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Research Article

Genetic Diversity of South Chadian Sorghum Landraces Assessed Through Quantitative and Qualitative Traits

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Abstract

Plant genetic resources and germplasm are fundamental sources for plant breeding, and the assessment of the genetic diversity among germplasm accessions is useful to facilitate the more efficient use of plant genetic resources. The current study was carried out to estimate genetic variability, heritability and genetic advance to select genotypes and traits for breeding. In the experiment undertaken, fifty-three sorghum landraces were evaluated for selected seven qualitative and fourteen quantitative traits using randomized complete block design in three repetitions. There were differences ($p< 0.001$) among landraces for all assessed traits indicating a high degree of variability. Higher genotypic coefficient of variation and phenotypic coefficient of variation were observed for grain weight of main panicle, number of leaf remain green and weight of main panicle. Estimates of phenotypic variances were higher than genotypic variance for all the studied quantitative traits. High heritability coupled with high genetic advance as per cent of mean was observed for majority of assessed traits. This study allowed noting a positive relationship between number of day to flowering with plant height and stay green, and a negative correlation between plant height and weight of main panicle. A dendrogram revealed four main clusters of genotypes. The D^2 statistics confirmed the highest inter-cluster distance between all clusters. This indicated existence of the possibility to improve genotypes through hybridization from any pair of clusters.

Keywords: agro-morphology; genetic diversity; *Sorghum bicolor*; heritability, genetic advance.

Introduction

Sorghum [*Sorghum bicolor* (L.) Moench] is a suitable crop for dry land farming agriculture owing to its wide adaptability and tolerance to adverse conditions as compared to other food crops. It is the fifth most important cereal crop worldwide after wheat, rice, maize and barley and is grown in at least 86 countries, in an area of 38 million hectares and with annual grain production of about 58 million tons (Tesfamichael *et al.*, 2015). Sorghum is a staple food crop in Chad with an annual grain production of about 946,295 tons (DSA, 2018).

Sorghum bicolor L. Moench was domesticated more than 5000 years ago, probably in the areas that now correspond to southern Sudan and Ethiopia (Doggett, 1988). The center of diversity both for the cultivated and wild sorghum lies in the Northeast quadrant of Africa, an area that extends from Ethiopia through the Sudan to Chad (Harlan, 1975; Mann *et al.,* 1983). In Chad, the landraces grown there are adapted to the multiple ecological conditions and the various production objectives of the farmers. But the grain sorghum yields are very low far below the genetic potential of the crop

The wide diversity plays an important role in domesticating, selecting, conserving and using plant genetic resources. Genetic variation in crop plants is essential for crop improvement. Maintenance of genetic diversity within and among crop species is crucial for sustainable agriculture, especially under low-input production conditions in marginal environments (Worede, 1993).

Unfortunately, there is a significant loss of genetic diversity of sorghum in Chad that can even reach, in some cases, a loss of 71% of overall diversity in a village (Gapili and Djinodji, 2016). Thus, in order to preserve sorghum landraces from Chad against genetic erosion and understanding methods for managing their diversity by the farmers in the Sudanese zone of Chad, surveys and collections have been carried out and allowed to collect grain sorghum accessions (Gapili and Djinodji, 2016), sweet sorghum accessions (Gapili *et al.*, 2016a) and dry-season sorghum accessions (Gapili *et al*., 2016b) managed by the farmer.

Genetic resources are the most valuable and essential basic raw material to meet the current and future needs for genetic improvement of any crop (Kaur *et al*., 2018). The phenotype is the first and easiest approach for the appraisal of genetic diversity in plant genetic resources and useful as a guide to follow up characterization and evaluation studies. Heritability estimates provide authentic information about a particular genetic attribute which will be transmitted to the successive generations and constitute an efficient guide for breeders in the choice of parents for crop improvement programs (Rafi and Nath, 2004).

The objective of this study was to assess the level of genetic diversity present among landrace of sorghum from Logone Oriental and Moyen Chari Region using morphological and agronomic traits.

Material and Methods

Plant Material

A total of 52 sorghum landraces, collected in the Sudanese zone collection, of which 33 are from Logone Oriental region and 19 from the Moyen Chari region were used in this current study (table 1). The genotypes of this collection were carried out in February 2015, with the objective of collecting, conserving and using plant genetic diversity and were conserved in the germplasm of Bébédjia. For each landraces only one panicle was sampled and gathered to constitute the collection (Gapili and Djinodji, 2016).

Table 1: Plant material and origin of genotypes

Regions prospected	**Villages**	**Number of accessions**
Logone Oriental	*Kamkoutou*	5
	Timbéri	9
	Mbanguirati 2	9
	Maïmbombaye	8
	Bekodo 2	2
Total 1		*33*
Moyen Chari	*Guilagonderé*	7
	Kobdogué	4
	Djoli	8
Total 2		*19*
Total 1+2		**52**

Experimental Design and Data Collection

The field experiment was conducted at the experimental station of Bébédjia, (9°55'N Latitude North and 15°8' Longitude East), at Chadian Institute for Research Agronomic for Development, under rain-fed conditions of 2016, with 1166 mm of main annual rainfall. The plants were grown in randomized block design with three repetitions and the plant received normal cultural operations and fertilizer applications (100 kg.ha^{-1} NPK-15-15-15). Thus, the seeds were planted at a depth of 5 cm in 80 cm inter row spacing and 30 cm intra row spacing. At growth stage, plants were thinned to one plant per hole.

