

## Genetic Diversity in Ethiopian Sorghum (*Sorghum bicolor* L.) Germplasm Accessions Based on Major Quantitative Morphological Traits

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### Abstract

In Ethiopia, sorghum exists in tremendous diversity with an extremely broad genetic base for trait improvement. However, so far only a small number of sorghum germplasms have been characterized. In the present study, a total of 275 sorghum germplasms collected from major growing areas were characterized using 13 major quantitative traits. The result indicated the presence of extensive genetic diversity among test germplasms. Accessions from Tigray region were characterized by early flowering and maturity, short plant height, small number of leaves per plant and small leaf area. The highest mean number of days to 50% flowering and numbers of days to maturity were obtained for accessions collected from Oromiya region. Cluster analysis grouped test genotypes into six distinct diversity groups irrespective of their region of origin. The genetic distances between most of the clusters were highly significant ( $P < 0.01$ ). Maximum genetic distances were obtained between cluster 4 and 6, cluster 4 and 5, and cluster 1 and 6 with pair wise generalized square distance ( $D^2$ ) of 86.62, 51.56 and 46.69, respectively. Moreover, the first four principal components with eigenvalues greater than one explained 62.09% of the variation indicating the existence of significant genetic diversity among Ethiopian sorghum germplasms. Interestingly, from six distinct diversity groups, 50 diverse sorghum germplasms with good yield and yield related morphological traits were identified. Therefore, these genotypes can be utilized by the breeding programs to identify diverse parental combination for crossing to develop best varieties to maximize the genetic gain of the breeding program.

**Keywords:** Ethiopia; Sorghum; Genetic; Diversity; Quantitative; Traits

### Introduction

Sorghum (*Sorghum bicolor* L.) Moench  $2n=20$  is a leading cereal in the arid and semi-arid regions of the world, ranking fifth in importance among the world's grain crops after wheat, maize, rice and barley [1]. Grain Sorghum serves as one of the most important staple cereals for millions of poor in semi-arid tropics of Africa and Asia, where annual rainfall is minimum and recurrent drought is common [2,3]. In Ethiopia, Sorghum is a major staple food crop, ranking second after maize in total production [4,5]. It is grown in almost all regions, covering a total land area of 1.84 million ha [6].

In Ethiopia Sorghum exists in tremendous diversity throughout the growing areas with an extremely broad and valuable genetic base for potential breeding and improvement program in the country and in the world [7-10]. However, only a small number of Sorghum germplasm collections have been characterized and the existence of considerable genetic diversity in both cultivated and wild Sorghum has been reported [5,10-16]. From more than 9,000 Sorghum accessions collected in Ethiopia, only a small number was characterized both at the morphological and molecular level [17].

Estimation of genetic diversity among genotypes can be based on quantitative traits [18,19]. Variation in most economically important quantitative traits of crop plants follows a continuous distribution caused by the action and interaction of many genes

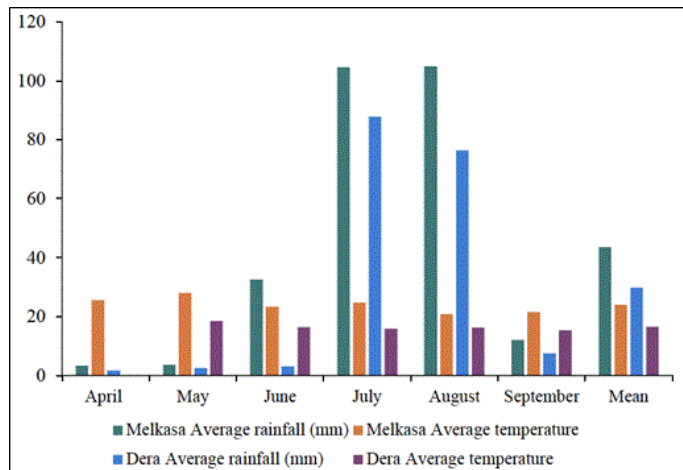
and various environmental factors. Statistical analysis of these quantitative traits, along with eco-geographic information is one of the earliest methods used for estimating genetic diversity in Sorghum [20]. It is widely used to quantify the amount and distribution of variation in large samples of Sorghum germplasm collections [11,14,19,21]. However, in Ethiopia extent of genetic diversity among Sorghum germplasm collections has not been well studied either with morphological or molecular markers [4,14,20,22].

