

African Crop Science Journal by African Crop Science Society is licensed under a Creative Commons Attribution 3.0 Uganda License. Based on a work at www.ajol.info/ and www.bioline.org.br/cs
DOI: <http://dx.doi.org/10.4314/acsj.v24i2.6>



GENETIC DIVERSITY AMONG SORGHUM LANDRACES OF SOUTHWESTERN HIGHLANDS OF UGANDA

R. AKATWIJUKA, P.R. RUBAIHAYO and T.L. ODONG
Makerere University, College of Agricultural and Environmental Sciences, School of Agricultural Sciences,
P. O.Box 7062, Kampala, Uganda

Corresponding author: akarogerz@gmail.com, akarogerz@yahoo.co.uk

(Received 6 January, 2016; accepted 14 May, 2016)

ABSTRACT

Sorghum (*Sorghum bicolor* L. Moench) is an economic and staple crop in sub-Saharan Africa. The genetic diversity in its germplasm is an invaluable aid for its crop improvement. The objective of this study was to assess the existing genetic diversity among sorghum landraces in the southwestern highlands of Uganda. A total of 47 sorghum landraces, collected from southwestern highlands of Uganda, were characterised using 12 qualitative and 13 quantitative traits. The study was conducted at Kachwekano Research Farm in Kabale District, at an altitude of 2,223 m above sea level, during growing season of December 2014 to August 2015. Panicle shape and compactness were the most varied qualitative traits. Grain yield (1.23 to 11.31 t ha⁻¹) and plant height (144.7 to 351.6 cm) were among quantitative traits that showed high variability. Days to 50% flowering (115 to 130 days) showed the least variability. Results of UPGMA cluster analysis generated a dendrogram with three clusters. Panicle weight, leaf width, stem girth, exertion length, peduncle length, panicle shape and compactness, glume colour and threshability were major traits responsible for the observed clustering (P<0.001). Principal Component Analysis revealed the largest variation contributors.

Key Words: Panicle morphology, *Sorghum bicolor*, traits

RÉSUMÉ

Le sorgho (*Sorghum bicolor* L. Moench) est une culture vivrière de grande consommation en Afrique au sud du Sahara. La diversité génétique au sein de son germplasm est d'une valeur incalculable pour la production de semences améliorées. L'objectif de la présente étude était d'évaluer la diversité existante au sein des cultivars des plateaux du Sud-ouest d'Ouganda. Au total, 47 accessions de sorgho, collectées des plateaux du Sud-ouest d'Ouganda, ont été caractérisées en se servant de 12 traits quantitatifs et de 13 traits qualitatifs. L'étude s'est déroulée à la ferme de recherche de Kachwekano dans le district de Kabalé, zone située à 2223m d'altitude, pendant la saison culturales de Decembre 2014 à Août 2015. La forme des panicules, et leur densité étaient les traits qualitatifs les plus diversifiés. Le rendement en grains (1,23 à 11,31 t ha⁻¹) et la hauteur des plants (144,7 à 351,6 cm) étaient les traits quantitatifs ayant présenté une grande variabilité. Le délai de 50% de floraison (115 à 130 jours) était le trait le moins variable. La classification numérique a généré un dendrogramme avec trois groupes. Le poids des panicules, la largeur des feuilles, la circonférence de la tige, la longueur des insertions, la longueur des pédoncules, la forme des panicules et leur densité, la couleur de la glume et la facilité au décorticage étaient les traits majeurs ayant contribué à la répartition en groupes (P<0.001). L'analyse en composantes principales a révélé les contributeurs à la plus grande variabilité.

Mots Clés: Morphologie de panicule, *Sorghum bicolor*, traits

INTRODUCTION

Sorghum (*Sorghum bicolor* L. Moench) is the fifth most commonly cultivated cereal crop in the world after wheat, rice, maize, and barley (Poehlman, 1994). It is adapted to a wide range of agro-ecologies and is produced from sea level to above 2,000 m elevation (Wortmann *et al.*, 2006). Sorghum has the largest genetic diversity of both cultivated and wild sorghum in Africa (de Wet and Harlan, 1971). Doggett (1970) reported that the great genetic diversity of *S. bicolor* was as a result of disruptive selection, isolation and recombination in the extremely varied habitats of northeast Africa and the movement of peoples carrying the species throughout the continent.

Watson and Eyzaguirre (2002) reported that genetic diversity is important in continuing the process of evolution, through farmer selection within crop diversity, to obtain suitable types under prevailing conditions and to ensure the crop's ability to adapt to changing conditions or requirements. Genetic diversity, therefore, is the foundation for crop improvement. Dudley and Moll (1969) reported three main phases in plant breeding programmes; namely the identification of the existing genetic variation in the breeding populations, selection of elites from the breeding populations and synthesis of the elite genotypes into a cultivar. Genetic diversity, therefore, provides the raw materials from which desirable alleles for improved agronomic traits of interest can be selected and subsequently incorporated into elite lines. Breeders need to decide on what combinations of traits to breed for, and for what environments; and all these depend on the available genetic diversity that confers the trait diversity in the breeding populations.