A total of 14 quantitative variables were observed throughout the plant development. Number of days to flowering (NDF) was measured on a plot basis as the number of days from planting to when approximately 50% of the plants in a plot reached half bloom stage. The following traits were measured from 6 randomly selected plants. Leaf length (LEL) was measured as the length between the collar and the tip of leaf; leaf width (LEW) was recorded as the width of the largest section of the leaf. Both LEW and LEL were measured on the top third leaf at dough stage. Number of leafs remaining green (NLG) were accounted at grain filling period. At maturity, following traits were measuring: plant height (PTH) measured from the base of the plant to the tip of the panicle in cm at maturity; number of internode (NIN); internode length (INL) was recorded as the mean of length of the third and fifth internodes; panicle length (PAL) measured from the base of the panicle to the tip (cm); panicle width (PAW) measured in the widest diameter of the panicle (cm); stay green (STG) represented the percentage of the number of leafs remaining green on the total number of leafs. Weight of main panicle (WPA) was measured as the weight of the un-threshed head, and grain weight of main panicle (GWP) was measured as the weight of the seed threshed from individual panicles. Thousand grain weight (TSW) was recorded as the weight of one thousand kernels from bulk seeds from all heads in each plot. Potential yield (PY) was obtained by multiply the mean value of grain weight of main panicle (GWP) by the number of plant per hectare.

The qualitative data includes type of panicle was categorized as straight or crossed. Panicle Compactness and shape was recorded as loose or compact. The colors of the grains and glumes were examined and recorded. Some variables, such as the exertion of the panicle, the shape of the peduncle, shape and endosperm texture of grain, length and hairiness of glumes and the rotation of grain, were used to determine botanical races of landraces studied, according to the keys of Harlan and De Wet (1972).

Statistical Analysis

An analysis of variance (ANOVA) was carried out to assess the genotype effect. R^2 was calculated for each trait to measure how close the data are to the fitted regression line. Relationships between these traits were investigated using the Pearson correlation test. All accessions were subsequently submitted to Principal Component analysis and then some traits were extracted to build the dendrogram based on Euclidean distance between individuals. Multivariate analysis was done with the Mahalanobis D^2 statistic. Phenotypic and genotypic variances (Vg and Vp), genotypic and phenotypic coefficients of variation (GCV and PCV), Heritability in broad sense (H^2), genetic advance (GA) and genetic advance as per cent of mean (GAM) were estimated following the formula given by Hosseini *et al.* (2012). All of genetic parameters were estimated using the following formula:

$$Vg = (MSg - MSe)/r$$

$$Vp = Vg + (MSe/r) = MSg/r$$

$$GCV\ (\%) = \frac{\sqrt{Vg}}{x} \times 100$$

$$PCV\ (\%) = \frac{\sqrt{Vp}}{x} \times 100$$

$$H^2\ (\%) = \frac{Vg}{Vp} \times 100$$

$$GA = H2 \times k\sqrt{Vp}$$

$$GAM = \frac{GA}{x} \times 100$$

Where, MSg = mean square of genotypes; MSe = mean square of error and r = number of replications; $\sqrt{Vg}$ = genotypic standard deviation; $\sqrt{Vp}$ = phenotypic standard deviation; X = general mean of the character and k = Selection differential which is equal to 2.06 at 5% intensity of selection. The software XLSTAT-pro version 7.1 and GenStat 12th Edition were used to perform the data analysis.

Results

Assessment of Agro-Morphological Traits

Table 2 presents the qualitative characteristics observed in the collection. The mostly straight panicles (94%) have various shapes, ranging from the loose type (4%) to the compact type (37%) with semi-loose or semi-compact forms (59%). Glumes range from red (47%) to black (30%) and straw (23%). The landraces with red color of grain were most large (67%). These grains of different colors were predominantly vitreous (78%). The landraces whose glumes had aristation represented 63% of the assessed collection. The landraces of this current study were divided into three races, of which *Bicolor* race (11%), *Caudatum* race (85%) and *Dura* race (4%).

