raj *et al.*, 2008).

To develop high yielding varieties of cotton, genetic information regarding different quantitative and qualitative traits is helpful to cotton breeders to improve genetic architecture of the crop in a particular direction, to improve and attain the proper production level of the crop (Nadeem and Azhar *et al.*, 2004; Ali & Khan, 2007 and Abbas *et al.*, 2008). The use of existing genetic variability in the breeding material and the creation of new variability along with the underlining knowledge on the genetic behavior are of crucial importance for this purpose in a breeding program (Basal and Turgut, 2005; Abbas *et al.*, 2008; Ali *et al.*, 2008; and Ali and Awan, 2009).

To address the current demand and supply gap targeted, intervention works in developing high yielding and excellent quality lint genotypes should be one of the main components to step forward the cotton sector through exploiting the available genetic resources. To set proper breeding strategy and exploit genetic potential of existing genotypes, understanding of genetic variability is very crucial.

Yield is a complex polygenic character which is final product resulting from the interaction of yield attributing characters. For rational improvement of seed cotton yield, the understanding of relationship of component traits with yield is very essential to make effective selection and also simultaneous improvement of most characters. Keeping the above facts in view, the present study was, therefore, planned with the following specific objectives:

1. To estimate heritability of quantitative and qualitative traits of cotton genotypes.
2. To analyze the correlation of seed cotton yield with yield attributing components.
3. To assess and select high yielding potential varieties for rain-fed areas.

## MATERIALS AND METHODS

### Description of the study area

The experiment was conducted at Homosha district in Benishangul Gumuz Regional State in the western part of Ethiopia during the main cropping season of 2017/18. It is one of the potential area for cotton production in the Region.

Homosha is located 38 km north of Assosa town and 701 km west of Addis Ababa with an altitude of 1390 meter above sea level and found at 10°18.764' N latitude and 034°38.630' E longitude. This district has also a uni-modal rainfall pattern, which starts at the end of April and extends to mid of October. Its maximum rainfall is received during June to October (AsARC Report, 2013) while its major soil type is Nitosol with a dark reddish brown color (AsARC Report, 2011). And also, its optimum temperature range is 28 to 32°C.

### Experimental Materials and Design

In this study, a total of 14 genotypes including 12 elite genotypes and two check varieties were evaluated at Homosha (Table 1). These genotypes were obtained from Werer Agricultural Research Center (WARC). The genotypes were organized in a randomized complete block design with three replications. Five rows of 5 m length were used for each plot. Inter-row and intra-row spacing of 90 cm and 20 cm, respectively, were used to make up plot sizes of 22.5 m<sup>2</sup> (5 rows x 5 m x 0.9 m) each. This translates to a population of about 55,000 plants on a per hectare basis.

**Table 1. List of 14 cotton genotypes used in the study in Benshangul-Gumuze Regional State.**

Item number	Name of Genotypes	Pedigree/description	Selection number
1	WARC-1	HTO#052 x Deltapine 90	21-7
2	WARC-2	Cucurova1518 x LG-450	35-4
3	WARC-3	Deltapine 90 x Cucurova1518	37-7
4	WARC-4	Deltapine 90 x Stam-59A	38-8
5	WARC-5	Del Cero x GL-7	8-2
6	WARC-6	ISA 205H x Stam-59A	11-4
7	WARC-7	ISA 205H x Beyazealtin/5	16-2
8	WARC-8	HS-46 x Stoneville 453	19-2
9	WARC-9	HS-46 x Stoneville 453	19-8
10	WARC-10	Stam-59 A x Cucurova 1518	30-2
11	WARC-11	Stam-59 A x Cucurova 1518	30-6
12	WARC-12	Stam-59A x Europa-5	-
13	Deltapine 90 (Check)	n.a.; Introduced from the USA in the 1980's	-
14	Stam-59A (Check)	n.a.; Imported from Mali in 2004 through technology shopping.	-

n.a = Pedigree not available.

### Management Practices

All recommended agronomic practices which included land preparation to harvesting were followed as per the recommendations from research. Plantings were carried out in June. Recommended DAP and urea fertilizers (each at 100 kg per hectare) were applied at sowing and later after plant establishment. All DAP was applied at sowing time while urea was applied in split, 2/3 at sowing and 1/3 at initial flowering stage. To control grass and broad leaf weeds, two hand weeding were performed at critical stages of crop development. The first hand weeding was carried out 35 days after seedling emergence and the second weeding 65 days after emergence or 30 days after the first weeding.

