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Genetic Variability and Association of Traits among Sorghum Genotypes [Sorghum bicolor (L.) Moench] Under Drought Stress Area

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Abstract

Drought is one of the most important factors that affect crop production worldwide and continues to be a challenge to plant breeders, despite many decades of research. Understanding the genetic variability among sorghum genotypes is the key objective to develop improved sorghum cultivars for drought-prone environments. The field experiment was conducted at miesso during the 2021 main cropping season. A set of 72 sorghum genotypes advanced from a pedigree breeding approach was used in this study. The experiment was laid out using a Row-Column design with two replications. R statistical software was used to analyze the data. The analysis of variance indicated that there were significant variations among the tested genotypes for the studied traits. Genotypic and phenotypic coefficient of variation ranged from 0.56% to 23.88% and 0.66% to 28.99% respectively. Broad sense heritability ranged from 25.56% to 86.87% while genetic advance as a percent of mean ranged from 1.11% to 43.40%. Principal component analysis (PCA) revealed that five principal components with Eigenvalue greater than unity accounted for 74.1% of the total variation. Cluster analysis grouped the test genotypes into five clusters. Cluster I, II, III, IV, and V accounted for 41.667%, 6.944%, 26.389%, 16.667%, and 8.333% of the tested genotypes in that order. The highest intra-cluster distance was observed for cluster V whereas the maximum inter-cluster distance was observed between cluster IV and V. The lowest intra-cluster distance was observed for cluster III, whereas clusters I and III showed the lowest inter-cluster distance. The overall study revealed the presence of wide genetic variability among the studied sorghum genotypes in the study area where moisture stress is a critical problem for sorghum production.

Keywords: *Genetic Advance, Heritability, and Cluster Analysis.*

INTRODUCTION

Sorghum *[Sorghum bicolor (L.) Moench]* is the fifth leading cereal crop grown in the tropical and subtropical regions with limited rainfall. It is stable food of poor and the most food-insecure people, living mainly in the semiarid tropics [1]. It is often cross pollinated, diploid crop species (2n=2x=20) which belongs to the Poaceae family with a genome size of 730 Mb [2]. While it is primarily grown as feed grain in the developed world, sorghum is a staple crop for more than 500 million people in 30 sub-Saharan African and Asian countries and is essential to the food security of over 300 million people in Africa [3]. Ethiopia is the second largest sorghum producing country in Eastern Africa next to Sudan. Of the cereals, sorghum covers 15% of the total area and contributed 16% of the total grain production in Ethiopia. It is an important food and feed crop grown in dry lowland areas, where soil moisture is limited.

In Ethiopia, many sorghum growing areas suffer from recurrent droughts due to shortage and uneven distribution of rainfall. Drought is one of the most important factors which affects crop production in the lowland areas of Ethiopia [4]. In many regions of the country, the rain comes late or stops early making the crop growing period very short leading to crop failures. The irregular rain pattern, coupled with subsistence farming system has made areas of the country vulnerable to drought and low productivity, leading to severe malnutrition and hunger. It acts as a serious limiting factor in agricultural production by preventing a crop from reaching the genetically determined theoretical maximum yield.

Due to the above listed problems, in the study area, the current sorghum production per unit area is not sufficient to meet the demand for human consumption, animal feed, fuel, and building material requirements of a rapidly growing population. Genetic improvement in sorghum yield depends on the magnitude of genetic variability, heritability, and genetic advance in the population. In planning a sorghum improvement program, knowledge of the variability of traits could be a key success. Genetic parameters like the genotypic coefficient of variation, phenotypic coefficient of variation, heritability, and genetic advance are useful biometric tools for measuring genetic variability [5]. Therefore, the present study was designed to estimate genetic variability among sorghum genotypes for drought tolerance and to determine the association of yield and yield related traits under drought stress condition.

MATERIALS AND METHODS

Description of The Study Area

The field experiment was conducted at Miesso, located in eastern Ethiopia, Oromia Region at 39°21'E longitude and 8°30'N latitude during the 2021 main cropping season. The altitude of Miesso is 1270 m.a.s.l. The area represents dry lowlands where sorghum is predominantly grown by smallholder farmers. The area also characterized by a semiarid climate with high rainfall variability and frequent drought events that affect crop productivity significantly. Long-term average maximum and minimum temperature of the area are 31.5°C and 16.2°C, respectively, and the total annual rainfall is about 571 mm. The study site has a bimodal rainfall distribution with very short rainfall season between March and May, and a main rainy season between end of June to September. Rainfall distributions are erratic and water scarcity is prevalent. The soil type of the experimental site is vertisol with a high clay content at the top 15cm [6]. The soil has a slightly basic pH (7.6–7.8) with relatively low organic matter content (0.9–1.5%).