Table 2: Frequency distribution of seven qualitative traits for 52 sorghum genotypes assessed

Traits observed	Score	Frequency
Type of panicle	Straight	94%
	Awry	6%
Panicle compactness	Compact	37%
	Semi compact	59%
	Loose	4%
Glume color	Straw	23%
	Black	30%
	Red	47%
Grain color	White	33%
	Red	67%
Endosperm texture	Floury	22%
	Vitreous	78%
Glume hairiness	Existing	63%
	None	37%
Race	*Bicolor*	11%
	Caudatum	85%
	Durra	4%

Descriptive statistics for different quantitative traits were given in Table 3. Highly significant differences ($p < 0.001$) were observed among the landrace for all traits assessed, except for the leaf width which showed significant difference at 1% probability. Most of this variability was well explained by the "accession" factor ($R^2 \geq 48\%$). The traits, panicle width (CV = 30.15%), number of leaf remaining green (CV = 34.13%), grain weight of main panicle (CV = 59.14%), weight of main panicle (CV = 34.71%) and yield potential (CV = 53.12%) showed the highest coefficients of variation (CV> 30%) indicating a large variation among accessions for these traits. Conversely, there was a mean value of coefficient of variation (10% < CV <30%) for the rest of traits showing a means variation between accessions for these traits.

The number of days to flowering ranged from 58 to 127 days with an average of 99.75 days. The mean plant height ranged from 101.11 to 462.22 cm. The number of internode varied from 5.44 to 24.56, with the length of third internode under panicle very variable ranging from 9.89 to 32.22 cm. The dimensions of the leaves vary between 45.89 and 83 cm (for length) and 5.06 to 11.22 cm (for width). The potential yield varied from 0.27 to 3.11 $Mg.ha^{-1}$, with an average of 1.3 $Mg.ha^{-1}$. The stay green, which measures the proportion of plant leaves that remain green during seed filling, ranged from 31% to 81% with an average of 57%.

Assessment of Heritability, Phenotypic and Genotypic Coefficients of Variations

Estimates of genotypic (Vg) and phenotypic variances (Vp), genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), broad sense heritability (H^2), genetic advance (GA) and genetic advance as percentage of the mean (GAM) varied for all traits (Table 4). The result showed in general the phenotypic variances were higher than the genotypic variances for all assessed traits. Higher genotypic and phenotypic variances where recorded with plant height, respectively 3542.2 and 4066.8, followed by number of day to flowering (224.75 and 229.35), weight of principal panicle (168.4 and 223.38), and grain weight of the main panicle (137.96 and 157.98). Genotypic and phenotypic coefficients of variation were ranged respectively from 5.92 to 38.61% and from 8.03 to 41.31%. The genotypic and phenotypic coefficients of variation were high for potential yield (38.61% and 41.31%), followed by grain weight of the main panicle (37.05 and 39.64), number of leaf stayed green (24.48% and 26.2%) and weight of main panicle (21.65% and 24.94%). Estimates of the phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV) for all traits.

The heritability in broad sense (H^2) estimate varied from 49.98 to 98.02%, respectively for leaf width and number of day to flowering. The high heritability was recorded for the number of days to flowering (98.02%), grain weight of main panicle (87.33%), potential yield (87.33%), number of leaf remaining green (87.26%), plant height (87.1%), number of internode (81.65%), thousand grains weight (78.95%), panicle length (76.7%), weight of main panicle (75.4%), panicle width (71.81%) and internode length (67.34%), while it was moderate for stay green (54.38%), leafs length (54.3%) and width (49.98%).

Genetic advance expressed as percent of mean (GAM) have values ranged from 8.98 to 74.32%, respectively for leaf length and potential yield. The highest genetic advance expressed as percent of mean (GAM > 20%) were recorded for all assessed traits except for thousand grains weight (19.76%), stay green (14.8%) and leaf width (13%) for which they were moderate (20% < GAM < 10%). The lower GAM in this study was only scored for leaf length (8.98%).

Table 3: Analysis of variance for 14 quantitative characters in 52 sorghum landraces

Traits	Minimum	Maximum	Mean	CV (%)	R² (%)	F
PTH (cm)	101.11	462.22	327.8±82.8	25.26	78	7.22^{***}
LEL (cm)	45.89	83	63.5±6.6	10.43	51	2.11^{***}
LEW (cm)	5.06	11.22	7.1±1.2	16.49	48	1.86^{**}
PAL (cm)	14.22	42.22	23.9±5.6	23.44	67	4.04^{***}
PAW (cm)	4.44	17.78	8.2±2.5	**30.15**	61	3.19^{***}
NIN	5.44	24.56	14.8±3.9	26.06	72	5.09^{***}
NLG	2.22	13.22	8.7±3	**34.13**	78	7.23^{***}
INL (cm)	9.89	32.22	18.2±4.2	23.39	60	2.97^{***}
STG (%)	31	81	57±0.1	17.18	52	2.15^{***}
WPA (g)	21.63	120	59.9±20.8	**34.71**	61	3.17^{***}
GWP (g)	6.44	98.98	31.7±18.7	**59.14**	66	3.88^{***}
TGW (g)	14.76	34.6	25.2±4	15.76	70	4.72^{***}
NDF (days)	58	127	99.7±19.7	19.74	96	47.30^{***}
PYI ($Mg.ha^{-1}$)	0.27	3.11	1.3±0.7	**53.12**	66	3.88^{***}