### Measurement of phenological and growth parameters

Data of different traits were collected and recorded either from randomly selected plants or on a plot basis. Days to seedling emergence (DSE) was recorded as the number of days from plating to the time when 50% of the seedlings have emerged in each plot. Days to initial squaring (DIS) was recorded as the number of days from seedling emergence to the appearance of first squares in each plot. Days to initial flowering (DIF) was recorded as the number of days from seedling emergence to the appearance of first flowers in each plot. Days to 50% flowering was recorded as number of days from seedling emergence to a growth stage when about 50% of plants have flowered in each plot. Days to 65% boll opening was recorded as days from seedling emergence to the appearance of open bolls on about 65% of the plants in each plot. Plant height (PHt) was recorded by measuring the height of 5 randomly selected plants at maturity from ground level to the tip of the main stem and taking mean of the total. Number of nodes to the first sympodial branch (NFSB) was recorded from 5 randomly selected plants on a plot basis and counting the number of nodes from the base of a plant to the first sympodial or fruiting

branch. Number of bolls per plant were counted from 5 randomly selected plants and then averaged for each plot. The average weight (g) of 30 bolls measured from randomly selected plants at maturity and the total weight of seed cotton yield harvested from each plot weighed in grams per plot and converted into kilogram per hectare. Number of monopodial and sympodial branches per plant were counted from 5 randomly selected plants and then averaged for each plot.

**Seed Cotton yield per plant (gm):** Seed cotton yield per plant was recorded by weighing total seed cotton of each plant recorded in grams.

**Lint Percentage (GOT):** From each plant 50gm dry seed cotton was weighed and was ginned on roller ginning machine. Lint percentage from each plant was recorded by following formula.

$$\text{Lint percentage} = \frac{\text{weight of lint sample}}{\text{weight of seed cotton sample}} \times 100$$

**Lint yield:** The product of total weight of seed cotton yield per plot multiplied by lint percentage value for that plot.

### Data Analysis

#### Analysis of variance

Analysis of variance, phenotypic and genotypic variance and coefficient of variation were computed with SAS statistical software (9.0); heritability and genetic advance were computed using the excel Microsoft program.

Mean separation was conducted using Duncan's multiple range test (DMRT) at 0.05 probability level. The simple correlation coefficients were computed to determine the degree of association between pair of characters using PROC CORR procedure of SAS (SAS, 2002) program based on across location mean data.

**Table 2. Analysis of variance in randomized complete block design and expected mean square.**

Source of Variation	Df	Mean Square	Expected Mean Square
Replication	r-1	MSr	$\sigma^2e + g\sigma^2r$
Genotypes	g-1	MSg	$\sigma^2e + r\sigma^2g$
Error	(r-1)(g-1)	MSe	$\sigma^2e$

Where,

r = number of replications;  
 g = number of genotypes;  
 MSr = mean square due to replications;  
 MSg = mean square due to genotypes;  
 MSe = mean square of error; and  
 $\sigma^2r$ ,  $\sigma^2g$ , and  $\sigma^2e$  are variances due to replication, genotype, and error, respectively.

Analysis of variance in a randomized complete block design was computed using the following model:  
 $Y_{ij} = \mu + r_j + g_i + \epsilon_{ij}$

Where,

$Y_{ij}$  = the response of trait Y in the  $i$ th genotype and the  $j$ th replication  
 $\mu$  = the grand mean of trait Y;  
 $r_j$  = the effect of the  $j$ th replication;  
 $g_i$  = the effect of the  $i$ th genotype; and  
 $\epsilon_{ij}$  = experimental error effect.

### Phenotypic and genotypic variances

The phenotypic and genotypic variances of each trait were estimated from the RCBD analysis of variance and the expected mean squares under the assumption of random effects model computed from linear combinations of the mean squares and the phenotypic and genotypic coefficient of variations, which were also computed as per the methods suggested by Burton *et al.* (1953).

$$\text{Genotypic variance } (\sigma^2g) = \frac{M_{sg} - M_{se}}{r}$$

$$\text{Environmental variance } (\sigma^2e) = M_{se}$$

Where,

MSg and MSe are the mean sum of squares for the genotypes and error in the analysis of variance, respectively.

r is the number of replications.

Then, the phenotypic variance was estimated as the sum of the genotypic and environmental variances:  
 Phenotypic variance ( $\sigma^2ph$ ) =  $\sigma^2g + \sigma^2e$

### Genotypic and phenotypic coefficient of variations

The genotypic and phenotypic coefficients of variability were estimated according to the formulae of Singh and Chaudhary, (1977) as follows

Genotypic Coefficient of Variation (GCV) =  $(\sigma g / \text{grand mean}) * 100$   
 Phenotypic Coefficient of Variation (PCV) =  $(\sigma ph / \text{grand mean}) * 100$

Where,  $\sigma g$  and  $\sigma ph$  are genotypic and phenotypic standard deviations, respectively.

