



doi: <https://doi.org/10.20546/ijcrar.2019.704.010>

Genetic Distance and Variation among Cotton (*Gossypium hirsutum*. L) Genotypes for Yield Traits in Kamashi District of Benishangul-Gumuz Regional State, Ethiopia

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Abstract

The present research was carried out to determine and record genetic distance and variation among cotton (*Gossypium hirsutum* L) genotypes for yield traits in Kamashi district of benishangul-gumuz regional state for fourteen upland cotton genotypes. The genotypes were evaluated for ten traits in randomized complete block design with three replications. Data were collected on days of 50% flowering, days to 65% boll opening, plant height, Number of monopodial branches per plant, Number of sympodial branches per plant, Boll number per plant, Boll weight Seed cotton yield per hectare, Lint yield and Ginning out turn. The data were subjected to analysis of variance. Genotypes were varied significantly for most of the traits studied and there were wide range variation on mean values for most of the traits which indicated the presence of variability among the tested genotypes.

Article Info

Accepted: 04 March 2019

Available Online: 20 April 2019

Keywords

Mean performance, Heritability, Genetic advance, upland cotton, Variability

Introduction

Cotton (*Gossypium* spp.) is an economically important crop around the world, providing the most natural fiber for the manufacture of textiles. *Gossypium* contains more than 50 recognized species belonging to eight genome groups (Wendel and Grover, 2015). Only four species, *G. herbaceum* (A1), *G. arboreum* (A2), *G. hirsutum* (AD1), and *G. barbadense* (AD2) have been domesticated and cultivated widely. *G. hirsutum* L. ($2n = 4x = 52$, genome size: 2.5 Gb; Li *et al.*, 2014a, 2015; Wendel and Grover, 2015), also called upland cotton, is cultivated worldwide and accounts for more than 95% of cotton production (Chen *et al.*, 2007; Zhang *et al.*, 2008).

The worldwide economic impact of the cotton industry is estimated at ~\$500 billion/year with an annual utilization of ~115 million bales or ~27 million metric tons of cotton fiber (Chen *et al.*, 2007). The top cotton producer in the world is China, U.S.A, India, Middle East, Australia and Pakistan (Spectrum Commodities, 2012). These countries are rich in climatic conditions for growth of the crop. Similarly, in terms of cotton production, the five most popular producers of European countries are Italy, Germany, France, Spain, and UK where they account nearly for three quarters of the E.U production of the textiles, and clothes (European Commission, 2011).

Estimation of the magnitude of variation within genotype for important plant attributes will enable breeders to exploit genetic diversity more efficiently. In breeding

programs, selection is an integral part by which genotypes with high productivity in a given environment could be developed. Indirect selection through related yield components will be more fruitful. Morphological traits are commonly used to evaluate genetic variation since their measurements are simple (Tsedeke, 2007).

Cotton is a crop of manifold merits in the world. Simultaneously it is used as a fiber, food and a feed; its lint is used for making cloth. Low quality lint is used as a raw material in the manufacture of high-grade writing paper and rayon, and in the chemical industry for making photographic and X-ray films (Berger, 1969). The oil is one of the most valuable products for cotton next to soybean. The refined oil is used in cooking and the oil cake residue as a protein feed for ruminant livestock (Lee, 2009). The edible-grade cotton seed flour can be used as human food in at least three ways: as a protein supplement in cereal grains and in vegetable protein mixtures; as an additive in bakery products, and as filler in meat-like products (Anonymous, 2008). In Africa, Asia and Latin America, cotton is contributing a lot towards overcoming food insecurity. In Africa, thirty-five of the fifty-five countries produce cotton. Twenty-two of these countries are known for exporting cotton (Valderrama, undated, 2007 online).

Production of cotton in Ethiopia has been increasing in the last few years in general and in Benisangul-Gumuze Regional State in particular, but productivity of cotton is generally low. SOFERCO (2016) reported that current world's productivity average of cotton lint is about 760 kg/ha (~ 2.054 tons/ha), and As the report, current cotton productivity of Ethiopia is estimated to 2.0-3.0 tons/ha (under irrigation) and 1.2-1.7 tons/ha (under rain-fed).

