Original Research Article

Physiochemical properties and identification of elite genotypes for improved sorghum breeding in Tanzania

Abstract

Variability in physiochemical properties in sorghum is critical in cultivar development for optimum grain quality and crop resistance against fungal and insect pests. These traits are not well studied. The objective of this study was to characterize sorghum genotypes based on kernel phenotypic and biochemical traits and identify promisinggenotypes for better utilization of these traits in sorghum breeding.98 sorghum genotypes comprised bythereleased varieties, breeding lines, hybrids and local cultivarswere studied usingqualitative and quantitative parameters.75.51% of these genotypes havethick pericarp, 33.67% have testa layer, and 7.0% showedmostly-corneous endosperm texture.Results revealeda wide variability among studied genotypes in terms ofphenotypic and biochemical properties ($p<0.001$).A cross IES11038 X A1GD 34553 recorded the highest 100 seed weight (6.2g). Patoand IESV 92174DL were the hardest genotypes with 110.33 and 108.4N respectively.Protein content rangedfrom 6.52 to 12.23%,of whichNaco Mtama 1 and IESV 24030SH were the promising genotypes.GenotypesICSA 88006 X IESV92172DL,ICSA15 x R8602 andGADAMrecorded the highest starch concentration (79 g/100g).The identified elite genotypes couldenable selection and hybridization of useful traits.

Key words: Phenotypic, biochemical, genotypes, variability, sorghum, kernel

Introduction

Sorghum is the main source of calories and protein to most people in Africa and Asia (Mohammed *et al.,* 2011), widely grown in semi-arid areas. The crop is known to withstand harsh environmental condition including drought (Tack *et al.,* 2017). Sorghum have a wide genetic diversity in its physical structure and or chemical composition and therefore presenting benefits in hybridization (Bean *et al.,* 2016).Variation in structure, nutritional composition and phytochemical composition is critical for selection of desired traits in sorghum breeding(Gerrano *et al.,* 2014). The inheritable qualitative traits in sorghum kernel consist ofpericarp color, pericarp thickness, presence of testa, testa color, and endosperm texture; while quantitative traits include grain size and weight(Chiremba, 2012;Guindo *et al.,* 2016).Literature indicated that starch is the largest portion of sorghum grain weight made up by amylose and amylopectin molecules held by hydrogen bonds(Ahmed *et al.,* 2016). Amylopectin is made up by large branched polymer unlike the amylose structure. Sorghum starch contain 70-80% amylopectin and 20-30% of amylose; mainly for feed and industrial use(Zhu, 2014). Moreover, Protein concentration in sorghum grain usually varied based on the genotype, water, temperature and soil fertility status of the soil. According toWaniska and Rooney (2000) drought condition is known to increase protein concentration while reducing starch content. Sorghum genotypes with higher yield is known to have smaller concentration of protein; while the application of nitrogenous fertilizer increases protein concentration particularlyprolamin, kafirns and glutelins in the sorghum endosperm(Almodares *et al.,* 2009).In addition, the germ portion comprised by albumin and globulins with highest concentration of lysine(Wong *et al.,* 2009).The physical appearance of sorghum kernel structure largely guided by its associated biochemical traits including the phenolic compounds. According to Dykes and Rooney (2007)Phenolic compounds consist of benzene ring and hydroxyl group. Plants materials contains phenolic compounds, which reflects the taste, color and appearance. Sorghums has a wide variability of phenolic acids. In addition, Dykes and Rooney (2007)screened a number of sorghum genotypes and found high phenolic content in high tannin sorghums. FurtherDykes *et al,* (2005) concluded the health

benefits derived from phenolic such as low digestibility, reduction of diseases like cardiovascular, anti-carcinogenic and lowering of cholesterol; This is due to antioxidant capacity of phenolic compounds as lowers amount of free radicals in the body. Some sorghum cultivars comprised by tannins or proanthocynidins which is genetically based controlled by genes B1,B2 in the testa (Dicko *et al.,* 2006). Dykes and Rooney (2006)characterized sorghum as Type I (sorghums without condensed tannins), Type II sorghums aregenotypes with extractable tannins using 1% acidified methanol and not the pure methanol and Type III sorghums that can be extracted using both one percent acidified methanol and the pure methanol.Sorghum tannins bind protein and makes it unavailable in the digestion through ionic, hydrogen, hydrophobic and covalent bonding (Butler et al, 1984).These compounds were also reported to protect plants against insects (War *et al.,* 2012). For this case breeders must screen large pool of germplasm to identify genotypes with higher levels of phenolic (Dykes *et al.,* 2014).