### Heritability analysis

Broad sense heritability values were estimated based on the formula of Falconer *et al.*, 1996 as follows:

$$\text{Heritability in broad sense } (H^2) = (\sigma^2g / \sigma^2ph) * 100$$

Then, the genetic advance for selection intensity (k) at 5% was estimated by the following formula (Allard, 1960):

$$\text{EGA} = k * \sigma ph * H^2$$

Where,

EGA represents the expected genetic advance under selection;  
 $\sigma ph$  is the phenotypic standard deviation;  
 $H^2$  is heritability in broad sense and k is selection intensity.

The genetic advance as percent of population mean was also estimated following the procedure of Johnson *et al.* (1955b):

$$\text{Genetic advance as percent of population mean} = (\text{EGA} / \text{grand mean}) * 100$$

### Correlation analysis

Estimations of genotypic and phenotypic correlation coefficients were done based on the procedure of Dabholkar (1992) as follows:

$$\text{Genotypic correlation coefficient } (r_g) = \frac{\text{COVg}(xy)}{\sigma g(x) * \sigma g(y)}$$

$$\text{Phenotypic correlation coefficient } (r_{ph}) = \frac{\text{COVph}(xy)}{\sigma ph(x) * \sigma ph(y)}$$

Where,

COVg(xy) and COVph(xy) are the genotypic and phenotypic covariance of two variables (X and Y), respectively;  $\sigma g(x)$  and  $\sigma g(y)$  are the genotypic standard deviations for variables X and Y, respectively, while  $\sigma ph(x)$  and  $\sigma ph(y)$  are the phenotypic standard deviations of variables X and Y, respectively.

The calculated phenotypic correlation values were tested for its significance using t-test:

$$t = r_{ph}/SE(r_{ph})$$

Where,

$r_{ph}$  = Phenotypic correlation;  $SE(r_{ph})$  = Standard error of phenotypic correlation obtained using the following formula (Sharma, 1998).

$$SE(r_{ph}) = \sqrt{(1-r_{ph}^2)/(n-2)}$$

Where,

$n$  is the number of genotypes tested,  
 $r_{ph}^2$  is phenotypic correlation coefficient.

The coefficients of correlations at genotypic levels were also tested for their significance by the formula described by Robertson (1959) as indicated below:

$$t = r_{gxy}/SE_{rgxy}$$

The calculated "t" values were compared with the tabulated "t" value at (n-2) degree of freedom at 5% level of significance. Where, n is number of genotypes.

$$SE_{rgxy} = \sqrt{(1-r_{gxy}^2)/2H^2x.H^2y}$$

Where,  $H^2x$  = Heritability of trait x; and  $H^2y$  = Heritability of trait y.

## RESULTS AND DISCUSSION

The analysis of variance results for the fourteen traits studied are given in Tables 3. Highly significant ( $P < 0.01$ ) differences among genotypes were observed days to seedling emergence, days to initial squaring, days to 50% flowering, days to 65% boll opening, plant height, number of nodes to first fruiting branch, number of monopodial branches per plant, number of sympodial branches per plant, number of bolls per plant, seed cotton yield, lint yield and lint percentage; while only boll weight showed non-significant difference among the tested genotypes.

The study results clearly showed that the presence of considerable variations among genotypes for many of the traits measured. This indicated the presence of appreciable variations among genotypes for most of the characters and justifies carrying out further genetic analysis and identifying important traits for future breeding work relevant to Benishangul-Gumuz Regional State and other similar cotton producing areas.

**Table 3. Analysis of variance (mean square) for 14 traits of 14 cotton genotypes**

Traits	Replication	Genotype	Error	CV (%)
DSE	0.21ns	1.13**	0.29	10.64
DIS	8.00ns	34.86**	3.77	4.39
DIF	0.17*	13.68**	0.68	1.21
D50F	0.93ns	6.95**	2.08	1.51
D65BO	39.59	66.36**	17.77	2.59
PHt	170.99*	431078.00**	53.09	7.56
NFSB	1.98**	0.47**	0.13	10.87
NMoB	3.32**	1.92**	0.51	13.36
NSyB	9.93**	3.48**	0.61	13.80
NBP	31.28**	8.50**	1.56	8.68
BWt	0.11ns	0.07ns	0.06	9.18
SCY	13004.87ns	70015.24**	18719.01	11.39
LY	1212.19ns	12746.82**	3030.50	11.52
L% (GOT)	0.94*	8.45**	0.22	1.19

\*, \*\* Indicate significant difference at  $P < 0.05$ ,  $P < 0.01$  levels, respectively; ns=Non-significant.