**: p< 0.01; ***: p< 0.001; CV: coefficient of variation; R^2: R squared; PTH: plant height; LEL: leaf length; LEW: leaf width; PAL: panicle length; PAW: panicle width; NIN: number of internode; NLG: number of leafs remaining green; INL: internode length; STG: stay green; WPA: weight of main panicle; GWP grain weight of main panicle; TGW: Thousand grain weight; NDF: number of days to flowering; PYI: Potential yield

Table 4: Estimate of genetic parameters of 52 sorghum landraces

Traits	**Vg**	**Vp**	**GCV (%)**	**PCV (%)**	**H^2 (%)**	**GA**	**GAM (%)**
PTH (cm)	3542.4	4066.8	18.16	19.46	**87.1**	114.43	**34.91**
LEL (cm)	14.09	25.96	5.92	8.03	54.3	5.70	8.98
LEW (cm)	0.4	0.81	8.95	12.66	49.98	0.9	13.0
PAL (cm)	14.21	18.52	15.78	18.0	**76.7**	6.80	**28.47**
PAW (cm)	2.59	3.60	19.72	23.27	**71.81**	2.81	**34.42**
NIN	7.29	8.93	18.21	20.1	**81.65**	5.03	**33.89**
NLG	4.50	5.16	24.48	26.20	**87.26**	4.08	**47.10**
INL (cm)	7.15	10.61	14.72	17.94	67.34	4.5	**24.89**
STG (%)	0.003	0.01	9.74	13.21	54.38	0.08	14.80
WPA (g)	168.4	223.38	21.65	24.94	**75.40**	23.21	**38.73**
GWP (g)	137.96	157.98	37.05	39.64	**87.33**	22.61	**71.32**
TGW (g)	7.42	9.40	10.80	12.15	**78.95**	4.99	19.76
NDF (days)	224.79	229.35	15.0	15.18	**98.02**	30.58	**30.65**
PYI ($Mg.ha^{-1}$)	0.24	0.27	38.61	41.31	**87.33**	0.94	**74.32**

PTH: plant height; LEL: leaf length; LEW: leaf width; PAL: panicle length; PAW: panicle width; NIN: number of internode; NLG: number of leafs remaining green; INL: internode length; STG: stay green; WPA: weight of main panicle; GWP grain weight of main panicle; TGW: Thousand grain weight; NDF: number of days to flowering; PYI: Potential yield; Vg: genotypic variance; Vp: phenotypic variance; GCV: genotypic coefficient of variation; PCV: phenotypic coefficient of variation; H^2: Heritability in broad sense; GA: genetic advance; GAM: genetic advance as per cent of mean

Correlation Among Traits Assessed

Pearson's Correlations among the traits assessed are reported in Table 5, based on the significant levels of 5% ($p < 0.05$) and 1% ($p < 0.01$). Plant height was significantly and positively correlated with panicle length (r=0.63), number of internode (r=0.75), internode length (r=0.36), stay green (r=0.32) and number of days to flowering (r=0.69); but was negatively and non-significantly correlated with leaf width (r=−0.22), weight of main panicle (r=−0.22) and potential yield (r=−0.23). The number of days to flowering was significantly and positively correlated with panicle length (r=0.3), number of internode (r= 0.85) and stay green (r= 0.69); but was negatively correlated with panicle width (r= −0.29). Potential yield was significantly and positively correlated with leaf width (r= 0.49), stay green (r= 0.32), weight of main panicle (r= 0.93) and grain weight of main panicle (r= 0.39). Stay green was positively correlated with plant height (r= 0.32), number of internode (r= 0.61), number of day to flowering (r = 0.69), potential yield (r = 0.32), but was negatively correlated with panicle width (r= −0.31) and internode length (r= −0.39).

Principal Component Analysis of Traits

Principal component (PC) analysis showed that out of the seven the first four explained majority of the total variation (table 6). These PCs with Eigenvalue > 1 contributed 80.36% of total variability. Than the PC I contributed maximum towards the variability (31.44 %), followed by the PC II (24.68 %), PC III (15.21 %) and PC IV (9.02 %). Number of leaves remaining green (r = 0.45), number of internode (r = 0.42), stay green (r = 0.4) and number of days to flowering (r = 0.39) were the traits that positively contributed most to the variation in the first PC. The traits weight of main panicle (r = 0.43), grain weight of main panicle (r = 0.39) and potential yield had (r = 0.42) relatively large positive influence on the second component, conversely, plant height (r = −0.38), panicle length (r = −0.33) and internode length (r = −0.23) had negative influence. Internode length (r = 0.38), panicles width (r= 0.4) and length (r = 0.38) were the traits that contributed most to the variation in the third PC. The fourth PC was explained mainly and positively by leaf width (r = 0.38) and length (r = 073) and negatively by thousand grains weight (r = −0.42).