Several studies attempted to characterize sorghum genotypes based on physical and biochemical composition. For instance,Subramanian & Jambunathan (1982) assessed the phytochemical properties of forty five sorghum genotypes based on weight, protein and sugar content;Gerrano *et al.* (2014) documented a wide variability in terms of nutritional and stalk sugar content in sorghum. Mabelebele *et al.* (2015)screened four improved sorghum varieties and observed considerable variability in terms of biochemical composition including mineral concentration, crude protein, starch, fat and even ash content. Thecurrent study therefore contributes to the general understanding of kerneltraits related to phenotypicand biochemical properties for effective utilization of these traits.In Tanzania,many sorghum genotypes were not previously evaluated and theirphenotypic and biochemicalpotential is not understood and or documented; therefore, it is important to characterize a broad range of sorghum genotypes. The study intended to characterize sorghum genotypes based on kernel phenotypic traits

and biochemical composition to establish potential of these traits in cultivar development. The study also identified promising sorghum genotypes to be used as parental materials during hybridization.

Materials and methods

Site and source of materials

Ninety eight (98) sorghum genotypes collected from TARI Ilonga center, Tanzania Gene bank and International Crops Research Institute for the Semi-arid Tropics (ICRISAT); comprised by commercial varieties, hybrids, local cultivars and breeding lines (Table 1). The known agronomic properties of these materials include high yielding, midge resistance, striga resistance, anthracnose, stay green and earliness.Materials were raised at Tanzania Agricultural Research Institute Ilonga in Kilosa, Morogoro Tanzania; located at latitude 06^{o}42'S, longitude 37^{o}02'E and altitude of 506 meters above sea level with a bimodal type of rainfall.Materials were planted in the cropping season 2017/18. All agronomic management including supplementary irrigation, weeding, fertilizer application and insect control were applied as per recommendation. Harvested grains were cleaned and sorted foranalysis of phenotypic and biochemical traits at the Nelson Mandela African Institution of science and Technology and food processing laboratory of the Sokoine University of Agriculture.

Determination of qualitative kernel traits

Ten sound kernel selected randomly for each physical analysis according to procedure described by (Gomez*et al.,* 1997). Pericarp thickness was determined by scratching sorghum kernel using scalpel and observe the pericarp thickness using a magnifying glass. The presence of testa layer and the associated color was recorded after removal of pericarp. Endosperm texture; was determined by cutting each kernel into half and observe the proportion of corneous material with the aid of magnifying glass; materials were characterized into starch, intermediate and pearly based on the score. Grain color was

determined through visual examination using color chart and codes as per sorghum descriptors guide (IBPGR and ICRISAT, 1993).

Determination quantitative kernel physical traits

100 sound sorghum kernels were manually counted and weight measured in replicates using analytical balance TPA 500.Kernel hardness (firmness)was observed using Brookfield CT3 Texture analyzer, using probe TA41 Cylinder 6mm D, 35mm L;with the recommended trigger value of 50g and Load Cell of capacity of50kg, test speed was set at 10mm/s, and deformation of 0.70mm.The average of six samples (kernels) per test was taken as hardness.Furthermore, the arithmetic mean diameters was taken as average of the major diameter, minor diameter, and intermediate diameter of sorghum kernel using automatic caliper (Adinoyi*et al.,* 2017).

Determination of nitrogen content

Total nitrogen and protein of sorghum genotypes was determined from grain through digestion, distillation and titration- with hydrochloric acid as per Micro KjeldahlMethod (Bradstreet, 1953). Grain was grindedand sieved using 0.5mm sieve;0.1 g was placed into a digestion tube. 1g Selenium catalyst mixture weighed and mixed with the sample; followed by addition of 5 ml of sulphuric acid (96%) into the tube. The tubes was heated slowly in the digestion apparatus until the digest is clear. The content was transferred to a 100 ml volumetric flask where distilled water was added into a 100 ml graduated flask. 5ml of boric acid indicator solution were placed into the distillation apparatus. 10ml of clear supernatant were then transferred into the apparatus where 10 ml of NaOH(46%) were added. Color change were observed when distillation drops mixed with the boric acid indicator. 150 ml of the distillate were titrated with sulphuric acids (0.0174N) where color change from green to pink was

observed, the titer volume was recorded. Finally, total nitrogen was determined using the following formula:

$$N\ (\text{percentage}) = a \times N \times Mw \times 100 \times 100\%\ b \times c$$

Where, a = ml of sulphuricacid, N = Normality of sulphuric acid (0.0174), a = Titer volume, Mw = Molecular weight of Nitrogen (0.014), b = gram sample taken for analysis (0.1 g)and c = ml digest used for distillation (10 ml). Thus, the percentage crude protein = 6.25 × % N.

