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Full Length Research Paper

Genetic variability and heritability studies of seed cotton yield and fiber quality in F5 segregating generation of upland cotton (*Gossypium hirustum* L.) in Ethiopia

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Sixteen genotypes were laid out in a Randomized Complete Block Design (RCBD) with four replications with the objectives of determining the genetic variability and heritability of seed cotton yield and quality traits in F5 lines. Genetic coefficient variability (GCV) ranged from 0.65% (degree of reflectance) to 12.02 (boll number plant^{-1}). Phenotypic coefficient variability (PCV) ranged from 0.87% (degree of reflectance) to 13.35% (boll number plant^{-1}). Most of the traits had fallen at low rank PCV and GCV which suggested that the breeders should go for source of high variability. Fiber Strength recorded the highest heritability (0.95), followed by hundred seed weight (0.94), upper half mean length (0.93), boll weight (0.89), ginning percentage (0.89), boll number plant^{-1}(0.81) indicating that these traits were affected less than days to emergence (0.58), seed cotton yield ha^{-1}(0.51) degree of reflectance (0.57)by the environmental conditions. The highest genetic advance in percent of the mean was exhibited by boll number plant^{-1}(22.28), followed by hundred seed weight (19.55). The study has highlighted the existence of low to moderate variability and high heritability for the traits so that new genetic diversity should be brought in through introduction, collection and by mutation breeding, to obtain high variability.

Keywords: phenotypic, genotypic, advance, variability, heritability

INTRODUCTION

The extent of genetic variability in a specific breeding population depends on the germplasm included in it and its selection history. When the genetic variability in a breeding program is insufficient to permit attainment of a specific goal it will be necessary to increase the variability by using either mutagenic treatment or introduction of a new germplasm (Hallawer, 1981).

The effectiveness of selection depends upon the variability present in the germplasm and the extent to which it is heritable. Variation is the occurrence of difference among individuals due to differences in their genetic composition and/or the environment in which they were raised (Allard, 1960).

The current cotton genetic pool is narrow and lacking variability for economically important agronomic and fiber traits (Bowman, 1999; Bowman *et al*., 2006; Paterson *et al*., 2004). Unless new genetic diversity is brought in, it may be difficult to maintain genetic gains. Studies clearly support the view that upland cotton is resting on a very

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narrow genetic base and is facing a risk associated with it (Campbell *et al*., 2009; Paterson et al., 2004; Zeng *et al*., 2011).

The knowledge of nature and magnitude of the variability among the genotypes for the traits is very important prerequisite for making simultaneous selection on more number of traits to make significant improvement in cotton. It is difficult to separate the heritable and non-heritable variation making difficulty in selection for the breeders. Hence it is very necessary for the breeder to separate the heritable portion from the non-heritable part to plan for proper breeding program.

Estimate of range, variance and genotypic and phenotypic coefficient of variability

Khurram *et al*. (2009) reported that the traits, number of monopodia per plant, seed cotton yield and number of bolls per plant showed high PCV and GCV indicating substantial variability for these characters. Dhamayanathi *et al.* (2010) found high genetic differences for sympodia, bolls per plant, and seed cotton yield and lint index, indicating ample scope for genetic improvement of these characters through selection. Results also revealed high heritability coupled with high genetic advance for yield and most of the yield components. As stated by Shivasubramanian and Menon, (1973) the PCV and GCV values are ranked as low, medium and high with 0 to 10%, 10 to 20% and >20%, respectively.

Heritability Estimate

In a population observed phenotypic variation is due to both factors i.e. genetics and environmental whereas the genetic variability is the only heritable from generation to the next generation so the heritability alone does not give an idea about the expected gain in the next generation but it has to be considered in conjunction with the genetic advance. The characters those have maximum heritability and high genetic advance as percentage of mean could be used as powerful tool in selection process such traits are controlled by the additive genes and less influenced by the environment (panse and Sukhatme, 1995). Panse (1957) also reported that low heritability accompanied with genetic advance is due to non-additive gene effects for the particular character and would offer less scope for selection because of the influence of environment (GxE). In this case simple selection may not be rewarding and in such cases breeders can go for selecting transgressive segregants. The successful breeding methods will be the ones, which will exploit the non-additive gene effects. High heritability associated with low genetic advance for these traits was probably due to non-additive gene (dominance and epistatasis). The degree to which the given trait is transmitted to next generation can be best visualized by the estimates of heritability, thus heritability coupled with genetic advance and genetic variability could be the suitable tool for plant breeder to select the suitable breeding method in order to improve the genetic makeup of cotton plant.