Determination of genetic diversity and relatedness has been achieved through use of morphological, biochemical and molecular characterisation approaches (Watson and Eyzaguirre, 2002). It was reported by Watson and Eyzaguirre (2002) that morphological characterisation is a highly recommended first step that should be made before in-depth biochemical or molecular studies are attempted. This is because of its various advantages, including the published descriptor lists which are readily available for most major crops, ability to

be carried out *in situ* (on-farm), being relatively inexpensive, and relatively easy to carry out. Watson and Eyzaguirre (2002) also reported that PCA of morphological characterisation results, could identify a few key or minimum descriptors that effectively account for the majority of the diversity observed, saving time and effort for future characterisation efforts. Bernardo (2010) reported that phenotypic characterisation is a quick tool in analysing the relative magnitude of additive, dominance and epistatic effects across unknown loci, without analysing for genotypic values of marker loci or quantitative trait loci.

In the highlands of southwestern Uganda, Nabimba *et al.* (2005) reported that, over 95% of the households grew sorghum for varying end uses that included production of alcohol, sweet beverage and local bread. Mbabwine *et al.* (2004) reported of the existence of many sorghum landraces in southwestern highlands of Uganda, which had never been characterised. Mbeyagala *et al.* (2012) in their study of molecular diversity among Sorghum landraces in Uganda, excluded sorghum in southwestern highlands of Uganda. So far, there is no available literature indicating previous characterisation of sorghum in the southwestern highlands of Uganda. The objective of this study, therefore, was to assess the existing genetic diversity among sorghum landraces in this agro-ecological zone so as to guide their future improvement and conservation strategies.

MATERIALS AND METHODS

The study area, the southwestern highlands of Uganda comprising of Kabale, Kisoro, Kanungu and Rukungiri districts, lie at 01 15 37S, 29 58 43E, and altitudes ranging from 1,100 to 4,000 m above sea level, with mean annual rainfall ranging from 700 to 2100 mm. The rainfall is bimodal and precipitation is usually gentle and evenly distributed. Temperatures range from 7 to 23°C. The region covers a total land area of approximately 5,180 Km² excluding open water (NEMA-Uganda, 2009).

The study materials consisted of 47 cultivars collected from farmers of the highlands of southwestern Uganda, during sorghum harvesting months of July and August 2013. Each

selected farmer, based on his/her experience in growing sorghum, was asked to provide 2 mature panicles of every type of sorghum grown. Each farmer named the sorghum type, source of seed and period of time the farmer has been engaged in growing the reported cultivar.

The collected materials were evaluated in a randomised complete block design at Kachwekano Zonal Agricultural Research and Development Institute (KAZARDI), during sorghum growing season of December 2014 to August 2015. KAZARDI is located in the highlands of southwestern Uganda, at an altitude of 2,223 m above sea level, with a mean annual rainfall of 1,400 mm and temperature of 15 °C (NEMA-Uganda, 2009)

Sowing of the collected sorghum seed for evaluation was done on 28th January 2015, on 2.4 m by 1.4 m plots and path length of 1.5 m, with inter-row spacing of 60 cm and intra-row spacing of 20 cm at a depth of 10 cm. Sorghum was overplanted with a sowing density of two seeds per hole. Manual weeding was done three times during the crops' vegetative stages, at three weeks (18th February 2015) during which thinning was done leaving one health plant per hole. This spacing resulted into an estimated plant population of 83,333 plants per hectare. Further weeding was done after seven weeks (19th March 2015) and after fourteen weeks (12th May 2015) when the early flowering varieties started to boot. Booting stage was manifested by the appearance of flag leaf collar with the head developed and enclosed in the flag leaf sheath (Gerik *et al.*, 2003).

Data collection. Qualitative data on panicle shape and compactness, grain colour and shape, dorsal view, grain shape profile view, grain covering (%), glume hairiness, glume colour, threshability, peduncle exertion, peduncle shape, leaf midrib colour and number of grains per glume were collected, on five randomly selected plants from middle rows in each plot, following sorghum descriptors (Bioversity International, 2010). From the same plants, quantitative data were recorded on days to 50% flowering, plant height, number of leaves, length and width of third leaf from top of each sampled plant, stem girth, exertion length, peduncle length panicle length and width, panicle weight, and 100-seed weight. Days to 50%

flowering were counted from the day of sowing to when 50% of the plants had entered flowering stage, manifested by the appearance of yellow anthers on the tip of the panicle (Gerik *et al.*, 2003). Plant height was taken from the base of the plant to the tip of the head at physiological maturity attained when a black-layer appeared above the point of grain attachment in the floret near the base of the grain (Gerik *et al.*, 2003). Number of leaves was determined by counting all leaves from first to the flag leaf. Leaf length data were taken from the base to tip of the leaf, leaf width on the widest part of the same leaf, exertion length from ligule of flag leaf to base of panicle; and peduncle length from the last node of the stalk to the base of the panicle. Panicle length was recorded by measuring each panicle from its base to its tip, with its width measurements recorded at the widest part in natural position. Panicle and 100 seeds weight were taken after harvest. Panicle weight was used to determine yield per hectare by multiplying the average grain weight per panicle with the total number of plants in a hectare, at the plant spacing of 20 cm by 60 cm. Fernandez *et al.* (2012), in their study on grain sorghum response to row spacing and plant populations in the Texas coastal bend region used average sorghum yield per plant in estimating yield for the entire hectare.

Data analysis. Qualitative data were converted into scores by assigning each qualitative trait category a numerical value (Bernardo, 2010). Each studied sorghum variety was considered as a measurement unit and qualitative traits as measured or observed variables. For traits that exhibited variations within varieties, a dominant form of the trait was considered to represent that variety. Frequencies of occurrence of each qualitative trait were computed, using Microsoft Excel computer programme, and their percentages recorded. Quantitative data were analysed using mean as a measure of central tendency, and coefficient of variation as a measure of dispersion.