Table 5: Pairwise correlation coefficient fourteen quantitative traits of fifty two sorghum landraces

	PTH	**LEL**	**LEW**	**PAL**	**PAW**	**NIN**	**INL**	**STG**	**WPA**	**GWP**	**NDF**
LEL	-0.19										
LEW	-0.22^{*}	**0.34^{*}**									
PAL	**0.63^{**}**	0.24^{*}	0.08								
PAW	0.07	0.05	0.02	**0.28**							
NIN	**0.75^{**}**	0.00	0.18	**0.5**	-0.15						
INL	**0.36^{*}**	0.16	0.01	**0.55^{**}**	**0.49^{**}**	0.07					
STG	**0.32^{*}**	-0.1	0.12	0.08	**-0.31^{*}**	**0.61^{**}**	**-0.39^{*}**				
WPA	-0.22^{*}	-0.01	**0.5^{**}**	-0.24^{*}	-0.17	0.16	-0.19	**0.39^{*}**			
GWP	0.18	-0.07	0.09	**0.3^{*}**	0.09	0.22^{*}	0.17	0.18	0.23^{*}		
NDF	**0.69^{**}**	-0.07	-0.09	**0.3^{*}**	**-0.29^{*}**	**0.85^{**}**	-0.22	**0.69^{**}**	0.04	0.12	
PYI	-0.23	-0.01	**0.49^{**}**	-0.16	-0.13	0.11	-0.11	**0.32^{*}**	**0.93^{**}**	**0.39^{*}**	-0.003

*: $p< 0.05$; **: $p< 0.01$; PTH: plant height; LEL: leaf length; LEW: leaf width; PAL: panicle length; PAW: panicle width; NIN: number of internode; INL: internode length; STG: stay green; WPA: weight of main panicle; GWP weight of grain of main panicle; NDF: number of days to flowering; PYI: Potential yield

Table 6: Eigenvalue and proportions of variability as assessed by traits contributed to four PCs

Principal Component	**F1**	**F2**	**F3**	**F4**
Eigen value	4.4	3.455	2.13	1.26
Proportion of variance (%)	31.44	24.68	15.21	9.02
Cumulative variance	31.44	56.12	71.33	80.36
PTH (cm)	0.28	**-0.38**	0.06	-0.17
LEL (cm)	-0.04	0.00	0.25	**0.73^{*}**
LEW (cm)	0.13	0.27	0.34	**0.38^{*}**
PAL (cm)	0.16	**-0.33**	**0.38^{*}**	0.09
PAW (cm)	-0.14	-0.14	**0.40^{*}**	-0.18
NIN	**0.42^{*}**	-0.19	0.04	0.09
NLG	**0.45^{*}**	-0.09	-0.07	0.09
INL	-0.07	**-0.23**	**0.51^{*}**	-0.12
STG	**0.40**	0.05	-0.19	0.03
WPA (g)	0.21	**0.43***	0.11	-0.05
GWP (g)	0.22	**0.39**	0.17	-0.14
TGW (g)	0.16	0.01	0.29	**-0.42^{*}**
NDF (days)	**0.39^{*}**	-0.20	-0.20	0.06
PYI ($Mg.ha^{-1}$)	0.21	**0.42^{*}**	0.22	-0.16

PTH: plant height; LEL: leaf length; LEW: leaf width; PAL: panicle length; PAW: panicle width; NIN: number of internode; NLG: number of leafs remaining green; INL: internode length; STG: stay green; WPA: weight of main panicle; GWP grain weight of main panicle; TGW: Thousand grain weight; NDF: number of days to flowering; PYI: Potential yield

Morphological Cluster Analysis

The hierarchical clustering using Euclidian distance with mean link method grouped 52 sorghum landraces into four clusters (Figure 1). The mean traits values of the genotypes in each cluster are given in table 7. Cluster I was composed of 6 landraces and was further subdivided into two sub clusters, each of them was composed of 3 genotypes. The comparison of traits between clusters showed that cluster I had productive genotypes which had wide leaf and panicles and with plant had intermediate height.

Cluster II was made up of 18 landraces, with were classified into two clusters, one of two clusters, sub-cluster IIa had 6 genotypes and sub-cluster IIb had 12 genotypes. The genotypes of this cluster had highest plant height, longest panicle length, late flowering, with lower grain weight of main panicle.

Cluster III was the largest cluster, which included 21 landraces and was categorized into two sub-clusters. The sub-clusters IIIa had seven genotypes and the sub-cluster IIIb had 14 genotypes. This cluster had the mean values of all assessed traits, but possessed the best grain weight of main panicle. The sub-cluster IIa was composed with genotypes had best grain weight of main panicle and the best potential yield. The genotype 48 had best grain weight of panicle (74.7 g) and best potential yield (3.114 $M.g^{-1}$) of collection, followed by the genotype 13 (59.9 g and 2.495 $M.g^{-1}$) and genotypes 47 (57.2 and 2.382 $M.g^{-1}$). This sub-cluster presented a real interest for a breeding program.

Cluster IV consisted of seven landraces and was subdivided into to sub-clusters. The first sub-cluster had six genotypes the other had only one genotypes. This cluster composed of genotypes which had weakness value of all traits assessed. The genotypes of this cluster were early flowering and had weakness grain weight of main panicle.