Experimental Materials

The experimental materials comprised of 72 different sorghum genotypes including three checks (Table 1.), which were released for moisture stress areas. The genotypes were obtained from Melkassa Agricultural Research Center (MARC). These genotypes were developed by the pedigree breeding method and with a subsequent selection of the derived segregating generation

Table 1. List of sorghum genotypes used for the experiment

Codes.	Genotypes	Pedigree	Seed Sources
G1	ETSC15437-2-2	14MILSDT7086/ “Gambella 1107”	MW21NVTSeedInc#1
G2	ETSC16087-23-1	235421/ICSTG2372	MW21NVTSeedInc#2
G3	ETSC16066-18-1	ETSL101851/Teshale	MW21NVTSeedInc#3
G4	ETSC16034-12-1	Argiti/ICSTG2372	MW21NVTSeedInc#4
G5	ETSC14573-5-4	Melkam/13sudanint10-1	MW21NVTSeedInc#5
G6	ETSC16091-10-1	235421/M204	MW21NVTSeedInc#6
G7	ETSC16032-4-1	05MW6073/M204	MW21NVTSeedInc#7
G8	ETSC15385-2-2	ETSC300301/Meko-1	MW21NVTSeedInc#8
G9	ETSC16034-10-1	Argiti/ICSTG2372	MW21NVTSeedInc#10
G10	ETSC15357-3-1	ICSV700/Meko-1	MW21NVTSeedInc#11
G11	ETSC14715-3-1	13MI5024/13sudanint13-2	MW21NVTSeedInc#12
G12	ETSC16005-9-1	14MWLSDT7310/M204	MW21NVTSeedInc#14
G13	ETSC15363-1-2	S35/ “Gambella 1107”	MW21NVTSeedInc#16
G14	ETSC14695-1-2	Debir/13sudanint27	MW21NVTSeedInc#17
G15	ETSC14225-4-2	“Gambella 1107”/S35	MW21NVTSeedInc#18
G16	ETSC16035-9-1	Argiti/B35 or 05MI5064/B35	MW21NVTSeedInc#19
G17	ETSC15312-3-1	Debir/(Hodem/Gobiye)	MW21NVTSeedInc#21
G18	ETSC17182-12-2	Local Bulk (White)/SRN39/E36-1/KariMatama1	MW21PYTSeedInc#22
G19	ETSC15363-1-2	WSV387/P-9403/ETSL101857	MW21NVTSeedInc#23
G20	ETSC17023-14-1	90BK4184/85MW5552/NTJ2	MW21PYTSeedInc#24
G21	ETSC17007-9-1	PGRCE6940/SAR24/Framida	MW21PYTSeedInc#25
G22	ETSC17240-8-1	(ICSV111/B35)/ICSV111/ “Gambella 1107”	MW21PYTSeedInc#26
G23	ETSC17268-7-1	MR812/B35/ “Gambella 1107”	MW21PYTSeedInc#27
G24	ETSC17073-6-2	(E-35-1)-4/CS3541derive5-4-2-1)/P9401/SRN39	MS20PYT#90
G25	ETSC17201-1-2	CR: 35:5/ICSV-1005/76T1#23/ “Gambella 1107”	MW21PYTSeedInc#29
G26	ETSC17258-13-1	ICSR24010/B35/SRN39	MS20PYT#95
G27	ETSC14804-4-2	SILA/13sudanint10-1	MW21PYTSeedInc#20