In order to determine the patterns of relationships between the evaluated sorghum landraces, Cluster Analysis using the unweighted Pair-group Method, using arithmetic averages (UPGMA) (Hair, 1995) was done, using the General Statistics (GenStat 14th Edition).

Clustering was based on Euclidean Distances among different sorghum landraces. In order to identify traits responsible for the largest variation, leading to different groupings in a dendrogram, Analysis of Variance (ANOVA) for the groups was carried out (Gelman, 2005). In order to identify the key contributors that effectively accounted for the majority of the observed diversity, Principal Component Analysis (PCA) was conducted (Jackson, 1991) for combined quantitative and qualitative data, and results of the first two PCs were used to generate a scatter plot based on PC coefficients (using GenStat 14th edition) as the first two PCs were reported by Jollie (2002) to account for the maximum amount of variation.

RESULTS

Qualitative traits. Morphological characteristics on the 47 sorghum landraces are presented in Table 1. There was high variability among 10 qualitative traits. The widest variability was recorded in panicle shape and compactness, with 53.1% of the evaluated landraces having semi-compact elliptic panicles. Grain was predominantly orange in colour, shaped convex when observed from dorsal view, and circular from profile view. Most of the cultivars had grain covered by glume to 50% level. Low haired and black glumes were observed in majority of the cultivars. Grain threshability was easy in most of the cultivars, with majority having erect peduncles. Leaf midrib colour and seeds per glume showed no variability

Quantitative trait variation. The results of descriptive statistics for quantitative traits are presented in Table 2. Exertion length, panicle weight, grain yield, plant height and panicle length were among the quantitative traits that showed high variability. Days to 50% flowering had the least variability.

The results of UPGMA hierarchical cluster analysis, based on both qualitative and quantitative traits are presented in Figure 1. All cultivars clustered into three groups at 82.5% similarity levels, with the smallest group having two cultivars. The largest group had 25 cultivars. Traits that caused the observed clustering are

presented in Table 3. Panicle weight, leaf width, stem girth, exertion length, peduncle length, panicle shape and compactness, glume colour and threshability significantly caused the observed clustering ($P < 0.001$).

Results of PCA are presented in Table 4. Seven PCs with Eigen values greater than one, accounted for 73.84% of the total variation. The first two PCs accounted for the largest variability (38.93%). The first PC accounted for 27.49% of variation and was loaded on exertion length, panicle weight, stem girth, width of third leaf from top and grain yield. Principal component 2 (PC2) accounted for 11.44% and was loaded on grain colour, peduncle shape, and plant height. Results of the scatter plot from the first two PCs are presented in Figure 2. The results indicated that the scattering of cultivars generally followed a similar trend with what was observed in the dendrogram (Fig. 1) under cluster analysis. For instance, cultivars 32 and 33, and cultivars 1 and 3 were grouped together in both the dendrogram (Fig. 1) and PCs plot (Fig. 2). Results of leaf midrib colour and seeds per glume were not included in the results of ANOVA (Table 3) and PCA (Table 4) because they showed no variability.

DISCUSSION

Qualitative traits. Variation in panicle morphology (Table 1) was a clear indicator for the existence of different sorghum races in this area. Harlan and De Wet (1972) classified sorghums into five races, bicolor, caudatum, kafir, durra and guinea with their hybrids on the basis of panicle, grain and spikelet morphology. Variation in panicle morphology also suggested cross pollination between cultivars growing together and a possibility of mutations. These races have overtime been subjected to farmer's selection based on perception for yield, adaptation and quality traits; giving rise to the variation exhibited in cultivar frequencies.

According to the principles of artificial selection (Yamasaki *et al.*, 2007), cultivars with preferred traits are selected by farmers, hence, their increased proportion relative to other cultivars. This may be the reason why 53.2% of the genotypes assessed had semi-compact elliptic panicles. The same reasons could have

TABLE 1. Frequencies of qualitative traits among sorghum landraces used in a study in the highlands of southwestern Uganda

Parameters	Qualitative trait	Score*	Percentage frequency
Panicle shape and compactness	Loose stiff branches	1	6.4
	Loose drooping branches	2	2.1
	Semi-loose stiff branches	3	19.2
	Semi-loose drooping branches	4	2.1
	Semi-compact elliptic	5	53.29
	Compact elliptic	6	4.3
	Compact oval	7	10.6
	Semi-compact oval	8	2.1
Grain Colour	Orange	1	51.1
	Red	2	42.6
	White	3	2.1
	Brown	4	4.3
Grain shape dorsal view	Dimple	1	2.2
	Convex	2	97.8
Grain shape profile view	Elliptic	1	8.5
	Circular	2	91.7
Grain covering (%)	Grain covering 25	1	2.1
	Grain covering 50	2	70.2
	Grain covering 75	3	23.4
	Grain covering 100	4	4.3
Glume hairiness	High	1	10.6
	Medium	2	6.4
	Low	3	66.0
	Absent	4	17.0
Glume colour	Black	1	70.2
	Brown	2	29.8
Threshability	Easy	1	76.6
	Medium	2	17.0
	Difficult	3	6.4
Peduncle exertion	Slightly exerted	1	21.3
	Exerted	2	44.7
	Well-exerted	3	19.2
	Panicle covered by leaf sheath	4	14.9
Peduncle Shape	Erect	1	78.7
	Bent	2	8.5
	Semi-bent	3	12.8
Leaf midrib colour	White	1	100
Number of grains per glume	Single	2	100

