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Genetic diversity study of sorghum (*Sorghum bicolor* (L.) Moenc) genotypes, Ethiopia

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Abstract. *Sorghum bicolor* is one of the most important cereal crops around the world, particularly in Africa, highly cultivated for dietary staple. For this reason, a good knowledge and usage of this genetic resource in sorghum accessions is highly vital for improving crop quality. Analysis of genetic variability among the accessions will enable accurate results in breeding. The research design used was augmented design, which is common in many gene banks. This research finding would be used later by plant breeders to select best performers for further evaluation of the crop and obtain a new variety of sorghum.

Keywords: genetic diversity, genetic variability

1. Introduction

Sorghum is ranked the fifth most produced food crop in the world, and it is a dietary staple for over half a billion people in over thirty countries, most of them being developing countries [1], [2]. It is also the second most cultivated cereal crop in Africa, where cultivation of farmer's variety of sorghum is the predominant form of agriculture next to maize [3]. Sorghum was domesticated in the African continent, particularly in East Africa, Ethiopia, from where it was believed to be introduced to other regions of the world with a wide agro-ecology [4]. It is one of most vital crops cultivated over a wide extreme ecological habitat in Ethiopia, in the range of low to high altitude (400–3,000 meters above sea level) [5]. It is well adapted to the range of environmental conditions in semi-arid Africa, with high variability [1], [6], [7]. Sorghum is the single most important cereal in the lowland areas because of its extreme resistance to water stress [8].

Sorghum bicolor contains both cultivated and wild relative races, and it provides a substantial amount of genetic diversity for traits of agronomic importance so as to develop the crop's different variety of interest for plant breeders [9].

Ethiopia is known to be one of the Vavilovian centres of origin, or diversity for many cultivated and wild species of crops, including sorghum [10], [11]. Sorghum is one of the cereal crops for which Ethiopia has been credited as being a centre of origin and/or diversity [10], [12]. In the high altitude areas, the landrace sorghum germplasm has often been the only well-adapted material that is easily accessible for use. There is a higher probability of genetic material exchange to occur between the wild (*Sorghum bicolor subsp. arundinaceum*) and the cultivated sorghum since both types mostly grow in sympathy with the wild and weedy relatives in most sorghum-growing parts of Ethiopia, mainly in the south-eastern and south-western part of the country [1]. A greater extent of genetic diversity existed within a species, often used as a measure of its ability to adapt to its new environment. Hence, biodiversity is like a wealth for coping with environmental fluctuations. Sorghum has one of the largest crop germplasm collections, consisting of more than 42,000 accessions worldwide [13], [14]. The largest diversity of the crop germplasm provides greater opportunities for improvement regarding its environmental adaptability and acquiring better agronomic traits from the crop species. Identifying and selecting the best varieties meeting specific local food and industrial requirements from this great biodiversity is of high importance for the food security assurance of any given country [14].

Having a good knowledge of the genetic diversity of a crop often enables the plant geneticist to select the desirable family for the breeding programme and gene introgression from distantly related germplasm. The more variable genotypes or accessions can be crossed to produce better varieties that can tolerate a range of environmental changes to abiotic and biotic stresses. Therefore, a better understanding of the genetic diversity in sorghum crop species will definitely facilitate the further improvement of this cereal crop concerning its genetic architecture [15].

Genetic diversity in the crop species is one of the precious gifts of nature to us, and it arises due to geographical isolation or genetic boundary to gene flow. Phenotypic traits are conventional tools to analyse the genetic diversity since studies of this type generally do not require complicated equipment and methodology. They are very simple and easy to score. These simple observable morphological characters are the useful tools for primary genetic diversity study as they provide a quick and useful approach for assessing the range of diversity in the crop species. Over the years, a number of studies have dealt with estimating genetic diversity in cultivated sorghum using morphological traits [16–22].

The use of phenotypic characters is the most advisable method most often used to estimate relationships between genotypes. The genetic variability of

cultivated crops and their wild relatives together form a potential and continued source for breeding new and better crop varieties. A better understanding of the genetic diversity in sorghum would greatly contribute to crop improvement with a view to food quality and other important agronomic traits. Therefore, there is a need to evaluate the available accessions for genetic diversity and identify the best accessions according to their performance.

There are around 11,353 sorghum accessions collected and conserved in Ethiopian Biodiversity Institute gene bank, of which 8,913 accessions were characterized by plant breeders and other researchers, and further 2,440 sorghum accessions are yet to be screened for their potentially useful characters. For this reason, the main objective of this research was to determine the range of variation among sorghum accessions in general and to classify them into clusters based on their similarity features regarding the traits under study (quantitative characters) and also to generate data on their performance for plant breeders for further evaluation of the crop in particular.