G28	ETSC17285-5-2	PGRCE69420/87PW3173/SRN39	MW21PYTSeedInc#32
G29	ETSC15312-3-1	14MWLSDT7324/ICSTG2372	MW21NVTSeedInc#21
G30	ETSC17140-9-1	WSV387/P9403/B35/KariMatama1	MW21PYTSeedInc#34
G31	ETSC17006-8-1	PGRCE6940/SAR24/SRN39	MW21PYTSeedInc#35
G32	ETSC17158-3-2	ICSR24010/B35/ “Gambella 1107”	MW21PYTSeedInc#36
G33	ETSC17323-24-2	90BK4184/85MW5552/M-204	MW21PYTSeedInc#37
G34	ETSC17300-4-2	PGRCE6940/SAR24/SRN39	MS20PYT#221
G35	ETSC17296-3-1	PGRCE6940/SAR24/ “Gambella 1107”	MW21PYTSeedInc#39
G36	ETSC17298-4-1	PGRCE6940/SAR24/ETSL101848	MW21PYTSeedInc#40
G37	ETSC17213-3-2	IESV92084/E36-1/Melkam	MW21PYTSeedInc#42
G38	ETSC17142-9-3	WSV387/P9403/B35/ETSL100307	MW21PYTSeedInc#43
G39	ETSC17156-1-4	MR812/76T1#23/ETSL101865	MW21PYTSeedInc#44
G40	ETSC17301-10-2	PGRCE6940/SAR24/B35	MW21PYTSeedInc#45
G41	ETSC17268-5-3	MR812/B35/ “Gambella 1107”	MW21PYTSeedInc#46
G42	ETSC17298-5-2	PGRCE6940/SAR24/ETSL101848	MW21PYTSeedInc#47
G43	ETSC17186-2-1	Local Bulk /SRN39/76T1#23/ “Gambella 1107”	MW21PYTSeedInc#48
G44	ETSC17106-6-1	WSV387/P9403/E-36-1/M-204	MS20PYT#355
G45	ETSC17328-8-1	90BK4184/85MW5552/SRN39	MW21PYTSeedInc#50
G46	ETSC17268-5-1	MR812/B35/ “Gambella 1107”	MW21PYTSeedInc#51
G47	ETSC17194-3-1	Local Bulk (White)/SRN39/76T1#23/NTJ2	MW21PYTSeedInc#52
G48	ETSC17043-8-1	(E-35-1)-4/CS3541Drv.5-4-2-1)/P9401/ETSL10865	MW21PYTSeedInc#41
G49	ETSC17354-12-1	WSV387/P-9403/ETSL101857	MW21PYTSeedInc#54
G50	ETSC17272-3-1	MR812/B35/SRN39	MW21PYTSeedInc#55
G51	ETSC17321-4-2	(E-35-1)-4/CS3541Drv.5-4-2-1)/P9401/ETSL10865	MW21PYTSeedInc#56
G52	ETSC17350-3-1	WSV387/P-9403/M-204	MW21PYTSeedInc#57
G53	ETSC17115-5-1	WSV387/P9403/E-36-1/ETSL102496	MW21PYTSeedInc#58
G54	ETSC17093-3-1	WSV387/76T1#23/ “Gambella 1107”	MW21PYTSeedInc#59
G55	ETSC17213-1-1	IESV92084/E36-1/Melkam	MW21PYTSeedInc#60
G56	ETSC14203-5-2	Karimtama1/N-13	MW21PYTSeedInc#61
G57	ETSC17071-6-2	(E-35-1)-4/CS3541Drv.5-4-2-1)/P9401/ETSL10848	MW21PYTSeedInc#62
G58	ETSC17111-3-1	WSV387/P9403/E-36-1/NTJ2	MW21PYTSeedInc#63
G59	ETSC17360-18-2	WSV387/P-9403/ETSL101853	MW21PYTSeedInc#67
G60	ETSC17257-6-1	ICSR24010/B35/ETSL101857	MW21PYTSeedInc#68
G61	ETSC17258-3-2	ICSR24010/B35/SRN39	MW21PYTSeedInc#70
G62	ETSC17354-9-1	WSV387/P-9403/ETSL101857	MW21PYTSeedInc#73
G63	ETSC17129-6-1	SDSL2690-2/76T1#23/NTJ2	MW21PYTSeedInc#77
G64	ETSC17175-5-4	MR812/B35/ETSL102496	MW21PYTSeedInc#78
G65	ETSC17113-6-1	WSV387/P9403/E-36-1/ETSL101853	MW21PYTSeedInc#80
G66	ETSC17360-5-1	WSV387/P-9403/ETSL101853	MW21PYTSeedInc#82
G67	ETSC17172-4-4	MR812/B35/NTJ2	MW21PYTSeedInc#83
G68	ETSC17032-6-1	90BK4236/87PW3173/ETSL101857	MW21PYTSeedInc#84
G69	ETSC16001-6-1	14MWLSDT7310/ICSTG2372	MW21PYTSeedInc#85
G70	Melkam	WSV387	MW21Breeder Seed
G71	Argiti	WSV387/P9403	MW21Breeder Seed
G72	Tilahun	2005MI5060/E36-1	MW21Breeder Seed

Experimental Design and Procedures

The experiment was laid out in an incomplete block of 24 rows by 6 columns in 2 replications according to the commonly used procedure by the National Sorghum Research Program of Ethiopia. The experimental plots consist of 2 rows, each 5 m in length with 75 cm between rows and 15 cm between plants. The experiment was planted on the 11th of July, 2021. Seeds were sown manually by hand drilling at a rate of 10 kgha^{-1}. Thinning was done three weeks after the date of planting to maintain the recommended plant population. Fertilizer was applied at a rate of 100 kgha^{-1} Di Ammonium Phosphate (DAP) and 50 kgha^{-1}of Urea. DAP was applied at sowing while urea was applied at knee height stage (around 35 days after Planting). The field was maintained free of weeds through hand weeding while chemical sprays were made to control insect pests.

Data Collection

The data were collected both on plot and individual plant basis as per descriptor for sorghum [7].

Data collection on plant basis

Plant height (cm): The average length of five randomly selected plants from the base of the plant to the tip of the panicle was taken at the time of maturity.
Panicle length (cm): The average length of five randomly selected plants from the base of the panicle to the tip was measured using barcode ruler.
Panicle weight (g): The average weight of five randomly selected panicles (un-threshed) / plot.
Panicle yield (g): The average yield of five randomly selected panicles (threshed) per plot.

Data collection on plot basis

Days to 50% flowering (days): The number of days from emergence to the date at which 50% of the plants in a plot started flowering.
Days to 90% physiological maturity (days): The number of days from emergence to the stage where 90% of the plants in a plot reached at physiological maturity which was recognized by a black layer formed on the bottom of the kernel.
Grain filling period (days): The numbers of days from dates of 50% flowering to dates of 90% physiological maturity.
Grain filling rate (kg/ha/days): It is calculated as the ratio of grain yield (kg/ha) to grain filling period (days) as: Grain filling rate (kg/ha/days) = Grain yield / Grain filling period [8].
Stand count at harvest (No.): The total number of main plants in a plot was counted when 90% of the plants in a row mature physiologically.
Harvest index (HI %): Calculated as the ratio of dried grain weight adjusted to 12% moisture content to the dried total above ground biomass weight and multiplied by 100. A 5m row of each plot was harvested, above ground biomass (stem and leaves) was dried for 10 days and weighed. Then the panicles were harvested, dried, threshed and weighed to compute the harvest index.

