Genetic Variability and Heritability Study of Cotton (*Gossypium hirstum* L.) Genotypes at Kamashi District of North-western Ethiopia

Kedir Wulchafo Hussen*

Ethiopian Institute of Agricultural Research, Wondogenet Agricultural Research Center, P.O.Box 198, Shashamen, Ethiopia

*Corresponding author

Abstract

Fifteen upland cotton (*Gossypium hirsutum* L.) genotypes were evaluated for eight traits in randomized complete block design in three replications at Kamashi district of Benishangul-Gumuze Regional State during the 2007 main cropping season. The overall objective was 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. Data were collected on seed cotton yield in kg ha-1 and yield-related traits and subjected to analysis of variance and subsequent estimation of variance components including coefficient of variations, heritability and genetic advance as percent of mean. Genotypes differed significantly for most of the traits and the relatively wide range of the mean values for most of the characters indicated the existence of variations among the tested genotypes. Estimates of phenotypic (PCV) and genotypic (GCV) coefficients of variations were generally laid under low, moderate and high ranges. The PCV values were slightly greater than the GCV values. Moderately high heritability was observed for Days to initial flowering, Days to 50% flowering, days to 65% boll maturity, plant height, boll number, boll weight and seed cotton yield. Estimated genetic advance as percent of the mean was generally low for the four traits and moderate to high for four traits. Among the traits plant height, boll number, boll weight and seed cotton yield had moderate to high genetic advance as percent of mean.

Introduction

Cotton (*Gossypium hirsutum* L.) is mainly grown for fiber and oil purposes and is crucial for the elevation of a country's economy and also called "White gold" (Komala *et al.,* 2018). The cotton fiber is used to spin into yarn which is further used for making socks, curtains, and towels, etc. Its fiber also consumed in textile industry for cloth making (Stewart and Rossi, 2010). The world population is increasing day by day; therefore, it is necessary to increase the productivity of crops to meet the requirement of textile industry. The utilization of various breeding tools is one method to meet the demand of textile industry (Farooq *et al.,* 2014). Understanding the genetic basis of important yield contributing traits is the pre-requisite and information about their relationship must be available to cotton breeders. All of the yield related traits are correlated with each other in a way that increases or decreases in one trait directly affects others. So, estimation of genotypic and phenotypic correlations among these traits are helpful to initiate the breeding programs. The knowledge

about association among various plant characters is useful in the selection of appropriate breeding methods (Teklewold *et al.,* 2000).

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 (Ali and 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).

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 study was planned with the following specific objectives:

To estimate heritability of quantitative and qualitative traits of cotton genotypes.

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 Assosa Agricultural Research Center's (AsARC) sub-testing site in Kamashi woreda in Benishangul Gumuz Regional State in the western part of Ethiopia during the main cropping season of 2007. Kamashi woredas is one of the main cotton cultivating areas in Benishangul-Gumuze.

The Kamashi sub-center of AsARC is located 250 km east of Assosa town and 560 km west of Addis Ababa with an altitude of 1247 meter above sea level at 09^0 31.172' N latitude, and at 035^0 35.488' E longitude. Kamashi woreda has a unimodal rainfall pattern, which starts at the end of April and extends to mid-November (AsARC Report, 2013). The major soil type is Nitosol with a dark reddish-brown color (AsARC Report, 2011).

Experimental Materials and Design

In this experimental study, a total of 15 genotypes including 13 elite genotypes and two check varieties were used (Table 1). These genotypes were obtained from Werer Agricultural Research Center (WARC).

Fifteen cotton genotypes including 13 elite genotypes and two check varieties 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 thus making a plot size of 22.5 m^2 (5 rows x 5 m x 0.9 m). The expectation is to achieve about 55,000 plants per hectare. The spacing between plots and blocks was 1 m and 2 m, respectively.

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.

Data Collection

Yield and yield related parameters and morphological and agronomic data were collected and recorded on a plot basis from the central three rows and on a plant basis from randomly selected plants from the central three rows in each plot.

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.

Measurement of Yield and Yield Related Parameters

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.

Data Analysis

Analysis of variance

The data collected were subjected to statistical analysis using the SAS computer program, version 9.0 (SAS, 2002). Mean separation was conducted using Least Significance Difference (LSD) at 0.05 probability level.