DSE=Days from planting to seedling emergence; DIS=Days from seedling emergence to initial squaring; DIF=Days to initial flowering; D50F=Days to 50% flowering; D65BO=Days to 65% boll opening; PHt=Plant height; NFSB=Number of nodes to first fruiting or sympodial branch; NMoB=Number of monopodial branches per plant; NSyB=Number of sympodial branches per plant; NBP=Number of bolls per plant; BWt=Boll weight in grams; LY=Lint yield in kg per ha; L%=Lint percentage or GOT (Ginning out turn); SCY=Seed cotton yield in kg per ha.

### Mean Performance of Cotton Genotypes

#### Crop phenology expressions

Range and mean values for 14 characters of 14 cotton genotypes are presented in Tables 4. Also, the mean performances of these genotypes are presented in Tables 6. Regarding phenological characters, days to 50% flowering ranged from 93.67 to 98.33 days and

days to 65% boll opening ranged from 155.3 to 170.3 days. The wide ranges in mean performance of the above traits among genotypes suggested the presence of variations that could be exploited to improve cotton genotypes through breeding and appropriate selection.

Analysis of variance showed highly significant differences among the genotypes for plant height ranged from 80.73 cm to 125.00 cm with the mean value of 96.42 and coefficient of variation of 7.56%



(Table 6). Minimum plant height was observed in genotypes WARC-10 (80.73 cm) followed by WARC-8 (82.30 cm), WARC-1 (84.13 cm), WARC-5 (89.00 cm) and Deltapine 90 (91.00 cm) while, Stam-59A (125.00 cm) exhibited maximum plant height which can lead the genotypes to lodging problems in areas where continuous rain fall exist as of the area where the present study was conducted.

The magnitude of genetic variability for number of monopodial branch per plant ranged from 4.20 to 7.03 with the mean value of 5.34 and the coefficient of variability is recorded as 13.36%. And, the means for number of sympodial branch per plant was ranged from 3.67 to 7.33 with the mean value of 5.67 and coefficient of variability is 13.80%. Maximum number of sympodial branch per plant (7.33) was recorded for the genotype WARC-12, while the minimum number of sympodial branch per plant (3.67) was recorded for the genotype WARC-9. The result of this study indicated that the monopodial branches follow the growth pattern of main stem and bear indirect fruit. And, genotypes with large number of monopodia lead to vegetative growth of the plant and delayed the time of maturity, hence it leads to terminal moisture stress. .

#### Yield and yield components of genotypes

Seed cotton yield (SCY) for genotypes ranged from 946.00 kg/ha to 1478.50 kg/ha, and the mean value was 1201.43 kg/ha (Table 4). As presented in Table 6, the top yielders included WARC 4, WARC-7, WARC-2 and WARC-3 with 1478.50 kg/ha, 1418.30 kg/ha, 1366.20 kg/ha and 1306.70 kg/ha, respectively. Lint is a major and important component of cotton yield, and a vital raw material for the textile industry. All of the above genotypes, except WARC-3, showed satisfactory SCY and lint yield (LY) potential. Boll number per plant (BNP) and boll weight (BWt) are important components that contribute to yield parameter. BNP of genotypes averaged 14.36. The top scorers were WARC-4, WARC-12, WARC-7 and WARC-1 (Tables 6). A combination of higher SCY and GOT is an advantage to harvest satisfactory lint yield which is needed by the textile industry. In this regard, genotypes WARC-7, WARC-4, WARC-2, WARC-10 and WARC-11 possessed higher combination of SCY and GOT for a better lint yield.