The effectiveness of selection is dependent on the magnitude of heritability. The heritability estimates express the reliability of phenotypic value, as a guide to the breeding value and its determination is obviously of fundamental importance in any breeding program (Aziz *et al.*, 2014).

According to Johnson *et al.* (1955) highly heritability coupled with high genetic advance could be useful in order to predict the behavior of segregating generation. It can be inferred that those traits can be selected in early generations and selection will prove true in the fixation of the said traits. Heritability values are categorized as low (0-30%), moderate (30-60%) and high (60% and above) as stated by Robinson *et al*., (1949).

Many investigators Khan and Azhar (2000), Chandio *et al*. (2003) and Bloach (2004) reported that high heritability for different agronomic traits of upland cotton helped cotton breeders to exploit different breeding procedures for enhancement of yield and quality related traits of upland cotton. Basal and Tuegut, (2005), Joshi *et al*. (2006), Rauf *et al*. (2006) observed high heritability and genetic advance for number of traits i.e. lint percentage, fiber length, seed cotton yield and number of bolls per plant. Similarly Elsiddig *et al*. (2007) and Ali *et al*.(2010) reported moderate to high heritability for seed cotton yield, seed index, boll weight, lint yield, bolls per plant, average boll weight and fiber fineness. Basbag and Gencer (2004) found that among yield related traits seed cotton weight per boll and 100 seed weight had high heritability, bolls per plant had low heritability, whereas other characters had moderate heritability. The characters with high heritability suggested some possibilities in obtaining required genotypes by selection in early segregating generations (F2, F3); while selection for improvement was delayed due to low heritability for some characteristics. Basbag and Gencer (2004) reported higher estimates of heritability for fiber fineness and strength but low for bolls per plant and seed cotton yield and recommended early generation selection for traits having higher heritability.

Mendez-Natera *et al*. (2012) reported higher values of broad sense heritability for fiber fineness but moderate values for plant height, fiber length and fiber strength and low values for bolls per plant, boll weight and seed cotton yield. Naveed *et al*. (2004) reported low values of heritability for lint percentage and boll weight.

Nistor and Nistor (1999) determined high broad-sense heritability (89%) for staple length. Ahmad *et al.* (2006) determined moderate to high heritability estimates and genetic advance for plant height and seed cotton yield per plant. Ulloa (2006) revealed that ginning out turn showed highest heritability (95%) followed by staple length (80%). Basal and Turgut (2005) mentioned that moderate heritability estimates were observed for fiber strength ratio(0.50), seed cotton weight per boll (0.42) and lint % (0.40), however, bolls per plant and seed cotton weight per plant showed low heritability estimates, 0.33 and 0.22, respectively. Lint percentage was reported to be a highly heritable trait and stable across environments (Desalegn *et al*., 2009; Lu and Myers, 2011; Percy *et al*., 2006).

Estimate of Expected Genetic Advance

Genetic advance in a population cannot be predicted from heritability alone, the genetic gain for specific selection pressure has to be worked out. Genetic advance as percent of mean classified as low (0 to 10%), moderate (10 to 20%) and high (20% and above) as stated by Johnson *et al*. (1955).

Heritability values are helpful in predicting the expected progress to be achieved through the process of selection; high heritability coupled with high genetic advance is an indicator of a greater proportion of the additive genetic variance and consequently a high genetic gain is expected from selection (Singh and Rai, 1981).

High heritability coupled with high response to selection was noticed for plant height, bolls per plant and lint yield per hectare, which revealed the additive gene action model in the inheritance of these characters and the scope for improvement of them through simple selection procedures (Vineela *et al.,* 2013). The studies conducted by Ravikesavan and Iyanar (2008) and Hussain *et al.* (2010) indicated that plant height and number of bolls per plant were under the control of additive gene action. High heritability along with moderate response to selection was observed in lint index, seed index and lint percentage, which revealed the involvement of both additive and non-additive gene action in the inheritance of these characters and offered the best possibility of improvement of these traits through progeny selection or any modified selection procedures (Vineela *et al.,* 2013).

Hybridization among cotton genotypes, followed by conventional pedigree selection is a predominant method utilized for cotton breeding. In such pedigree system the best F2 plants and the best plants within the best lines in the following segregating generations are visually selected. Many investigators stated that visual selection in early segregating generations for yield is inefficient and that the evaluation of some strains in such programs begins from F5 generation and continue, until satisfactory genetic stability is achieved (El-Hoseiny, H. A**.**, 2013).