Analysis of variance in a randomized complete block design was computed using the following model:

$$Y_{ij} = \mu + r_j + g_i + \varepsilon_{ij}$$

Where,
Y_{ij} = the response of trait Y in the ith genotype and the jth replication

μ = the grand mean of trait Y;

r_j = the effect of the jth replication;

g_i = the effect of the ith genotype; and

ε_{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).

$$\text{Genotypic variance } (\sigma^2 g) = \frac{Msg - Mse}{r}$$

Environmental variance $(\sigma^2 e) = MSe$

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 $(\sigma^2 ph) = \sigma^2 g + \sigma^2 e$

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) = (σg/grand mean) *100

Phenotypic Coefficient of Variation (PCV) = (σph/grand mean) *100
Where,
σg and σph 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:

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

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

$$EGA = k*\sigma ph*H^2$$

Where,

EGA represents the expected genetic advance under selection;

σph 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):

Genetic advance as percent of population mean = (EGA/grand mean) *100

Results and Discussion

Analysis of variance

The analysis of variance results for the eight traits studied are given in Tables 3. Highly significant (P<0.01) differences among genotypes were observed at the testing site for, days to initial flowering, plant height, number of bolls per plant and seed cotton yield. However, three traits namely days to initial squaring, days to 50% flowering and days to 65% boll opening at the <0.05 probability level.

Mean Performances of Experimental Cotton varieties Crop phenology expressions

Range and mean values for 8 characters of 15 cotton genotypes evaluated in 2007/8 cropping season is presented in Tables 4. Also, the mean performances of these genotypes are presented Tables 5. Regarding phenological characters, days to 50%flowering ranged from 76 to 78 days; and days to 65% boll opening ranged from 137 to 164.23 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 significant differences among the genotypes for plant height, which ranged from 118.32 cm to 162.53 cm with the mean value of 138.1 and coefficient of variation of 8.94% (Table 4& 5). Minimum plant height was observed in genotypes Deltapine 90 (120.53 cm) followed by CCRI 12 (124.23 cm), 5800 (128.27 cm) and BEYAZ ALTIN /5/ (128.6 cm), whileStam-59A (162.53 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.

Yield and Yield Components of Experimental Cotton genotypes

Seed cotton yield (SCY) for genotypes ranged from 1296.3 to 2465.2 kg/ha, and the mean value was 1934.9kg/ha (Table 4 & 5). As presented in Table 4, the top yielders included CCRI 12, 5800, 5794 and the ZHONG 521 with 2465.2, 2583.70, 2332.3, 2234.3 and 2131.6 kg/ha, respectively.

Seed cotton yield (SCY) is a major and important component of cotton yield, and a vital raw material for the textile industry. All of the above genotypes, except China cotton, showed satisfactory SCY potential. Low SCY performing genotypes were China cotton, MYRTO and STAM 59A while intermediate yielders were JIMIAN 1, LU MIAN 6, LU MIAN 1 and BEYAZE ALTINE /5/ all with seed cotton yield of slightly lower than the mean value of 1934.9 kg/ha.

Boll number per plant (BNP) and boll weight (BWt) are important components that contribute to yield parameter. BNP of genotypes averaged 11.93. The top scorers were JIMIAN 1, 5800, CCRI 12 and SHAN MIAN 4, (Tables4 & 5) have good adaptability across locations.

The lower performance of genotypes may be attributed to differences in soil fertility, land preparation; higher early season rainfall compared to insufficient rainfall late in the season. These factors plus the uneven topography, especially have affected the mean performance of the genotypes and their traits unfavorably.

Table.1 List of 15 cotton genotypes used in the study in Benshangul-Gumuze Regional State.

Trt	Trt names
1	BEYAZE ALTIN/5/
2	BEYAZE ALTIN 320
3	MYRTO
4	5800
5	5794
6	JIMIAN 8
7	CCRI 12
8	ZHONG 521
9	CHINA COTTON
10	LU MIAN 1
11	LU MIAN 6
12	SHAN MIAN 4
13	JI MIAN 1
14	DELTAPINE-90
15	STAM 59A

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	$\sigma^2 e + g\sigma^2 r$
Genotypes	g-1	MSg	$\sigma^2 e + r\sigma^2 g$
Error	(r-1) (g-1)	MSe	$\sigma^2 e$

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

$\sigma^2 r$, $\sigma^2 g$, and $\sigma^2 e$ are variances due to replication, genotype, and error, respectively.

