Article

Assessment of Genetic Variability in Sorghum Genotypes under Dry Low Land Areas of Ethiopia

Yirgalem Gidey [1,2,*], Kassahun Bantte [3], Fetien Abay [1], Taye Tadesse [4], Alemu Tirfessa [5]

[1] Department of Dryland Crop and Horticultural Sciences, College of Dryland Agriculture and Natural Resources, Mekelle University, Mekelle 1000, Ethiopia
[2] Tigray Agricultural Research Institute, Mekelle 1000, Ethiopia
[3] Department of Horticulture and Plant Science, College of Agriculture and Veterinary Medicine, Jimma University, Jimma 188, Ethiopia
[4] Ethiopian Institute of Agricultural Research, Addis Ababa 1165, Ethiopia
[5] Melkassa Agricultural Research Center, Ethiopian Institute of Agricultural Research, Addis Ababa 0000, Ethiopia
* Correspondence: Yirgalem Gidey, Email: yirgatsehaye@gmail.com.

ABSTRACT

Sorghum (*Sorghum bicolour* (L.) Moench) is an important source of food in many semi-desert and tropical areas of the world that are usually affected by drought, resulting in reduced yield. Despite its relatively better adaptation to moisture stress environments, yield loss in sorghum due to drought is very high. This investigation was undertaken to estimate components of genetic variability amongst Ethiopian's landraces for yield and yield related traits under moisture stress conditions. Two hundred Ethiopian sorghum landrace collections selected based on adaptation to moisture stress environment and two hundred genotypes from the reference of the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) were evaluated during the 2018 growing seasons at two locations, Sheraro and Miesso that represent dry lowland agro-ecologies. Analysis of variance revealed highly significant differences amongst the germplasms at Sheraro and Miesso for seven traits, showing that there is a broad range of genetic variability among them. The highest grain yield values (kg/ha) were 7701.33 and 3106.67 for Sheraro and Miesso respectively under rain fed.

Depending on the trait studied, the values for coefficient of variance for phenotypes were higher than that of coefficient of variance for genotype at both sites, indicating that the environmental effect had a crucial role in the manifestation of these characters. Likewise, heritability ranged from 30.57% (for panicle length) to 75.83% (for grain yield from 47.4% (for leaf area) to 96.72% (for days to maturity) at Miesso. The extent of phenotypic correlation coefficients for most of the traits were smaller than their corresponding genotypic correlation coefficients, except for a few cases, which indicates the camouflaging effect of the environment in the total manifestation of the traits. Out of the total six and eight components from

Open Access

Received: 01 June 2023
Accepted: 20 November 2024
Published: 27 November 2024

both Sheraro and Miesso respectively, the first three principal components described most of the total variations. At both sites, the D^2 analysis grouped the four hundred germplasms into six clusters with variable number of entries in each cluster. Based on the data from both sites, selecting germplasms with high thousand grain weight and long panicle length could be used to select genotypes with high grain yield. Accessions 239130, 220255, 235810 and 220253 were identified as best performers in drought tolerance. With further evaluation, these genotypes could be used as varieties and/or breeding materials in developing drought tolerant sorghum varieties.

KEYWORDS: genetic variability; heritability; genetic distance; sorghum

INTRODUCTION

Sorghum (*Sorghum bicolour* (L.) Moench) serves both as food for humans and animal feed. Its grain is the main staple food especially for the poverty-stricken and the majority food-in need society, residing primarily in the semi-desert tropics [1,2]. According to [3], report sorghum is 5th in the globe next to wheat, maize, rice and barley.

Moisture stress is a challenge in almost half of the globe's arable land is a main determinant to the crop productivity worldwide [4]. According to different research studies moisture deficiency at key phases like tillering, seedling setting up and reproductive phases may result in a significant yield reduction and even fatal to the in cereal crops [5,6].

In addition to that, moisture deficient at reproductive stage reduces grain yield more than the moisture stress at another growth phases. Variations in water balance and soil accessible moisture are decisive to crop productivity since they directly interrupt plant physiological growths and responses [7,8]. Although sorghum grows well under unsuitable soil and weather conditions as contrasted to other crops [9]. It can grow in desert and semi-desert regions is affected by moisture deficit at terminal growth phases like flowering and post-flowering that renders the most adverse effect on its yield [10,11]. Gebrekidan [12] reported that it has large genetic diversity in East African countries like Ethiopia, Sudan and Eritrea. It was reported that the presence of significant genetic variability among tested genotypes by [13]. Studies in Ethiopia also revealed that more than 95% of sorghum production area was covered by landraces and with limited use of improved varieties [14]. This implies that the Ethiopian breeding program has not yet efficiently utilized the available genetic variability for genetic improvement. Phenotypic selection based on important characters with bigger heritability along with higher genetic advance (GA) is efficient for the success of breeding to develop best genotypes for sorghum breeding program [15].

Genotypic and phenotypic coefficient of variations, heritability estimates, and genetic advance are important information to an efficient genetic improvement [16]. Hence, searching for sources of extra genetic diversity and largest exploitation of the in-situ genetic variability for selection and development of best and high yielding genotypes can help to increase the yield of sorghum. Godbharle et al. [17] also concluded that quantifying the magnitude and pattern of genetic variability is a precondition to develop best varieties for different objectives of sorghum production. This investigation was conducted to assess the genetic variability in sorghum for yield and yield components under drought conditions.

MATERIALS AND METHODS

Experimental Sites

The research was implemented at two research sites specifically Sheraro (14°24'N/37°45'E) and Miesso (9°14'N/40°45'E); where sorghum is the major crop (Figure 1). The experiments were conducted during the 2018 growing season. The altitudes for Sheraro and Miesso are 1010 and 1470 meters above sea level, respectively. The soils in both Sheraro and Miesso are dark clay vertisols. The agro-ecology of Sheraro and Miesso is SM1 (SM1-4) sub-moist hot warm lowland and SM1 (SM1-1) hot to warm sub-moist plains, respectively [18]. The range of temperature during the growing season was from 14.38 to 37.76 ℃ and the average of rainfall was 653.9 mm at Sheraro (Supplementary Figure S1). Whereas the temperature range and average rainfall at Miesso during the same period were 16–31 ℃ and 355.3 mm (Supplementary Figure S2).

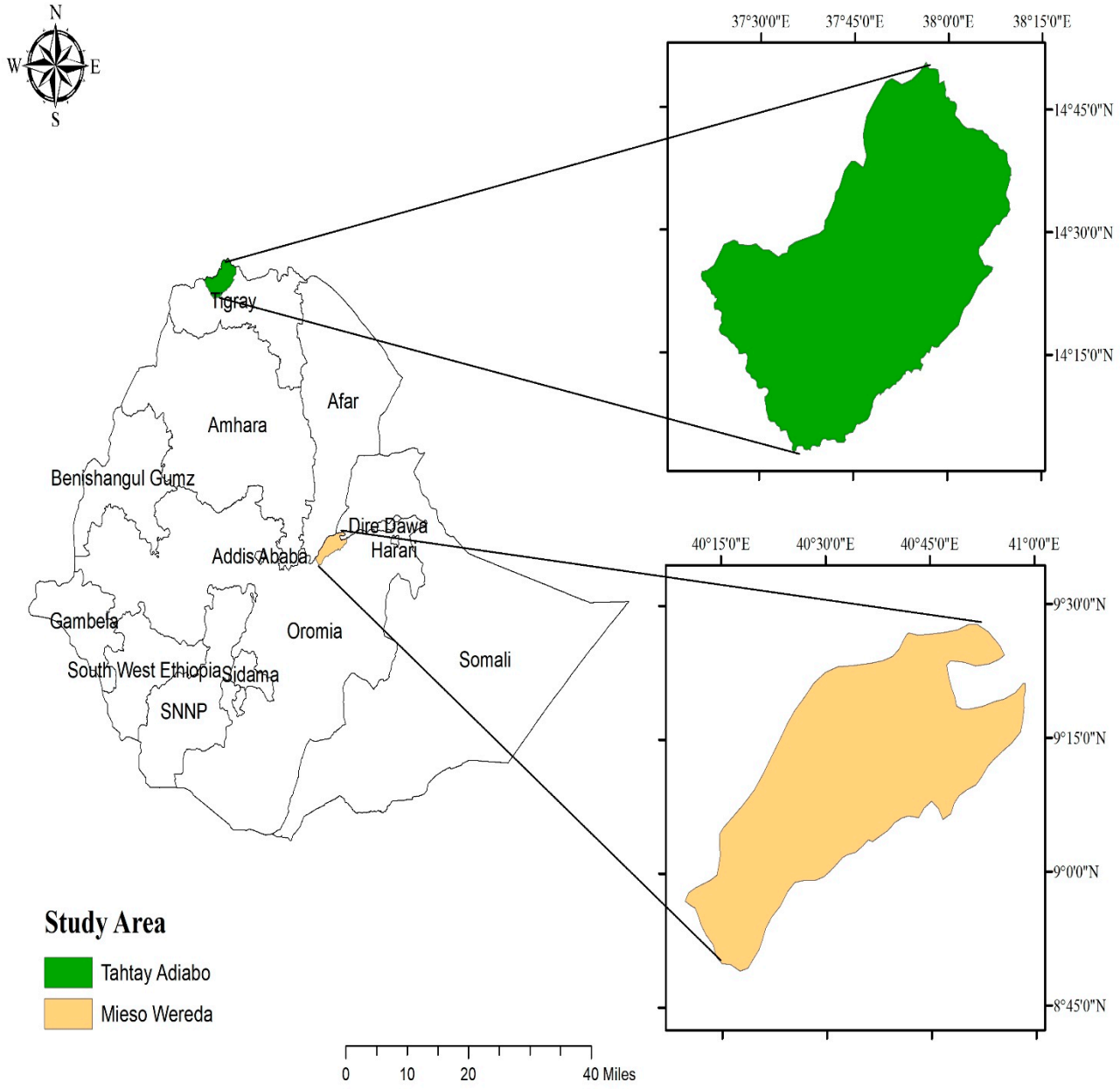

Figure 1. Map of the experimental sites.