2. Materials and methods

The study on sorghum was conducted in Oromia Regional State, Arsi Zone, Arsi Negale Research sub-centre in the summer of 2014/15, during the main cropping season. This region is located in the Western Oromia Regional State, with an altitude of 1,960 meters above sea level and 7°20'N latitude and 38°09'E longitude. 117 Sorghum accessions and two standard checks (Geremew and Baji), which were obtained from Melkasa Agricultural Research Centre (MARC), were used for yield and drought resistance traits comparison for the research, respectively. The research design used was augmented design with no replication among the sorghum accessions, except for the two standard checks replicated in every block due to insufficient seed availability. The sorghum genotypes were planted in two rows with a spacing of 75 cm × 30 cm between and within rows respectively, with a row length of 5m. DAP, Urea, and other management practices were applied as per recommended for the site.

Morphological data was recorded with the help of the International Plant Genetic Resources Institute (IPGRI), nowadays known as "Bioversity International", based in Italy, Rome. The characterization descriptor list for sorghum (E and F, 1993) was used by randomly selecting and tagging 20 individual plants for diversity study research from each accession. For each selected plant, the quantitative trait to be studied in the accession was coded as Basal tiller (BT), Nodal tiller (NT), Leaf number at maturity (LN), Plant height (PH) in cm, Panicle length (PL) in cm, Panicle width (PW) in cm, thousand grain weight (GY) in gm, Days to 50% flowering (DF), and Days to 50% maturity (DM). The collected data were calculated by statistical analysis of

variance using MINITAB (version 13.0) and SAS (9.2). Variances and coefficient variation were calculated as per formula, as it was suggested [23].

Table 1. List of the sorghum accessions and the two standard checks used for the study, obtained from the Ethiopian Biodiversity Institute

No	Acc. Number	No	Acc. Number	No	Acc. Number	No	Acc. Number	No	Acc. Number
1	9125	28	219976	55	233816	82	237778	109	241689
2	9161	29	219982	56	233819	83	237784	110	241690
3	9630	30	223513	57	233820	84	238379	111	241692
4	15817	31	223533	58	233821	85	238382	112	242029
5	15821	32	223581	59	233822	86	238384	113	242030
6	70940	33	226053	60	233830	87	238385	114	242034
7	71806	34	227098	61	233832	88	238387	115	242035
8	71889	35	227202	62	233835	89	238388	116	242038
9	73657	36	227203	63	233836	90	238392	117	69057
10	74788	37	227205	64	233837	91	238407	118	Germew (ck 1)
11	73957	38	227206	65	234056	92	238410	119	Baji (ck2)
12	200117	39	227208	66	234057	93	238438		
13	200646	40	227213	67	234067	94	238453		
14	200774	41	228091	68	234081	95	241197		
15	201444	42	228111	69	235468	96	241199		
16	201768	43	228544	70	235476	97	241218		
17	201817	44	228548	71	235597	98	241221		
18	201923	45	228741	72	235615	99	241235		
19	201936	46	228743	73	235624	100	241237		
20	201956	47	231201	74	235626	101	241240		
21	206944	48	233686	75	236728	102	241245		
22	206950	49	233689	76	237033	103	241246		
23	216827	50	233693	77	237037	104	241247		
24	217694	51	23699	78	237278	105	241248		
25	217697	52	233700	79	237281	106	241251		
26	217698	53	23707	80	237769	107	241273		
27	219974	54	233808	81	237771	108	241275		

3. Results and discussions

3.1 Analysis of variance

The analysis of variances (ANOVA) table revealed that there is diversity among the accessions of sorghum for all characters studied; in other words, there were significant differences ($p < 0.05$), as it was indicated in *Table 2*.

Table 2. The mean square of the tested sorghum accessions for the nine quantitative characters

Source of variation	Degree of freedom	Mean squares								
		BT	NT	LN	PH	PL	PW	GY	DF	DM
Between Groups	7	0.674	1.462	30.27	5.14	130.76	9.29	110.30	157.41	200.36
Within Groups	111	0.25	0.773	4.19	3.41	42.42	4.53	98.36	33.48	64.44
Mean		0.26	0.77	9.21	2.67	24.69	6.88	23.41	102.7	71.06
SE		0.48	0.08	0.22	0.17	0.63	0.20	0.56	0.99	0.78

3.2 Mean and range values

The mean values of the genotypes indicated that there are some genotypes performing better than the two standard checks, “Geremew and Baji”, for some of the traits studied. Only one genotype matured earlier than the two standard checks, which was ACC No 238453 (51 days), while some others matured at the same time as the two standard checks, e.g. ACC No 9161 (54 days) and ACC no 9630 (54 days), ACC No 237769 (59 days), ACC No 234056 (59 days), and ACC No 241275 (59 days), whereas the two checks matured after 54 days (Geremew) and 59 days (Baji) respectively.