Generally, to develop suitable varieties, it is essential to know the extent of genetic variability in the existing recurrent crossing parents and their offspring of upland cotton germplasm. Therefore, the present study was conducted with objectives of studying the genetic variability and heritability of seed cotton yield, yield components and lint quality traits in F5 lines of cotton.

MATERIALS AND METHODS

Description of the testing Site

The study was conducted at Werer Agricultural Research Center (WARC), Amibara District, Gebiresu zone of Afar National Regional State during 2016 cropping season (May to November, 2016). WARC is located at 9° 27' N and 40° 15' E in north eastern part of Ethiopia. It is about 280 km away from Addis Ababa. The altitude of WARC is 740 m.a.s.l. Fourteen (1970 - 2014) years of the average minimum and maximum temperature of WARC was19 °C and 34 °C, respectively. Its annual average rainfall is about 571 mm which is erratic in its nature. The soil is predominantly vertisol with porosity and bulk density (0-25cm depth) of 49.06% and 1.35gm/cm^2, respectively (Wendemagegn and Abere, 2012).

Experimental Materials

Fourteen *Gossypium hirsutum* F_5 lines obtained from a cross betweenDeltapine-90 and Delcero were used for the study along with the two parents (Table 1).

Experimental Design and Layout

The experiment was laid out in a Randomized Complete Block Design (RCBD) with four replications. Each treatment had five rows, each five meters long with spacing of 90 cm between rows and 20cm between plants. The plot size was 5 x 5m x 0.9m =22.5m^2. Net plot size was 3 rows x 5m x 0.9m=13.5 m^2.

Statistical Analysis

Analysis of variance

The data was subjected to analysis of variance using the general linear model (GLM) procedure of SAS (SAS Institute, 2002). Genotype effect F tests were performed against their error source. Means were separated using Fisher's protected least significance difference test (LSD) at p=0.05.

The ANOVA model of the data is given below at Table 2 and the linear model equation of analysis of variance is as follows:-

$Y_{ij} = Mean + Trt_i + Block_j + Error_{ij}$,

(Or $Y_{ij} = \mu + \alpha_i + \rho_j + e_{ij}$) Mean is the overall mean (μ); Trt_i (α_i) is the fixed effect of the ith variety; Block (ρ_j) is the random effect of the jthblock. $Error_{ij}$ (e_{ij}) is the error term specific to the variety identified assigned to theith treatment within the jth block.

Table 1. List of cotton genotypes used in the study and their pedigree.

TreatmentNo	Treatment code	Treatments/pedigrees
1	A	Delcero X Deltapine-90 #F5-5-3-2-1-1
2	B	Delcero X Deltapine-90 #F5-5-3-2-2-1
3	C	Delcero XDeltapine-90 #F5-5-3-2-2-Bulk
4	D	Delcero XDeltapine-90 #F5-5-3-3-1-1
5	E	Delcero XDeltapine-90 #F5-5-3-3-1-2
6	F	Delcero X Deltapine-90 #F5-5-4-2-1-Bulk
7	G	Delcero X Deltapine-90 #F5-5-4-2-2-1
8	H	Delcero X Deltapine-90 #F5-5-4-2-3-2
9	I	Delcero X Deltapine-90 #F5-5-4-2-3-3
10	J	Delcero X Deltapine-90 #F5-5-4-2-3-Bulk
11	K	Delcero X Deltapine-90 #F5-5-4-3-1-Bulk
12	L	Delcero XDeltapine-90 #F5-5-4-3-2-1
13	M	Delcero X Deltapine-90 #F5-5-4-3-3-Bulk
14	N	Delcero XDeltapine-90 #F5-5-7-1-1-1
15	O	Deltapine-90 (Parental line)
16	P	Delcero (Parental line)

Estimate of variance, PCV and GCV, heritability and genetic advance

The genotypic and phenotypic coefficients of variation were computed according to Burton and Devane (1953). Broad sense (H^2) and heritability magnitude of genetic advance from selection for a character in a cross under 5% selection intensity (2.063) and genetic advance as a percent of the sample were calculated for each character in F5 generations according to (Breese 1972 and Robinson *et al.*, 1955).

$$\text{Genetic variance } (\sigma^2 g) = \frac{(\text{MSG} - \text{MSE})}{r}$$

$$\text{Phenotypic variance } (\sigma^2 \text{ph}) = \frac{(\text{MSG})}{r}$$

$$\text{Genotypic coefficient of variance (GCV)} = \frac{\sqrt{\sigma^2 g}}{\bar{X}} * 100$$

$$\text{Phenotypic coefficient of variance (PCV)} = \frac{\sqrt{\sigma^2 \text{ph}}}{\bar{X}} * 100$$

$$\text{Broad sense Heritability } [h^2(\text{bs})]\ (\%) = \frac{\sigma^2 g}{\sigma^2 \text{ph}} * 100$$