Genetic Materials

Two hundred Ethiopian sorghum landrace collections selected based on adaptation to the moisture stress environments and two hundred genetic lines were used along with known stay-green genotypes such as B-35 (Supplementary Table S1).

Experimental Design and Agronomic Management

Row column experimental design (50 rows × 8 columns) with two replications was used at each site. It was planted based on the onset of rain in the two test sites, which started from end of June until first week of July 2018 crop season. Seeds were planted direct into a three meters plot length

with single row with seventy-five centimeters spacing from one row to the next row and fifteen centimeters spacing between plants. Seedlings were thinned to an interplant spacing of 15 cm in two weeks after emergence. Fifty kilograms of urea and 100 kilograms di-ammonium phosphate per hectare of fertilizer was applied as per the national fertilizer recommendation. Half of the urea altogether the Di-ammonium phosphate was applied on planting. Urea was top dressed at the 6 to 8 leaf stage. Each suggested agronomic management (weeding, cultivation, etc.) was used uniformly for both stress and non-stress conditions.

Morphological evaluation of genotypes was done using the sorghum (*Sorghum bicolor* (L.) Moench) descriptors as perBPGR/ICRISAT descriptor list. The traits used for morphological evaluation are leaf area (cm^2), thousand grain weight (g), days to fifty percent flowering, days to seventy five percent maturity, panicle length (cm), plant height (cm) and grain yield (kg/ha). Randomly selected five plants per genotype were used for observations and measurements. Yield was evaluated plot wise.

Data Analysis

Analysis of variance (ANOVA): Row column design was used to estimate analysis of variance for seven traits. Fit linear mixed-effects models *lmer* function in *lmerTest* R package was used for the analysis of variance. Genotypes as fixed effect and replications, row and column as random effect [19,20]. Random effect ANOVA was evaluated using ANOVA-like table for random-effects chi-square test *rand* function in *lmerTest* R package [21]. Before computing the analysis of variance homogeneity test for error variance was done.

Estimation of variance components: META-R software [22] was used to calculate genotypic and phenotypic variances and their coefficients of variations as per the formula recommended by [23] as cited by [24] as follows:

$$\text{Environmental variance } (\sigma_e^2) = Mse \quad (1)$$

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

Where Msg is for mean square due to genotypes, Mse is for mean square of error (Environmental variance), r = number of replication.

$$\text{Phenotypic variance } (\sigma_p^2) = \sigma_g^2 + \sigma_e^2 \quad (3)$$

Where, σ_g^2 is for genotypic variance and σ_e^2 is for environmental variance.

$$\text{Phenotypic coefficient of variation (PVC)} = \frac{\sqrt{\sigma_p^2}}{\overline{X}} \times 100 \quad (4)$$

$$\text{Genotypic coefficient of variation (GCV)} = \frac{\sqrt{\sigma_g^2}}{\overline{X}} \times 100 \quad (5)$$

Where, σ_p^2 is for phenotypic variation, σ_g^2 is for genotypic variation and $\overline{X}$ is for grand mean of the character studied.

Estimation of heritability in broad sense: The ratio of the genotypic variance (σ_g^2) to the phenotypic variance (σ_p^2) was calculated to give broad sense heritability (h^2) expressed on genotype mean as recommended by [25] and as cited in [24] as follows:

$$h^2 = \frac{\sigma_g^2}{\sigma_p^2} \times 100 \quad (6)$$

Estimation of correlation coefficients: As suggested by [26], phenotypic and genotypic correlation coefficients were estimated out of the consequent variance and covariance components as:

$$\text{Phenotypic correlation coefficient } (r_p) = \frac{PCovxy}{\sqrt{\sigma_p^2 x \times \sigma_p^2 y}} \quad (7)$$

$$\text{Genotypic correlation coefficient } (r_g) = \frac{gCovxy}{\sqrt{\sigma_g^2 x \times \sigma_g^2 y}} \quad (8)$$

Where, $PCovxy$ is for phenotypic covariance between variables x and y. Similarly $gCovxy$ is genotypic covariance between variables x and y; $\sigma_p^2 x$ and $\sigma_g^2 x$ are phenotypic and genotypic, variances for variable x; and $\sigma_p^2 y$ and $\sigma_g^2 y$ are phenotypic and genotypic variances for the variable y respectively. The coefficients of correlation were tested using 'r' tabulated value at $n-2$ degrees of freedom, at 5% and 1% probability level, where n is the number of treatments (accessions) as cited by [24].

Path coefficient analysis: was done considering grain yield per hectare as dependent variable and the test characters as independent (causal) variables. Based on [27] path coefficient analysis was evaluated using the phenotypic and genotypic correlation coefficients to determine the direct and indirect effects of yield components on grain yield based on the following relationship:

$$r_{ij} = p_{ij} + \sum r_{ik} \times p_k \quad (9)$$

Where r_{ij} is for mutual correlation between the independent character (i) and dependent character (j) as estimated by the genotypic correlation coefficients. Whereas p_{ij} is for components of direct effects of the independent character (i) on the dependent character (j) as calculated by the genotypic path coefficients. $\sum r_{ik} \times p_{kj}$ is for summation of components of indirect effect of a given independent character (i) on a given dependent character (j) via all other characters (k). The contribution of the remaining unknown factor was measured as the residual factor (P_R), which was calculated as:

$$P_R = (\sqrt{\Sigma r_{ij} p_{ij}} \quad (10)$$

The level of P_R indicates how best the causal factors account for the variability of the dependent factor [23]. That is, if P_R result is small (for instance, nearly zero), the dependent character considered (grain yield) is

fully clarified by the variability in the independent characters, whereas higher P_R value implies that some other factors which have not been considered, need to be included in the analysis to account fully the variation in the dependent character (grain yield) [24].

Clustering and principal component analysis: Average linkage was used to analyze clustering of genotypes using SAS software using seven morphological descriptors that were found significantly different among the genotypes at least at one location. To decide the number of clusters pseudo-F statistics and pseudo t^2 statistics were examined [24]. Mahalanobis D^2 statistics was used to calculate distances between clusters:

$$D^2_{ij} = (X_i - X_j)\, S^{-1}(X_i - X_j) \quad (11)$$

Where: D^2_{ij} = distance between cases i and j, X_i and X_j is the vectors of the values of the variables for cases i and j S^{-1} = inverse of the pooled variance covariance matrix.

Statistical Analysis System (SAS) software [28] was also used to calculate principal components based on correlation matrix. The D^2 values analyzed for pairs of clusters were considered as the calculated values of Chi square (χ^2) and were tested for significance both at 1 and 5% probability levels against tabulated value of χ^2 for P degree of freedom, where P is the number of characters considered [23,24].

RESULTS

Analysis of variance (ANOVA)

Analysis of variance showed highly significant differences among the sorghum genotypes both at Sheraro and Miesso for seven traits, indicating the existence of broad genetic variability among them (Table 1).

Table 1. Variance of fixed and random effects with significant values among sorghum landraces evaluated at Miesso and Sheraro under rain fed conditions (2018/19).

Traits	Miesso					Shiraro				
	Fixed	Random effect				Fixed	Random effect			
	Gen	σ_r^2	σ_b^2	σ_c^2	σ_e^2	Gen	σ_r^2	σ_b^2	σ_c^2	σ_e^2
DTF	3.69×10^{-12}**	0.00ns	0.3403ns	0.00ns	8.6938	3.88×10^{-6}**	9.04×10^{-9}	1.074	4.13×10^{-9}	40.91
PHT	4.24×10^{-12}**	0.00ns	0.3028ns	0.1685ns	9.7173	1.38×10^{-4}**	0.00	0.00	61.04	1461.02
DTM	6.63×10^{-6}**	0.00ns	0.9278ns	1.272**	69.3200	2.81×10^{-6}*	0.03464ns	0.39032ns	0.06921	29.72200
TGW	3.06×10^{-6}**	0.00ns	0.9999*	0.00ns	31.8413	3.80×10^{-6}**	0.1113ns	1.2260ns	0.6413ns	39.7758
LA	1.35×10^{-3}**	0.00	0.00	847.4	14275.4	5.138×10^{-4}**	206.43ns	71.21ns	1315.00**	5339.95
PL	4.63×10^{-6}**	0.00	0.00	0.0853	49.3595	3.80×10^{-6}**	0.1113ns	1.2260*	0.6413ns	39.7758
Yld	5.54×10^{-2}**	0.00ns	1899ns	0.00ns	375691	6.00×10^{-2}**	0.00ns	19954*	10446ns	627122

Note: σ_r^2 = variance due replication, σ_b^2 = variance due to row, σ_c^2 = variance due to column, σ_e^2= residual variance, ns = non-significant, * = significant at 5%, ** = significant at 1%.