Table.3 Analysis of variance (mean square) for 8 traits of 15 cotton genotypes grown at Kemashi testing site.

Traits	Rep (2)	Gen (14)	Error (28)	CV (%)
DIS	0.8ns	1.8ns	1.80	3.81
DIF	0.47ns	8.68*	3.80	2.76
D50F	0.27ns	1.23ns	0.93	1.26
D65BO	26.6ns	1.44.29ns	95.10	6.76
PHt	311.71ns	501.09*	152.42	8.94
BN	0.8ns	8.87*	4.32	17.42
BWt	40.32ns	43.40*	20.44	11.12
SCY	166334.01ns	286462.95*	128218.98	18.51

*, ** Indicate significance at the 0.05 and 0.01 levels, respectively; ns=non-significant.

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; NBP=Number of bolls per plant; BWt=Boll weight in grams; SCY=Seed cotton yield in kg per ha.

Table.4 Minimum and maximum values, mean and standard error of mean (SE) for the 14 traits of 14 cotton genotypes grown in Kamashi testing site.

Traits	Min. value	Genotypes with Min. value	Max. value	Genotype with Max. value	Mean	SE	CV (%)
DIS	34	LU MIAN 1	36.3	China cotton	35.13	0.60	3.81
DIF	68	Delta Pine 90	74.67	China cotton	70.73	1.27	2.76
D50F	76	5794 & Delta Pine 90	78	BEYAZE ALTIN/5/& China cotton	76.93	0.31	1.26
D65BO	137	JIMIAN 8	164.33	China cotton	144.33	31.70	6.76
PHt	118.37	Deltapine 90	162.53	BEYAZE ALTIN/5/	138.1	50.81	8.94
NB	9	China cotton	15	JI MIAN 1	11.93	1.44	17.42
BWt	34	ZHONG 521	46.87	5794	40.66	6.81	11.12
SCY	1298.3	China cotton	2465.2	CCRI 12	1934.9	42739.66	18.51

*, ** Indicate significance at the 0.05 and 0.01 levels, respectively; ns=non-significant.
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; NBP=Number of bolls per plant; BWt=Boll weight in grams; SCY=Seed cotton yield in kg per ha.

Table.5 Mean performance of the eight traits of fifteen genotypes.

S/N	Genotype name	DIS	DIF	D50F	D65BO	PHT	BN	BWT	SCY
1	BEYAZE ALTIN/5/	36ba	71.67bdac	78a	141.67b	118.37g	11.67ebdac	36.67edc	2085.7bac
2	BEYAZE ALTIN 320	36ba	70.33bdec	77.33ba	140b	128.6edfg	11.67ebdac	35.73ed	1849.1bdc
3	MYRTO	34.33ba	68.67de	76.3333	144.67b	131.17edcg	11.33ebdc	38.67ebdc	1593.3dc
4	5800	35.67ba	71.33bdc	77.33ba	142b	128.27edfg	14.67ba	38.86ebdc	2332.3ba
5	5794	36ba	69.67bdec	76b	139.67b	137.7ebdfcg	12ebdac	46.87a	2234.3ba
6	JIMIAN 8	34.33ba	71.67bdac	76.67ba	137b	146.87bdac	11.67ebdac	43.13bdac	2057.3bac
7	CCRI 12	35ba	69dec	76.67ba	139b	124.23efg	13.33bac	37.33edc	2465.2a
8	ZHONG 521	35.33ba	71bdec	77ba	148b	155.87ba	12ebdac	34.8e	2131.6bac
9	CHINA COTTON	36.3a	74.67a	78a	164.33a	143.57ebdac	9e	39.2ebdc	1296.3d
10	LU MIAN 1	34b	70.33bdec	76b	151.33ba	140.33ebdfc	9.67ed	45.06ba	1883bdac
11	LU MIAN 6	34.33ba	72.67ba	77.33ba	146.67b	143ebdac	13bdac	41.93ebdac	1807.7bdc
12	SHAN MIAN 4	35ba	70.33bdec	77ba	146.67b	139.67ebdfc	13.33bac	45ba	2017.8bac
13	JI MIAN 1	34.33ba	72bac	77ba	138.6b7	150.83bac	15a	43.86bac	1811.9bdc
14	DELTAPINE-90	34.67ba	68e	76b	139b	120.53fg	10.33ebc	43.8bac	1921.7bac
15	STAM 59A	35.67ba	69.67bdec	77.33ba	146.33b	162.53a	10.33ebc	38.93ebdc	1536.5dc
	Mean	35.13	70.73	76.93	144.33	138.1	11.93	40.66	1934.9
	CV%	3.81	2.76	1.26	6.76	8.94	17.42	11.12	18.51
	LSD (0.05)	2.24	3.26	1.62	16.31	20.64	3.48	7.56	598.89