Determination of starch content

Starch concentrationwas determined using(AOAC, 2002) official method 996.11 whereby, 100mg of finely ground sample were taken into 15ml centrifuge tubes. 0.2ml 80% ethanol was added and vortexed. 3ml of 10% α – amylase enzyme in mM sodium acetate buffer were addedand incubated in a boiling water bath for 6 minutes with 2 minutes shaking intervals. The tubes placed in a water bath at 50^{o}C and 0.1ml of amyloglocosidase enzyme was added; the tubes was stirred using vortex and incubated for 30 minutes. The contents were then centrifuged for 10 minutes at 3000 rpm. A duplicate of 0.1ml aliquot was placed into 15ml test tube. 3.0ml of ρ-hydroxybenzoic acid and sodium azide mixture (1:1) and left to stand for 20 minutes at 20^{o}C.

5.0g of D-glucose powder was taken into 100ml volumetric flask, dissolved with sodium acetate buffer to make stock solution of 50mg/ml. Serial dilution of 0 – 40mg/ml prepared into 100ml volumetric flask. 0.1ml of diluted standard solution were taken into 15ml test tube. 3.0ml ρ-hydroxybenzoic acid and sodium azide mixture (1:1) and left to stand for 20 minutes at 20^{o}C. Absorbencies of samples and standards was read at 510nm using X-ma 3000 UV/Visible spectrophotometer.

Data analysis

Qualitative data including pericarp thickness, testa presence, corneous, and endosperm color was analyzed using excel program; where frequencies and percentage presented in bar chart.Data on mean kernel diameter, 100seed weight, kernel hardness, protein and starch concentration were subjected into analysis of variance (ANOVA) using GenStat version 15 software and means were compared using Duncan new multiple test. Pearson correlation employed to determine the association between quantitative traits. MINTAB version 14 software were used in multivariate analysis such asprincipal component and cluster analysis.

Results and discussion

Qualitative traits

Most of sorghum genotypes studied (75.51%) had thick pericarp (Figure 1), while the rest possessed thin pericarp. Other researchers;Earp & Rooney, (1982) reported a variation in pericarp thickness in sorghum using electron microscope consisting of very thin (8 to 32 µm) to very thick (40 to 160 µm).

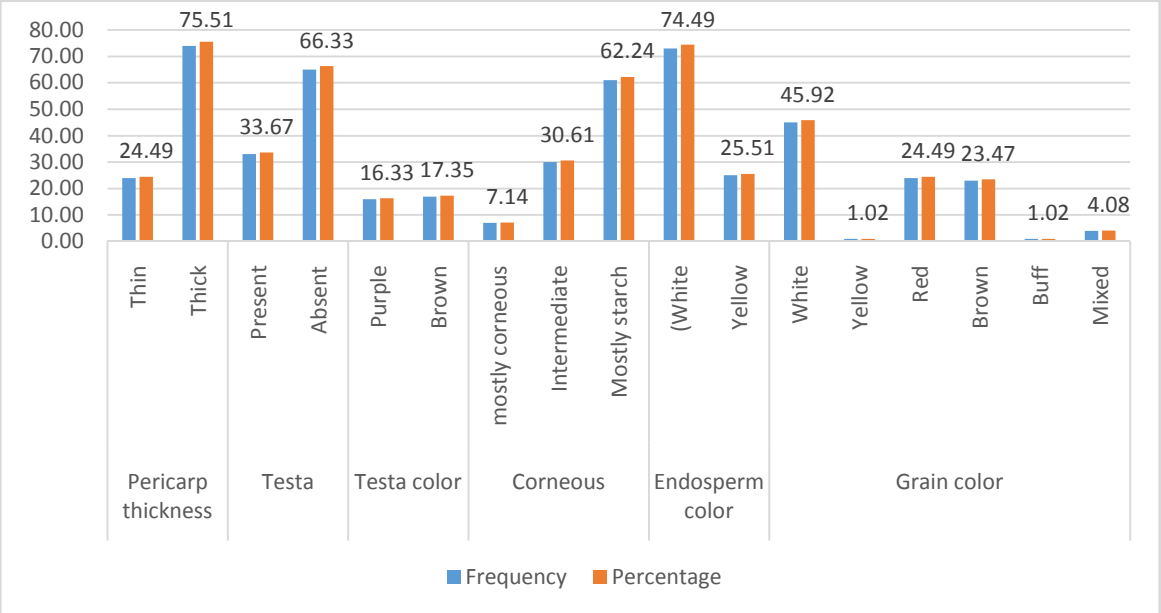

Figure 1: Frequencies and percentages among qualitative kernel traits

Only 33.67% of sorghum genotypes had either purple or brown testa, while the rest of genotypes had no testa. Genotypes with testa indicates the possibility of having higher levels of tannin concentration