Mean, Variances and Heritability of Different Traits Under-Study

As indicated in Table 2, the range and mean values for leaf area (cm^2) were from 241 to 805 and 416.39, respectively at Sheraro whereas these values for the same trait at Miesso were 213.00–2004.95 and 354.17, respectively (Table 3). The range and mean values for thousand grain weight (g) at Sheraro were 7–51 and 24.3, respectively but at Miesso they were 10–60 and 20.54, respectively. The range and mean of days to maturity (DM) at Sheraro were 85–122 and 106.75 whereas these values at Miesso were 90–138 and 112.23, respectively. The range and mean for plant height (cm) were 22–327 and 226.07, respectively at Sheraro and at Miesso, they were 17–296 and 201.73, respectively. For panicle length (cm) the range and mean values were 7.8–75.4 and 21.87 at Sheraro and 6–35 and 20.88, respectively at Miesso. The range and mean grain yield (kg/ha) values were 216.53–7701.33 and 1914.14 at Sheraro whereas at Miesso they were 10.67–3106.67 and 997, respectively. Range and mean for days to 50% flowering at Sheraro were 50–95 and 73.63, respectively whereas at Miesso they were 52–100 and 73.19, respectively. The range for days to 50% flowering among germplasm was almost a month at both research sites.

Analysis results of phenotypic (σ_p^2) and genotypic (σ_g^2) variances and phenotypic (PCV) and genotypic coefficients of variation (GCV) are presented in Table 2 for the Sheraro site and in Table 3 for Miesso. The genetic coefficient of variation at Sheraro ranged from 24.6% for panicle length to 44.49% for grain yield. The range of genetic coefficient of variance at Miesso was from 29.64% for leaf area to 89.58% for thousand-grain weight. Similarly, the range for phenotypic coefficient of variation at Sheraro was from 44.49% for panicle length to 92.88% for grain yield. The phenotypic coefficient of variation at Miesso varied from 38.57% for DM to 91.98% for thousand-grain weight. The GCV values were lower than that of PCV in this study, signifying that the environment had more effect on the expression of these traits. All the seven traits studied at Sheraro and Miesso had high phenotypic and genotypic coefficients of variance. This reveals that selection may be efficient based on these characters and could be a good indicator of genetic potential.

The heritability estimation for traits under research is presented in Tables 2 and 3. Heritability values are useful in forecasting the expected progress to be achieved through the process of selection. Genetic coefficient of variation along with heritability estimation provides a reliable estimate of the amount of genetic advance anticipated through phenotypic selection. Heritability at Sheraro extended from 30.57% for panicle length to 75.83% for grain yield. The heritability estimates at Miesso varied from 47.4% for leaf area to 96.72% for days to maturity. Days to maturity, days to fifty percent flowering, thousand-grain weight, plant height, and panicle length had high heritability at Miesso. This shows that selection using these traits could effectively select high-yielding genotypes. This is because there would be a close correspondence between the

genotypes and the phenotype due to the relatively small contribution of the environment to the total variability. Characters, like plant height, leaf area and grain yield at Sheraro had moderately high heritability. Traits like thousand grain weight, DF, and DM at Sheraro had medium heritability. A character that had low heritability was panicle length at Sheraro. Grain yield had moderately high heritability at Miesso whereas leaf area had medium heritability at Miesso.

Table 2. Estimates of genetic parameters for traits of sorghum genotypes evaluated at Shararo in 2018.

Characters	Range	Mean ± SE	σ_g^2	σ_p^2	GCV (%)	PCV (%)	H (%)
LA	241–805	416.39 ± 3.92	120886	83890	53.9000	69.5592	69.3960
TGW	7–51	24.30 ± 0.24	250.608	440.706	65.1465	86.3909	56.8651
DF	50–95	73.63 ± 0.23	1901.520	4303.280	59.2237	89.0933	44.1876
DM	85–122	106.75 ± 0.19	4567.720	8057.160	63.3114	84.0859	56.6914
PH	22–327	226.07 ± 1.38	13802.600	22845.300	51.9682	66.8583	60.4178
PL	7.8–75.4	21.87 ± 0.24	28.953	94.680	24.6036	44.4918	30.5798
GY	216.5–7701.3	1914.14 ± 28.85	30551.700	40285.300	80.7234	92.6947	75.8383

Note: LA (leaf area, cm^2), TGW (thousand grain weight, g), DF (days to 50% flowering), DM (days to maturity), PH (plant height, cm), PL (panicle length, cm) and GY (grain yield, kg/ha), standard error (SE), phenotypic (σ_p^2), genotypic (σ_g^2) components of variances, coefficients of phenotypic (PCV) and genotypic (GCV) variability and broad sense heritability (H).

Table 3. Estimates of genetic parameters for traits of sorghum genotypes evaluated at Mieso in 2018.

Characters	Range	Mean ± SE	σ_g^2	σ_p^2	GCV (%)	PCV (%)	H (%)
LA	213.00–2004.95	354.17 ± 4.17	11020.100	23247.49	29.640	43.0500	47.40
TGW	10–60	20.54 ± 0.21	338.550	356.96	89.580	91.9800	94.84
DF	52–100	73.19 ± 0.29	1227	1288.32	47.850	49.0400	95.23
DM	90–138	112.23 ± 0.31	1812.600	1873.92	37.930	38.5716	96.72
PH	17–296	201.73 ± 1.39	5824.210	6315.96	37.830	39.3900	92.21
PL	6–35	20.88 ± 0.25	269.042	310.11	78.556	84.3300	86.75
GY	10.67–3106.67	997.33 ± 21.71	502652	697022.70	71.080	83.7100	72.11

Note: LA (leaf area, cm^2), TGW (thousand grain weight, g), DF (days to 50% flowering), DM (days to maturity), PH (plant height, cm), PL (panicle length, cm) and GY (grain yield, kg/ha), standard error (SE), phenotypic (σ_p^2), genotypic (σ_g^2) components of variances, coefficients of phenotypic (PCV) and genotypic (GCV) variability and broad sense heritability (H).

Correlation

Estimates of phenotypic and genotypic correlation coefficients between each pair of characters are presented in Tables 4 and 5. The amount and pattern of genotypic correlation coefficients for most of the characters were higher than their corresponding phenotypic correlation coefficients, except for a few cases, which show the masking effect of the environment in the total expression of the genotypes.

The phenotypic and genotypic correlations of grain yield with other characters are presented in Tables 4 and 5. The scope of genotypic correlation of grain yield with other characters starts from 0.809 for thousand grains weight to 0.173 for days to maturity at Sheraro. At Miesso, it ranged from 0.843 for a thousand grain weight to 0.166. Traits that correlate significantly with grain yield may be crucial grain yield predictors in improving grain yield in sorghum. Grain yield showed highly significant and positive genotypic correlation with thousand-grain weight, leaf area, DF, DM, plant height, and panicle length at both sites. Grain yield with panicle length, days to maturity with days to 50% flowering, and grain yield with thousand grain weight had significant positive associations. In contrast, the rest of the correlations among morphological descriptors were non-significant.

The genotypic associations among the agronomic traits at Sheraro were as follows (Table 4): Leaf area had a positive significant genotypic correlation with 1000-grain weight, days to physiological maturity, and panicle length. Thousand grain weight had a positive significant genotypic correlation with DM, plant height, and panicle length. There was a positive significant genotypic correlation of days to maturity with DF, plant height, and panicle length. Similarly, the genotypic associations between yield attributing traits at Miesso were as follows (Table 5): Leaf area had a positive significant genotypic association with thousand-grain weight, days to 50% flowering, and days to physiological maturity. Thousand grain weight was a descriptor with significant and positive genotypic correlation with days to fifty percent flowering, days to physiological maturity, plant height, and panicle length. Days to maturity had a positive-significant genotypic correlation with days to fifty percent flowering, plant height, and panicle length. Days to 50% flowering had a positive-significant association with plant height and panicle length. The range of phenotypic correlation started from 0.89 for grain yield/thousand grain weight up to 0.002 for plant height/panicle length at Sherro whereas at Miesso it was from 0.789 for grain yield/panicle length to 0.01 for thousand-grain weight/leaf area.

Table 4. Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients for traits of sorghum genotypes evaluated at Sheraro in 2018.

Characters	LA	TSW	DF	DM	PH	PL	Yld
LA	1	0.33024**	0.03842	0.62680**	0.036	0.655**	0.521**
TGW	0.070	1	0.00250	0.10702*	0.345**	0.188**	0.809**
DF	0.016	0.01100	1	0.87300**	0.001	0.064	0.198**
DM	0.015	0.08900	0.76000**	1	0.430**	0.106*	0.173**
PH	0.002	0.12800**	0.01000	0.05500	1	0.071	0.291**
PL	0.031	0.07700	0.02600	0.00900	0.027	1	0.258**
Yid	0.041	0.89000**	0.48100**	0.80100**	0.053	0.730**	1

Note: Simple linear correlation coefficients r, at *5% and **1% levels for this table are 0.098 and 0.128 respectively. LA: leaf area (cm^2), TGW: thousand grain weight (g), DF: days to 50% flowering, DM: days to maturity, PH: plant height (cm), PL: panicle length (cm) and Yld: grain yield (kg/ha).

Table 5. Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients for traits of sorghum genotypes evaluated at Miesso in 2018.