**Table 4. Minimum and Maximum values, mean and standard error of mean (SE) for the 14 traits of 14 cotton genotypes.**

Traits	Min. value	Genotypes with Min. value	Max. value	Genotype with Max. value	Mean	SE	CV (%)
DSE	4.33	WARC-5, -9, & -12	6	WARC-4	5.07	0.31	10.64
DIS	39	WARC-12 & Deltapine 90	51.33	WARC-1	44.02	0.41	4.39
DIF	64	WARC-7	71.33	WARC-9	67.95	0.47	1.21
D50F	93.67	WARC-6	98.33	WARC-5	95.43	0.83	1.51
D65BO	155	WARC-5	170.33	Stam-59A	162.31	2.42	2.59
PHt	80.73	WARC-10	125	Stam-59A	96.42	4.2	7.56
NFSB	2.6	WARC-9	4.07	WARC-8	3.37	0.21	10.87
NMoB	4.2	WARC-9	7.03	WARC-4	22.16	0.41	13.36
NSyB	3.67	WARC-9	7.33	WARC-12	5.67	0.45	13.8
NBP	10.47	WARC-9	16.97	WARC-4	14.36	0.72	8.68
BWt	2.56	WARC-6	3.02	WARC-4	2.76	0.14	9.18
SCY	946	WARC-1	1478.5	WARC-4	1201.43	78.99	11.39
LY	358.9 1	WARC-1	585.4	WARC-8	478	31.78	11.52
L% (GOT)	37.33	Deltapine-90	42.17	Stam-59A	39.77	0.27	1.19

DSE=Days from planting to seedling emergence; DIS=Days from seedling emergence to initial squaring; DIF=Days to initial flowering; D50F=Days to 50% flowering; D65BO=Days to 65% boll opening; PHt=Plant height; NFSB=Number of nodes to first fruiting or sympodial branch; NMoB= Number of monopodial branches per plant; NSyB=Number of sympodial branches per plant; NBP=Number of bolls per plant; BWt=Boll weight in grams; LY=Lint yield in kg per ha; L%=Lint percentage or GOT (Ginning out turn); SCY=Seed cotton yield in kg per ha.

### Phenotypic and genotypic coefficients of variation (PCV)

Higher phenotypic and genotypic variances were obtained from days to initial squaring, days to 65% boll opening, plant height, seed cotton yield and lint yield, indicating high influence of the environment on these traits.

High phenotypic coefficient of variation (PCV) values was noted on number of days to seedling emergence, plant height, number of nodes to the first fruiting branch, number of monopodial branch per plant, number of sympodial branch per plant, number of bolls per plant, seed cotton yield and lint yield. The PCV values for days to initial squaring and boll weight were medium (10-20%). Days to initial flowering, days to 50% flowering, days to 65% boll opening and lint percentage (GOT) had low values (< 10 %).

### Estimation of broad-sense heritability

Estimates of heritability in broad sense ranged from 45% for average boll weight to 97% for lint percentage (GOT) (Table 6). Pramoda and Gangaprasad (2007) generally classified heritability estimates as low (< 40%), medium (40-59%), moderately high (60-79%) and very high (80-100%). If heritability were 100 %, which is genotypic variance ( $s^2_g$ ) is equal to phenotypic variance ( $s^2_p$ ), and then phenotypic performance would be a perfect indication of genotypic value (Johnson *et al.*, 1955). Based on this bench mark, moderately high heritability (60-79%) was noted for days to seedling emergence, days to 50% flowering, days to 65% boll opening, number of nodes to first fruiting branch, number of monopodial branches per plant, seed cotton yield and lint yield. And genotypes which have high range of heritability (80-100%) were noted for days to initial squaring, days to initial flowering, plant height, number of sympodial branches per plant, number of bolls per plant and lint percentage. This result agrees with Amir *et al.*, (2012) and Ali *et al.*, (2011).

Moderately high heritability (60-79%) but low genetic advance as percent of mean was observed for the traits days to initial flowering, days to 50% flowering and days to 65% boll opening. For both testing sites, high heritability and yet low genetic advance as percent of mean indicated the involvement of non-additive gene actions for expression of the traits.

Generally, most of the traits studied showed moderately high to high heritability estimates indicating the possibility of improving these traits through selection. According to Poehlmon and David (1995) if a trait has high heritability accompanied with high genetic advance as percent of mean value, it indicates that the influence of the environment on the trait is less and selection for that trait becomes easy. The present study results are also in agreement with those obtained by Abbas *et al.*, (2013), Dhivya *et al.*, (2014) and Farooq *et al.*, (2013).

### Genetic advance as percent of mean

The genetic advance as the percentage of the mean (GAM) at 5% selection intensity is presented in Tables 3. It ranged from 4.68 for days to 50% flowering to 60.62 for sympodial branches per plant followed by monopodial branches per plant (44.98), lint yield (41.68), plant height (41.02), seed cotton yield (38.13) and number of bolls per plant (37.12).

Plant height and sympodial branches per plant showed moderately high heritability coupled with high genetic advance as percent of mean. These results indicate that there is good opportunity to improve these traits through crossing and selection.

In general, plant height, monopodial branch per plant, sympodial branch per plant, boll number per plant, seed cotton yield and lint yield showed moderately high heritability coupled with high genetic advance as percent of mean value.