This study was, therefore, designed to examine the magnitude of genetic diversity among Sorghum germplasm accessions collected from the major growing areas of Ethiopia based on the quantitative morphological traits.

### Materials and Methods

A total of 275 Sorghum germplasm accessions collected from different drought-prone areas of Ethiopia were used in this study. Accessions were evaluated in two major Sorghum growing areas of Ethiopia, at Melkassa Agricultural Research Center and Dera Research station. Melkassa Agricultural Research Center is located in the Rift Valley at  $39^{\circ}21'$  E longitude,  $8^{\circ}24'$  N latitude and with an altitude of 1550 meter above sea level. Dera is also located at  $39^{\circ}0'$  N latitude and  $08^{\circ}04'$  E longitudes with an altitude 1600 meter above sea level. Test accessions were planted at Melkassa and Dera after the onset of the summer rain in June (Figure 1). Each test accession was planted in single row of 4.5 m and every plot contains 30 individual plants. The spacing between plants and between rows was 0.15 meter and 0.75 meter, respectively. At planting 100 kg/ha DAP and the

same rate of urea was applied. All the recommended agronomic practices such as weeding, cultivation and thinning were applied as required regularly.



**Figure 1:** Average rainfall and temperature during growth and development stages of sorghum germplasms at Melkasa and Dera.

**Data collected**

Sorghum Descriptor IBPGR/ICRISAT was used for characterization of test germplasms based on major quantitative morphological traits [23]. Accordingly, data were collected on Leaf Number per plant (LN), Leaf Length in cm (LL), Leaf Width in cm (LW), Leaf Area in cm<sup>2</sup> (LA), Internode Length in cm (IL), Plant Height in cm (PH), Panicle Length in cm (PL), Panicle Width in cm (PW), Days to Maturity (DM), Number of Primary Branches Per Panicle (NPBP), 1,000 Seed Weight in gram (TSWt), Grain Yield Per Panicle in gram (GYPP). All data were recorded from the middle row on ten randomly selected individual plants; except for percent stand establishment, days to 50% flowering and number of days to maturity which were recorded on plot basis. To estimate leaf area, a procedure developed by Stickler et al. was applied [24]. Before measuring thousand seed weight and grain yield per panicle, the grain moisture content was recorded for individual plants and the moisture content of the grain was adjusted to 12.5%.

**Statistical data analysis**

Data were inspected for normality of residuals and outliers, and subjected to Analysis of Variance (ANOVA) using SAS

computer software [25]. The combined over locations mean of all quantitative traits were used to assess the correlations of each traits using SAS computer software. For multivariate analysis, the data were standardized to a mean of zero and standard deviation of one to avoid differences in scales used for recording data on the different quantitative characters Sneath and Sokal, before undertaking a series of multivariate analyses using the appropriate procedures of SAS computer programme [26]. Principal Component Analysis (PCA) was computed on the standardized data using the correlation matrix using SAS computer software [25]. Using average linkage method of SAS software all Sorghum accessions were clustered based on their differences and similarities on the quantitative traits. The numbers of clusters were determined based on the pseudo F and the pseudo t<sup>2</sup> statistics. The relationships among the clusters were assessed by measuring the genetic distances between clusters as D<sup>2</sup> (Mahalanobis's distance).

$$D^2_{ij} = (x_i - x_j)' cov^{-1} (x_i - x_j)$$

Where, D<sup>2</sup><sub>ij</sub> is the distance between cases i and j; x<sub>i</sub> and x<sub>j</sub> are vectors of the values of the variables for cases i and j; and cov<sup>-1</sup> is the pooled within groups variance-covariance matrix. The D<sup>2</sup> values obtained for pairs of clusters was considered as the calculated values of Chi-square and tested for significance both at 1% and 5% probability levels against the tabulated value of (x<sup>2</sup>) for 'N' degree of freedom, where N, is the number of characters considered.

**Results**

Mean comparison revealed the existence of significant difference among test accessions for all 13 quantitative traits considered in this study (Table 1). Based on the over location mean, the variation between the accessions was much greater for plant height, leaf area, grain yield per panicle, number of primary branches per panicle, number of days to maturity and number of days for 50% flowering. Similarly, Sorghum accession collected from different regions showed significant difference for all most quantitative morphological traits (Table 2). Accessions from Tigray region showed the lower record for most of the traits, mainly for days to 50% flowering; number of days to maturity, plant height, leaf number, leaf length, leaf width and leaf area. On the other hand, the highest mean number of days to 50% flowering and numbers of days to maturity were observed for Sorghum accessions collected from Kemise.