Many factors including biotic (disease, insects, and weeds), and abiotic factors (drought, low soil fertility, salinity, etc.); also, not using appropriate technologies (improved variety and fertilizer) do contribute to the low productivity. Therefore, developing improved varieties is one of the measures to alleviate these constraints. In this regard, studying is the primary precondition that breeders look into for the development of new varieties. So far no studies on genetic distance and variation of different cotton traits contributing to yield parameters have been carried out in Kamashi district of Beneshangul-Gumuz Regional State, Ethiopia. In view of these gaps, the present investigations were carried out to determine and record genetic distance and variation among cotton (*Gossypium hirsutum*. L) genotypes for yield traits in kamashi district of benishangul-gumuz regional state.

Materials and Methods

Description of the Study Area

The field experiments were conducted at Kamashi sub-testing site of Assosa agricultural research center to determine and record genetic distance and variation among cotton (*Gossypium hirsutum*. L) genotypes for yield traits. For this purpose, fourteen upland cotton genotypes were studied (Table 1). The experiment was conducted in 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 m² (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.

Data Collection

For agronomic and yield parameters, data were recorded for the following traits; Days to 50% flowering, Days to 65% boll opening, Plant height (PHt), Number of monopodial, sympodial branches per plant, Number of bolls per plant. The average Boll weight (g), Seed Cotton yield per plant (gm), Lint Percentage (GOT) and Lint yield

Data Analysis

Analysis of variance

The data collected were subjected to statistical analysis. First, the analysis was done using the SAS computer program, version 9.0 (SAS, 2002). Mean separation was conducted Duncan's multiple range test (DMRT) at 0.05 probability level

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

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

Where,

Y_{ij} = the response of trait Y in the i th genotype and the j th replication

μ = 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

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).

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

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

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:

$$\text{Phenotypic variance } (\sigma^2ph) = \sigma^2g + \sigma^2e$$

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

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

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

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:

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

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;

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.*, (1955).

Genetic divergence analysis

Genetic divergence analysis was computed based on multivariate analysis using Mahalanobis's D^2 statistic (Mahalanobis, 1936) by using SAS Computer Software Program.

As Sneath and Sokal (1973) indicated, Euclidean distance (ED) were computed from the 10 morph-physiological traits of 14 cotton genotypes after standardization (subtracting the mean value and dividing it by the standard deviation) as follows:

$$\text{ED}_{jk} = \sqrt{\sum_{i=1}^n (x_{ij} - x_{ik})^2}$$

Where,

EDjk = distance between cultivars j and k; x_{ij} and x_{ik} = morph-physiological traits values of the i^{th} character for genotype j and k, respectively; and n = number of morph-physiological traits used to calculate the distance.

The distance matrix from morph-physiological traits was used to construct dendrograms based on the Un-weighted Pair-group Method with Arithmetic means (UPGMA). The results of cluster analysis were presented in the form of dendrogram. In addition, mean ED was calculated for each genotype by averaging of a particular genotype to the other 14 varieties. The calculated averages distance (ED) was used to estimate which genotype is closest or distant to the others based on their mean performance.

Results and Discussions

The mean square from analysis of variance showed highly significant ($P < 0.01$) differences among cotton genotypes were observed for days to 50% flowering,

days to 65% boll opening, plant height, number of monopodial branches per plant, number of sympodial or fruiting branches per plant, number of bolls per plant, for average boll weight, seed cotton yield, lint yield, and lint percentage or ginning outturn (GOT).