Thousand seed weight (g): is the weight of 1000 seeds and adjusted to 12.5% moisture level.
Grain yield (kg/ha): After harvesting, the panicles from each row were threshed, cleaned and weighed after adjusted to 12.5% moisture content. Then the raw grain yield (g/plot) was converted to total grain yield (kg/ha).
Stay-green score: Visual stay-green rating was done at physiological maturity using a scale of 1 to 5. Rating 1 indicates completely green normal size leaves (no leaf death), 2 = 25% of the leaves died, 3 = 26 to 50% of the leaves died, 4 = 51 to 75% are dead, 5 = 76 to 100% of the leaves and stem are dead (complete plant death).

Drought tolerance score: This was recorded at the time of physiological maturity with a scale of 1 to 5 where 1 = poor, 2 = fair, 3 = good, 4 = very good and 5 = excellent.

Chlorophyll content of leaves: At the flowering stage, the amount of chlorophyll in the leaves of five randomly chosen plants per plot was measured. A chlorophyll content meter, SPAD -502 plus (Konica Minolta Sensing, Inc. Japan, Osaka), was used to measure two leaves per plant. The second and fourth leaves were measured from the top at the base of their leaf lamina using a chlorophyll meter (SPAD values).

Data Analysis

Analysis of Variances (ANOVA)

The data were subjected to analysis of variance by using the R- statistical software version 4.3 [9]. The experimental design was described by the model: $\boldsymbol{y_{ijkl} = \mu + \alpha_i + \beta_j + \gamma_k + \delta_l + \varepsilon_{ijkl}}$ where y_{ijkl}=the observation of i^{th} treatment applied in the j^{th} row and k^{th} column for l^{th} replication, μ is the grand mean effect, α_i is the i^{th} treatment effect, β_j is the j^{th} row effect, γ_k is the k^{th} column effect, δ_l replication effect and ε_{ijkl} are uncorrelated random errors with zero mean and constant variance (δ^2) (Table 2).

Table 2. Analysis of Variance (ANOVA)

Source of Variations	Degrees of Freedom (DF)	Sum of Squares (SS)	Mean of Squares (MS)	F-Values
Rows	R-1	SSR	SSR/DFR	MSR/MSE
Columns	C-1	SSC	SSC/DFC	MSC/MSE
Treatments	Trt-1	SSTrt	SSTrt/DFTrt	MSTrt/MSE
Error	(RC-1) - (R-1) - (C-1) - (Trt-1)	SSE	SSE/DFE	
Total	R*C-1	SST		

DF = Degree Freedom, R = Rows, C = Columns, Trt = Treatments, DFE = Degree Freedom of Error, DFR = Degree Freedom of Rows, DFC = Degree Freedom of Columns, DFTrt = Degree Freedom of Treatments, SSR = Sum Squares of Rows, SSC = Sum Squares of Columns, SSTrt = Sum Squares of Treatments, SSE = Sum Squares of Error, SST = Sum Squares of Total, MSE = Mean Squares of Error, MSR = Mean Squares of Rows, MSC = Mean Squares of Columns, MSTrt = Mean Squares of Treatments.

Estimation of Variance Components

The phenotypic and genotypic variability of each quantitative trait was estimated as phenotypic and genotypic variances and coefficients of variation. These variance components were computed using the formula suggested by [10].

Heritability and Genetic Advance

The proportion of phenotypic variance that is attributable to an overall genetic variance for the genotypes was estimated using broad sense heritability values by the formula adopted from [11].

Expected genetic advance under selection (GA)

Genetic advance (GA) in absolute unit and as percent of the mean (GAM), assuming selection of superior 5% of the genotypes were estimated in accordance with the methods illustrated as: - $GA = K * SDp * H^2b$ Where, GA = Genetic advance, SDp = Phenotypic standard deviation on mean basis; H^2b = Heritability in the broad sense. K = the standardized selection differential at 5% selection intensity (K=2.063).

Genetic advance as percent of mean (GAM)

Genetic advance as percent of mean was estimated as $GAM = \frac{GA}{\bar{X}} * 100$ Where, GAM = Genetic advance as percent of mean GA = Genetic advance, $\bar{x}$ = Mean. The GAM was categorized as low (<10%), moderate (10-20%) and high (>20%) [12].

Clustering of Genotypes

The cluster analysis was performed based on the Unweight Pair Group Method with Arithmetic Means (UPGM) clustering method from the Euclidean distance matrix.

Principal Component Analysis

Principal component analysis (PCA) based on a correlation matrix was computed to find out the characters, which accounted for much of the total variation. Based on the principal component analysis the inter-relationship among a large set of variables in terms of a relatively small set of variables or components was assessed without losing any essential information of original data set.

RESULTS AND DISCUSSIONS

Analysis of Variances

From the analysis of variance, the tested genotypes exhibited significant variation for days to flowering (DTF), stay green score (SGs), days to maturity (DTM), stand count (SC), drought tolerance score (DTs), plant height (PH), chlorophyll content (CHLc), grain filling period (GFP), panicle length (PL), harvest index (HI), panicle weight (PW), panicle yield (PY), thousand seed weight (TSW), grain filling rate (GFR) and grain yield (GY) (Table 3). The result indicates that the tested genotypes were different in their potential to perform for variable characteristics at the tested location. Highly significant differences among sorghum genotypes with respect to days to flowering, days to maturity, plant height, head weight per plot, hundred seed weight, and grain yield also reported [13] . Similarly, significant differences in plant height, days to flowering, days to maturity, grain filling period, thousand seed weight, stay green, panicle exertion, panicle length, days to emergency, panicle width and grain yield were reported [8].