Genetic advance (GA) = K. $\sqrt{\sigma^2 \text{ph}}.\,H^2$

$$\text{GAM} = \frac{\text{G.A}}{\bar{X}} * 100$$

Where, MSG = Genetic mean square of genotypes in ANOVA Table, MSE = Environmental (error) mean squares from ANOVA, r = Number replications, σ^2ph=Phenotypic Variance; $\bar{X}$ = Grand mean of the character; K = selection intensity at 5% with a value of 2.063;σph=Phenotypic standard deviation (square root of σ^2ph); H^2 (bs) =Heritability in broad sense GAM= Genetic advance as Percent of mean

RESULTS AND DISCUSSION

Results of ANOVA

Analysis of variance

Results of Variability Analysis

Quantitative traits

Estimates of means and ranges

The results pertaining to mean, range, component of variance, genotypic and phenotypic coefficient of variability, heritability, genetic advance and genetic advance expressed as percent of mean of 16 genotypes of cotton has been presented at Table 3.

Range of variation for days to emergence ranged from 5-6, while its grand mean was 5.55. The variation to the

Table 2. Analysis of variance (ANOVA) model for quantitative characters.

Source of variation	DF	MS	EMS
Block (rep)	r-1	MSb	$\sigma^2e + g\sigma^2r$
Genotypes	(g-1)	MS_G	$\sigma^2e + r\sigma^2g$
Error	(g-1)(r-1)	MSe	σ^2e
Total	gb-1		

Where b (r) =blocks/replications, g= genotypes; DF= degree of freedom, MSb= mean square of blocks, MS_G= mean square of genotypes, MSe = mean square of error,σ^2G= genotype variance components,σ^2e=error variance, σ^2g= (MSg-MSe)/r, σ^2e = MSe.

number of days taken to emerge was minimum which shows narrow base variation among the tested genotypes. The variation ranged from 9.73 to 17.27 for sympodial branches and its grand mean was 12.66. This range gives an opportunity to select genotypes of interest for this trait. The minimum and maximum plant height was recorded from 65.07to 131.53cm, respectively. According to Rathinavel *et al*. (2005) plant height characterizations, the studied genotypes have been categorized under short, medium and tall type; this variation creates a good chance for the breeder to choose based on the breeding program. The grand mean of plant height recorded was 102.5 cm. The lowest and highest range recorded for boll number plant^{-1} was 9 to 20.8, respectively. Since BOP is the main component of seed cotton yield and lint yield; there might be a possibility to select boll number from the existing range of variability to increase the yield (Smith and Coyle, 1997; Zeng and Meredith.Jr., 2009a, 2009b).Its grand mean was 14.92 bolls plant^{-1}.The grand mean of boll weight (BOW) was recorded 5.21gand the maximum and the minimum boll weight also ranged from 4.25 to 6.63 g, respectively. According to Rathinavel *et al*. (2005) boll weight characterization, the studied genotypes have been categorized under medium to large BOW. Thus, this indicated that there was variability between genotypes for boll weight. Seed cotton yield varied from 2696to 5681kgha^{-1}and its mean was 4536.16g.Seed cotton yield range suggested that there is a considerable variation between these traits. This gives an opportunity for the breeder to carefully select better genotypes.

Ginning percentage (GP)of the studied genotypes ranged from 34.22 to 42.29 and its grand mean was 39.47.Economically, GP is desirable trait and it is useful indicator to evaluate the performance of genotype. According to Rathinavel *et al*. (2005) GP characterization, for the studied genotypes all have been classified under Medium, high and very high.

The lowest and highest range was recorded for lint yield from 1073 to 2334 kgha^{-1}, respectively. The variation was ample to select superior genotypes among the studied genotypes. The grand mean for this trait was 1791.77 kg/ha indicating that the general performance of the genotypes is good.

Hundred seed weight (HSW) ranged from 7.37 to 12.62g while the grand mean of hundred seed weight was 8.82 g. According to Rathinavel *et al*. (2005) HSW characterization, the genotypes have been classified under medium, bold and very bold. Thus, this indicating a potential that seed weight could be improved through selection.

Estimates of PCV and GCV

The trait seed cotton yield plot^{-1} exhibited the highest genetic and phenotypic variance i.e. 138,851.46 and 269,805, respectively and followed by lint yieldplot^{-1}that had genetic variance of 38,130.39 and phenotypic variance of 58,424.73.The lowest genetic and phenotypic variance was recorded for the trait number of nodes to first fruiting branch i.e. 0.03 and 0.04, respectively (Table 3).