Table 8 showed the repartition of cultivar in different cluster. The cultivars of Bekodo 2 were found only in cluster 2, the rest of cultivar from others villages were found in all clusters or at least in two clusters. It has specific distribution of cultivars in cluster regardless of their origin.

Inter-cluster divergences existed (Table 9). In fact, the high inter-cluster distance occurred between clusters IV and II, indicating greater diversity between genotypes belonging to these clusters. The minimum inter-cluster distance was between clusters III and II, indicating a close relationship between members of these clusters. However, the study showed too there were not the intra-cluster divergences, indicating a close relationship among members of same group. The statistical value of Fisher showed the significant difference ($p < 0.0001$) between all groups indicating that each cluster was statistically different of the others clusters. Each cluster constituted by the genotypes which had a close relationship.

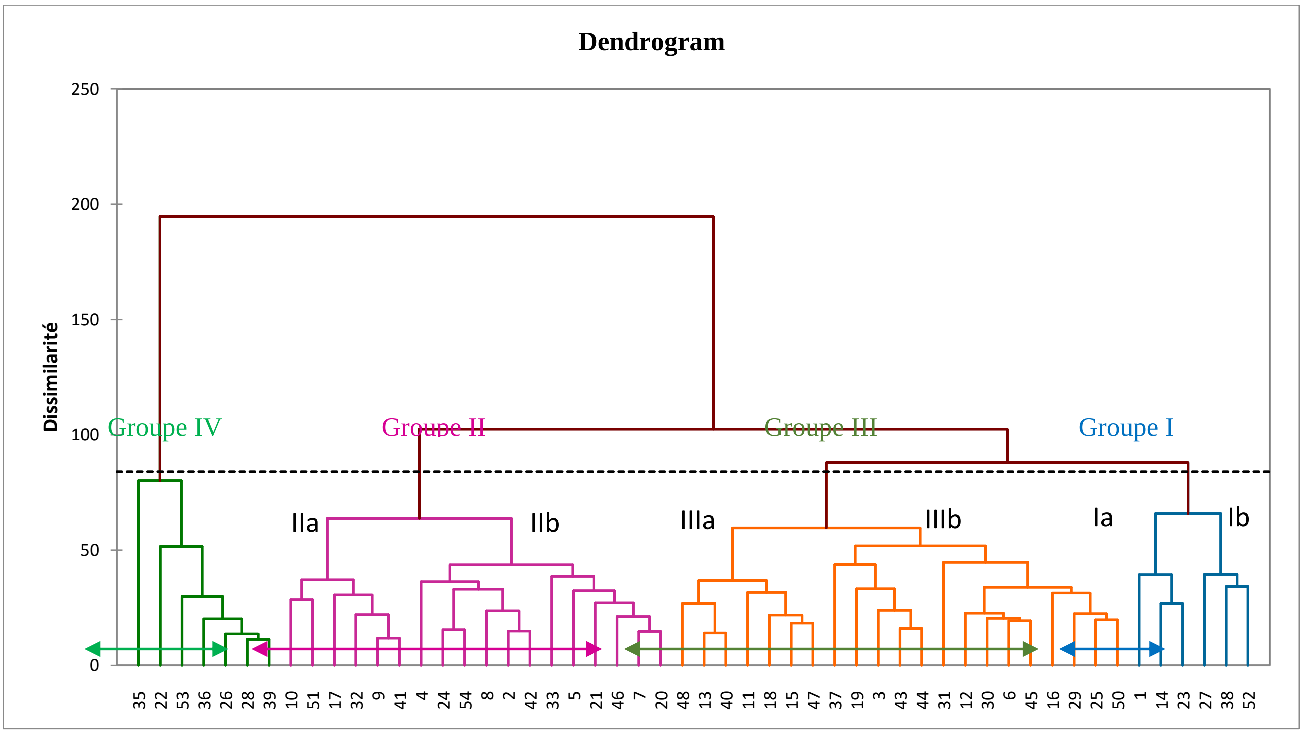

Fig. 1: Grouping of 52 sorghum landraces on the basis of the standardized squared Euclidean distance using mean link's hierarchical clustering method.

Table 7: Comparison of agro-morphological traits in four clusters from Factorial Discriminant Analysis

Traits	**Cluster 1**	**Cluster 2**	**Cluster 3**	**Cluster 4**
PTH	263.1 ± 21.4	**409.5 ± 30.5**	336.6 ± 24	**167.3 ± 33.6**
LEL	66.6 ± 5.4	62.6 ± 4.8	62.6 ± 8.2	65.6 ± 4.7
LEW	7.5 ± 1.2	6.5 ± 1.1	7.4 ± 1.2	7.2 ± 1.2
PAL	20.9 ± 1.9	**27.7 ± 5.2**	23.8 ± 5.3	17.9 ± 1.8
PAW	9.3 ± 4.9	8.2 ± 2.1	7.8 ± 1.7	8.2 ± 2.9
INL	16.4 ± 7.5	**18.8 ± 3.4**	**18.8 ± 3.9**	16 ± 3.3
STG	0.6 ± 0.1	0.6 ± 0.1	0.6 ± 0.1	0.4 ± 0.1
GWP	29.9 ± 15	**16.8 ± 7.6**	**40.3 ± 16**	27.7 ± 7.4
TGW	25.3 ± 4.2	24.6 ± 3.7	**26.4 ± 4.1**	**22.6 ± 3**
NDF	92.2 ± 21.5	**111.8 ± 11.2**	104.5 ± 11.2	**63.5 ± 5.3**
Number of accessions	6	18	21	7