Range and mean values of cotton genotypes

Range and mean values for tested cotton genotypes are presented in Table 3. Traits like days to 50% flowering ranged from 82.67 to 93.00 days while days to 65% boll opening ranged from 145 to 167 days. Shorter number of days to flower setting and boll opening indicated earliness of certain tested lines. The early flowering entry was the check Deltapinee-90 with 82.7 days from emergence followed by WARC-4 with 88.3 days. The late flowering lines were WARC-5 and WARC-1 with 93.0 and 92.7 days, respectively. The remaining entries were intermediate and ranged from 90.0 to 91.3 days. Deltapinee-90 was also the early boll opener at 145 days and WARC-12 was the latest at 165.7 days after emergence (Table 3). Ali and Khan (2003) have taken to flowering is considered as an important determinant of earliness. (Iqbal and Jabbar, 2011) also found positive linkage between first flower formation and earliness. Hence, delay in flowering is a sign of late maturity which may be okay in non-moisture stress areas. Plant height ranged from 99.60 cm to 186.53 cm with the mean value of 133.48 and indicated a wide variation among genotypes. Variations of genotypes for other traits are demonstrated in Table 3.

Seed cotton yield (SCY) ranged from 1601.20 to 2724.70 kg/ha with a mean value of 2207.20 kg/ha. The top yielders, as shown in Table 5, included WARC-4, WARC-8, WARC-3, WARC-9, WARC-11 and the check Deltapinee-90 with 2724.9, 2583.7, 2564.9, 2433.1, 2353.1 and 2413.3 kg/ha, respectively. These entries with the exception of WARC-3 have satisfactory levels of lint percentages and could serve as good source for cotton variety improvement. Lint is a major and most important component of cotton production, and a vital raw material for the textile industry.

Boll number per plant (BN) and boll weight (BWt) are important yield components that contributed to increased seed cotton (Table 5). Entries with higher boll number than the trial mean (3.62 g) included WARC-2, WARC-5, WARC-6, WARC-10 and the two checks Deltapinee-90 and Stam-59A. These test entries also had ball weights larger than the mean with the exception of WARC-6 and Stam-59A (Table 5). Larger number of bolls indicated

the capacity of certain entries to retain more productive bolls under stress or otherwise.

Estimation of broad-sense heritability

GCV alone is not helpful for effective selection, but together with heritability estimates could determine the extent of selection response (Mahaingam *et al.*, 2013). Estimate of broad sense heritability for 10 traits of Cotton genotypes were ranged from 63% to 92% for days to 65% boll opening and days to 50% flowering respectively (Table 5). In this study heritability's of genotypes were categorized as high, moderately high and low heritability ranges. High heritability were noted for plant height, number of monopodial branch per plant, number sympodial branches per plant, boll number per plant and ginning out turn indicating these traits affected less than others by the environmental factor (Amir *et al.*, 2012 and Ali *et al.*, 2011) have similar findings. Moderately high heritability was observed for days to 65% boll opening, boll weight, seed cotton yield and lint yield. And heritability estimates for number of monopodial branches per plant (6.67%) and plant height (20.60%) were low. Killi *et al.*, (2005) also agree with this findings.

Euclidean Distance of *Gossypium hirsutum* Genotypes

Estimates of genetic distance were ranged from 2.3 to 97.7 with a mean of 14.17. The highest distance was observed for WARC-4 and Stam-59A (97.7) followed by Deltapinee 90 and Stam-59A (97.1) and the lowest distance was noted for WARC-6 and WARC-9, (2.3), followed by WARC-5 and WARC-11 (3.3) (Table 6).

Cluster analysis based on the Euclidean distance (ED) matrix is presented in Figure 1. From the Figure two groups were formed each with a sub-group and the third cluster is solitary and comprised a single genotype which is Stam-59A (7.15%). The remaining 13 cotton varieties (92.85%) including one standard check variety Deltapinee 90 formed two larger groups. The first large group consisted WARC-5, WARC-11, WARC-12 and Deltapinee 90. The second larger group had two sub-groups; the first sub-group consisted of WARC-1, WARC-6, WARC-10 and WARC-9, while the second sub-group comprised WARC-7, WARC-2, WARC-3, WARC-4 and WARC-8.

The solitary genotype, Stam-59A, is characterized by tall stem and long monopodial branches; under high rainfall and windy conditions, it has a tendency to lodge. The

presence of genetic diversity among the tested genotypes is appreciable, and crossing of lines from the different clusters could produce heterotic F₁'s and a wide range of variability in subsequent segregating populations from which to select and advance promising types. According to Ghaderi *et al.*, (1984) increasing parental distance

implies a great number of contrasting alleles at the desired loci, and then to the extent that these loci recombine in the F₂ and F₃ generation following a cross of distantly related parents and the greater will be the opportunities for the effective selection for yield factors.