### Correlations of seed cotton yield and yield related traits

As shown in the Table 7, seed cotton yield had highly significant and positive phenotypic correlation with days to 50% flowering ( $r_p = 0.61$ ), days to 65% boll opening ( $r_p = 0.69$ ), plant height ( $r_p = 0.89$ ), number of sympodial branches per plant ( $r_p = 0.87$ ), number of bolls per plant ( $r_p = 0.81$ ) boll weight ( $r_p = 0.79$ ), lint yield ( $r_p = 0.86$ ) and lint percentage (0.83). Days to initial flowering, number of nodes to the first fruiting branch and number of monopodial branches per plant also showed significance and positive correlation with seed cotton yield. Days to initial squaring had positive association with seed cotton yield but not significant correlation.

At genotypic level, days to 50% flowering, plant height, number of sympodial branches per plant, number of bolls per plant, lint yield and lint percentage were observed to have positive and highly significant ( $p \leq 0.01$ ) correlations with seed cotton yield. At genotypic level seed cotton yield was significantly and positively correlated with days to initial flowering ( $r_g = 0.51^*$ ), number of nodes to the first fruiting branch ( $r_g = 0.63^*$ ) and Number of monopodial branch per plant ( $r_g = 0.57^*$ ). The strong positive correlation of days to 50% flowering, plant height, sympodial branch per plant, number of bolls per plant, lint yield and lint percentage with seed cotton yield indicated that these characters might be utilized as selection criteria for improving seed cotton yield in upland cotton (*G. hirsutum*. L.).

**Table 5. Range, mean, SE,  $\sigma^2p$ ,  $\sigma^2g$ ,  $\sigma^2e$ , GCV, PCV,  $h^2$ , GA and GAM% for the 14 characters of *G. hirsutum* L. genotypes**

Traits	Range	Mean	SE	$\sigma^2 P$	$\sigma^2 G$	$\sigma^2 e$	PCV%	GCV%	$h^2$	GA	GAM%
DSE	4.33-6.00	5.07	0.31	1.33	1.04	0.29	22.78	20.14	0.78	1.86	36.73
DIS	39.00-51.33	44.14	0.41	37.37	33.60	3.77	13.85	13.13	0.90	11.34	25.69
DIF	64.00-71.33	67.95	0.47	14.13	13.46	0.67	5.53	5.40	0.95	7.39	10.87
D50F	94.00-98.00	95.43	0.83	8.34	6.26	2.08	3.03	2.62	0.75	4.47	4.68
D65BO	155.00-170.00	162.31	2.42	77.91	60.31	17.60	5.44	4.78	0.77	14.10	8.68
PHt	82.33-125.00	96.41	4.20	464.96	413.40	51.56	22.37	21.09	0.89	39.55	41.02
NFSB	2.60-4.07	3.37	0.21	0.56	0.43	0.13	22.21	19.37	0.76	1.17	34.85
NMoB	4.20-7.03	5.34	0.41	2.26	1.75	0.51	28.15	24.77	0.77	2.40	44.98
NSyB	3.67-7.30	5.66	0.45	3.88	3.28	0.61	34.85	32.00	0.84	3.43	60.62
NBP	10.47-16.97	14.36	0.72	9.54	7.98	1.56	21.50	19.67	0.84	5.33	37.12
BWt	2.53-3.02	2.76	0.14	0.11	0.05	0.06	12.02	8.10	0.45	0.31	11.27
SCY	946.00-1478.50	1201.43	78.99	82495.00	63775.60	18719.01	23.91	21.02	0.77	458.08	38.13
LY	358.31-584.91	478.00	31.78	14767.15	11736.65	3030.50	25.42	22.66	0.79	199.25	41.68
L% (GOT)	37.33-42.13	39.77	0.27	8.60	8.38	0.22	7.38	7.28	0.97	5.89	14.82

DSE=Days from planting to seedling emergence; DIS=Days from seedling emergence to initial squaring; DIF=Days to initial flowering; D50F=Days to 50% flowering; D65BO=Days to 65% boll opening; PHt=Plant height; NFSB=Number of nodes to first fruiting or sympodial branch; NMoB= Number of monopodial branches per plant; NSyB=Number of sympodial branches per plant; NBP=Number of bolls per plant; BWt=Boll weight in grams; LY=Lint yield in kg per ha; L%=Lint percentage or GOT (Ginning out turn); SCY=Seed cotton yield in kg per ha.