Characters	LA	TSW	DF	DM	PH	PL	Yld
LA	1	0.121*	0.576**	0.530**	0.059	0.084	0.407**
TGW	0.010	1	0.141**	0.098*	0.173**	0.431**	0.843**
DF	0.238**	0.079	1	0.842**	0.185**	0.184**	0.451**
DM	0.081	0.042	0.755**	1	0.293**	0.174**	0.375**
PH	0.043	0.097	0.149**	0.090	1	0.104*	0.166**
PL	0.042	0.190**	0.109*	0.070	0.070	1	0.701**
Yld	0.058	0.782*	0.061	0.044	0.020	0.789*	1

Note: Simple linear correlation coefficients r, at *5% and **1% levels for this table are 0.098 and 0.128 respectively. LA: leaf area (cm^2), TSW: thousand grain weight (g), DF: days to 50% flowering, DM: days to maturity, PH: plant height (cm), PL: panicle length (cm) and Yld: grain yield (kg/ha).

Path-Coefficient

Path co-efficient analysis delivers an efficient method of splitting direct and indirect causes of correlation. It permits a determinant look to recognize the specific forces acting to produce a given association and measures the relative importance of each causal factor. The genotypic direct and indirect effect of different characters on grain yield kg/ha is presented in Tables 6 and 7. thousand grain weight pursued by leaf area, panicle length, and DM exerted a positive prominent direct effect on grain yield at Sheraro whereas days to fifty percent flowering, 1000-grain weight, and panicle length showed direct positive effect on grain yield at Miesso. Thousand grain weight and panicle length exerted a direct positive effect on grain yield at both sites. Thus, according to both sites, selecting sites selecting genotypes having large thousand grain weight and long panicle length could be used to improve grain yield in sorghum genotypes because of their direct effect on yield.

Days to fifty percent (DF) and plant height at Sheraro and DF, panicle length, and thousand grain weight at Miesso showed a high indirect positive effect via days to maturity on the grain yield kg/ha. Days to maturity and panicle length revealed a high positive indirect effect via leaf area on grain yield at Sheraro. Leaf area and panicle length had a high positive indirect effect on grain yield at Miesso. Therefore, yield can be improved by selecting a1000-grain weight, panicle length, leaf area, plant height, and days to maturity as these traits have an indirect effect on grain yield. The residuals (0.33431 and 0.40460) indicate that traits involved in the path analysis expounded 66.56% and 59.54% of the total variation in grain yield Sheraro and Mieso, respectively. The results from the genetic variability, character association, and path coefficient analyses revealed that morphological descriptors such as thousand grain weight and panicle length were useful concerning genetic variability, correlation, and path-coefficient analysis. The larger variability in these traits could give a main scope for the development of high-yielding lines through selection in the segregating generations.

Table 6. Estimates of direct (bold diagonal) and indirect (off diagonal) genotypic effects of traits on grain yield in sorghum genotypes evaluated at Sheraro in2018.

Characters	LA	TSW	DF	DM	PH	PL	Rg
LA	**0.500**	0.172	−0.037	−0.440	0.006	0.320	0.521
TGW	−0.165	**0.522**	0.345	0.075	−0.060	0.092	0.809
DF	−0.019	0.191	**−0.662**	0.815	−0.096	−0.031	0.198
DM	0.313	0.056	0.056	**0.372**	−0.572	−0.052	0.173
PH	0.018	0.180	0.001	0.302	**−0.175**	−0.035	0.291
PL	0.327	−0.098	−0.198	−0.274	0.013	**0.488**	0.258

Note: Residual Effect: 0.33431, LA leaf area (cm^2), TGW: thousand grain weight (g), DF: days to 50% flowering, DM: days to maturity, PH: plant height (cm), PL: panicle length (cm) and Rg: genotypic correlation of grain yield with the yield components.

Table 7. Estimates of direct (bold diagonal) and indirect (off diagonal) genotypic effects of traits on grain yield in sorghum genotypes evaluated at Miesso in 2018.

Charaters	LA	TGW	DF	DM	PH	PL	Rg
LA	**−0.44**	0.490	−0.210	−0.07	0.400	0.237	0.407
TSW	0.05	**0.710**	−0.540	0.38	0.063	0.180	0.843
DF	−0.55	−0.500	**0.840**	0.90	0.041	−0.280	0.451
DM	0.23	0.075	0.860	**−0.40**	−0.460	0.070	0.375
PH	0.03	−0.120	0.316	0.14	**−0.240**	0.040	0.166
PL	0.04	0.301	−0.710	0.68	−0.020	**0.410**	0.701

Note: Residual Effect: 0.4046052, LA: leaf area (cm^2), TGW: thousand grain weight (g), DF: days to 50% flowering, DM: days to maturity, PH: plant height (cm), PL: panicle length (cm) and Rg: genotypic correlation of grain yield with the yield components.

Principal Component Analysis (PCA)

The first six PCAs from Sheraro data are presented in Table 8. Sixty-three and 69/100 percent (63.69%) of the total variability among the four hundred genotypes evaluated for different morphological traits was scored by the first three principal components with Eigenvalue > 1. The remaining PCAs provided only 36.31% of the total morphological diversity among the genotypes studied. PCA 1 provided the greatest variability of 25.03% pursued by PCA 2, which donated a total phenotypic variability of 23.53%, and PCA 3 supplied 15.13% of the total variation. The useful morphological descriptors in PCA 1 that were the main contributors to the variations among the accessions were days to maturity, 1000-grain weight, plant height, days to fifty percent flowering, and grain yield which had positive factor loading value. PCA 2 was related to diversity among genotypes due to days to fifty percent flowering, days to maturity, and panicle length. Similarly, PCA 3 expressed positive loading values for variations among genotypes due to panicle length, and plant height.

The principal component analysis on data from Miesso (Table 9) showed that out of eight components, three principal components scored most the genetic variance. Sixty-one and 6/10 percent of the total variability among the four hundred genotypes evaluated for seven morphological traits was scored by the first three principal components with Eigenvalue > 1. Only 38.4% of the total morphological diversity among the genotypes studied was scored by the remaining PCAs. The main morphological traits in PCA 1 that contributed to the variations among the accessions were days to maturity (DM), days to 50% flowering (DF), leaf area, panicle length, and plant height which had positive factor loading value whereas grain yield and thousand grain weight had contributed negatively. PCA 2 was related to diversity among sorghum genotypes due to thousand-grain weight, plant height, grain yield, DM, DF, and leaf area. Panicle length had a negative factor loading value.

Table 8. Percentage, cumulative variance and Eigen vectors on the first six principal components for characters of sorghum genotypes evaluated at Sheraro in 2018.

Characters	Eigenvectors					
	PC1	PC2	PC3	PC4	PC5	PC6
Grain yield (Kg/ha)	0.309	−0.533	−0.042	0.231	0.193	0.725
Thousand grain weight (g)	0.452	−0.400	−0.024	0.215	0.378	−0.647
Days to 50% flowering	0.424	0.500	−0.263	−0.009	0.054	0.200
Days to maturity	0.506	0.431	−0.185	0.090	0.094	−0.005
Plant height (cm)	0.444	−0.072	0.528	0.077	−0.713	−0.043
Panicle length (cm)	−0.045	0.303	0.776	0.125	0.524	0.109
Eigen Value	1.75207	1.64717	1.05939	0.93624	0.67446	0.54539
Total Variance (%)	25.03	23.53	15.13	13.37	9.64	7.79
Cumulative Variance (%)	25.03	48.56	63.69	77.07	86.7	94.5

Note: Where PC1 to PC6 indicates for principle component 1 up to 6.

Table 9. Percentage, cumulative variance and Eigen vectors on the first six principal components for characters of sorghum accessions evaluated at Miesso in 2018.

Characters	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
Days to 50% flowering	0.600	0.131	0.064	−0.091	−0.156	0.253	0.150	0.707
Days to Maturity	0.599	0.150	0.069	−0.088	−0.143	0.246	0.157	−0.707
Plant Height (cm)	0.180	0.318	−0.347	0.713	−0.003	0.035	−0.487	0.002
Panicle length (cm)	0.195	−0.482	−0.221	0.441	0.418	−0.070	0.553	0.001
Grain yield (Kg/ha)	−0.315	0.306	0.381	0.213	0.365	0.675	0.169	0.007
Thousand grain weight (g)	−0.148	0.614	0.010	0.181	−0.240	−0.424	0.575	0.012
Leaf Area (cm^2)	0.292	0.111	0.619	0.051	0.482	−0.483	−0.225	0.009
Eigenvalue	2.438	1.438	1.054	0.984	0.773	0.671	0.625	0.017
Total Variance (%)	30.5	18.0	13.2	12.3	9.7	8.4	7.8	0.2
Cumulative Variance (%)	30.5	48.5	61.6	73.9	83.6	92.0	99.8	100.0

Note: Where PC1 to PC8 indicates for principle component 1 up to 8.

Clustering

At Sheraro, the D^2 analysis of the 400 genotypes grouped them into six clusters with different numbers of genotypes in each cluster (Table 10). Cluster I had the largest number of entries, which is 181 (45.25%), followed by Cluster IV with 102 (25.5%) genotypes, cluster II with 67 (16.75%) genotypes, and cluster III with 41 (10.25%) genotypes. The remaining clusters (cluster V and cluster VI) had eight (2%) and one (0.25%) genotype, respectively. The D^2 analysis for the data from Miesso showed that the 400 germplasms were grouped into six clusters (Table 11). Clusters II and I had the highest number of genotypes with 156 (39%) genotypes each, and Cluster III is next with 44 (11%) genotypes, cluster IV with 38 (9/5%) genotypes, cluster V with 4 (1%) genotypes and cluster VI with 2 (0.5%) genotypes. A cluster with a single genotype may be due to total isolation preventing the gene flow or intensive natural/human selection for diverse adaptive complexes. From the breeding point of view, these genotypes are very important. They can have very important genotypes with desirable characteristics.