PTH: plant height; LEL: leaf length; LEW: leaf width; PAL: panicle length; PAW: panicle width; INL: internode length; STG: stay green; GWP grain weight of main panicle; TGW: Thousand grain weight; NDF: number of days to flowering

Table 8: Distribution of cultivars by origin in different clusters

Region	**Village**	**Cluster I**	**Cluster II**	**Cluster III**	**Cluster IV**	**Total**
Logone Orientale	Kamkoutou	1	3	1	0	5
	Timberi	1	4	4	0	9
	Mgamguirati 2	1	3	4	1	9
	Maïbombaye	1	1	4	2	8
	Bekodo 2	0	2	0	0	2
Moyen Chari	Guilagonderé	1	1	2	3	7
	Kodogué	0	1	3	0	4
	Djoli	1	3	3	1	8
Total		6	18	21	7	52

Table 9: Average intra- (bold) and inter cluster divergence, Fisher distance and P-value

Cluster (from/To)	**D^2 value**	**F-value**	**P-value**
Cluster I – Cluster II	45.084	15.984	< 0.0001
Cluster I – Cluster III	16.485	6.374	< 0.0001
Cluster I – Cluster IV	27.136	7.123	< 0.0001
Cluster II – Cluster III	12.935	9.917	< 0.0001
Cluster II – Cluster IV	122.863	48.611	< 0.0001
Cluster III – Cluster IV	75.044	32.722	< 0.0001

Discussion

The primary objective of the current study was to assess the agronomical and phenotypic diversity of sorghum landrace of South of Chad. The phenotype is the first approach to appreciate the genetic diversity in plant genetic resources. The result for qualitative traits indicated that the accessions of this collection belonged in three of the five cultivated global sorghums as proposed by Harlan and de Wet (1972). Most of them were from *Caudatum* represented 85 % of the landraces assessed, so the *Kafir* and *Guinea* races did not find in the collection. The presence of the three races in the small amount of landraces (52 genotypes) indicates the presence of high genetic diversity in these two regions. According to Teshome *et al.* (1997), farmers deliberately maintain a wide diversity of Sorghum landraces. Farmers' practices may also influence the handling and conservation of the genetic material on their fields (Mofokeng *et al.*, 2017).

The current study showed that the majority of landraces had straight panicle, possessed white grains, which were most vitreous. Trouche *et al.* (2001) reported that farmers' demand for new varieties is higher for white sorghum. Sorghum is used in human food, and consumer taste is more pronounced for vitreous white sorghum.

The analysis of variance showed high variability well explained by the “accession” factor, and all of the quantitative traits assessed allowed to seeing the high genetic diversity ($p < 0.001$) between landraces indicating the sufficient amount of variability existed for all the traits and considerable improvement could be achieved in most of these traits by selection (Yogeshkumar *et al.*, 2018).

For all the traits under study, phenotypic variances were higher than the corresponding genotypic variances showing the environmental factors influence the expression. According to Ram and Sigh (1993) the difference between genotypic and phenotypic variance indicates the contribution of environmental variance. The smaller the difference in values between phenotypic and genotypic variance, the lesser will be the environmental effect on the character. Similarly, the higher the values, the greater will be the environmental effect.

Coefficient of variations measures the amount of variability present in the characters but it alone is not sufficient to determine the expected progress that could be made in quantitative traits (Falconer, 1981). High PCV and GCV for the traits such as potential yield, grain weight of main panicle, number of leaf remaining green and weight of main panicle, indicating large scope of selection for these characters; while other characters had moderate (10-20%) or low GCV and PCV values indicating less variability and need for creation of variation through hybridization (Singh and Verma, 2018). Phenotypic coefficient of variance was found higher than genotypic coefficient of variance for all studied traits indicates the environmental influence on the expression of these traits. However, the presence of comparatively little difference between PCV and GCV estimates for all characters indicated that variability was primarily due to genotypic differences and that scope for selection based on these components would be much greater in sorghum. According to Adhikari *et al.* (2018), small difference between GCV and PCV indicated that there was very little environmental influence on these traits and cannot be improved by providing favorable environment. In other hand, phenotypic variability is a reliable measure of genotypic variability (Kaur *et al.*, 2018).