*Scoring was done based on standard sorghum descriptors (Bioversity International, 2010). Whereby: 1 = Loose stiff branches, 2 = Loose drooping branches, 3 = Semi-loose stiff branches, 4 = Semi-loose drooping branches, 5 = Semi-compact elliptic, 6 = Compact elliptic, 7 = Compact oval and 8 = Semi-compact oval

TABLE 2. Descriptive statistics for 13 quantitative traits of sorghum landraces from the highlands of southwestern Uganda

Quantitative trait	Minimum	Maximum	Mean± SEM	CV (%)
Days to 50% flowering (d)	115	130	124.32±0.44	3.0
Plant height (cm)	144.70	351.60	211.98±6.71	21.7
Stem girth (cm)	3.64	9.04	5.74±0.03	18.3
Number of leaves	7	13	10±0.17	11.6
Length of third leaf from top (cm)	41.20	77.70	64.86±1.13	11.9
Width of third leaf from top (cm)	5.00	10.60	7.97±0.18	15.8
Panicle length (cm)	8.60	26.70	18.67±0.55	20.0
Panicle width (cm)	3.60	12.10	8.15±0.21	18.0
Panicle weight (g)	23.54	154.88	80.57±4.05	34.5
100-seed weight (g)	1.47	2.96	2.35±0.05	13.3
Grain yield (t ha ⁻¹)	1.23	11.31	5.48±0.2.7	34.1
Exertion length (cm)	0.00	21.17	5.84±0.81	94.8
Peduncle length (cm)	28.69	51.38	39.46±0.89	15.5

SEM = standard error of the mean, CV = coefficient of variation

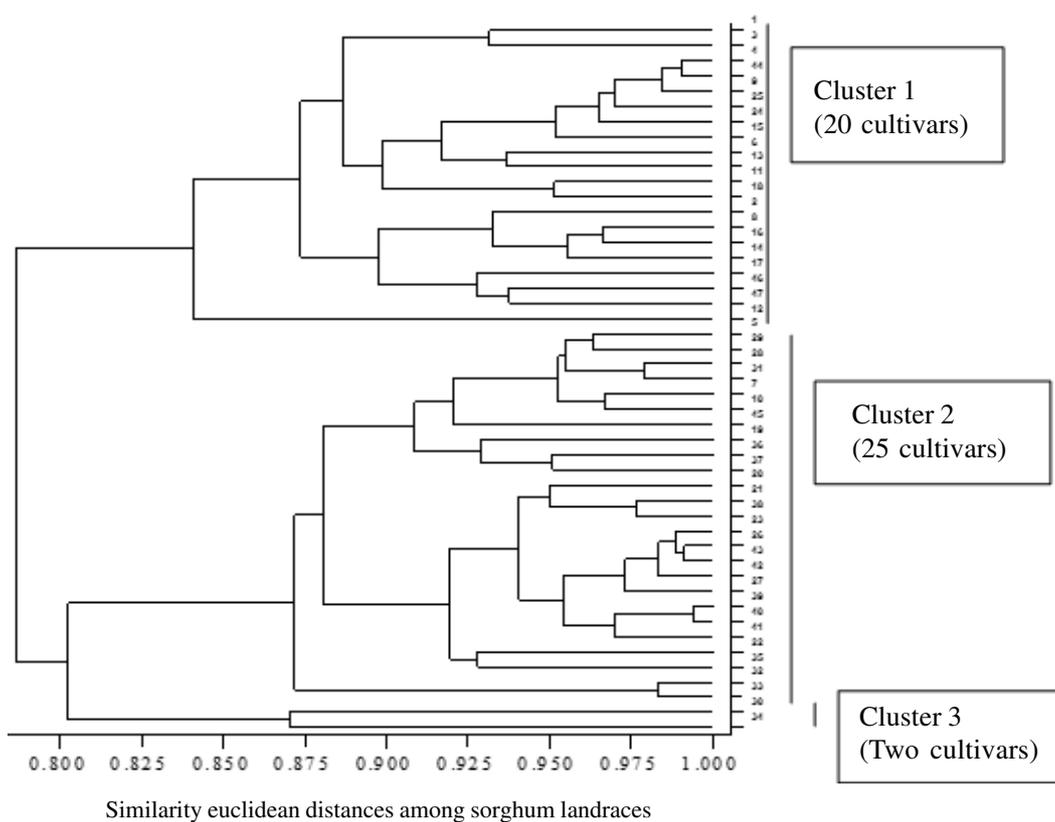


Figure 1. Dendrogram of clustering patterns of sorghum landraces based on 12 qualitative and 13 quantitative traits.