Characters	Melkassa			Dera			Over locations		
	LSD	Sig.	CV%	LSD	Sig.	CV%	LSD	Sig.	CV%
Leaf number	0.75	*	9.88	0.97	*	17.57	0.58	*	12.8
Leaf length	3.22	**	6.33	4.49	**	10.7	2.7	**	8.37
Leaf width	0.48	*	8.37	1.03	*	19.07	0.51	*	13.21
Leaf area	37.04	**	12.38	49.03	**	21.81	29.52	**	16.21
Plant height	17.61	**	16.71	25.67	**	21.51	15.28	**	19.56
Internodes length	2.26	**	22.21	1.76	**	19.58	1.31	**	19.73
Panicle length	2.21	**	16.8	1.72	**	15.22	1.27	**	14.99

Panicle width	0.9	*	20.42	0.75	*	17.01	0.53	*	17.45
Days to 50% flowering	3.56	**	6.03	4.5	**	7.51	3.09	**	7.48
Days to maturity	5.54	**	5.98	3.68	**	4.7	3.37	**	5.68
Number of primary branches/panicle	6.79	**	17.83	7.85	**	23.96	4.76	**	19.35
1000 seed weight	2.55	**	8.36	4.17	**	21.33	2.34	**	13.45
Grain yield/panicle	18.79	**	37.12	10.58	**	31.54	10.4	**	34.22

**Note:** LSD=Least Significant Difference; Sig.=Significance level ; \*, \*\* corresponds to the significance level at p=0.05 and p=0.01 probability level, respectively.

**Table 1:** Statistical analysis of 13 major quantitative traits in 275 sorghum accessions evaluated at Melkassa and Dera.

Origin	LN	LA	PH	IL	PL	DF	DM	NPBP	TSWt	GYPP
Tigray	11.1c	384.7ab	221.5c	16.2b	17.7ab	87.7e	129.7c	60.1b	31.4ab	49.5ab
Wello	11.8bc	424.8a	240.7b	16.5ab	17.1ab	96.1c	139a	57.8bc	30.2b	56.0a
Shewa	11.1c	396ab	262.5a	15.1c	13.5c	93.4d	135.0b	60.2b	30.0b	36.6c
Gamogofa	11.9b	409.6a	249.1a	16.6ab	18.7a	100b	136.6b	43.4d	28.4bc	58.2a
Kemise	12.1b	412.2a	235bc	17.8a	17.6ab	105.4a	141.3a	69.3a	27.6c	52.2a
Hararge	13.3a	423.1a	266.6a	18.9a	16.1b	101.5b	131.8c	60.7b	32.1ab	54.9a
Gondar	10.4d	384.9ab	230.9b	16.5d	18.7a	92.1d	133.8c	60.6b	33.6a	51.4a
LSD	0.58	29.52	15.29	1.31	1.27	3.1	3.371	4.76	2.34	10.4

**Note:** Levels not connected by same letter are significantly different.

Leaf Number per plant (LN), Leaf Area in cm<sup>2</sup> (LA), Internode Length in cm (IL), Plant Height in cm (PH), Panicle Length in cm (PL), Days to Maturity (DM), Number of Primary Branches Per Panicle (NPBP), 1,000 Seed Weight in gram (TSWt), Grain Yield Per Panicle in gram (GYPP).

**Table 2:** Mean comparison for regions of origins of 275 sorghum accession based on major quantitative traits.

Accessions from Hararge showed relatively higher leaf number per plant, leaf area, and plant height and internodes length. Accessions from Gamogofa and Wello gave relatively the higher grain yield per panicle than the rest of the regions. Moreover, most accessions from Shewa showed an intermediate value for almost all the quantitative traits considered in this study (Table 2).

The correlation coefficient between most of the quantitative characters is highly significant ( $P \leq 0.01$ ) and positive (Table 1). The highest significant positive correlation was obtained between leaf area and leaf width. Number of days to 50% flowering significantly correlated with plant height, leaf area, leaf length and number of leaves per plant.