Table 3. Mean squares from the analysis of variance (ANOVA) for 15 traits of 72 sorghum genotypes evaluated at Miesso Agricultural Research Station in 2021

		Mean Squares				
S/N	Traits	Trt. (T-1) (Df=71)	Row (R-1) (Df=23)	Col (C-1) (Df=5)	Err (R*C)-T (Df=44)	CV (%)
1	DTF	38.77***	16.24***	9.13*	3.25	6.24
2	CHLc	13.39.	50.76‘.’	15.75***	8.89	7.12
3	SGs	1.0671***	1.5987***	1.0501*	0.4485	29.66
4	DTM	32.23***	43.64***	20.72**	4.92	4.15
5	SC	124.84***	74.06‘.’	27.71ns	40.56	19.96
6	DTs	0.7094*	1.2276***	0.4836ns	0.4205	37.20
7	GFP	33.32***	42.99***	24.95**	7.26	11.14
8	PH	1095.16***	654.96***	393.56*	152.43	13.74
9	PL	8.65***	8.07**	0.75ns	3.17	12.27
10	PW	12230.9***	12800***	12805.9*	3715.5	19.92
11	PY	5853.4***	7737.7***	27263***	2192	22.38
12	HI	70.98***	76.26***	150.29***	21.32	28.93
13	GY	1399848***	851509***	1232283***	178278	22.63
14	GFR	812.39***	503.34***	225.90**	63.70	24.24
15	TSW	29.79***	31.401‘.’	31.11ns	4.86	14.83

The significant codes indicate that if the P- value was in the range (0, 0.001), (0.001, 0.01), (0.01,0.05), P>0.05, it had a significance code of ***, **, *, . and ns

Mean Performance of Genotypes

The range and mean values for 15 traits of 72 studied sorghum genotypes are indicated in Table 4. Grain yield ranged from 2102.82 Kg/ha to 6322.95 Kg/ha with an average value of 4253.4 Kg/ha. In general, three genotypes had a mean value greater than the best standard check (Melkam= 4260 Kg/ha) for grain yield. Similar ranges and means for days to flowering, days to maturity, grain filling period and plant height are also reported.

Table 4. Range and mean values for yield and agronomic traits of the test genotypes and standard check varieties.

	Test Genotypes			Check Varieties			Overall
Traits	Minimum	Maximum	Average	Melkam	Argiti	Tilahun	Mean
DTF	64.00	86.00	75.00	72.00	82.00	76.00	77.00
CHLc	45.47	60.92	53.19	54.78	51.00	48.10	52.24
SGs	1.00	5.00	3.00	4.00	3.5.0	2.00	2.61
DTM	112.00	135.00	124.00	116.00	126.00	119.00	123.00
DTs	1.00	4.00	2.50	1.00	1.00	1.00	1.73
SC	25.00	70.00	48.00	46.00	58.00	53.00	47.00
GFP	37.00	61.00	49.00	40.50	45.00	42.50	46.00
PH	131.67	246.33	189.00	147.00	215.00	163.70	193.94
PL	13.17	26.00	19.59	26.00	20.67	20.50	21.08
PW	295.00	816.70	555.50	408.30	641.70	333.30	494.93
PY	184.46	525.90	355.18	323.60	409.80	217.20	339.65
HI	15.52	46.70	31.11	33.46	24.72	17.61	26.62
GY	2102.82	6322.92	4212.87	4.26	5.74	3.59	4253.40
GFR	43.34	140.91	92.16	105.19	132.15	84.45	93.50
TSW	17.60	36.30	26.95	30.85	28.55	24.15	28.03

DTF=days to flowering, CHLc=chlorophyll content, SGs=stay green score, DTM=days to maturity, DTs=drought tolerance score, SC=stand count, GFP=grain filling period, PH=plant height, PL=panicle length, PW=panicle weight, PY=panicle yield, HI=harvest index, GY=grain yield, GFR=grain filling rate and TSW=thousand seed weight.

Estimates of Variance Components

Phenotypic and Genotypic Coefficient of Variation

Genotypic and phenotypic coefficient of variation ranged from 0.56% (stay green score) to 23.88% (harvest index) and 0.66% (stay green score) to 28.99% (harvest index), respectively (Table 5). High PCV and GCV values were observed for harvest index, grain filling rate and grain yield. High PCV values indicate that selection on the basis of phenotype would be effective for most of the characters [14]. Traits with high GCV indicate the basic prerequisite on which positive response due to selection depends. Low GCV values were recorded for stay green score, grain filling period, panicle length, days to flowering, chlorophyll content and days to maturity indicating that improvement of these traits through selection would be less effective due to lack of genetic variability. Low PCV values were recorded for days to flowering, stay green score, chlorophyll content, drought tolerance score and days to maturity. These traits contribute a low magnitude of heritable genetic (additive) factor to the next generation, which indicates no need for investment to improve these traits aiming for sorghum improvement. The lower GCV and PCV values for different traits in the current study was in agreement with findings reported [15].