TABLE 3. Analysis of variance for the three clusters of the dendrogram

Trait	ANOVA				Means			
	S.S	M.S	V.R	F pr.	Grand mean	Cluster 1	Cluster 2	Cluster 3
Panicle weight (g)	12251.5	6125.7	11.55	<.001	80.6	97.1	65.5	104.3
Leaf width (cm)	27.4	13.7	13.27	<.001	8.0	8.7	7.3	9.7
Stem girth (cm)	20.4	10.2	14.78	<.001	5.7	6.3	5.1	7.3
Exertion length (cm)	533.7	266.9	13.46	<.001	5.8	2.3	9.0	1.5
Peduncle length (cm)	886.7	443.3	23.53	<.001	39.5	35.1	43.5	32.5
Panicle shape and compactness	36.0	18.0	9.47	<.001	4.6	5.4	3.8	6.5
Glume colour	3.6	1.8	12.66	<.001	1.3	1.0	1.5	2.0
Threshability	4.3	2.2	8.26	<.001	1.3	1.7	1.0	1.0
Panicle width (cm)	21.8	10.9	6.22	0.004	8.2	8.8	7.5	9.6
Grain yield (t ha ⁻¹)	33.5	16.8	5.82	0.006	5.5	6.3	4.7	7.2
Peduncle shape	4.4	2.2	5.35	0.008	1.3	1.5	1.1	2.5
Grain colour	4.6	2.3	4.9	0.012	1.6	2.0	1.4	1.0
Peduncle exertion	9.2	4.6	4.27	0.02	2.4	1.9	2.8	2.5
Days to 50% flowering	87.8	43.9	3.5	0.039	124.3	123.2	124.8	129.5
Number of leaves	6.8	3.4	2.73	0.076	9.8	10.2	9.4	10.5
Leaf length (cm)	254.4	127.2	2.24	0.119	64.9	67.4	62.7	67.2
Grain shape profile view	0.3	0.1	2.23	0.12	1.9	1.9	2.0	2.0
Plant height (cm)	7025.0	3,513.0	1.71	0.193	212.0	197.8	222.1	227.2
Grain covering	0.5	0.2	0.67	0.515	2.3	2.4	2.2	2.0
Grain shape dorsal view	0.0	0.0	0.67	0.519	2.0	2.0	2.0	2.0
100-seed weight (g)	0.1	0.1	0.49	0.616	2.3	2.4	2.4	2.1
Glume hairiness	0.0	0.0	0.02	0.98	2.9	2.9	2.9	3.0
Panicle length (cm)	0.3	0.1	0.01	0.991	18.7	18.7	18.6	19.0

led to the observed variation among other key qualitative traits, including grain colour. Grain colour, for instance, was predominantly orange and red because farmers associated them with good culinary qualities for making alcoholic and sweet beverage (House, 1985). Indeed, farmers in the highlands of southwestern Uganda were reported to grow sorghum largely for the production of alcoholic drinks and sweet beverages whose superior qualities are linked to orange and red sorghum grains (Nabimba *et al.*, 2005). White sorghum landraces were the least grown because they were reported not produce the preferred alcoholic drinks and sweet beverages and were highly susceptible to bird's damage, resulting into reduced yield (Mbabwine *et al.*, 2004).

Less variability among some traits such as glume colour, glume coverage, glume hairiness, grain shapes, threshability and peduncle exertion revealed that the genes controlling these traits

were tending towards fixation as a result of farmers' selection. Lack of variability among midrib colour and number of seeds per glume (Table 1) meant that the genes controlling these traits were already fixed, implying that only their respective gene variants were present in the populations. Less or lack of variability could have been the result of excessive conscious selection, in which farmers preserved the most valued, and discarded genotypes with less valued traits. Valued traits, therefore, ended up increasing in the population and may have led to their fixation.

Zohary (2004) reported that in conscious selection, desirable phenotypes are selected, while less desirable phenotypes are neglected or actively removed leading to their frequency decreasing in the population. This, according to Darwin (1875) could also gradually produce unintended reduction in variation in traits associated with those characters that were consciously selected for. For instance, farmers

TABLE 4. Principal components based on correlation matrix of both qualitative and quantitative traits

Variable	PC1	PC2	PC3	PC4	PC5	PC6	PC7
Exertion length (cm)	-0.36474	0.02444	0.02915	-0.03005	0.00383	0.16771	-0.00073
Panicle weight (g)	0.35888	0.07197	0.01707	0.05504	0.10107	0.20192	-0.05789
Stem girth (cm)	0.33854	0.00495	-0.15302	0.00417	0.00544	-0.03751	0.07102
Width of third leaf from top (cm)	0.32134	-0.03883	-0.17329	-0.04133	-0.05362	0.09827	0.2355
Grain yield tons (ha)	0.32048	0.14709	0.04222	0.03902	0.11341	0.26317	-0.11561
100 seed weight (g)	0.12562	0.28955	0.31753	0.19977	0.11412	0.02577	0.20272
Days to 50% flowering	0.0087	0.1235	-0.15599	-0.54746	-0.17039	0.02879	-0.19302
Glume colour	-0.09321	0.2276	-0.23592	-0.24736	0.01799	0.1454	-0.14645
Glume hairiness	0.02359	-0.00313	0.34127	-0.31549	-0.05466	0.28463	0.32446
Grain colour	0.00616	-0.36428	0.29001	0.15577	0.11064	0.02544	-0.1342
Grain shape dorsal view	-0.05298	0.18732	-0.30346	0.07613	0.48514	-0.23115	0.07641
Grain shape profile view	-0.08452	0.29182	-0.2094	0.24276	0.37972	-0.04682	0.08225
Length of third leaf from top (cm)	0.27128	0.17579	0.20628	0.03004	-0.12144	-0.21393	0.15836
Number of leaves	0.21566	0.15285	0.15336	-0.23068	0.22223	-0.31621	-0.33153
Panicle length (cm)	0.15305	0.24972	0.01712	0.36077	-0.25518	0.03138	0.05122
Panicle shape and compactness	0.12538	-0.29387	0.16394	-0.16218	0.40464	-0.01032	0.15561
Panicle width (cm)	0.26796	0.02435	-0.25044	0.05013	-0.17188	0.26879	-0.24364
Peduncle exertion	-0.19776	0.09627	-0.02505	0.00556	0.32808	0.47008	-0.13342
Peduncle length (cm)	-0.29962	0.1974	0.25507	0.1482	-0.10791	0.03771	0.05402
Peduncle shape	0.07476	-0.3265	-0.13672	-0.16699	0.15692	-0.16892	0.27611
Plant height (cm)	0.00728	0.33873	0.37271	-0.25499	0.08525	-0.24056	-0.22607
Threshability	0.12139	-0.2445	0.20496	0.16302	0.19329	0.21179	-0.44695
Grain covering	-0.04688	-0.18511	-0.07102	0.22119	-0.16059	-0.34367	-0.34362
Latent loots (Eigenvalues)	6.324	2.632	2.021	1.795	1.602	1.475	1.138
Percentage variation	27.49	11.44	8.79	7.8	6.96	6.41	4.95
Cumulative percentage variation	27.49	38.93	47.72	55.52	62.48	68.89	73.84