Number of days to maturity is highly correlated with most of the characters including number of leaves per plant, leaf length, leaf width, leaf area, plant height and number of days to 50% flowering. Grain yield per panicle is significantly correlated ( $P \leq 0.01$ ) with all other characters except for number of days to maturity. However, thousand seed weight is negatively correlated with most of the quantitative traits considered in this study. Thousand seed weight is not significantly correlated

with all quantitative traits considered in this study except with leaf number, leaf length, number of days for 50% flowering and number of days to maturity.

### Cluster analysis

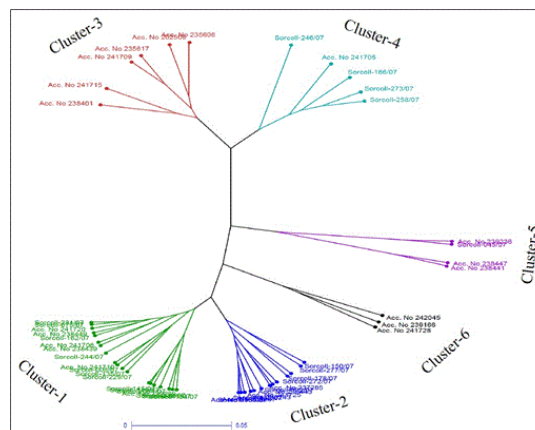
Grouping of Ethiopian Sorghum germplasm accessions is very important to select best accessions from diverse clusters groups for crossing. Cluster analysis based on 13 quantitative traits grouped the 275 accessions in to 6 major cluster groups irrespective of their region of origin (Table 3). Accessions within a cluster are assumed to be more closely related to each other in terms of the trait under consideration than those accessions in different clusters. Cluster one (C-1), is the largest cluster containing 119 accessions. The majority of the accessions in this cluster (62.2%) were Tigray collections. Many Sorghum cultivars which are preferred by farmers for their reasonable yield in the drought affected areas were members of this cluster.

Cluster two (C-2) is the second largest cluster consisting of 51 accessions from different regions of origin. However, in this cluster accessions collected from Gamogofa were more abundant than those from the rest of the regions. Cluster six (C-6) was the smallest cluster with 6 accessions collected only

from Wello. The rest of the clusters contained different number of accessions from all regions. Moreover, cluster mean analysis indicated that cluster six (C-6) contained Sorghum germplasms with the highest values of most morphological traits such as leaf length, leaf width, leaf area, internode length, plant height, panicle length, panicle width, days to maturity and grain yield per panicle (Table 2). However, cluster-1 and cluster-4 represented with Sorghum germplasms with least values of most morphological traits (Table 2).

In this study, the contribution of most adaptive quantitative morphological characters such as plant height and number of days to 50% flowering and maturity in cluster analysis is very high. Many early flowering and early maturing Sorghum accessions with relatively short plant height from different regions were fall in the same clusters. Moreover, as recognized during collection different Sorghum cultivars preferred by farmers to give reasonable yield during the drought season were members of this cluster. In most cases, many accessions collected from the same region were clustered together. On the other hand, number of accessions collected from different regions was also clustered together. Besides, in this study, 50 promising and

very diverse Sorghum germplasm accessions representing the six cluster groups were identified for trait improvement in the breeding program (Figure 2 and Table 3).



**Figure 2:** UPGMA dendrogram of 50 Sorghum germplasm accessions representing the six distinct diversity groups (clusters).

Region of origin	Cluster-1	Cluster-2	Cluster-3	Cluster-4	Cluster-5	Cluster-6
Tigray	74	11	7	19	14	0
Wello	23	14	11	3	5	6
Gamogofa	6	16	12	7	7	0
Shewa	5	3	0	8	0	0
Kemisie	6	3	0	1	1	0
Harergie	2	3	3	0	0	0
Gonder	3	1	0	1	0	0
Total	119	51	33	39	27	6

**Table 3:** Distribution of 275 sorghum accessions into 6 clusters based on 13 quantitative traits.

Moreover, the pair wise generalized square distance ( $D^2$ ) between each cluster is shown in (Table 4). The genetic distance between most of the clusters was found highly significant ( $P < 0.01$ ). Crossing of accessions belonging to different clusters of wide Mahalanobis distance ( $D^2$ ) maximize the opportunity

for transgressive segregation. In the current study, maximum genetic distances were obtained between C4 and C6, C4 and C5 and C1 and C6 with  $D^2$  of 86.62, 51.56 and 46.69, respectively. The lowest genetic distances between the clusters were observed between C3 and C5, and C1 and C4 with  $D^2$  of 9.15 and 9.19