Table.1 Fourteen Cotton seed materials used in the study

Entry number	Codes	Pedigree/Designation	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	(Check-1)	Deltapine 90 (na ⁺)	-
14	(Check-2)	Stam-59A (na ⁺)	-

na⁺ = Pedigree not available

Table.2 Analysis of variance (mean square) for 10 traits of 14 experimental cotton varieties

Traits	Replication	Genotypes	Error
D50%F	1.50ns	18.35**	1.60
D65%BO	141.07*	111.53**	37.56
PHt	2483.62**	1545.68**	291.53
NMB	0.74ns	3.91**	0.45
NSyB	0.57ns	2.65**	0.32
NB	1.87ns	6.48**	0.81
BWt	0.21ns	0.22**	0.08
SCY	235570.91ns	332418.31**	96973.04
LY	45356.15ns	56175.97**	17464.58
GOT	6.60**	7.93**	0.89

*, ** Indicate significance and highly significance difference at the 0.05 and 0.01 levels, respectively; ns=non-significant; D50%F=Days to 50% flowering, D65%BO=Days to 65% boll opening, PHt= Plant height, NMB=Number of monopodial branches/plant, NSyB=Number of sympodial branches/plant, NB=Number of bolls per plant, BWt=Boll weight in grams, SCY=Seed cotton yield in kg per ha, LY= Lint yield in kg per ha and GOT=Ginning out turn

Table.3 Minimum and maximum values with the corresponding genotypes for ten traits of cotton genotypes

Traits	Min. Value	Genotypes with Min. value	Max. value	Genotype with Max. value	Mean	SE	CV (%)
D50%F	82.67	Deltapine-90	93.00	WARC-5	90.29	0.73	1.42
D65%BO	145.00	Deltapine-90	167.00	Stam-59A	159.29	3.51	3.72
PHt	99.60	Deltapine-90	186.53	Stam-59A	133.48	9.86	12.79
NMB	6.21	WARC-2	10.22	WARC-3	8.76	0.39	7.66
NSyB	7.46	WARC-11	10.98	WARC-6	8.89	0.33	6.33
NB	20.00	WARC-7	24.69	Deltapine-90	22.17	0.52	4.05
BWt	2.95	Stam-59A	3.95	WARC-10	3.62	0.16	7.82
SCY	1601.00	WARC-1	2725.00	WARC-4	2207.20	180	14.11
LY	645.00	WARC-1	1140.00	WARC-4	914.45	76.3	14.45
GOT	37.60	WARC-3	43.62	WARC-10	41.46	0.54	2.27

D50%F=Days to 50% flowering, D65%BO=Days to 65% boll opening, PHt= Plant height, NMB=Number of monopodial branches/plant, NSyB=Number of sympodial branches/plant, NB=Number of bolls per plant, BWt=Boll weight in grams, SCY=Seed cotton yield in kg per ha, LY= Lint yield in kg per ha and GOT=Ginning out turn