consciously selecting for good culinary qualities aimed at making good alcoholic beverages, may end up affecting grain colour which is always associated with culinary qualities. Less variability could also have been brought about by mutation in which case, a mutant gene, having a positive selection was slowly replacing the other forms of the gene. Under positive selection, certain factors in the environment apply consistent pressure over generations in favour of a mutant gene (Hartl and Clark, 2007). If mutation happens to be beneficial to the species, it will spread to the population immediately by selection (Nielsen, 2005). Lack of variability, on the other hand, could mean that the mutant gene had already replaced all other variants of the gene.

Kimura (1983) reported that fixation of the gene is dependent on selection coefficients and chance fluctuations in allelic proportions. Innan and Kim (2004) reported that during crop domestication, strong selective pressure cause

traits of interest to be fixed in founder populations in quite a short time. Clearly, variable social habits concerning the use of sorghum acting on the principles of artificial selection together with forces of natural selection, could have contributed to the observed trait variations in the sorghum land races in the southwestern highlands of Uganda.

Quantitative traits. The high coefficient of variation values for different quantitative traits, except days to 50% flowering (Table 2), could be an indication of high variability that exists in the genes of the evaluated sorghum cultivars. Coefficient of variation is an ideal device for comparing the variation in a series of data measured in different units and that the higher the CV, the greater the dispersion in the variable (Tian, 2005; Mohmoudvand *et al.*, 2007).

The observed high variability is an indicator of the high variation in genes controlling their