Since the variation depends upon the magnitude of the measuring units of the traits; coefficient of variation is independent of the measuring units so it is more useful in comparing the population.

The genetic coefficient of variability ranged from 3.03 for ginning percentage to 12.02 for boll number plant^{-1}. The maximum genetic coefficient of variability was observed for boll number per plant (12.02%) followed by hundred seed weight (9.78) (Table 3).

The result of phenotypic coefficient of variability was in agreement with genetic coefficient of variability for the traits. The phenotypic coefficient of variability ranged from 3.27% for ginning percentage to 13.35% for boll number plant^{-1}. The maximum phenotypic coefficient of variability was observed for boll number plant^{-1}(13.35%) followed by hundred seed weight (10.08%) (Table 3).

In this study, the phenotypic coefficient of variability was greater than genetic coefficient of variability. However, the differences between phenotypic and genotypic coefficient for most of the traits were lower in magnitude. This indicates that there was small effect of environment on those characters and selection might be effective.

Table 3.1. ANOVA for cotton phenology.

S.variation	DTE	DIS	DIF	D50F	DIBO	D65BO
Genotypes	0.474^{**}	12.591^{ns}	12.563^{ns}	13.329^{ns}	49.891^{ns}	29.232^{ns}
Replication	0.057	19.266	99.854	87.354	613.099	8.766
Error	0.191	7.688	9.887	16.632	66.232	19.921
CV	7.871	8.644	6.324	7.238	8.596	3.049
LSD	0.622	3.949	4.478	5.8	11.59	6.357
R-square	0.460	0.416	0.532	0.382	0.465	0.341

*, ** and *** are significance levels of p-value at 5%, 1% and 0.1%, respectively and ns= non significance, S. variation: source of variation, CV: coefficient of variability, LSD: least significance difference, DTE: days to emergence, DIS: days to initial squaring, DIF: days to initial flowering, D50F: days to 50% flowering, DIBO: Days to initial boll opening, D65BO: days to 65% boll opening.

Table 3.2. ANOVA for growth parameters.

S.variation	SYM	MON	NFFB	PLH
Genotypes	4.468^{***}	0.064^{ns}	0.163^{***}	253.212^{**}
Replication	2.413	0.193	0.044	336.981
Error	1.415	0.06	0.053	97.879
CV	9.397	54.88	4.54	9.646
LSD	1.694	0.348	0.328	14.09
R-square	0.538	0.364	0.519	0.522

SYM: number of Sympodial branchplant^{-1}, MON: number of monopodial branchplant^{-1}, NFFB: number of nodes to first fruiting branch, PLH: plant height (cm)

PCV % was higher in magnitude than GCV% for all the traits which are in accordance with the results of Mendez-Natera *et al*. (2012). The current study agreed with Sambamurty *et al*. (2004) and Gumber *et al*. (2005) who also reported greater PCV values than GCV values for the characters.

Medium genetic and phenotypic coefficient of variation was observed for the traits boll number plant^{-1}, and hundred seed weight. It indicates that rigorous selection can be applied on the traits to isolate more promising lines.

Lint yield exhibited low PCV and GCV indicating that there was little potential for improvement within the population.

As stated by Shivasubramanian and Menon (1973), the PCV and GCV values are ranked as low, medium and high with 0 to 10%, 10 to 20% and >20%, respectively. Based on this ranking most of the traits under this study, had fallen at low rank PCV and GCV which suggested that the breeders should go for source of high variability for these traits to make improvement.

Estimates of Heritability

In this study hundred seed weight recorded the highest heritability (0.94) followed by boll weight (0.89), ginning percentage (0.89),boll number plant^{-1}(0.81), nodes to first fruiting branch (0.75),number of sympodial branchplant^{-1}(0.68), lint yield plot^{-1} (0.65), lint yield ha^{-1} (0.65) and plant height (0.61) (Table 3). These traits were affected less than the other trait by the environmental conditions and thus selection will be the best step for selecting genotypes having traits high and moderate heritability. Most of the traits in this study exhibited high heritability estimates and few traits had moderate heritability estimates. The result in this study agrees with Ahmad *et al*. (2006) who found moderate to high heritability estimates and genetic advance for plant height and seed cotton yield per plant. Ulloa (2006) also revealed that ginning out turn showed highest heritability (95%) followed by staple length (80%).This study agrees with Desalegn *et al*. (2009), Lu and Myers (2011) and Percy *et al*. (2006) who found as lint percentage was reported to be a highly heritable trait. The current study is

Table 3.3 ANOVA for yield and yield related traits.