In the same column, means followed by the same letter are not significantly different at the 5% level of significance.
 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; NB=Number of bolls per plant; BWt=Boll weight in grams; SCY=Seed cotton yield in kg per ha.

Table.6 $\sigma 2p$, $\sigma 2g$, $\sigma 2e$, GCV, PCV, h2, GA and GAM% for the 8 characters of *G. hirustum* L. genotypes.

Traits	σ2p	σ2g	σ2e	PCV%	GCV%	h2 %	GA	GAM (%)	CV%
DIS	3.00	1.20	1.80	2.92	1.85	0.40	1.43	4.07	3.81
DIF	11.17	7.37	3.80	3.97	3.23	0.66	2.76	3.90	2.76
D50F	1.85	0.92	0.93	1.55	1.09	0.50	1.12	1.46	1.26
D65BO	207.69	112.59	95.10	12.00	8.83	0.54	11.89	8.24	6.76
PHt	602.70	450.28	152.42	20.89	18.06	0.75	20.26	14.67	8.94
BN	11.75	7.43	4.32	9.92	7.89	0.63	2.83	23.71	17.42
BWt	57.03	36.59	20.44	11.84	9.49	0.64	6.23	15.33	11.12
SCY	371942.27	243723.29	128218.98	138.65	112.23	0.66	503.27	26.01	18.51

σ2p=Phenotypic variance, σ2g=genotypic variance, σ2e=environmental variance, PCV%=phenotypic coefficient of variation, GCV%=genotypic coefficient of variation, h2 %= heritability, GA=genetic advance, GAM (%) =genetic advance as percent of mean, CV%=percent of coefficient of variation.

Estimates of Variance Components

Phenotypic and genotypic coefficients of variation

The phenotypic and genotypic variations calculated for the 15 traits are presented in Tables 6. The phenotypic and genotypic variances (> 20 %), were obtained from days to 65% boll opening, plant height, seed cotton yield and lint yield indicating high influence of the environment on these traits.

The high phenotypic coefficient of variation (PCV) values was noted on plant height and seed cotton yield. The PCV values for days to 65% boll opening and boll weight were medium (10-20%). Days to initial squaring, Days to initial flowering, days to 50% flowering, Boll number had low values (< 10 %).

Estimation of broad-sense heritability

Estimate of broad sense heritability for the eight traits of *G. hirustum* genotypes ranged from 40% for days to initial squaring to 75% for plant height (Table 6).
Under a range of moderately high heritability, but low genetic advance as percent of mean were observed for the trait days to initial flowering (66%, 3.9%); days to 50% flowering (50%, 1.46%), and days to 65% boll opening (54%, 8.24%).

The high heritability may have been exhibited due to the influence of favorable environmental conditions rather than genotypic influences and selection for such traits may not be rewarding. The GCV values of most of the heritable traits were also relatively high in magnitude. Moreover, as the value of broad sense heritability becomes high it is used as an indicator of the ease of phenotype-based selection particularly when it is accompanied by a relatively high variability and genetic advance as percent of mean value.

Genetic advance as percent of mean

The genetic advance as the percentage of the mean (GAM) at 5% selection intensity is presented in Tables 6. In this testing site, it ranged from 1.46 for days to 50% flowering to 26.01 for seed cotton yield. Relatively higher genetic advance was observed for seed cotton yield, and plant height. Likewise, estimates of genetic advance (as percent of the mean) for number of days for 65% boll opening were also considerably high.