Heritability is a useful quantitative parameter, which considers the role of heredity and environment determining the expression of a trait (Allard, 1960). Selection is favored when a major proportion of a large amount of phenotypic variability is due to heritable variation. H^2 is hence classified as low, below 30%), medium between 30 and 60% and high, above 60% (Reddy *et al.*, 2013). In the present study high estimates of heritability in broad sense ($H^2 > 60\%$) was observed for almost all the traits except for stay green, leaf length and leaf width, which exhibited moderate heritability (49-60%). High H^2 in broad sense indicated that, environment factors did not affect greatly the phenotypic performance of these traits and the traits are under genetic control (Mukesh *et al.*, 2019) and expected to give constant results under simple selection. Even though heritability estimates represent the heritable portion of variation, they do not indicate the effectiveness with which selection of a phenotype could be made based on the phenotypic performance (Johnson, 1955). High heritability alone is not enough to make efficient selection in advanced generations unless accompanied by substantial amount of genetic advance (Burton, 1952).

The genetic advance is a useful indicator of the progress that can be expected as result of exercising selection on the pertinent population (Reddy *et al.*, 2013). H^2 coupled with genetic advance would give a more reliable index of selection value (Johnson *et al.* 1955). Higher heritability and genetic advance were recorded by plant height, panicle length and width, number of internode, number of leaf remaining green, internode length, weight of main panicle, grain weight of main panicle, number of days to flowering and potential yield, indicating the importance of additive gene action controlling these traits and hence selection based upon these characters would be effective. Simple selection therefore could be effective for improvement of these traits (Barcchiya *et al.*, 2018; Kumar *et al.*, 2019). High heritability (78.95%) with moderate genetic advance (19.76%) observed for thousand grain weights indicated the presence of both additive and non-additive gene effects. Atter *et al.* (2009) reported high heritability accompanied with moderate genetic gain pointed towards additive gene action which gave credence for successful breeding of these traits through selection. The last traits leaf length had moderate heritability with low genetic gain indicating the influence of environment.

The knowledge of correlation existing between different plant traits help the breeders to understand how the improvement of one trait can't influence the other, and how they finally affect grain yield. Information on significant correlation among the characters is important for initiation of breeding program as it provides an opportunity for selection of desirable genotypes with desirable traits concurrently (Mofokeng *et al.,* 2017). This study allowed noting marked relationships between the various traits measured. A positive relationship was found between plant height and number of day to flowering, and between stay green and number of day to flowering. This suggests that it is possible to develop hybrids with these traits. A negative correlation between plant height and weight of main panicle is beneficial when the goal is to develop short plant with the weighty panicle. Plant height was negative correlation with potential yield; this suggests that it is difficult to predict grain yield based on height of plant. This corroborates the earlier observations of Zongo (1991) and Barro-Kondombo (2010) but is contrary to those of Tesso *et al.* (2011) and Mofokeng *et al.* (2017), which found that grain yield was found to be positively correlated with plant height.

The foregoing results indicate that the Sorghum landraces are variable populations which group into four clusters. The dendrogram allowed observing a structuration of diversity. The different groups however did not correspond to the different origins. The clustering of cultivars regardless of origin showed the presence of genetic diversity among the accessions within and among the village studied. According to Manzelli *et al.* (2005), the clustering regardless of origin may also be due to gene flow from neighboring areas/provinces and sharing of seeds by farmers amongst themselves. Moreover, farmers share seeds and name the same accessions differently in various areas or regions (Chakauya *et al.,* 2006). Cluster III was the largest cluster, which included 21 landraces and was categorized into two sub-clusters. One of the two clusters, sub-cluster IIIa had seven genotypes which had the best grain weight of main panicle and the best potential yield. In sub-cluster IIIa, genotype 48 had best grain weight of panicle (74.7 g) and best potential yield (3.114 $M.g^{-1}$), followed by the genotype 13 (59.9 g and 2.495 $M.g^{-1}$) and genotypes 47 (57.2 and 2.382 $M.g^{-1}$). This cluster presented a real interest for a breeding program.

Conclusion

This study revealed high variability for both qualitative and quantitative traits between sorghum landraces. The high variability assessed in this collection is a good source of diversity to use in sorghum breeding programs. High heritability along with high genetic advance as per cent over mean for almost all traits assessed indicates involvement of additive gene in controlling gene responsible for these traits. Therefore, these characters could be improved through selection in segregating generations. Pearson correlation coefficient analysis revealed positive association between plant height and number of day to flowering and between stay green and number of day to flowering and a negative correlation between plant height and weight of main panicle, which could be beneficial when the goal is to develop short plant with the weighty panicle. The comparison of traits between clusters showed that cluster III had productive genotypes which had mean values of all assessed traits, but possessed the best grain weight of main panicle. This cluster presented a real interest for a breeding program.

Author's Contribution

G. Naoura and D. Reoungal designed the research plan; G. Naoura & M.A. Hassane performed experimental works & collected the required data. G. Naoura analysed the data; G. Naoura prepared the manuscript. All authors critical revised, finalized and approved the final form of the manuscript.

Conflict of Interest

The authors declare that there is no conflict of interest with present publication.

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