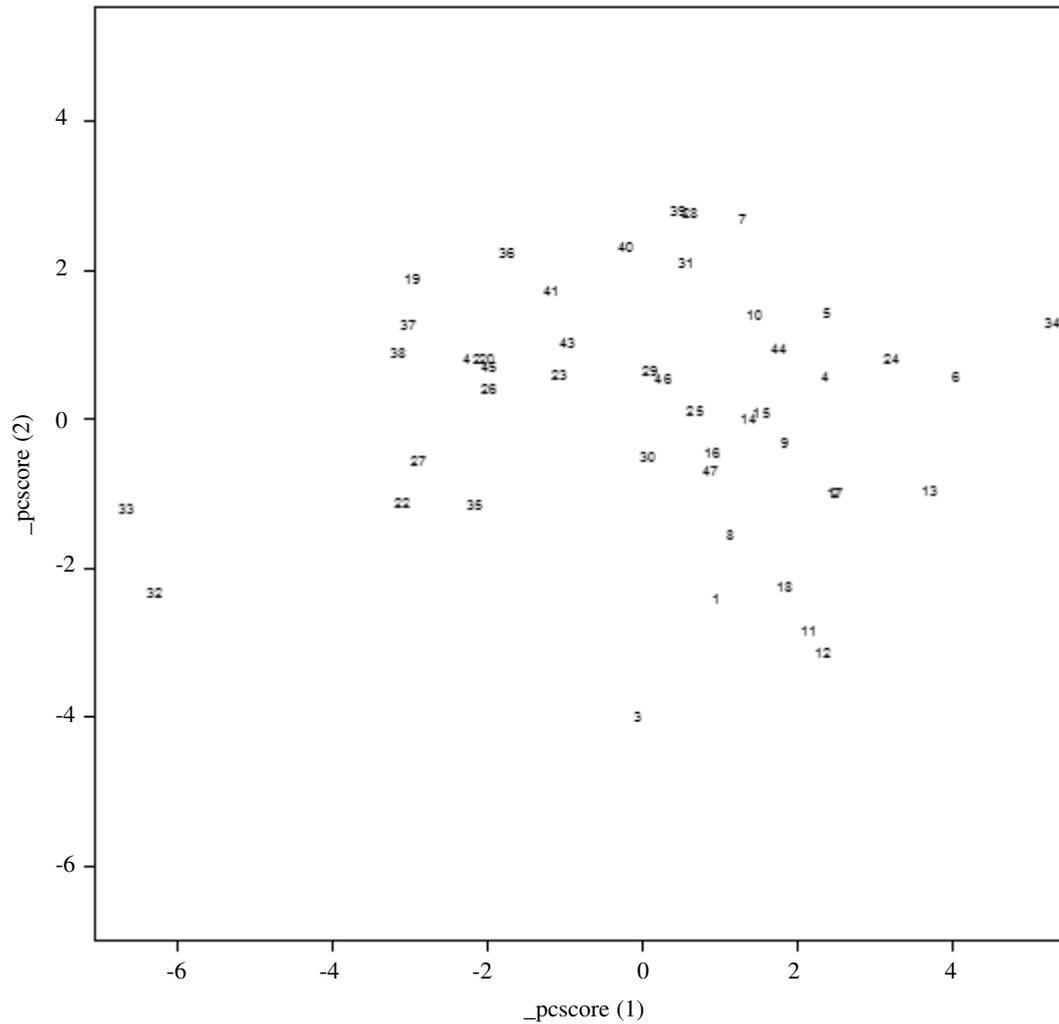


Figure 2. Scatter plot of the first two principal components for both qualitative and quantitative traits of sorghum in the highlands of southwestern of Uganda.

expression. This high variability offers diverse parental combinations, resulting in progenies with maximum genetic variability for further selection (Barrett and Kidwell, 1998). Superior cultivars among the materials could form the breeders' initial material for developing cultivars.

The observed high variability for panicle length, width and weight; grain yield, exertion length, peduncle length, width and length of third leaf from top and stem girth were similar to earlier reports in sorghum by Elangovan *et al.* (2013) and Dossou-Aminon *et al.* (2015). Less variability in days to 50% flowering (115 to 130 days, CV

3%) could mean that farmers have overtime, been selecting cultivars that fit in the same growing season. The 15 days flowering differences observed between the earliest and the latest cultivars in this study, imply that all the evaluated sorghum cultivars fit in the same growing season. The 15 days differences though is so critical, especially when faced with acute water stress (Rooney, 2004). Cultivars that do not fit within the major sorghum growing season (early or late) may face a challenge of birds' damage, since birds concentrate on the cultivars that tend to mature outside the normal season (House, 1985).

Cluster analysis grouped the 47 cultivars into three groups (Fig. 1). The more the cultivars grouped together to the right of the dendrogram near 100% similarity (such as cultivars 39 and 40), the more similar and genetically closer to each other they were. On the other hand, cultivars that clustered to the left of the dendrogram, far from the 100% (for instance cultivars 30 and 34), were different and genetically distant from each other (Fig. 1). ANOVA using means of cultivars per cluster identified which traits greatly contributed to the observed variation and clusters formed. ANOVA using means of cultivars per cluster (Table 3) identified which traits greatly contributed to the observed variation and clusters formed. This information could be useful in sorghum improvement when selecting suitable parents with appropriate trait variability, depending on the objectives of the improvement programme.

PCA was able to identify few key traits that accounted for the largest variability (Table 4). Sharma (1998) reported that PCA reflects the importance of the largest contributor to the total variation at each axis of differentiation. It was further reported by Fenty (2004) that PCA reduces a large set of variables to come up with smaller sets of components that summarise the correlations. In this study, the traits revealed by the first two PCs account for the largest variability (Table 4) and were similar to those identified under cluster analysis using ANOVA (Table 3). A scatter plot from the first two PCs (Fig. 2) generally grouped the cultivars in a similar way to cluster analysis (Fig. 1), using the entire data from all the traits. This showed that PCA is a reliable method in identifying few key traits contributing to the largest variation and could be a reliable method in predicting the important traits influencing clustering of different cultivars observed in Figure 1 under cluster analysis.

ACKNOWLEDGEMENT

This study was funded by Carnegie of New York and EU-supported Outreach project (FED/2009/217080) through the Regional Universities Forum for Capacity Building in Agriculture (RUFORUM). Dr. Alex Barekye, Director KAZARDI, provided experimental plots.

REFERENCES

- Barrett, B.A. and Kidwell, K.K. 1998. AFLP-based genetic diversity assessment among wheat cultivars from the Pacific Northwest. *Crop Science* 38(5):1261-1271.
- Bernardo, R. 2010. Breeding for quantitative traits in plants. Second Edition. University of Minnesota-Twine cities. *Stemma Press*, Woodbury, Minnesota, USA.
- Bioversity International. 2010. Key access and utilization descriptors for sorghum genetic resources. *International Sorghum and Millets Newsletter* 47:9.
- Darwin, C. 1875. The variation of animals and plants under domestication. Ed . 2 . 2 vols. *Murray*, London .
- de Wet, J.M.J. and Harlan, J.R. 1971. The origin and domestication of *Sorghum bicolor*. *Economic Botany* 25:128-135.
- Doggett, H. 1970. Sorghum. Tropical Agriculture Series. Longmans, London, UK.
- Dossou-Aminon, I., Yêyinou, L.I., Arlette Adjatin, A. and Eben-Ezer B.K. 2015. Genetic divergence in northern Benin sorghum (*Sorghum bicolor* L. Moench) landraces as revealed by agromorphological traits and selection of candidate genotypes. Hindawi Publishing Corporation. *The Scientific World Journal* Volume 2015, Article ID 916476.
- Dudley, J.W. and Moll, R.H. 1969. Interpretation and use of estimates of heritability and genetic variances in plant breeding. *Crop Science* 9:257-262
- Elangovan, M., Jain, S.K. and Patel, N.V. 2013. Characterisation of sorghum germplasm collected from Gujarat. *Indian Journal of Plant Genetic Resources* 26(1): 42-46.
- Fernandez, C.J., Dan, D., Fromme, D.D., James, W. and Grichar, J.W. 2012. Grain sorghum response to row spacing and plant populations in the Texas Coastal Bend region. *International Journal of Agronomy*, Article ID 238634. Hindawi Publishing Corporation.
- Fenty, J. 2004. Analysing distances. *The Strata Journal* 4: 1- 26.
- Gelman, A. 2005. Analysis of variance? Why it is important than ever. *Annals of Statistics* 33:1-53.