Generally, a considerable mean range value was observed for all the traits (*Fig. 1*). Mean ranges of 0 to 2.5, 0 to 3.1, 4.75 to 14.66, 1.45 to 4, 11.34 to 45.6, 4.3 to 10.3, 12 to 36.4, 79 to 131, and 51 to 88 were recorded for BT, NT, LN, PH, PL, PW, GY, DF, and DM, respectively, which clearly shows genetic diversity in the sorghum accession for the studied traits.

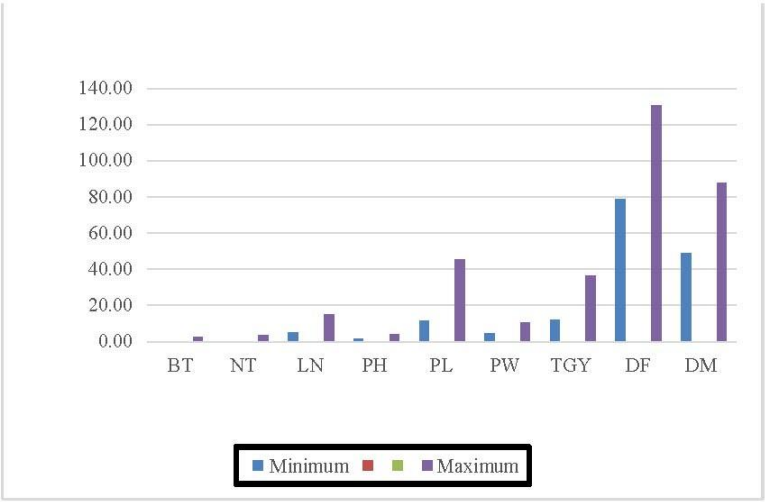

Figure 1. Minimum and maximum values of nine quantitative traits of 119 Sorghum genotypes

3.3 Phenotypic and genotypic coefficients of variation

Low PCV and GCV values were calculated for the traits considered according to [23]. This showed that there is no wide variation among genotypes for the traits considered, except for thousand grain yields (GY) and panicle length (PL), as it was illustrated in the bar graph (*Fig. 2*).

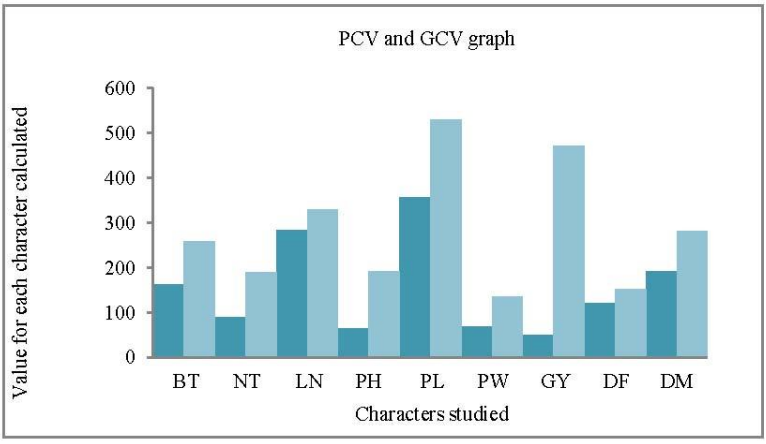

Figure 2. Phenotypic and genotypic coefficient of variation of all characters considered

3.4 Principal component analysis

Principal component analysis was performed in order to reduce a large set of phenotypic traits to a more meaningful smaller set of traits and to know which trait is contributing to maximum variability, because genetic improvement depends on the magnitude of genetic variation. The first four principal components (PCs), with eigenvalues greater than 1, explained about 71.9% of the total variation among accessions for all traits, as it was given in *Table 4*. The first principal component (PC1) obtained was 26.9% of total variance and had high contributing factor loading from LN and PH, which were the most important contributing traits for the relative magnitudes of eigenvectors for the first principal component, while the second principal component (PC2) had high contributing factor loading from PL, GY, and DF, which was 18.9%; thirdly, it had a high contributing factor loading from BT and NT for the third principal component (14.6%), and, finally, it had a high contributing factor loading from PW and DM for the fourth principal component (11.6%).