**Table 6. Mean values of 14 traits of 14 cotton genotypes tested at Homosha in 2017.**

Genotypes	DSE	DIS	DIF	D50F	D65BO	Pht	NFSB	NMoB	NSyB	NBP	BWt	LY	L%	SCY
WARC-1	5.67ba	51.33a	71.00ba	96.33ba c	161.00edfc	84.13ge	3.47bac	6.30ba	5.27bde c	15.06ba	2.86bac	358.31e	37.867e	946.00f
WARC-2	5.00bd	47.67b	67.00gfe	94.00dc	161.33edfc	100.00cbd	3.40bc	4.60ecd	5.00de	13.00dc	2.78bac	537.81ba	39.36d	1366.20ba
WARC-3	5.33ba	47.00bc	66.00g	96.67ba	169.00ba	103.73cbd	3.33bc	5.30bcd	5.73bde c	14.40bc	2.88bac	490.78bc	37.50e	1306.70bd
WARC-4	6.00a	47.00bc	66.67gf	94.00dc	159.67edf	91.73gefd	3.47bc	7.03a	6.47bac	16.97a	3.02a	583.47a	39.47d	1478.50a
WARC-5	4.33d	45.67d	68.67dc	98.00a	155.33f	89.07gef	3.67dc	4.40ed	7.20a	14.67bc	2.97ba	483.60dc	41.30bc	1172.70fc
WARC-6	4.67dc	41.00f	66.67gf	93.67d	162.30ebdf	94.07cefd	3.80ba	5.20bcd	4.53fe	13.53dc	2.56bc	454.00bd	40.74c	1114.30fe
WARC-7	5.33ba	45.33ed	69.67bc	94.00dc	163.67edac	91.80gefd	3.30bc	6.27ba	6.47bac	16.07ba	2.89bac	584.91a	41.27bc	1418.30ba
WARC-8	5.66ba	44.33e	64.00h	97.33ba	158.00ef	82.33ge	4.067a	5.30bed	4.93fde	14.33bc	2.62bac	485.40dc	38.86d	1248.40bc
WARC-9	4.33d	41.00f	71.33a	97.00ba	159.67edf	103.73cbd	2.60d	4.20e	3.67f	10.47e	2.62bac	451.10bd	41.67ba	1083.20e
WARC-10	5.67ba	41.33f	67.67dfe	94.00dc	167.67bac	80.73g	2.87dc	4.60ecd	4.67fe	12.13ed	2.62bac	505.4bac	41.02bc	1231.90bd
WARC-11	4.67dc	46.00cd	70.67ba	95.30bc	161.33edfc	104.07cb	3.00dc	5.40bcd	6.20bda c	14.60bc	2.77bac	499.60ba	40.53c	1232.40bc
WARC-12	4.33d	39.00g	68.33dc e	94.00dc	166.67bdac	108.467b	3.47bc	5.40bcd	7.33a	16.20ba	2.73bac	413.30dc	37.71e	1096.50fd
Deltpine 90	4.33d	39.00g	67.67dfe	95.00bd c	155.67f	91.00gef	3.87ba	5.73bc	5.20dec	14.80bc	2.71bac	394.08ed	37.33e	1057.80fe
Stam-59A	5.67ba	40.67f	66.00g	96.67ba	170.33a	125.00a	3.40bc	4.93ecd	6.53ba	14.87bc	2.57bc	450.00bd	42.17a	1067.20fe
Mean	5.07	44.14	67.95	95.43	162.26	96.41	3.37	5.34	5.66	14.36	2.76	478	39.77	1201.43
LSD	0.91	3.26	1.38	2.42	7.08	12.23	0.61	1.2	1.31	2.09	0.43	92.39	0.79	229.63
CV%	10.64	4.39	1.21	1.51	2.59	7.56	10.87	13.36	13.8	8.68	9.18	11.51	1.19	11.39

In the same column, means followed by the same letter are not significantly different at the 5% level of significance.

DSE=Days from planting to seedling emergence; DIS=Days from seedling emergence to initial squaring; DIF=Days to initial flowering; D50F=Days to 50% flowering; D65BO=Days to 65% boll opening; Pht=Plant height; NFSB=Number of nodes to first fruiting or sympodial branch; NMoB= Number of monopodial l branches per plant; NSyB=Number of sympodial branches per plant; NBP=Number of bolls per plant; BWt=Boll weight in grams; LY=Lint yield in kg per ha; L%=Lint percentage or GOT (Ginning out turn); SCY=Seed cotton yield in kg per ha.