S. variation	BOP	BOW	SPL	SPO	SHA	GP	LPL	LPO	LHA	HSW	SNPB
Genotype	15.872^{***}	0.665^{***}	174.456^{ns}	1079220.0^{*}	591986.1^{*}	6.454^{***}	40.658^{ns}	233698.902^{**}	128217.68^{**}	3.159^{***}	2.673^{ns}
Replication	9.440	0.147	217.320	517987.5	283973	1.902	25.056	48452.812	26557	0.022	6.716
Error	3.011	0.075	156.137	523814.17	287442	0.732	24.779	81177.333	44562.44	0.183	3.908
CV	11.627	5.277	13.657	11.819	11.819	2.167	13.777	11.779	11.782	4.855	6.43
LSD	2.471	0.391	17.796	1030.8	763.56	1.218	7.089	405.77	300.64	0.61	2.815
R-square	0.663	0.574	0.318	0.429	0.429	0.757	0.381	0.5	0.5	0.852	0.255

BOP: boll plant^{-1},BOW: boll weight (g), SPL: seed cotton yield plant^{-1} (g): SPO: seed cotton yield plot^{-1} (g)SHA: seed cotton yield ha^{-1} (kg), GP: ginning percentage, LPL: Lint yield plant^{-1}(g), LPO: lint yieldplot^{-1}(g), LHA: lint yield ha^{-1}(kg), HSW: hundred seed weight (g), SNPB: seed number boll^{-1}

Table 3.4. ANOVA for fiber quality traits

S. variation	Mic	Uhml	Ui	Sf	Str	Rd	+b
Genotype	0.174^{***}	7.128^{**}	4.722^{ns}	3.544^{**}	24.636^{***}	2.033^{*}	0.303^{***}
Replication	0.129	0.625	1.340	1.74	0.618	1.177	0.194
Error	0.034	0.524	2.677	1.350	1.311	0.88	0.076
CV	4.1	2.465	2.01	11.553	4.142	1.139	3.263
LSD	0.263	1.031	2.33	1.655	1.631	1.336	0.393
R-square	0.661	0.822	0.383	0.49	0.863	0.462	0.6

Mic: micronaire (units), Uhml: upper half mean length (mm), Ui: length uniformity (%), Sf: short fiber content (%), Str: fiber strength (gram/tex), Rd: degree of reflectance (units), +b: yellowness (units).

in partial agreement with the Authors Mendez-Natera *et al*. (2012).

Nevertheless, the present finding disagrees with the findings of Basbag and Gencer (2004) who found that among yield related traits; bolls per plant had low heritability.

High heritability estimates for bolls per plant indicated the additive/ additive x additive genes were more effective than non- additive effects. Moderate broad sense heritability was also observed for traits days to emergence (0.58),seed cotton yield plot^{-1} (0.51), and seed cotton yield ha^{-1}(0.51).The results of this study confirms the reports presented by Elsiddig *et al*. (2007) and Ali *et al*. (2010) who reported moderate to high heritability for seed cotton yield, lint yield, bolls plant^{-1}and average boll weight.

Estimates of Genetic Advance

The genetic advance as percentage of the mean for the traits under study ranged from 5.52(number of nodes to first fruiting branch) to 22.28 (boll number plant^{-1}) (Table 3). As stated by Johnson *et al*.(1955)genetic advance as percent of mean classified as low (0 to 10%), moderate (10 to 20%) and high (20% and above) .

The highest genetic advance as a percentage of mean was exhibited by boll number plant^{-1}(22.28) followed by hundred seed weight (19.55), boll weight (14.31), lint yield plot^{-1} (13.43) and lint yield ha^{-1}(13.43) (Table 3).The high heritability and high genetic advance that was observed for boll number plant^{-1}is in agreement with the findings of Basal and Tuegut (2005), Joshi *et al*.(2006), Rauf *et al*.(2006) who found high heritability and genetic advance for number of traits including number of bolls per plant, which revealed the additive gene action model in the inheritance of this character and the scope for improvement through simple selection procedures (Vineela *et al*., 2013).This trait is highly reliable during selection process of the genotypes.

High heritability and moderate genetic advance was obtained in traits like hundred seed weight, boll weight, number of sympodial branchesplant^{-1}, lint yield plot^{-1}and lint yield ha^{-1},which revealed the involvement of both additive and non-additive gene action in the inheritance of these characters and offered the best possibility of improvement of these traits through progeny selection or any modified selection procedures (Vineela *et al*.,2013).