Table.4 Mean values of 10 traits of 14 cotton genotypes

Cotton Genotypes	Mean values of tested Cotton genotypes									
	D50%F	D65%BO	PHt	NMB	NSyB	NBP	BWt	SCY	LY	L%
WARC-1	92.7ba	158.0bdac	103.6d	7.1ef	8.8ced	21.6dce	3.75dac	1601.2e	644.6d	40.26ed
WARC-2	90.7bc	161.3bdac	120.7cd	6.2fa	9.8b	24.2a	3.52dac	2202.2bc	917.4ba	41.66bdc
WARC-3	90.7bc	167.0a	142.3cb	10.2a	8.0fg	21.2dce	3.93ba	2564.9ba	965.4ba	37.64f
WARC-4	88.3d	156.7bdc	116.5cd	7.8ecd	9.0ebd	21.1dce	3.84bac	2724.9a	1139.5a	41.82bdc
WARC-5	93.0a	152.3de	119.1cd	7.7ed	8.8ebd	22.2bc	3.59dac	2017.5edc	856.9bcd	42.47bac
WARC-6	90.0dc	159.3bdac	144.3cb	9.6ba	11.0a	24.0a	3.33de	1668.1ed	686.0cd	41.13edc
WARC-7	91.0bac	160.7bdac	135.8cb	8.9bc	8.4egd	20.1e	3.61bdac	1958.5edc	844.4bcd	43.12ba
WARC-8	90.7b	154.7dec	134.5cb	8.6bcd	7.7g	20.7de	3.87bac	2583.7ba	1049.0ba	40.60ed
WARC-9	91.3bac	156.7bdc	155.0ba	9.5ba	8.9ebd	22.0dc	3.71dac	2433.1bac	1056.4ba	43.42a
WARC-10	90.0dc	162.3bdac	120.9ba	9.5ba	9.7cb	22.3bc	3.95a	2160.0bdc	942.2ba	43.62a
WARC-11	91.0bac	163.0bac	137.7cb	8.9bc	7.5g	20.4e	3.44dc	2353.1bac	1004.1ba	42.67bac
WARC-12	90.3dc	165.7dcdc	152.1b	9.5ba	8.2feg	22.0dc	3.74dac	2184.7bdc	869.5bc	39.80e
Deltapine-90	82.7e	145.0e	99.6d	9.7ba	9.7cb	24.7a	3.47bdc	2413.3bac	976.2ba	40.45ed
Stam-59A	91.7bac	167.3a	186.5a	9.4ba	9.3cbd	23.7ba	2.95e	2035.3edc	850.7bcd	41.80bdc
Trial mean	90.3	159.3	133.5	8.76	8.9	22.16	3.62	2207.20	914.44	41.46
CV (%)	1.42	3.85	12.79	7.66	6.33	4.05	7.82	14.11	14.45	2.27
LSD _(0.05)	2.16	10.29	28.66	1.13	0.95	1.51	0.48	522.60	221.8	14.45

* Within columns, values having a letter in common are not significantly different at the 5% significance level.

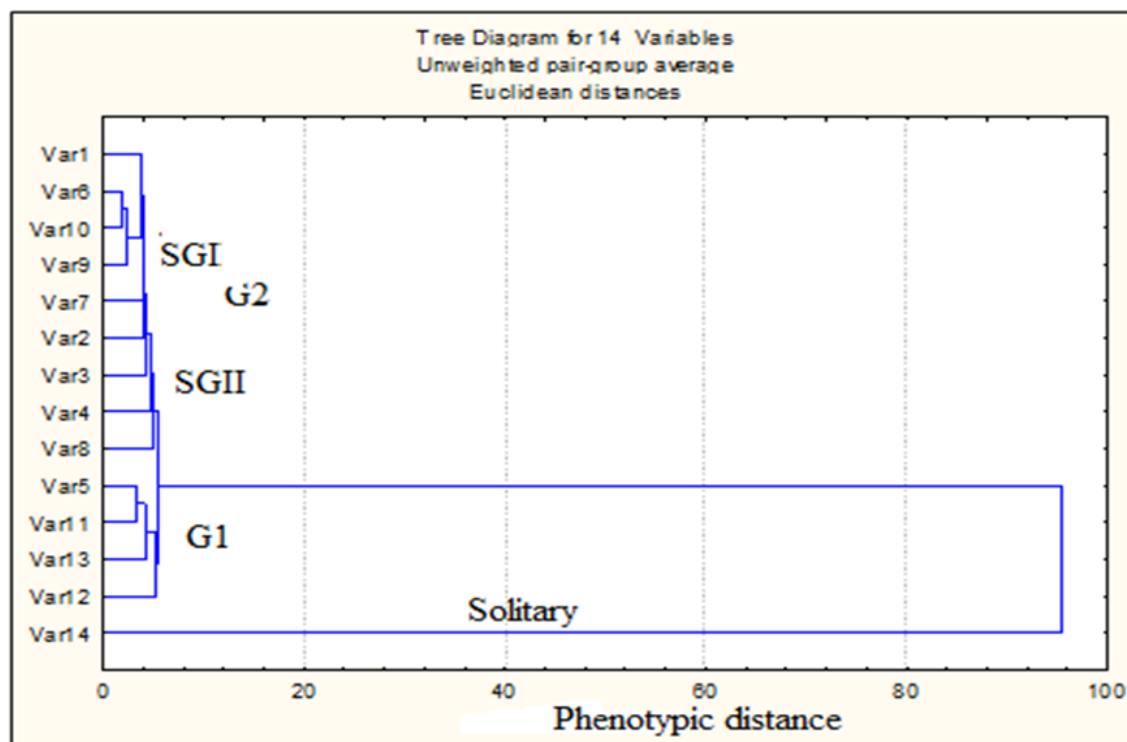
D50%F=Days to 50% flowering; D65%BO=Days to 65% boll opening; PHt=Plant height; NMB= Number of monopodial branches per plant; NSyB=Number of sympodial branches per plant; NB=Number of bolls per plant; BWt=Boll weight in grams; SCY=Seed cotton yield in kg per ha; LY=Lint yield in kg per ha; L%= GOT (Ginning out turn).