Table 10. Grouping of sorghum genotypes into different diversity classes based on data from the Sheraro trial (2018).

Cluster	No. of genotypes	Genotypes
I	181	10234, 10876, 11119, 11960, 12169, 12447, 13791, 13845, 14206, 14830, 15443, 15478, 15526, 15752, 17531, 17536, 17593, 18698, 18835, 19026, 19053, 19455, 19615, 19622, 19685, 19847, 20064, 20351, 20700, 20710, 20762, 210952, 211193, 21124, 21519, 216736, 216739, 216744, 220000, 220001, 220009, 220011, 220012, 220013, 220016, 220017, 220223, 220236, 220237, 220238, 220242, 220245, 220249, 220260, 220263, 220264, 220265, 220268, 220276, 22040, 222285, 22287, 222881, 222888, 22330, 22334, 223589, 226049, 226067, 226069, 226087, 227085, 227090, 229831, 229844, 22986, 23254, 234066, 234074, 234089, 234092, 234102, 234103, 234106, 234110, 234111, 234112, 234113, 234115, 235763, 235789, 235790, 235791, 235792, 235794, 235798, 235803, 235809, 235814, 23635, 23637, 23640, 23644, 23650, 23651, 23653, 23654, 23777, 238440, 238442, 238444, 238445, 25442, 25702, 26224, 26735, 26833, 27287, 27599, 27911, 2814, 28553, 28556, 28557, 28688, 2873, 28740, 29310, 29375, 29409, 29472, 29870, 29876, 29977, 30175, 30205, 30207, 30317, 30405, 30409, 30443, 30492, 30619, 30898, 31299, 31559, 31852, 33173, 3583, 3675, 4821, 5106, 5867, 5972, 69212, 69217, 69498, 69499, 69504, 69507, 69508, 69568, 69570, 7314, 8218, 8347, 9577, 9600, 9830, 9883, 9911.Girana-1.Kem Kem, Malt sorghum-1, Malt sorghum-2, Malt sorghum-3, Malt sorghum-4, Malt sorghum-5, Malt sorghum-6, Melkam, Merewey
II	67	10978, 15428, 15964, 16044, 16173, 20387, 20665, 20713, 20842, 220010, 220227, 220239, 220240, 220244, 220246, 220247, 220248, 220250, 220256, 220257, 220259, 220262, 220267, 220273, 22074, 222882, 22325, 22506, 229843, 230065, 231230, 234096, 235023, 235793, 235801, 235806, 235812, 235813, 23601, 238431, 238447, 239130, 2416, 25596, 2787, 2848, 28545, 28549, 28550, 28551, 28991, 29798, 30001, 30469, 3073, 36524, 36633, 5622, 6193, 69046, 6928, 69572, 7125, 8685, Malt sorghum-7, Malt sorghum-8, Malt sorghum-9
III	41	14963, 19126, 19262, 19418, 20205, 20782, 211022, 220241, 220243, 220251, 220253, 220254, 220255, 220266, 220269, 220270, 220272, 220274, 220275, 220277, 220278, 220279, 220281, 23048, 23053, 235804, 235805, 235807, 235808, 235810, 235811, 239238, 28546, 28547, 28548, 3443, 69513, 69571, 69573, 9713, Wedi Aker
IV	102	1127, 12931, 13827, 14298, 15965, 18874, 18919, 18922, 19041, 19132, 19627, 20016, 20624, 20681, 20697, 20709, 20724, 20749, 20763, 21849, 220014, 220015, 220018, 220224, 22239, 22282, 22291, 225837, 2260681, 226086, 226088, 2262, 2263, 227086, 227091, 227092, 22909, 23033, 231229, 23178, 234070, 234079, 234087, 234101, 234104, 234105, 235797, 23636, 23638, 23639, 23642, 23643, 23645, 23652, 2398, 24072, 24083, 24481, 25733, 25848, 26110, 26815, 27490, 27791, 27855, 27919, 28332, 29496, 303, 30318, 30335, 30397, 30422, 30441, 30503, 31179, 31202, 3121, 3147, 31681, 31693, 33209, 33353, 33423, 35, 3971, 5720, 6094, 6351, 6413, 6723, 69506, 69512, 69558, 69560, 7277, 7463, 9527, 9597, B-35, Malt sorghum-10, Wanze
V	8	216735, 216737, 220252, 220261, 235817, 29911, 32087, Argiti
VI	1	20727

Table 11. Grouping of sorghum genotypes into different diversity classes based on data from the Miesso trial (2018).

Cluster	No. of genotypes	Genotypes
I	156	10876, 12169, 13827, 13845, 14206, 15443, 16044, 17531, 17536, 17593, 18835, 19041, 19132, 19418, 19627, 19847, 20064, 20351, 20697, 20700, 20713, 20724, 20749, 20762, 20842, 210952 ,21124, 21519, 216735, 216736, 216737, 220000, 220011, 220014, 220223, 220227, 220236, 220238, 220239, 220242, 220243, 220246, 220247, 220250, 220251, 220253, 220255, 220260, 220263, 220268, 220269, 220270, 220272, 220273, 220278, 220279, 22239, 22282, 222882, 22291, 22506, 225837, 226049, 226067, 226069, 2262, 227086, 227091, 227092, 229831, 229843, 229844, 23033, 231229, 231230, 23178, 234074, 234092, 234096, 234101, 234102, 234103, 234111, 234115,235023, 235763, 235797, 235801, 235814, 235817, 23601, 23637, 23640, 23644, 23650, 23652, 23654, 23777, 239238, 24072, 25848, 26224, 26815, 26833, 28549, 28550, 28551, 29310, 29472, 29496, 29870, 29911, 30001, 30175, 30205, 30317, 30405, 30898, 31202, 31299, 31693, 33173, 33353, 33423, 3443, 3971, 5720, 6094, 6193, 6413, 69212, 69217, 69498, 69499, 69504, 69507, 69512, 69513, 69560, 69568, 69570, 7277, 7463, 8347, 8685, 9600, 9713, 9883, Argiti, Kem Kem, Malt sorghum#1, Malt sorghum#10, Malt sorghum#5, Malt sorghum#6, Malt sorghum#8, Wanze
II	156	10234, 11119, 11960, 12931, 13791, 14298, 14830, 15478, 15964, 15965, 18698, 18874, 18919, 18922, 19026, 19053, 19126, 19262, 19455, 19615, 19622, 19685, 20016, 20387, 20624, 20665, 20681, 20709, 20710, 20727, 20763, 20782, 211193, 21849, 220001, 220009, 220010, 220012, 220013, 220015, 220016, 220017, 220018, 220224, 220240, 220245, 220249, 220256, 220257, 220262, 220267, 220274, 220275, 22287, 222881, 22325, 22330, 22334, 223589, 2260681, 226086, 226087, 2263, 227085, 227090, 22909, 22986, 230065, 23053, 23254, 234066, 234070, 234079, 234087, 234089, 234104, 234105, 234106, 234110, 234112, 235794, 235798, 235806, 235807, 235810, 23635, 23636, 23639, 23642, 23643, 23645, 23651, 23653, 238431, 2398, 24083, 2416, 24481, 25442, 25596, 25733, 26110, 27287, 27490, 27791, 27855, 2787, 27911, 27919, 28332, 28553, 28556, 28557, 28688, 2873, 29375, 29798, 29876, 29977, 30207, 303, 30397, 30409, 30422, 30469, 30492, 30503, 30619, 31179, 3121, 3147, 31681, 33209, 35, 3583, 3675, 4821, 5106, 6351, 6723, 69046, 69506, 69508, 69558, 69572, 69573, 7125, 9527, 9597, 9830, 9911, B-35, Girana-1, Malt sorghum#4, Merewey, Wedi Aker
III	44	1127, 12447, 14963, 15752, 20205, 211022, 216739, 220244, 220248, 220254, 220259, 220265, 220276, 220281, 222285, 222888, 226088, 235792, 235793, 235805, 235808, 235812, 23638, 238440, 238444, 239130, 25702, 27599, 2814, 28548, 28991, 29409, 30318, 30335, 30443, 3073, 32087, 36524, 36633, 5622, 7314, 9577, Malt sorghum#2, Malt sorghum#9
IV	38	10978, 15428, 15526, 220237, 220241, 220252, 220261, 220264, 220266, 220277, 22040, 23048, 234113, 235789, 235790, 235791, 235803, 235804, 235809, 235811, 238442, 238445, 238447, 26735, 2848, 28545, 28547, 28740, 30441, 31852, 5867, 5972, 6928, 69571, 8218, Malt sorghum#3, Malt sorghum#7, Melkam
V	4	16173, 216744, 22074, 28546
VI	2	235813, 31559

Genetic Distance and Cluster Mean

The mean inter-cluster D^2 values for Sheraro are given in Table 12. The χ^2-test for the 6 clusters showed that there was a statistically highly significant difference (P = 0.1%) in all traits except for cluster I with II (7.825), I with III (29.27), I with IV (12.84), II with III (6.922) and III with V (14.05). The topmost mean inter-cluster D^2 was recorded between cluster IV with cluster VI (D^2 = 301.5) followed by cluster I with cluster IV (D^2 = 197.6) and cluster IV with cluster V (D^2 = 159) which had shown the largest inter-cluster distance. Likewise, the average inter-cluster D^2 values for Miesso are presented in Table 13. The χ^2-test for the six clusters indicated that there was a statistically highly significant difference (P = 0.1%) probability level in all characters except cluster I with II (7.645), I with III (5.884), I with IV (27.43), II with III (26.04), III with IV (8.999) and IV with V (8.523). The highest average inter-cluster D^2 was recorded between cluster V with cluster VI (D^2 = 202.9) followed by cluster IV with cluster VI (D^2 = 158.5) and cluster III with cluster VI (D^2 = 126) which had shown the largest inter-cluster distance. These clusters were genetically more divergent from each other than any other clusters.