From the results of the present study it can be concluded that direct selection cannot be made for most of the yield contributing traits since they exhibited low to moderate genetic variability.

Fiber Quality Traits

Estimates of Means and Ranges

The minimum and maximum micronaire values ranged from 3.57 to 5.06. This range variation could be exploited to obtain interesting micronaire values which fulfill the domestic and world micronaire standards. The grand mean of micronaire value was 4.5 that satisfied world acceptable standards.

Upper half mean length ranged from 26.09 mm to 33.68 mm and its general mean was 29.35mm. This variation of length indicated that there has been ample chance to exercise selection.

Fiber strength varied from 23.5 gram/tex to 37.7 gram/tex and its grand mean result was 27.64 gram/tex, indicating that genotypes grand mean has not met domestic and world standards. Most of the inbred lines were below the standards in fiber strength. Short fiber content ranged from 6.8 % to 13.3% and grand mean 10.06% (Table 4). Short fiber content suggested that there has been considerable potential to drag down to the minimum percentage. High short fiber content (%) in cotton leads to many problems in spinning process such as high end breaks, excessive yarn defects, low machine efficiency and higher worker turnover.

Estimates of PCV and GCV

The lowest genotypic and phenotypic variance was recorded for the trait micronaire which is 0.03and 0.04, respectively. The highest genotypic and phenotypic variance was observed for fiber strength i.e. 5.83 and 6.16, respectively (Table 4).

The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) for micronaire recorded 4.62 and 4.14, respectively. The following PCV and GCV results were found for the different fiber quality parameters; Uhml (PCV=4.55) and GCV=4.38), Sf (PCV=9.36 and GCV=7.36), Str (PCV=8.98 and GCV=8.74), Rd (PCV=0.87 and GCV=0.65) and +b (PCV=3.25 and GCV=2.82) (Table 4).

The genetic coefficient of variability ranged from 0.65% for degree of reflectance to 8.74% fiber strength. The maximum genetic coefficient of variability was recorded for fiber strength (8.74%), followed by short fiber content (7.36%) (Table 4).

The phenotypic coefficient of variability ranged from 0.87% for degree of reflectance to 9.36% for short fiber content. The maximum phenotypic coefficient of variability was observed for short fiber content (9.36%) followed by fiber strength (8.98%) (Table 4).

In this study, the phenotypic coefficients of variability were greater than genetic coefficients of variability. The differences between them for most of the traits were lower in magnitude, i.e. They were more or less close to each other. This indicates that there was small effect of environment on characters and therefore selection might be effective.

Traits exhibited low PCV and GCV indicating that there has been little potential for fiber quality improvement within the population. In fact, some lines exhibited the desirable combination of fiber length and micronaire.

Thus, based on this ranking all of the fiber quality traits under this study have fallen under low rank PCV and GCV which suggested that the breeders should go for source of high variability for these traits to make improvement.

Estimates of Heritability

The highest heritability was recorded for fiber strength (0.95), followed by upper half mean length (0.93), micronaire (0.75), yellowness (0.75), short fiber content(0.62) and degree of reflectance (0.57).Most of the traits exhibited high heritability estimates; few had moderate heritability estimates (Table 4). The present

Table 4. Range, variance, PCV, GCV, H^2, mean, GA and GAM for 18 characters of16 genotypes.

Traits	Range	Genv	EV	PHV	PCV	GCV	H^2	GA	MEAN	GAM
DTE	5-6	0.07	0.05	0.12	6.21	4.80	0.58	0.42	5.55	7.64
SYM	9.73-17.27	0.76	0.35	1.12	8.35	6.90	0.68	1.49	12.66	11.75
NFFB	4.6-6.0	0.03	0.01	0.04	3.98	3.27	0.75	0.28	5.08	5.52
PLH	65.07-131.53	38.83	24.47	63.30	7.76	6.08	0.61	10.05	102.56	9.80
BOP	9-20.80	3.22	0.75	3.97	13.35	12.02	0.81	3.33	14.92	22.28
BOW	4.25-6.63	0.15	0.02	0.17	7.83	7.38	0.89	0.75	5.21	14.31
SPO	3640-7670	138851.46	130953.54	269805.0	8.48	6.09	0.51	550.67	6123.75	8.99
SHA	2696-5681	76136.03	287442	147996.5	8.48	6.08	0.51	404.95	4536.16	8.93
GP	34.22-42.29	1.43	0.18	1.61	3.22	3.03	0.89	2.32	39.47	5.88
LPO	1449-3152	38130.39	20294.33	58424.73	9.99	8.07	0.65	324.97	2418.85	13.43
LHA	1073-2334	20913.92	44562	32054.42	9.99	8.07	0.65	240.2	1791.77	13.40
HSW	7.37-12.62	0.74	0.05	0.79	10.08	9.78	0.94	1.72	8.82	19.55
Mic	3.57-5.06	0.03	0.01	0.04	4.62	4.14	0.75	0.35	4.51	7.65
Uhml	26.09-33.68	1.66	0.13	1.79	4.55	4.38	0.93	2.55	29.35	8.70
Sf	6.8-13.30	0.55	0.34	0.89	9.36	7.36	0.62	1.20	10.06	11.93
Str	23.5-37.7	5.83	0.33	6.16	8.98	8.74	0.95	4.84	27.64	17.51
Rd	79.7-84.1	0.29	0.22	0.51	0.87	0.65	0.57	0.83	82.37	1.01
+b	7.5-9.2	0.06	0.08	0.08	3.258	2.82	0.75	0.425	8.45	5.04