Estimates of Heritability and Genetic Advance

Broad sense heritability ranged from 25.56% for drought tolerance score to 86.87% for grain filling rate. High heritability values were noticed for grain filling rate, days to flowering, grain yield, thousand seed weight, plant height, days to maturity, harvest index and grain filling period (Table 5). These variables' high heritability values suggested that genetics accounted for the majority of the variance seen and that environmental factors had less of an impact. Thus, under stressful situations, these characteristics could be employed as selection criteria. Because the environment masks the genotypic effects, selection may be extremely difficult or even impossible for a character with low heritability. Accordingly, choosing genotypes based on grain yield and attributes related to yield would be a more satisfying way to enhance the performance of sorghum genotypes, according to the results of the current study [16].

Genetic advance as a percentage of mean ranged from 1.11% for drought tolerance score to 43.4% for grain filling rate (Table 5), indicating selection of the top 5% base population could result in an advance of 1.11% and 43.4% over the respective population. High genetic advance as percentage of mean was recorded for grain filling rate, harvest index, stand count, thousand seed weight, grain yield, panicle yield, panicle weight and plant height. High value, given as a percentage of mean, of the projected genetic advance observed for plant height and harvest index. When selection is based on characteristics with a sufficiently substantial genetic advancement as a percentage of mean, varieties will perform better for those traits [17].

Table 5. Estimates of variability components for fifteen traits of 72 sorghum genotypes evaluated at Miesso Agricultural Research Station during the 2021 growing season

Traits	Range	Mean ±SEM	σ^2g	σ^2p	σ^2_e	GCV (%)	PCV (%)	H^2b (%)	GA	GAM (%)
DTF	64.00-86.00	77.00±1.29	19.95	23.26	3.31	5.88	6.26	85.76	8.52	11.06
CHLc	45.47-60.92	52.24±2.26	4.30	13.73	9.42	3.97	7.09	31.34	2.39	4.58
SGs	1.00-5.00	2.61±0.47	0.31	0.76	0.45	0.56	0.66	40.82	0.73	1.14
DTM	112.00-135.00	123.00±1.92	17.56	24.96	7.40	3.48	4.05	70.86	7.24	5.96
SC	25.00-70.00	47.00±4.50	47.95	88.51	40.56	14.71	19.99	54.17	10.58	22.31
DTs	1.00-4.00	1.73±0.46	0.14	0.56	0.42	0.78	0.60	25.56	0.39	1.11
GFP	37.00-61.00	46.00±2.28	16.75	26.38	9.63	8.83	11.17	63.38	6.78	14.56
PH	131.67-246.33	193.94±8.96	553.48	714.03	160.74	12.13	13.88	77.50	42.75	21.99
PL	13.17-26	21.08±1.32	3.13	6.64	3.51	8.39	12.22	47.17	2.50	11.87
PW	295.00-816.00	494.93±44.75	5781.08	9786.22	4005.14	15.36	19.99	59.07	120.38	24.32
PY.	184.46-525.90	339.65±36.56	3107.68	5781.09	2673.41	16.41	22.38	53.76	84.19	24.79
HI	15.52-46.70	26.62±3.09	40.43	59.57	19.15	23.88	28.99	67.86	10.79	40.53
GY	2102.82-6322.95	4253.4±300.64	752491.82	933261.16	180769.34	20.36	22.67	80.63	1604.6	37.66
GFR	43.34-140.91	93.50±5.81	446.88	514.29	67.51	22.61	24.25	86.87	40.58	43.40
TSW	17.60-36.30	28.03±1.56	12.47	17.33	4.86	12.59	14.85	71.96	6.17	22.02

SEM = Standard error of mean, σ^2g =genotypic variance, σ^2e =environmental variance, σ^2p =Phenotypic variance, PCV=Phenotypic coefficient of variation, GCV=Genotypic coefficient of variation, H^2b= Broad sense heritability GA=Genetic advance in absolute unit, GAM= Genetic advance as percentage of mean, DTF=days to flowering, CHLc=chlorophyll content, SGs=stay green score, DTM=days to maturity, DTs=drought tolerance score, SC=stand count, GFP=grain filling period, PH=plant height, PL=panicle length, PW=panicle weight, PY=panicle yield, HI=harvest index, GY=grain yield, GFR=grain filling rate and TSW=thousand seed weight.

Clustering of Genotypes

Most breeding programs utilize diverse parents which are genetically far apart from one another; cluster analysis usually finds the extent of genetic diversity and groups the crop with similar parents into one cluster [18]. The analysis was based on an unweighted pair group method with an arithmetic means clustering method from euclidean distances matrix which grouped the 72 sorghum genotypes into five major clusters, consisting of 5 to 30 genotypes (Figure 1 and Table 6). Cluster I was the largest cluster consisting of 30 genotypes and accounted for 41.667 % of the total genotypes. Cluster III was the second largest cluster followed by cluster IV which consists of 19 genotypes (26.389%) and 12 genotypes (16.667%) of the total genotypes respectively. Cluster II and V have the lowest number and percentage of the genotypes. Such genetic divergence among sorghum genotypes indicated that crossing between distantly related genotypes of these clusters might provide desirable recombinants.