Table.5 Genotypic, phenotypic and environmental variance and coefficient of variation, broad sense heritability and genetic advance. For 10 traits of Cottons genotypes in Kamashi district

Traits	Range	Mean	SE	PV	GV	EV	PCV%	GCV%	H ²	GA	GAM%
D50%F	82.66-93.00	90.28	0.73	19.40	17.82	1.60	4.88	4.68	0.92	8.34	9.24
D65%BO	145.00-167.33	159.80	3.51	99.30	62.40	36.90	6.24	4.94	0.63	12.92	8.08
PHt	99.60-186.53	133.48	9.86	1740	1448.50	291.53	31.25	28.51	0.83	71.64	53.67
NMB	6.21-10.22	8.76	0.39	4.20	3.76	0.45	23.42	22.14	0.89	3.78	43.16
NSyB	7.46-10.97	8.89	0.33	2.90	2.54	0.32	19.03	17.94	0.89	3.10	34.88
NB	20.11-24.68	22.16	0.52	7.00	6.22	0.81	11.96	11.25	0.88	4.84	21.84
BWt	2.95-3.93	3.62	0.16	0.30	0.19	0.08	14.44	12.15	0.71	0.76	21.07
SCY	1601.20-2724.70	2207.20	179.79	397067.00	300094.00	96973.00	28.55	24.82	0.76	883.98	40.05
LY	644.60-1139.50	914.44	76.30	67819.03	50354.45	17464.58	28.48	24.54	0.74	365.33	39.95
GOT	37.64-43.43	41.45	0.54	8.53	7.64	0.89	7.04	6.67	0.90	4.10	9.88

D50%F=Days to 50% flowering; D65%BO=Days to 65% boll opening; PHt=Plant height; NMB= Number of monopodial branches per plant; NSyB=Number of sympodial branches per plant; NB=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.

Figure.1 Dendrogram generated based on UPGMA clustering method depicting genetic relationships among 14 cotton varieties based on 10 morphological traits



Note: Var1=WARC-1, Var2=WARC-2, Var3=WARC-3, Var4=WARC-4, Var5=WARC-5, Var6=WARC-6, Var7=WRC-7, Var8=WARC-8, Var9=WARC-9, Var10=WARC-10, Var11=WARC-11, Var12=WARC-12, Var13=Daltapine-90, Var14=Stam-59A

Table.6 Euclidean distance of 14 cotton genotypes measured from 14 phenological traits