Cluster	Cluster-1	Cluster-2	Cluster-3	Cluster-4	Cluster-5	Cluster-6
Cluster-1	0	-	-	-	-	-
Cluster-2	11.99	0	-	-	-	-
Cluster-3	9.92	12.43	0	-	-	-
Cluster-4	9.19	22.14	34.48**	0	-	-
Cluster-5	19.37	36.65**	9.15	51.56**	0	-
Cluster-6	46.69**	32.57**	16.05	86.62**	27.86**	0

**Note:** \*, \*\* significant at  $p = 0.05$  and  $p = 0.01$  probability level, respectively

**Table 4:** Mahalanobis distance ( $D^2$ ) of the six clusters of 275 sorghum germplasms.

respectively.

### Principal component analysis

The first four principal components with eigenvalues greater than one accounted for a cumulative variation of 62.09% (Table 3). Some characters have greater importance in determining the existing variability than others. In the present study, leaf length, days to 50% flowering, plant height, leaf area and days to maturity were the most important traits contributing to the first principal components. The contribution of internodes length, panicle length and grain yield per panicle in the second principal component analysis was also very high. Leaf width, number of primary branches per panicle and thousand seed weight were the most important traits in the third, fourth and fifth principal components, respectively.

### Discussion

This study indicated the existence of high genetic diversity among Ethiopian Sorghum germplasm accessions collected from the major growing areas of Ethiopia. The highest significant positive correlation was obtained between most of the quantitative traits. The correlation that exists between different characters is very important in plant breeding program as it helps in the identification of easily measured characters that could be used as indicators of the more important and complex characters [13]. Moreover, high correlation coefficients between characters show that the characters share common element of genetic control between genes.

The significant positive correlation between the number of days for 50% flowering, leaf number, leaf area, plant height and number of days for maturity is in agreement with the result of the previous study [13]. This significant positive correlation between plant height and number of days for 50% flowering, which is observed in the present study and in the previous studies of Ayana and Bekele suggests that the transfer of genes for maturity and plant height into the farmers' preferred cultivars would be successful [13].

In the present study, clustering of the Sorghum accessions based on quantitative traits produced six diversity classes irrespective of their geographical origin. Many early flowering and early maturing Sorghum accessions with relatively short plant height from different regions fall in the same clusters together with many farmer-preferred cultivars with good yield and yield related morphological traits. Maximum genetic distances were obtained between clusters 4 and 6, clusters 4 and 5, and clusters 1 and 6 with  $D^2$  of 86.62, 51.56 and 46.69, respectively. In any crop, crosses among parents with maximum genetic distances are more responsive to improvement for a given trait of interest [9,10,19,27]. Therefore, there is a high possibility to get several promising crossing parents from each cluster based on desirable quantitative morphological traits.

Maximum genetic recombination and variation in subsequent generation is expected from crosses that involve parents from those clusters characterized by maximum genetic distance [10,19,28]. Crosses between Sorghum accessions selected from those clusters with maximum  $D^2$  are expected to provide relatively better genetic recombination and segregation in their progenies. Besides, the selection of individual parents from such

clusters must consider the special advantage of each cluster. Sorghum germplasms to be considered as best crossing parent, in addition to genetic diversity, should express the optimum level of desired traits. Therefore, the identified 50 diverse Sorghum germplasms with best yield and yield related morphological traits can be used as best crossing parent to generate different Sorghum varieties with economically important yield related morphological traits.

### Conclusion

In Ethiopia, Sorghum exists in tremendous genetic diversity with an extremely broad genetic base for trait improvement. However, so far only a small number of Sorghum germplasms have been characterized. This study indicated the existence of high genetic diversity among Ethiopian Sorghum germplasm accessions collected from the major growing areas of Ethiopia. Therefore, the identified diverse Sorghum germplasm accessions can be utilized by the breeding programs to identify diverse parental combination for crossing to develop best varieties to maximize the genetic gain of the breeding program.

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### Conflicts of Interest

The author declare that there no conflict of interest.

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