In the case of Sheraro, the mean value of the quantitative morphological descriptors in each cluster is shown in Table 14. Cluster I had the description of the shortest days to maturity and shortest plant height. The remaining traits were reasonable in magnitude. Cluster II was described by moderate magnitudes of all the characters. The smallest panicle length characterized cluster III and the remaining traits were modest in magnitude. The smallest grain yield, smallest thousand-grain weight, and the longest DF illustrated cluster IV. Cluster V was characterized by the largest thousand-grain weight; the following features characterized Cluster VI: largest grain yield, shortest DF, longest DM, tallest plant height, and largest panicle length. The average value of the quantitative characters at Miesso is given in Table 15. All the traits in cluster I showed moderate results in magnitude. The longest DF, longest DM, largest panicle length, smallest grain yield, and smallest thousand grain weight characterized cluster II. The shortest DF, shortest DM, and largest thousand grain weight characterized cluster III. Cluster IV was characterized by the shortest plant height whereas. Cluster V was characterized by grain yield and tallest plant height; the smallest panicle length characterized Cluster VI.

Table 12. Pairwise generalized squared distance (D^2) among sorghum accessions in six clusters at Sheraro (2018).

Cluster	I	II	III	IV	V	VI
I	-	7.825	29.270	12.84	82.42***	197.60***
II	-	-	6.922	40.04***	39.77***	132.40***
III	-	-	-	79.78***	14.05	88.34***
IV	-	-	-	-	159.50***	301.50***
V	-	-	-	-	-	42.54***

χ^2 = 26.30, 32.00 and 39.25 at 5%, 1% and 0.1% probability level respectively. *** indicates significance at 0.1% probability level.

Table 13. Pairwise generalized squared distance (D^2) among sorghum accessions in six clusters at Miesso (2018).

Cluster	I	II	III	IV	V	VI
I	-	7.645	5.884	27.430	63.010***	122.3***
II	-	-	26.040	63.480***	113.200***	124.5***
III	-	-	-	8.999	32.940	126.0***
IV	-	-	-	-	8.523	158.5***
V	-	-	-	-	-	202.9***

χ^2 = 26.30, 32.00 and 39.25 at 5%, 1% and 0.1% probability level respectively. *** indicates significance at 0.1% probability level.

Table 14. Cluster means for six characters of sorghum accessions evaluated at Sheraro in 2018.

Traits	I	II	III	IV	V	VI
Grain yield (kg/ha)	1847.21	2452.94	3013.40	1058.12*	3841.13	4755.73**
Thousand grain weight (g)	23.31	26.49	30.45	21.60*	31.31**	23.00
Days to 50% flowering	73.75	72.90	72.61	74.39**	72.94	68.00*
Days to maturity	106.39*	106.52	106.66	107.46	106.69	117.50**
Plant height	219.12*	234.74	243.42	224.05	243.66	258**
Panicle length	21.68	21.43	19.21*	23.70	19.45	28.10**

*, ** indicates for the lowest and largest value.

Table 15. Cluster means for six characters of sorghum accessions evaluated at Miesso in 2018.

Traits	I	II	III	IV	V	VI
Days to 50% flowering	74.03	74.64**	68.93*	69.01	71.17	71.75
Days to maturity	113.17	113.73**	107.45*	108.01	111.17	111.25
Plant height (cm)	199.92	202.67	207.24	196.56*	228.33**	214.90
Panicle length (cm)	20.25	22.46**	19.62	18.76	20.50	17.25*
Grain yield (kg/ha)	1054.76	432.97*	1595.23	2208.60	2963.56**	820.00
Thousand grain weight (g)	21.00	19.17*	23.14**	21.38	20.00	20.00

*, ** indicates for the lowest and largest value.

DISCUSSION

The analysis of variance for different traits including yield and yield components was highly significant at both research sites, indicating the presence of a significant amount of variability for these traits among the genotypes, which provides an opportunity for selection of desirable genotypes for further genetic improvement. Similarly, [29] reported significant differences for days to flowering, plant height, grain yield per panicle, panicle length, number of tillers per plant, panicle weight, and panicle exertion at Kobo; and days to flowering, days to maturity, plant height, grain-filling period, grain yield per panicle, panicle length, panicle harvest index at Miesso. Likewise, [30] reported that analysis of variance showed significant differences among fifty-two sweet sorghum genotypes for days to 50% flowering, days to physiological maturity, plant height, stem girth, internode length, number of leaves, stay green trait, brix content, fresh cane weight, mill-able cane weight, juice weight, juice volume, sucrose percentage, juice extractability percentage, cane yield, juice yield, and sucrose yield. The range of days to flowering period among genotypes was almost a month at both research sites and this might be attributed to the diversity of genotypes with different genetic backgrounds and adaptations.

In this study, the GCV values were lower than that of PCV, indicating that the environment had an important role in the expression of these characters. Generally, quantitative or agronomic traits are highly influenced by the environment. Adane et al. [31] reported a similar result that the phenotypic variances were slightly higher than the genotypic variance for days to 50% flowering, plant height, hundred seed weight, and overall agronomic aspect, signifying the influence of environment on these traits. All the seven traits studied at the Sheraro and Miesso sites had high phenotypic and genotypic coefficients of variance. This indicates that selection may be effective based on these characters and their phenotypic expression would be a good indication of genetic potential. There is a large scope for selection based on these traits and the diversity in the genotypes provides a huge potential for future breeding programs. Yaqoob M et al. [32] reported similar higher estimates of PCV and GCV for plant height, leaf area index, and grain yield, suggesting that environmental influence was moderate for these traits as the experiment was managed under uniform input level to all the genotypes. Elangovan and Babu [33] also reported higher PCV and GCV values for days to 50% flowering, plant height, and 100-seed weight. On the contrary, [34] reported a low coefficient of variation for plant height, days to flowering, thousand seed weight, and medium value for grain yield.

The estimate of GCV and PCV alone is not very helpful in determining the heritability of a trite portion. The amount of genetic advance to be expected from the selection can be achieved by estimating heritability along with the coefficient of variability [35]. Heritability values help

predict the expected progress to be achieved through the process of selection. The genetic coefficient of variation along with the heritability estimate provides a reliable estimate of the amount of genetic advance to be expected through phenotypic selection. Days to maturity, days to 50% flowering, thousand seed weight, plant height, and panicle length had high heritability at the Miesso site. This indicates that selection using these traits could be effective. This is because there would be a close correspondence between the genotypes and the phenotype due to the relatively small contribution of the environment to the total variability. Characters, like plant height, leaf area and grain yield at the Sheraro site had moderately high heritability. Traits like thousand seed weight, days to flowering, and days to maturity at the Sheraro site had medium heritability. The character that had low heritability was panicle length at the Sheraro site. Heritability for grain yield was moderately high at Miesso. However, leaf area had medium heritability at Miesso.

Although variability estimates provide information on the extent of improvement, they do not throw much light on the extent and nature of the relationship, which exists between the characters [36]. This could be obtained from simple association analysis. Knowledge of the association of component characters with single plant yield may greatly help in making selection precise and accurate. The greater the magnitude of correlation coefficients, the stronger the association. The magnitudes of genotypic correlation coefficients for most of the characters were higher than their corresponding phenotypic correlation coefficients, except in few cases, which indicates the influence of the environment in the total expression of the genotypes was low. Such results are in concurrence with the results of [37].

Traits significantly correlated with grain yield may be important yield predictors in sorghum breeding. Grain yield showed positive and highly significant genotypic association with thousand seed weight, leaf area, days to 50% flowering, days to physiological maturity, plant height, and panicle length at both sites. Grain yield with panicle length, days to maturity with days to flowering, had significant positive associations while the rest of the associations were non-significant. Similarly, [37–40] reported that seed yield exhibited a positive and significant correlation with thousand seed weight. In contrary to the present study, [29] reported that thousand grain weight had a non-significant association with grain yield. Khandelwal et al. [37] also reported that grain yield had a non-significant positive genotypic correlation with the thousand grain weight of sorghum.