Table 3. Eigenvectors and eigenvalues of the nine principal components of the 119 sorghum accessions

Traits	Eigenvectors								
	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9
BT	0.214	0.416	-0.491	-0.134	-0.297	-0.139	0.199	-0.610	-0.042
NT	-0.041	0.405	-0.630	0.036	0.172	0.140	-0.078	0.614	0.064
LN	-0.589	0.147	0.010	0.181	0.080	0.007	0.045	-0.231	0.773
PH	-0.527	0.016	-0.123	0.398	0.252	0.099	0.206	-0.197	-0.627
PL	0.244	-0.504	-0.277	0.270	0.005	0.083	0.688	0.093	0.220
PW	-0.0372	-0.156	-0.101	-0.458	-0.056	-0.708	0.241	0.218	-0.086
GY	-0.026	0.490	0.446	-0.273	-0.018	0.285	0.611	0.171	-0.042
DF	-0.033	-0.177	-0.092	-0.044	0.829	0.356	-0.063	0.154	-0.080
DM	0.136	0.303	0.229	0.656	0.349	-0.485	0.042	0.221	-0.007
Eigenvalue	2.4174	1.6985	1.3098	1.0468	0.8261	0.6778	0.4942	0.4133	0.1161
% of total variance explained	0.269	0.189	0.146	0.116	0.092	0.075	0.055	0.046	0.013
% cumulative variance explained	0.269	0.457	0.603	0.719	0.811	0.886	0.941	0.987	1.000

The score plot of 119 accessions based on the first two principal components is presented in *Figure 3*. Accessions (arranged by their plot number) were distributed in different groups, which clearly showed genetic diversity among sorghum accessions.

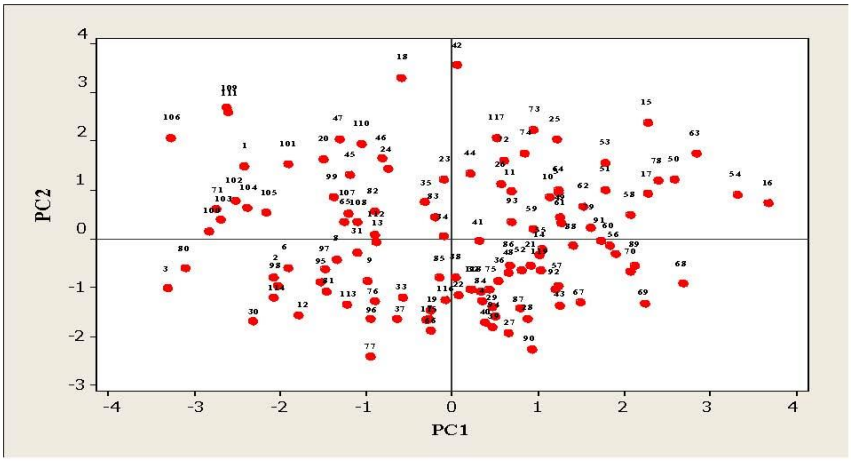

Figure 3. Distribution of sorghum accessions for the first two principal components (PC1 and PC2) based on nine quantitative traits given in their order of arrangement

3.5 Phenotypic and genotypic variation

Low phenotypic and genotypic values were calculated for the traits considered, as it was explained in *Figure 4* [23]. This indicated that there is no wide variation among genotypes for the traits studied, except for TGY, PL, and DM, which showed variability among the sorghum accessions for the traits considered.

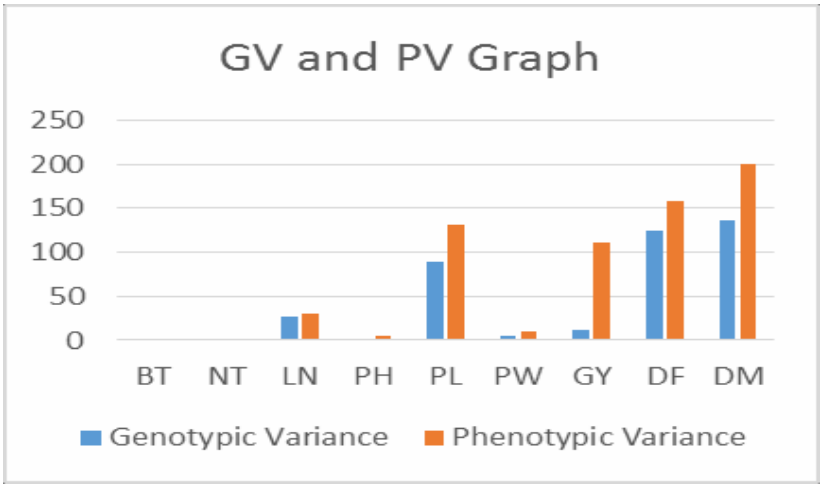

Figure 4. Genotypic and phenotypic variation bar graph of sorghum accessions considered for the nine quantitative traits