**Table 7. Estimates of genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients for 14 traits of 14 cotton genotypes.**

Traits	DSE	DIS	DIF	D50F	D65BO	PHt	NFSB	NMoB	NSyB	NBP	BWt	LY	L%	SCY
DSE		0.43*	0.65*	0.84**	0.08	0.27	0.53	0.23ns	0.06ns	0.08	0.01	0.21ns	-0.31ns	0.42ns
DIS	0.52**		0.89**	0.75*	0.53*	-0.57*	-0.48**	-0.35ns	-0.37*	0.45*	0.25ns	0.24ns	0.25ns	0.32ns
DIF	0.53**	0.55**		0.64*	0.51*	0.47	0.41*	0.57*	0.47	0.56*	0.38ns	0.19ns	0.41*	0.35*
D50F	0.45**	0.58*	0.65**		0.72*	0.74*	0.09	-0.83**	0.36*	0.63**	0.67**	0.26ns	0.35*	0.75**
D65BO	0.24ns	0.31ns	0.54*	0.51*		0.84*	0.43	-0.79*	0.33*	-0.42*	0.79**	-0.52ns	0.31ns	0.59*
PHt	0.13ns	0.18ns	0.19ns	0.65*	0.59*		0.53	0.37**	-0.22	0.36**	0.25ns	0.66**	0.62*	0.83**
NFSB	0.09ns	0.23	0.25	0.55*	0.87**	-0.59*		0.38**	0.68*	0.52*	0.23ns	0.53*	0.45*	0.57*
NMoB	0.21ns	0.87*	-0.58*	-0.54*	-0.66*	0.68*	0.35**		0.59*	0.65*	0.54*	-0.38*	-0.66*	-0.69*
NSyB	0.33ns	0.26ns	0.53*	0.82**	0.73*	0.59*	0.98**	-57*		0.38*	0.57*	0.61*	0.59**	0.89**
NBP	0.24ns	0.29ns	0.08ns	0.25ns	0.79**	0.37**	0.86**	0.51*	0.93**		-0.59*	0.48**	0.67**	0.78**
BWt	0.35ns	0.35ns	0.07ns	0.56**	0.84**	0.69*	0.71*	0.55	0.88*	-0.66*		0.26	-0.23	0.48*
LY	0.37ns	0.22ns	0.56*	0.55*	0.61*	0.78**	0.56*	-0.35*	0.66*	0.78**	0.37		0.94**	0.88**
L%	0.18ns	-0.28	0.45*	0.49*	0.65*	0.71*	0.48*	0.47*	0.58**	0.79**	-0.19	0.79**		0.65**
SCY	-0.33ns	0.38ns	0.51*	0.61**	0.69**	0.89**	0.63*	0.57*	0.87**	0.81**	0.79**	0.86**	0.83**	1

\*, \*\*Indicate significant at the 0.05 and 0.01 probability levels, respectively.

DSE=Days from planting to seedling emergence; DIS=Days from seedling emergence to initial squaring; DIF=Days to initial flowering; D50F=Days to 50% flowering; D65BO=Days to 65% boll opening; PHt=Plant height; NFSB=Number of nodes to first fruiting or sympodial branch; NMoB= Number of monopodial branches per plant; NSyB=Number of sympodial branches per plant; NBP=Number of bolls per plant; BWt=Boll weight in grams; LY=Lint yield in kg per ha; L%=Lint percentage or GOT (Ginning out turn); SCY=Seed cotton yield in kg per ha.

## CONCLUSION

The analysis of variance showed significant differences among the tested genotypes for all characters considered in the study; this indicated the existence of variability among the tested genotypes. Phenotypic variances and phenotypic coefficients of variation were higher than their respective genotypic variances and genotypic coefficients of variation for all the traits considered in the study. This indicated the presence of environmental influence to some degree in the phenotypic expression of the traits.

Estimates of heritability in a broad sense ranged from 45% for boll weight to 95% for days to initial flowering. Moderately high heritability values were noted for days to seedling emergence, days to 50% flowering, days to 65% boll opening, number of nodes to the first fruiting branch, number of monopodial branches per plant, seed cotton yield and lint yield. Genotypes with high heritability values were noted for days to initial squaring, days to initial flowering, plant height, number of sympodial branches per plant, and number of bolls per plant, indicating that these traits are less affected by environmental conditions. High heritability but low genetic advance as percent of mean revealed the involvement of non-additive gene actions for the expression of the traits. The high heritability estimates suggested that the traits are primarily under genetic control and selection for them can be achieved through their phenotypic performance. Generally, most of the traits studied showed moderately high to high heritability estimates indicating the possibility of improving these traits through selection.

Correlation analysis among the characters studied revealed that positive and significant association of seed cotton yield and its components were more explained at phenotypic than at genotypic level. This implies that the correlation of these characters is reasonably expressed as a result of environmental factors rather than their genetic characteristics.

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