Path co-efficient analysis provides an effective means of partitioning direct and indirect causes of association. It permits a critical look to recognize the specific forces acting to produce a given correlation and measures the relative importance of each causal factor. In the present study, thousand grain weight followed by leaf area, panicle length, and

days to maturity exerted a positive prominent direct effect on grain yield at Sheraro. Days to flowering, thousand seed weight, and panicle length also showed a positive direct effect on seed yield at the Miesso site In line with the present study, [41] reported panicle length having a direct effect on grain yield. Patel et al. [42] reported that thousand grain weight had a direct effect on sorghum grain yield. Similarly, [43] also reported that panicle length had a direct effect on sorghum grain yield. This information would be of greater value in selecting the useful traits and thus optimize the data recording by taking observations on a few related traits in the preliminary trials involving a large number of genotypes [44]. Therefore, according to the data from both sites, selecting genotypes having high seed weight and long panicle length could be used to improve grain yield in sorghum. Similar to this study, [45] reported that days to maturity, panicle length, and thousand grain weight had shown a positive direct effect on grain yield. It was reported that panicle length had a positive direct effect on seed yield [37,43]. Iyanar et al. [41] also reported a direct effect of thousand grain weight on grain yield. However, days to 50% flowering and plant height at Sheraro; leaf area, days to maturity, and plant height at Mieso showed a negative direct effect on grain yield. These traits only contributed to seed yield mainly via their positive indirect effect with other characters. Plant height had a negative direct effect on seed yield at both sites. A similar result, that plant height had a negative direct effect on seed yield, was reported by [45] and [46]. Days to flowering and plant height at Sheraro and days to flowering, panicle length, and thousand grain weight at Miesso showed a high positive indirect effect via days to maturity on the grain yield/ha. Days to maturity and panicle length showed a high positive indirect effect via leaf area on seed yield at the Sheraro site. Leaf area and panicle length revealed a high positive indirect effect on seed yield at the Miesso site Therefore, yield can be improved by selecting for thousand seed weight, panicle length, leaf area, plant height, and days to maturity due to their indirect effect on yield. The residuals (0.3343)1 for Sheraro and (0.40460) for Miesso indicate that characters included in the genotypic path analysis explained 66.56% at Sheraro and 59.54% at Mieso of the total variation in seed yield which indicates that there may be some more components that are contributing towards seed yield.

The association between the characters and their contribution to the diversity can also be confirmed by PCA analysis. The principal component analysis (PCA) using the mean values of the genotypes provides a reduced dimension model that would indicate measured differences among the germplasm. In this study, only PCAs with eigenvalues greater than one, which determines as a minimum of ten percent of the variation, was considered as recommended by [47]. The largest eigenvalues have the largest attributes in principal components. The results at Sheraro showed the importance of the first three principal components (PC) with

eigenvalue > 1 in discriminating the entire germplasm. The percentage of variation explained by these PCs was more than 63.69% of the total variability among the four hundred sorghum genotypes evaluated for different morphological traits. The remaining components contributed only 36.31% towards the total morphological diversity among the genotypes studied. Similarly, [48] reported that the first three principal components with eigenvalue > 1 contributed about 66.35% of the total variability among the 100 sorghum germplasm genotypes evaluated for different morphological traits. For the Mieso site, the principal component analysis revealed that out of eight components, three principal components scored most the genetic variance. The first three principal components with eigenvalue > 1 contributed about 61.6% of the total variability among the four hundred sorghum genotypes evaluated for seven morphological traits. Jain and Patel [49] also reported in line with this report.

Genetic divergence in a population, especially in relation to important traits, is necessary and an indispensable pre-requisite for successful plant selection work. Different members within a cluster are assumed to be more closely related in terms of the traits under consideration with each other than those members in different clusters. Similarly, members in clusters with no significant distance are assumed to have more close relationships with each other than they are with those in significantly distant clusters. A better understanding of the genetics of morphological characteristics is required by the breeder to increase the efficiency of the selection of more diverse and adapted parents for crop improvement [50]. The success of any crop-breeding program is based on the knowledge and availability of genetic variability for efficient selection [2]. At both research sites, the cluster analysis of the 400 genotypes grouped them into six clusters with a variable number of entries in each cluster, indicating the presence of a wide range of genetic diversity among the genotypes under investigation. The formation of solitary clusters in the present study may be due to total isolation preventing the gene flow or intensive natural/human selection for diverse adaptive complexes. These genotypes may be unique and useful from a breeding point of view. This genetic diversity can be due to the geographic diversity of the collection sites of the sorghum landraces used in this study. In line with this study, [51] reported six clusters based on D^2 statistics among one hundred fifty sorghum genotypes. Vijaylaxmi et al. [52] also reported six hierarchical clusters containing one to sixty-one sorghum genotypes. Similar results were observed by [53–60] who had reported 14, 13, 23, 10 and 14 clusters of sorghum genotypes, respectively.

Maximum inter-cluster distances were observed between cluster 4 and cluster 5 at Sheraro and between clusters 5 and 6 at Miesso, indicating that genotypes belonging to these groups were genetically most divergent. Such genetically diverse sorghum genotypes could be effectively utilized as

parents in the hybridization program. This type of hybridization would be useful for obtaining the highest number of valuable segregates along with maximized vigor. Kadam et al. [61], Shridher et al. [55], and Yirgalem et al. [24] reported similar instances of inter-cluster distances.

In conclusion, the overall genetic diversity analysis and phenotypic evaluation have identified four common genotypes that are consistently superior in all experiments, having unique alleles and drought tolerance traits. The genotypes that showed promising results for drought tolerance include Acc#239130, Acc#220255, Acc#235810 and Acc#220253. It is therefore recommended that these four genotypes be used as breeding material for further improvement of the crop.

SUPPLEMENTARY MATERIALS

The following supplementary materials are available online at https://doi.org/10.20900/cbgg20240008. Supplementary Table S1: Sorghum (*Sorghum bicolor* (L.) Moench) genotypes (accessions) used in this study (2018); Supplementary Figure S1: Monthly rainfall amount at Sheraro (2018); Supplementary Figure S2. Monthly rainfall amount at Miesso (2018).

DATA AVAILABILITY

All data supporting the findings of this study will be available on paper and its supplementary materials published online. The original breeding data is uploaded to the Journal through online uploading system. The data is uploaded to the publisher consumption only. The original data can't be shared to any third party. Seed of the breeding lines can be obtained from Melkassa Agricultural Research Center and it can be shared.

AUTHOR CONTRIBUTIONS

Conceptualization, YG; Methodology Formulation, YG; Software Analysis, YG; Writing—Original Draft Preparation, YG, KB, FA, TT and AT; Writing—Review & Editing, YG, KB, FA, TT and AT; Supervision, KB, FA, TT and AT.

CONFLICTS OF INTEREST

The authors declare that they have no conflicts of interest.

FUNDING

This work was supported by TERRA project coordinated in by Ethiopian Institute of Agricultural Research Institution. TERRA project is among the projects financed by Bill & Melinda Gates Foundation. The project has terminated after the fieldwork.

ACKNOWLEDGEMENTS

We thank to Melkassa Agricultural Research Center and Shire Maitsebri Resesarch center for providing experimental site. We especially thank to the sorghum research national coordination center staff based at Melkassa Agricultural Research Center, Adama, Ethiopia for providing planting material, technical support during data collection.

REFERENCES

1. Bibi A, Sadaqat HA, Akram HM, Mohammed MI. Physiological markers for screening sorghum (*Sorghum bicolor*) germplasm under water stress condition. Int J Agric Biol. 2010;12:451-5.
2. Ali MA, Abbas A, Niaz S, Zulkiffal M, Ali S. Morpho-physiological criteria for drought tolerance in sorghum (*Sorghum bicolor*) at seedling and post-anthesis stages. Int J Agric Biol. 2009;11:674-80.
3. Food and Agriculture Organization (FAO). Food and agriculture data. Available from: http://www.fao.org/faostat/en/#data/QC. Accessed on 21 Mar 2023.
4. Boyer J. Plant productivity and environment. Science. 1982;218:443-8.
5. Westgate M, Grant D. Water deficits and reproduction in maize: Response of the reproductive tissue to water deficits at anthesis and mid-grain fill. Plant Physiol. 1989;91:862-7.
6. Ludlow M, Muchow R. A critical evaluation of traits for improving crop yields in water-limited environments. Adv Agron. 1990;43:107-53.
7. Kramer P, Boyer J. Water Relations of Plants and Soils. London (UK): Academic Press; 1995.
8. Miyashita K, Tanakamaru S, Maitani T, Kimura K. Recovery responses of photosynthesis, transpiration, and stomatal conductance in kidney bean following drought stress. Environ Exp Bot. 2005;53:205-14.
9. Ejeta G, Knoll JE. Marker-assisted selection in sorghum. In: Varshney RK, Tuberosa R, editors. Genomic-assisted crop improvement: Vol. 2: Genomics applications in crops. Dordrecht (Netherlands): Springer Publications; 2007. p. 187-205.
10. Tuinstra M, Grote E, Goldsbrough P, Ejeta G. Genetic analysis of post-flowering drought tolerance and components of grain development in *Sorghum bicolor* (L.) Moench. Mol Breed. 1997;3:439-48.
11. Prasad P, Pisipati S, Mutava RN, Tuinstra M. Sensitivity of grain sorghum to high temperature stress during reproductive development. Crop Sci. 2008;48:1911-7.
12. Gebrekidan B. Utilization of accession in sorghum improvement. Sorghum in the eighties. Patancheru (India): ICRISAT; 1982.
13. Amare K, Zeleke H, Bultosa G. Variability for yield, yield related traits and association among traits of sorghum (*Sorghum bicolor* (L.) Moench) varieties in Wollo. Ethiop J Plant Breed Crop Sci. 2015;7(5):125-33.