- Gerik, T., Bean, B. and Vanderlip R. 2003. Sorghum growth and development, Texas Cooperative Extension Service University of Arkansas 2301 S. University, Little Rock, Arkansas 72203. Arkansas Printing Services, USA.
- Hair, J. R., Anderson, R.E., Tatham R.L. and Black, W.C. 1995. Multivariate data analysis with readings. 4th edition, Prentice-Hall, Englewood Cliffs, NJ, USA.
- Hartl, O.L. and Clark, A.G. 2007. Population genetics, fourth edition. Sinauer Associates, 23 Plumtree Road, Sunderland, MA 01375, U.S.A.
- House, L.R. 1985. A guide to sorghum breeding. 2nd Edition. Patancheru, A.P.502324, India: International Crop Research Institute for Semi-Arid Tropics. 216 pp. 45 ref. ISBN 92-9066-084-8.
- Innan, H. and Kim, Y. 2004. Pattern of polymorphism after strong artificial selection in a domestication event. *Proceedings Nationall Academy of Science, USA* 101:10667-72.
- Jackson, J.E. 1991. A User's guide to principal components (Wiley).
- Jollie, I.T. 2002. Principal component analysis. Springer, New York, USA.
- Kimura, M. 1983. The neutral theory of molecular evolution. The Edinburgh Building, Cambridge University Press. ISBN 978-0-521-23109-1.
- Mbabwine, Y., Sabiiti, E. N. and Kiambi D. 2004. Assessment of the status of plant genetic resources in Kabale highlands, Uganda: A case of cultivated crop species. Plant Genetic Resources Institute (IPGRI). Bioversity International Via dei Tre Denari, 472/a 00057 Maccarese Rome, Italy. <http://www.sweetpotatoknowledge.org>
- Mbeyagala, E.K., Kiambi, D.D., Okori, P. and Edema, R. 2012. Molecular diversity among sorghum (*Sorghum bicolor* (L.) Moench) Landraces in Uganda. *International Journal of Botany* 8 (3):85-95,2012. ISSN 1811-9700/DOI:10.3923/ijb.2012.8.95. Asian Network for Scientific Information
- Mohmoudvand, R., Hassani, H. and Wilson, R. 2007. Is the sample coefficient of variation a good estimator for the population coefficient of variation? *World Applied Sciences Journal* 2(5):519-522
- Nabimba, F., Kashaia, I.N., Wagoire, W.W., Bamwerinde W.M., Kakuhenzire R., Kikafunda, J. and Kamanyi, J. 2005. Significance of sorghum in the south western highlands agro-ecological zone of Uganda. *African Crop Science Conference Proceedings* 7:971-978.
- NEMA (National Environment Management Authority) - Uganda. 2009. Atlas of Our Changing Environment. P. O. Box 22255 Kampala Uganda.
- Nei, M. 1972. Genetic distances between populations. *The American Naturalist* 106: 282-292.
- Nielsen, R. 2005. Molecular signatures of natural selection. *Annual Rev Genetics* 39:197-218.
- Poehlman, J.M. 1994. Breeding sorghum and millet. In: Poehlman, J.M. (Ed.). Breeding field crops, 3rd Edition. *Iowa State University Press*, Ames. pp. 508-541.
- Rooney, W. L. 2004. Sorghum improvement - Integrating traditional and new technology to produce improved genotypes. *Advances in Agronomy* 83:10.1016/S0065-2113(04)83002-5.
- Saitou, N. and Nei, M. 1987. The neighbour-joining method: A new method for reconstructing phylogenetic trees. *Molecular Biology and Evolution* 4:406-425.
- Sharma, J.R. 1998. Statistical and biometrical techniques in plant breeding. *New Age International (P) Limited Publishers*, New Delhi, India. 432 p.
- Tian, L. 2005. Inferences on the common coefficient of variation. *Statistics in Medicine* 24:2213-2220.
- Watson, J.W. and Eyzaguirre, P.P.B. 2002. Home gardens and in situ conservation of plant genetic resources in farming systems. *Proceedings of the second international home gardens workshop*, 17-19th July 2001, Witzenhausen, Federal Republic of Germany. International Plant Genetic Resources Institute, Rome, Italy.
- Wortmann, S.C., Martha, M., Mburu, C., Letayo, E., Abebe, G., Kaizzi, M., Kayuki, C., Chisi, M., Munyaradzi, M., Xerinda, S. and

- Ndacyayisenga, T. 2006. Atlas of sorghum (*Sorghum bicolor* (L.) Moench). Production in Eastern and Southern Africa. The Board of Regents of the University of Nebraska, USA.
- Yamasaki, M., Wright, S.I. and McMullen, M.D. 2007. Genomic screening for artificial selection during domestication and improvement in maize. *Annals of Botany* 100:967-973.
- Zohary, D. 2004. Unconscious selection and the evolution of domesticated plants. *Economic Botany* 58:5-10.