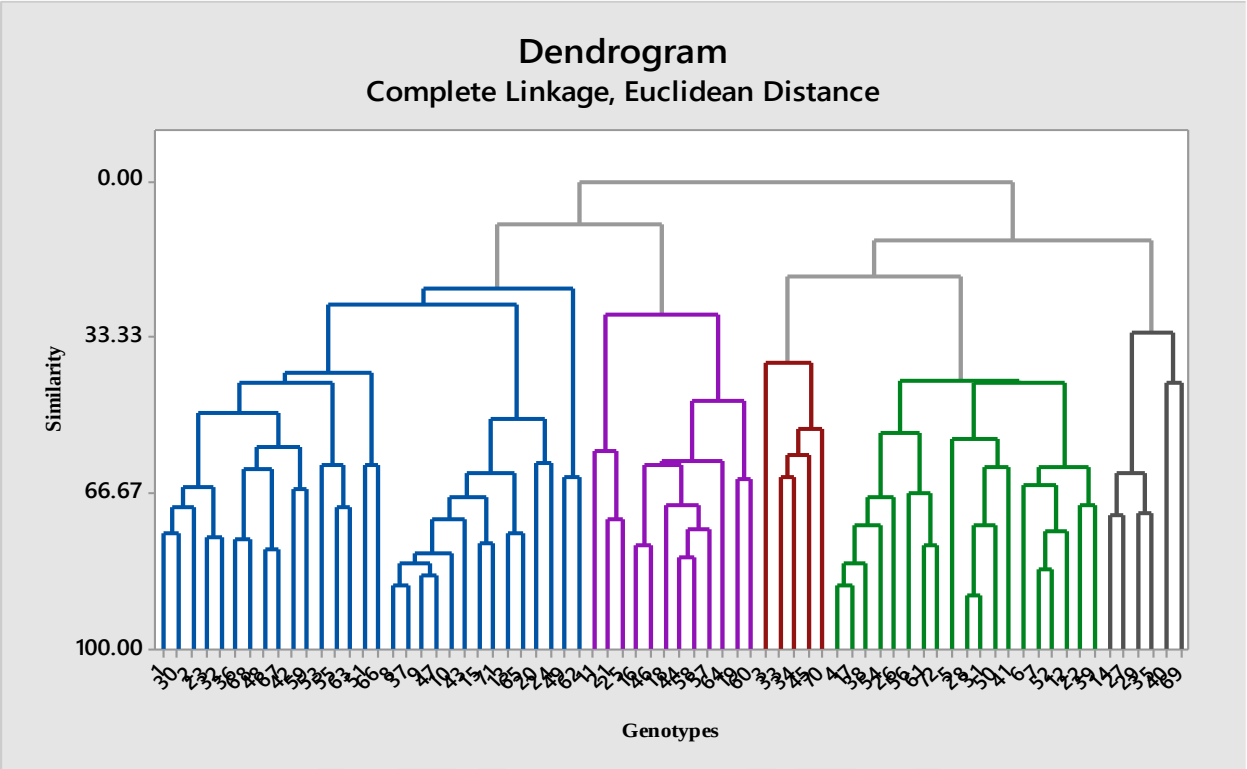

Figure1. Dendrogram depicting similarity of 72 sorghum genotypes by unweighted pair group method with arithmetic means (UPGMA) clustering method from Euclidean distances matrix estimated for 15 quantitative traits

Table 6. Distribution of 72 sorghum genotypes in to five different clusters based on fifteen quantitative traits

Number of Clusters	Proportion of Genotypes	List of Genotypes.
Cluster-I	30 (41.667%)	G1, G30, G2, G23, G32, G36, G68, G48, G67, G42, G59, G53, G55, G63, G51, G66, G8, G37, G9, G47, G10, G43, G15, G71, G13, G65, G20, G24, G49, G62
Cluster-II	5 (6.944%)	G3, G33, G34, G45, G70
Cluster-III	19 (26.389%)	G4, G17, G38, G54, G26, G56, G61, G72, G5, G28, G31, G50, G41, G6, G7, G52, G12, G22, G39
Cluster-IV	12 (16.667)	G11, G21, G25, G16, G46, G18, G44, G58, G57, G64, G19, G60
Cluster-V	6 (8.333%)	G14, G27, G29, G35, G40, G69

Cluster Mean Analysis

The mean values of fifteen quantitative characters distributed in to five clusters are presented in Table 7. Cluster I had mean values greater than overall mean for all traits except for days to flowering and stand

count. Cluster II was distinguished from the others by having lower mean values than over all means for all traits except for panicle length, panicle weight, thousand seed weight and grain filling rate. The genotypes in cluster III had higher mean values for panicle weight, thousand seed weight, harvest index, panicle yield, grain filling rate and grain yield, which can be selected for further evaluation and could be suitable for improvement of sorghum yield under drought conditions. The low values of days to maturity and grain filling period in cluster II and days to flowering in cluster IV indicate the presence of early maturing genotypes, Thus, further evaluation of members of this cluster to develop early maturing variety would be promising option to improve the yield of sorghum for the area.

Table 8. Mean values of five clusters based on fifteen studied traits of 72 sorghum genotypes

Traits	Cluster-I	Cluster-II	Cluster-III	Cluster-IV	Cluster-V	GM
DTF	77.00	77.00	77.00	78.00	74.00	77.00
CHLc.	53.08	498.82	52.42	51.41	55.20	52.24
DTM	124.00	118.00	123.00	123.00	128.00	123.00
SC	44.00	41.00	45.00	50.00	57.00	47.00
GFP	47.00	41.00	47.00	45.00	54.00	46.00
PH	195.06	152.00	192.09	195.01	241.67	193.94
PL	2122.53	22.67	20.86	20.82	24.00	21.08
PW	579.17	816.67	495.24	415.70	550.00	494.93
PY	418.81	306.81	348.21	278.14	184.46	339.65
TSW	30.25	40.21	26.29	22.63	15.52	26.10
HI	28.99	26.65	28.16	27.25	26.85	28.03
GFR	100.05	94.02	93.83	87.33	78.71	93.00
GY	4643.00	3847.00	4333.00	3909.00	4205.00	4261.00

DTF=days to flowering, CHLc=chlorophyll content, SGs=stay green score, DTM=days to maturity, DTs=drought tolerance score, SC=stand count, GFP=grain filling period, PH=plant height, PL=panicle length, PW=panicle weight, PY=panicle yield, HI=harvest index, GY=grain yield, GFR=grain filling rate and TSW=thousand seed weight.