14. Adugna A, Tirfessa A. Response of stay-green quantitative trait locus (QTL) introgression sorghum lines to post-anthesis drought stress. Afr J Biotechnol. 2014;13(49). doi: 10. 5897/ AJB20 14. 14157
15. Rao M, Patil S. Variability and correlation studies in F2 population of kharif × rabi crosses of sorghum. Karnataka J Agric Sci. 1996;9(1):78-84.
16. Atta BM, Haq MA, Shah TM. Variation and inter-relationships of quantitative traits in chickpea (*Cicer arietinum* L.). Pak J Bot. 2008;40:637-47.
17. Godbharle A, More A, Ambekar S. Genetic variability and correlation studies in elite 'B' and 'R' lines in Kharif sorghum. Electron J Plant Breed. 2010;1(4):989-93.
18. Ethiopian Institute of Agricultural Research (EIAR) Coordination of National Agricultural Research System, Ethiopia. Addis Ababa (Ethiopia): EIAR; 2011.
19. Kuznetsova A, Brockhoff P, Christensen R, Haubo B. lmerTest Package: Tests in Linear Mixed Effects Models. J Stat Softw. 2017;82(13). doi: 10.18637/jss.v082.i13
20. Bates D, Mächler M, Bolker B, Walker S. Fitting linear mixed-effects models using lme4. J Stat Softw. 2015;67(1):1-48.
21. R Core Team. R: A language and environment for statistical computing. Available from: https://www.R-project.org/. Accessed on 11 Jun 2023.
22. Alvarado B, Rodríguez F, Pacheco G, Burgueño J, Crossa J, Vargas-H P, et al. META-R: A software to analyze data from multi-environment plant breeding trials. Crop J. 2020;8(5):745-56.
23. Singh RK, Chaudhary B. Biometrical Methods in Quantitative Genetics Analysis. New Delhi (India): Kalyani Publishers; 1999.
24. Yirgalem T, Sintayehu A, Geremew T. Assessment of genetic variability, genetic advance, correlation and path analysis for morphological traits in sesame genotypes. Int J Plant Breed Genet. 2013;7(1):21-4.
25. Burton GW. Quantitative inheritance in grasses. Proc 6th Int Grasslands Congr. 1952;1:227-83.
26. Miller P, Williams J, Robinson H, Comstock R. Estimates of genotypic and environmental variances and covariances in upland cotton and their implications in selection. Agron J. 1958;50:126-31.
27. Dewey DR, Lu K. A correlation and path-coefficient analysis of components of crested wheatgrass seed production. Agron J. 1959;51:515-8.
28. SAS. Statistical Analysis Software, Version 9.2. Cary (US): SAS Institute Inc.; 2008.
29. Techale B, Kassahun B, Andrew P, Mihrete G, Aregash G. Evaluation and genetic analysis of a segregating sorghum population under moisture stress conditions. J Crop Sci Biotechnol. 2014;23(1):29-38.
30. Tomar SS, Sivakumar S, Ganesamurthy K. Genetic variability and heritability studies for different quantitative traits in sweet sorghum [*Sorghum bicolor* (L.) Moench] genotypes. Electron J Plant Breed. 2012;3(2):806-10.
31. Adane G, Taye T, Amare S, Habte N, Amare N, Tsegau S, et al. Genetic variability in agronomic traits and associations in sorghum [(*Sorghum bicolor*

(L.) Moench)] genotypes at intermediate agro-ecology sorghum growing areas of Ethiopia. Afr J Agric Res. 2018;49:2780-7.

32. Yaqoob M, Hussain N, Rashid A. Genetic variability and heritability analysis for yield and morphological traits in sorghum (*Sorghum bicolor* (L.) Moench) genotypes. J Agric Res. 2015;53(3):321-6.
33. Elangovan M, Babu PK. Genetic variability and diversity of sorghum landraces collected from Uttar Pradesh, India. Indian J Plant Genet Resour. 2015;28(2):213-21.
34. Dhutmal R, Kalpande H, More A. Genetic variability and heritability studies in rabi sorghum drought-tolerant genotypes. Ann Plant Soil Res. 2015;17(4):391-4.
35. Warkad Y, Potdukhe N, Dethe A, Kahate P, Kotgire R. Agril Sci Digest. 2008;28:202-5.
36. Seetharam K, Ganesamurthy K. Characterization of sorghum genotypes for yield and other agronomic traits through genetic variability and diversity analysis. Electron J Plant Breed. 2013;4(1):1073-9.
37. Khandelwal V, Shukla M, Jodha B, Nathawat V, Dashora S. Genetic parameters and character association in sorghum (*Sorghum bicolor* (L.) Moench). Indian J Sci Technol. 2015;8(22):73902.
38. Ezeaku I, Mohammed S. Character association and path analysis in grain sorghum. Afr J Biotechnol. 2006;5(14):1337-40.
39. Swamy N, Biradar B, Sajjanar G, Ashwathama V, Sajjan A, Biradar A. Genetic variability and correlation studies for productivity traits in Rabi sorghum [*Sorghum bicolor* (L.) Moench]. J Pharmacol Phytochem. 2018;7(6):1785-8.
40. Ambachew T. Variability and association studies among the sorghum genotypes for seed yield and yield related traits under rainfed condition of Ethiopia. J Genet Genomics Plant Breed. 2020;4(1):9-19.
41. Iyanar K, Gopalan A, Ramasamy P. Correlation and path analysis in sorghum. Ann Agric Res. 2001;22(4):495-7.
42. Patel RH, Desai KB, Raj KRV, Parikh RK. Estimates of heritability and genetic advance and other genetic parameters in an F2 population of sorghum. Sorghum Newslett. 1980;23:22-3.
43. Mahajan R, Wadikar P, Pole S, Dhuppe M. Variability, correlation and path analysis studies in sorghum. Res J Agric Sci. 2011;2(1):101-3.
44. Upadhyaya HD, Sharma S, Ramulu B, Bhattacharjee R, Gowda CLL, Reddy VG, et al. Variation for qualitative and quantitative traits and identification of trait-specific sources in new sorghum germplasm. Crop Pasture Sci. 2010;61:609-18.
45. Santosh K, Girish G, Yashoda Y. Character association and path analysis studies in germplasm lines of rabi sorghum (*Sorghum bicolor* (L.) Moench). J Appl Nat Sci. 2017;9(1):206-10.
46. Goswami S, Patel PG, Gami R, Patel R, Khatri A. Correlation and path analysis study of different characters for grain yield and fodder purpose in sorghum [*Sorghum bicolor* (L.) Moench]. Electron J Plant Breed. 2020;11(4):1053-61.

47. Brejda J, Moorman T, Karlen DL, Dao TH. Identification of regional soil quality factors and indicators. I. Central and Southern High-Plains. Soil Sci Soc Am J. 2000;64:2115-24.
48. Kavithamani D, Yuvaraja A, Selvi B. Principal component analysis and grouping of sorghum (*Sorghum bicolor* L. Moench) gene pool for genetic diversity. Electron J Plant Breed. 2019;10(4):1426-34.
49. Jain SK, Patel PR. Principal component and cluster analysis in sorghum (*Sorghum bicolor* (L.) Moench). Forage Res. 2016;42(2):90-5.
50. Billot C, Ramu P, Bouchet S, Chantereau J, Deu M, Gardes L, et al. Massive sorghum collection genotyped with SSR markers to enhance use of global genetic resources. PLoS One. 2013;8(4):e59714.
51. Vikas K, Keerthika A, Meenakshi D. Genetic divergence studies for morphological traits in sorghum [*Sorghum bicolor* (L.) Moench] over the environments. Curr J Appl Sci Technol. 2019;38(6):1-7.
52. Vijaylaxmi S, Pahuja K, Pummy K, Joshi U. Genetic divergence studies for agro-morphological, insect pest and quality parameters in mini core collection of forage sorghum. Forage Res. 2019;44(4):237-41.
53. Sarwate C. Genetic analysis of yield and yield contributing characters in sorghum. Part II. The Study of Genetic Divergence in Sorghum [dissertation]. Rahuri (India): MPKV; 1985.
54. Barhate K. Genetic divergence, combining ability and stability studies in sorghum [dissertation]. Rahuri (India): MPKV; 1996.
55. Shridher K, Gangaiah B, Ramesh C. Genetic diversity studies in forage sorghum. Sorghum Res Rep. 2003;44:3-6.
56. Patankar A, Sonone A, Patil J, Sarode N. Genetic divergence in sweet sorghum. J Maharashtra Agric Univ. 2005;30(2):175-7.
57. Ganesamurthy D, Punitha K, Elangovan M. Genetic diversity among the land races of sorghum collected in Tamil Nadu. Electron J Plant Breed. 2010;1(6):1375-9.
58. Damor H, Parmar H, Parmar D. D2 analysis in forage sorghum [*Sorghum bicolor* (L.) Moench]. Int J Chem Stud. 2017;5(4):337-41.
59. Ahalawat N, Arya V, Kumar P, Singh S. Genetic divergence in forage sorghum (*Sorghum bicolor* (L.) Moench). J Appl Nat Sci. 2017;10(1):439-44.
60. Karadi A, Kajjidoni S. Genetic variability and diversity for productivity traits and grain quality including nutritional quality traits in selected mini core and promising released varieties of sorghum. J Pharmacog Phytochem. 2019;8(4):2091-7.
61. Kadam D, Patil F, Bhor T, Harer P. Diversity studies in sweet sorghum. J Maharashtra Agric Uni. 2001;26(2):140-3.

How to cite this article:
Gidey Y, Bantte K, Abay F, Tadesse T, Tirfessa A. Assessment of Genetic Variability in Sorghum Genotypes under Dry Low Land Areas of Ethiopia. Crop Breed Genet Genom. 2024;6(4):e240008. https://doi.org/10.20900/cbgg20240008