Genv: Genotypic variance, EV: Environmental variance, PHV: Phenotypic variance, PCV: phenotypic coefficient of variance, GCV: Genotypic coefficient of Variance, H^2: broad sense heritability, GA: Genetic Advance, GAM: Genetic advance expressed as percent of mean, DTE: Days to emergence, SYM: Symbodial branch plant^{-1}, NFFB: Number of nodes to first fruiting branching, PLH: plant height (cm), BOP: bollplant^{-1}, BOW: Boll weight (g), SPO: seed cotton yield plot^{-1} (g), SHA: seed cotton yield ha^{-1} (kg), GP: Ginning percentage, LPO: lint yieldplot^{-1}(g), LHA: Lint yieldha^{-1}(kg), HSW: Hundred seed weight (g), Mic: Micronaire (units), Uuml: Upper half mean length (mm), Sf: Short fiber content(%), Str: Strength (gram/tex), Rd: Degree of reflectance (units), +b: Yellowness (units), and the selection differential 2.06 at 5% selection intensity was used.

finding is in agreement with Nistor and Nistor (1999) who determined high broad-sense heritability (89%) for staple length and also agreed with Ali *et al*. (2010) who reported moderate to high heritability for fiber fineness (micronaire).

Estimates of Genetic Advance

The highest genetic advance was relatively recorded for the trait fiber strength (17.51) and the lowest was fordegree of reflectance (1.01). The following genetic advance results were obtained: short fiber content (11.93), upper half mean length (8.70), micronaire (7.65) and degree of reflectance(5.04).Fiber strength and short fiber content have fallen in moderate rank, while the remaining traits have been categorized under low ranking.

Fiber strength and short fiber content exhibited high heritability and moderate genetic advance, which revealed the involvement of both additive and non-additive gene action in the inheritance of these characters and offered the best possibility of improvement of these traits through progeny selection or any modified selection procedures (Vineela *et al*., 2013).

SUMMARY, CONCLUSION AND RECOMMENDATION

As indicated by phenotypic and genotypic coefficients of variability, the genotypes possessed moderate variability for boll number plant^{-1}, hundred seed weight, and lint yield plot^{-1} indicating moderate scope for improvement through selection. Fiber Strength recorded the highest heritability (0.95) followed by hundred seed weight (0.94), upper half mean length (0.93), boll weight (0.89), ginning percentage (0.89), boll number plant^{-1}(0.81) indicating these traits were affected less than the others by the environmental conditions.

Most of the traits exhibited high heritability estimates, few had moderate heritability estimates. The highest genetic advance as a percentage of mean was exhibited by boll number plant^{-1}(22.28) from quantitative parameters and fiber strength (17.51) from fiber quality parameters suggesting that the genotypes under consideration are a good source of material to develop varieties with high yield and strong strength.

In conclusion, the present study has highlighted the existence of low to moderate variability, high heritability and weak to strong associations for the traits understudy of upland cotton.

The information obtained about genetic variability, heritability, genetic advance of characters on lint yield and fiber strength in G. *hirustum* population can profitably be exploited in formulating efficient selection programme for synthesis and development of new cotton genotypes with improved yield and yield contributing traits.

In the present study, low to moderate variability among the 16 genotypes has suggested that exhaustive study should be cared out on the existing germplasm across the country to obtain novel variability. Predominantly introduction, collection, hybridization, mutation breeding and marker assisted selection of cotton in Ethiopia should be a crucial task to enhance genetic variability.

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