Genetic Distance among Clusters

The range of variation present between genotypes determines the extent of improvement gained through selection and hybridization. The larger the distance between two clusters, the wider the genetic variability between them, for inclusion in the hybridization program [19]. The intra cluster distances ranged from 2.59702 to 3.12876 estimated by using Euclidian's distance methods, indicating that the hybrids in clusters have dissimilarity in morphological features and performance (Table 8). The intra-cluster distance was significantly smaller than the inter-cluster one, indicating that the groupings were heterogeneous inside and homogeneous between them. Cluster V exhibited the maximum intra-cluster distance, whilst cluster III displayed the lowest intra-cluster distance. The highest inter cluster distance was observed between cluster II and IV while the lowest inter cluster distance was observed between cluster I and IV. Lowest inter cluster distances were indicative of close relationship and similarity for most traits in the genotypes hence selection of parents from these clusters is to be avoided [20].

Maximum inter cluster distance indicates that genotypes falling in these clusters had wide diversity and can be used for improvement program to get better recombinants. Genotypes that were both agronomically excellent and genetically varied were chosen using inter-cluster distances. More opportunities for crossing over would result from dissimilar groups coming together, which breaks up unwanted links and releases latent potential variability [21]. It is anticipated that offspring from these kinds of varied crossings will exhibit a broad range of genetic variability, which will increase the opportunity to identify transgressive segregants in later generations. From the mean analysis genotypes, G34, G45, G3, G50 and G39 are the most promising genotypes based on a combination of multiple studied traits.

Table 8. Average intra (bold) and inter (off diagonal) cluster distance among five clusters of 72 sorghum genotypes

No. of cluster	Cluster-I	Cluster-II	Cluster-III	Cluster-IV	Cluster-V
Cluster-I	**2.90645**	4.02052	2.78664	3.02085	3.90981
Cluster-II		**3.00575**	4.01958	5.29924	4.14042
Cluster-III			**2.59702**	2.95493	3.76775
Cluster-IV				**2.68495**	5.18341
Cluster-V					**3.12876**

CONCLUSION

The genotypes employed for the evaluated characters showed a wide range of genetic diversity in this investigation, suggesting a high potential for use in trait enhancement. Furthermore, the presence of predicted GAM% and significant high heritability (H2) suggested possibilities for improving the traits through selection. From the principal component analysis, the first two principal components accounted for a cumulative of 39.5% of total variation indicating most of the important yield and yield attributing traits were present in these first two principal components. Cluster analysis based on unweighted pair group method with arithmetic means method grouped the 72 sorghum genotypes into five distinct clusters based on fifteen quantitative characters. Such genetic divergence among sorghum genotypes indicated that crossing between genotypes of these clusters might provide desirable recombinants and high yielding segregants. In general, based on the mean performance of genotypes, G14, G15 and G27 had a yield advantage over the best standard checks (Melkam). Genotypes, G34, G24, G40, G5, G29, G50, G27 and G49 are the most promising genotypes based on the combination of multiple traits. The overall study revealed the presence of wide genetic variability among the 72 sorghum genotypes evaluated which can be exploited to develop high-yielding varieties with desirable grain yield and early maturity in the study area where moisture stress is a critical problem for sorghum production.

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Significance Statement

In Ethiopia sorghum is predominantly grown in arid and semi-arid areas. However, the yield of sorghum is affected by severe and recurrent drought where rainfall is inadequate, non-uniform and erratic. Development of high yielding varieties require detailed knowledge of variation among the traits and the association among yield components. There is a need of conducting genetic variability to generate information for further breeding work to develop varieties for the moisture stressed areas. Therefore, the present study was designed to estimate genetic variability among sorghum genotypes for drought tolerance, and to determine the association of yield and yield related traits under drought stress condition.

Author's contribution

The following tasks have been confirmed as being within our purview as the research paper's authors: study idea and design; data collecting; analysis and interpretation of findings; and article writing. [Author 2] and [Author 3] designed the research study and secured funding. [Author 1] conducted the experiments, collected and analyses the data. The Author has the rights: (1) to use the manuscript in the Author's teaching activities; (2) to publish the manuscript, or permit its publication, as part of any book the Author may write; (3) to include the manuscript in the Author's own personal or departmental (but not institutional) database or on-line site.

Conflict of interest

Conflicts of interest, often known as "competing interests," arise when external factors influence or are thought to influence the impartiality or neutrality of research. It can occur at any point during the research cycle, including when a manuscript is being written, conducting experiments, or preparing an article for

publication. Nonetheless, none of the research paper's authors had any conflicts of interest to declare. Each and every author says that they have no competing interests.

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