	V1	V2	V3	V4	V5	V6	V7	V8	V9	V10	V11	V12	V13	V14	Mean
V1		4.9	4.5	4.1	4.9	4.2	4.5	5.9	4.2	3.8	4.8	5.9	6.4	95.6	11.8
V2			4.5	6.0	5.8	4.0	4.1	5.7	4.4	4.0	4.2	6.4	6.9	96.6	11.7
V3				5.3	5.9	3.6	4.2	6.6	4.6	4.7	5.0	4.9	7.4	96.7	11.5
V4					5.2	4.0	5.3	5.1	4.5	4.6	5.3	6.2	6.4	97.7	11.1
V5						4.1	5.4	6.4	4.9	4.3	3.3	4.3	3.9	95.2	10.1
V6							4.0	4.7	2.3	3.4	4.3	5.3	5.5	97.0	9.7
V7								5.2	4.4	3.9	5.3	5.4	6.7	95.9	9.8
V8									4.3	3.6	6.3	7.3	6.9	96.8	9.6
V9										3.7	5.3	6.0	6.3	95.9	9.0
V10											3.8	5.5	5.5	96.3	8.5
V11												4.6	4.7	96.6	8.1
V12													6.9	94.1	7.8
V13														97.1	13.1
V14															96.3

Note: -V1=WARC-1, V2=WARC-2, V3=WARC-3, V4=WARC-4, V5=WARC-5, V6=WARC-6, V7=WARC-7, V8=WARC-8, V9=WARC-9, V10=WARC-10, V11=WARC-11, V12=WARC-12, V13=Deltapine90, V14=Stam-59A

The magnitude and structure of genetic variation detected from the diversity analysis could be used in breeding programs (Koutis *et al.*, 2012). Generally, the more distant the parents are for crossing, the better the chance to obtain heterotic hybrids, and the broader the genetic base of the varieties to be developed.

Conclusions

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. Higher phenotypic coefficients of variation were recorded for plant height, number of monopodial branches per plant, seed cotton yield and lint yield traits.

Heritability estimates for genotypes were found to be moderately high for days to 65% boll opening, boll weight, seed cotton yield and lint yield. And genotypes

which have high range of heritability were noted for plant height, number of monopodial branches per plant, number of sympodial branches per plant, number of bolls per plant and lint percentage, indicating that these traits are less affected by environmental conditions. Plant height, number of monopodial branches per plant and number of bolls per plant showed high heritability (83%, 89% and 89%, respectively) with high genetic advances in percent of mean (53.67, 43.16, and 54.45, respectively). The integration of high heritability with high response to selection will provide high reliability in selection of those specific traits

Euclidean genetic distance of the genotypes was estimated based on means of genotypes. The distance analysis classified 14 cotton genotypes into two classes. This indicates the presence of diversity among the tested genotypes. Clusters I (7.15%) was the least cluster containing one genotype and Cluster II contained the largest groups of genotypes (92.85%). Thus, crossing of genotypes from these two clusters may produce heterotic F₁'s and wide range of variability in subsequent segregating (F₂) populations.

The top four genotypes that performed better than the released check varieties for seed cotton yield were WARC-4, WARC-8, WARC-3, and WARC-9, with seed cotton yields of 2724.9, 2583.7, 2564.9, and 2433.1 kg per hectare, respectively. Seed cotton yields of the standard checks were 2035.3 kg per hectare for Deltapine 90 and 2413 kg per hectare for Stam-59A.

In this study, looking at the mean seed cotton yield, the lint percentage and mean lint yield, six top performing entries deserve variety verification evaluations in BenshangulGumuze and other similar rain-fed areas. Finally adaptation, demonstration and promotion on farmers' fields should follow if any or all of these lines meet the national variety release requirements during the verification process.

Conflict of interest

There are no conflicts of competition of interests in this paper.

Acknowledgments

My special appreciation and deepest thanks go to Dr. Bedada Girma and to Dr. GudetaNepir for their encouragement, suggestions, guidance and overall assistance during my study period. And I want to express my deepest gratitude and appreciation to EIAR for sponsoring my study through provision of research grant. My thanks also go to Werer Agricultural Research Center for providing me with seeds of cotton varieties for my research work.

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How to cite this article:

Kedir Wolchafo Hussien. 2019. Genetic Distance and Variation among Cotton (*Gossypium hirsutum* L) Genotypes for Yield Traits in Kamashi District of Benishangul-Gumuz Regional State, Ethiopia. *Int.J.Curr.Res.Aca.Rev.* 7(4), 91-100. doi: <https://doi.org/10.20546/ijcrar.2019.704.010>