In general, days to initial flowering, days to 50% flowering, number of days for 65% boll opening, plant height, number of bolls, boll weight and seed cotton yield showed moderately high heritability coupled with high genetic advance as percent of mean value. These results indicate that there is good opportunity to improve these traits through crossing and selection. The analysis of variance showed significant differences among the tested genotypes for most of the 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. Higher phenotypic coefficients of variation were recorded for plant height and seed cotton yield traits.

Heritability estimates were found to be moderately high for days to initial squaring, days to initial flowering, days

to 50% flowering, days to 65% boll opening, plant height, boll numbers, boll weight and seed cotton yield, indicating that these traits are less affected by environmental conditions. The integration of high heritability with high response to selection will provide high reliability in selection of those specific traits

In this study area, moderately high heritability but low genetic advance as percent of mean revealed the involvement of non-additive gene actions for the expression of the traits. Generally, most of the traits studied showed moderately high heritability estimates indicating the possibility of improving these traits through selection.

References

Abbas A, Ali M. A., and Khan T. M (2008). Studies on gene effects of seed cotton yield and its attributes in five American cotton cultivars. *J. Agric. Social Sci.* 4:147-152.

Ali M A., Awan S. I (2009). Inheritance pattern of seed and lint traits in *Gossypium hirsutum* L. *Int. J. Agric. Biol.* 11: 44-48.

Ali M. A., Khan I. A. (2007). Assessment of genetic variation and inheritance mode in some metric traits of cotton (*Gossypium hirsutum* L.) *J. Agri. Social Sci.* 3:112-116.

Ali M. A., Khan I. A., Awan S. I., Ali S, Niaz (2008. Genetics of fiber quality traits in cotton (*Gossypium hirsutum* L.).*Aust. J. Crop. Sci.* 2: 10-17.)

Allard R. W. 1960. Principles of Plant Breeding. John Wiley and Sons. Inc. New York.

Assosa Agricultural Research Center (AsARC), 2011. Farming system survey document.

Assosa Agricultural Research Center (AsARC), 2013. Farming system survey document

Basal H., Turgut I (2005). Genetic analysis of yield components and fiber strength in upland Cotton

(G. *hirsutum* L.), *Asian J. Plant Sci.*, 4(3): 293-298 http://dx.doi.org/10.3923/ajps.2005.293.298.

Burton G. W. and Devane E. H. 1953. Estimating heritability in tall Fescue (*Festuca arundinacea*) from replicated clonal materials. *Agron. J.* 45:487-488.

Falconer D. S. and Trudy F. C. Mackay. 1996. Introduction to Quantitative Genetics. 4th Ed., Longman Group Limited, Malaysia. 464p.

Farooq J, Anwar M, Riaz M, *et al.,* Correlation and path coefficient analysis of earliness, fiber quality and yield contributing traits in cotton (*Gossypium hirsutum* L.). J Anim Plant Sci. 2014;24(3):781–90.

Johnson H. W., Robinson H. F. and Comstock R.E. 1955. Estimate of genetic and environmental variability in soya bean. *Agronomy Journal*, 47:314-8.

Komala M, Ganesan N M, Kumar M, *et al.,* Genetic variability, heritability and correlation analysis in F2 populations of ratoon upland cotton hybrids. Int J Agric Environ Biotechnol. 2018

Raj A., Oudenaarden V., Alexander A (2008). Nature, nurture, or chance: *Stochastic gene expression and its consequences.* Cell, 135 (2): 216–226.

Singh R. K. and Chaudhary B. D. 1977. Biometrical methods in quantitative genetic analysis. Kalyani publishers, New Delhi, Ludhiana, India. 318p.

Stewart L, Rossi J. Using cotton byproducts in beef cattle diets. Bulletin 1311. Cooperative Extension, the University of Georgia College of Agricultural and Environmental Sciences. 2010; 1–8. http://cotton.tamu.edu/General%2Production /Georgia%20Cotton%20Byproducts%20for%20 Beef%20Cattle%20B%201311_2.pdf. Accessed 27 Feb 2020.

Teklewold A, Jayaramaiah H, Jagadeesh B N. Correlations and path analysis ofphysio-morphological characters of sunflower (*Helianthus annuus* L.) as related to breeding method. Helia. 2000;23(32):105–14.