3.6 Cluster analysis

Cluster analysis was performed on the Euclidean distance matrix utilizing Ward's linkage method, and the resulting dendrogram is given in *Figure 5*, using MINITAB software version 14. The 117 sorghum accessions along with the two standard checks formed 13 clusters at a 40.88% similarity level. The result of the hierarchical cluster analysis indicated that 119 sorghum accessions were grouped into thirteen different clusters with a range of accessions that are categorized because of their similar performance for the trait under study (i.e. 5, 51, 4, 15, 8, 9, 13, 7, and 3 accessions per cluster respectively) from cluster number 1 up to 9, while the rest of the cluster numbers, 10, 11, 12, and 13, have only one accession per cluster. The clustering pattern indicated the existence of a significant amount of variability among the sorghum species. The two standard checks used were grouped into cluster 8 along with five other sorghum genotypes that performed in a similar way for the studied quantitative characters. Cluster 7 and 12 have the largest distance between them (56), while cluster 3 and cluster 5 have the smallest distance (13.5).

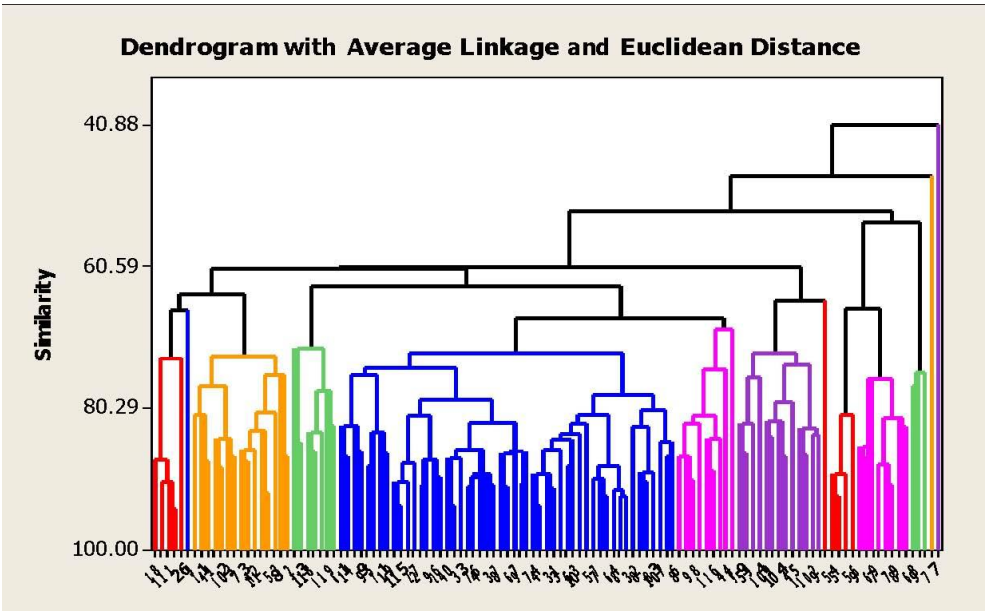

Figure 5. Cluster analysis of 119 sorghum genotypes

4. Conclusions

The diversity study of sorghum clearly indicates a diversity among the accessions. Landraces on a farm are acknowledged as the main source of genetic diversity for gene banks and breeding programmes, yet many studies have shown that genetic erosion is occurring on farmer varieties because of the utilization of high-yielding varieties. It has also been suggested, however, that only landraces which are not used for specific reasons are subjected to genetic erosion, while those which are (and have been for years) selected by farmers for certain desirable traits are likely to survive on a farm alongside improved varieties.

Based on all the parameters used to see if there was diversity among the sorghum accessions, the tested genotypes showed genetic variability for the traits considered. 119 genotypes are grouped into 13 cluster groups, which consists of 51 genotypes for the largest cluster and a single accession for four cluster groups (clusters 10, 11, 12, and 13), having different values of squared distance for each cluster group ranging from 13.5 to 56, which clearly shows that there exists a diversity of the sorghum genotypes.

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