compared to non-testa genotypes.Dykes and Rooney (2006)characterized sorghum into three different groups namely; Type I sorghumsthat lacking pigmented testa and have no tannin, Type II sorghums having pigmented testa with tannin and Type III sorghums having tannin in the testa and pericarp of the kernel.(74.49%)of the evaluated sorghum genotypes had white color endosperm, while the rest were yellowish.While, 7.14% of all genotypes had mostly corneous endosperm texture, 30.61% had intermediate corneous indicating a relative balance between floury content and corneous; while the majority of genotypes were floury or complete starch.Endosperm texture is related to kernel hardness; such that mostly corneous endosperm referring to hard kernel and floury endosperm referring to soft kernel(Anglani, 1998). Great variation were also observed in terms of grain color;where,45.92% of the evaluated genotypes were white in color,24.49% were red, 23.47% of thegenotypes were brown; the rest in small fraction were yellow, buff and mixed colors. However, qualitative traits in sorghum play bigger role in processing and flour quality; for instance, genotypes producing grains of uniform sizes is most preferred in milling than non-uniform because smaller kernels normally taken out with bran.

Analysis of variance (ANOVA)

Analysis of variance indicated a highly significant difference ($p<0.001$) among evaluated genotypes, showing greater genetic variability among traits under consideration (Table 1).Kernel mean diameter ranged between 2.29mm to 4.61mm. LinesICSx152 002-SB-13-2, F2Striga16 and IESH 22017 had the greater mean kernel diameter and genotypes IS 21055 had the lowest mean kernel diameter. 100 seed weight ranged between1.81to 6.2 g. Genotypes F2Striga 5, P9537A x MACIA and IES11038 x A1GD 34553recorded the highest hundred seed weight; while genotype TZA 3983 had the least weight. Kernel hardness varied between 14.94 newton to 110.33newton; GenotypesPATO, IESV 92174DL, and IESV 92028 DL recorded the highest kernel hardness, while genotypes IESV 92043DL, F2Striga15 and

TZA3993had the least kernel hardness. Subramanian & Jambunathan (1982) reported hardness range of 3kg to 12kg using forty-five sorghum genotypes.

Protein concentration ranges between 6.52 to 12.23%; where genotype Naco Mtama 1 and IESV 24030SH recorded the highest concentration and genotypes F2 Striga 13 and ICS x 152 001-SB-4-2 had the lowest concentration. This finding corresponds with results from other studies. For instance, Afripro, (2003)reported crude protein range of 6% to 16.6%.Dicko *et al.*(2006) reported protein content range from 7 -15% using data from FAO and other studies. Mofokeng *et al.*(2018) reported protein range of 7.16- 16.18% using 59 sorghum genotypes from South Africa.However,Mutwali*et al.*(2018) confirm the fact that protein contents varies due to environment and genotype.

The mean total starch concentrationranged between 21.88 to 79.05 g/100g. The higher concentration observed on genotypes ICSA 88006 X IESV92172DL, ICSA15 x R8602 and GADAM; while Tegemeo and ASARECA 18-3-1recorded the least concentration.Some genotypes recorded either lower or higher starch concentration due tohigh diversity of genotypes used in the present study. Dicko et al, (2006)reported starch concentration range of 60-75g/100g; Gerrano *et al.*(2014) reported starch concentration range of 44.39% to 68.08% using 22 sorghum accessions mostly from Ethiopia and South Africa.However, it was suggested that starch concentration in sorghum is highly affected by genotype and environment (Boudries *et al.,* 2009). According toFAO (1995) sorghum starch is resistant impairing digestion making it useful to people with obesity and diabetic. The higher variability among studied genotypes in terms of kernel phenotypic and biochemical traits is critical in selection of appropriate traits during cultivar development.

Table 1: Simple statistics

Variable	MKD	100Swt	Hardness	Protein	Starch

Mean	3.02	3.713	70.02	8.656	45.95
SE	0.1	0.075	1.377	0.08	1.116
Minimum	4.6050	1.8083	14.94	6.515	21.88
Maximum	2.2850	6.2000	110.33	12.229	79.05
CV	4.7	2.9	2.8	1.3	3.4
F prob	<0.001	<0.001	<0.001	<0.001	<0.001

MKD = mean kernel diameter, 100Swt =100 seed weight;
SE= Standard error of mean, CV= coefficient of variation,

Correlation between quantitative traits

Table 2: Pearson correlation among the studied traits in terms of phenotypic and biochemical properties

	Mean diameter	100 Seed weight	Kernel hardness	Protein
100Seed weight	0.169			
Kernel hardness	0.143	0.250*		
Protein	0.140	0.132	0.225*	
Starch	-0.200*	-0.158	-0.064	-0.087

*significant at p<0.05

Pearson correlation analysis indicated a weakpositive significant correlation between 100 seed weight and kernel hardness (r=0.250, p=0.013) (Table 2); while kernel hardness had apositive butweaksignificant correlation with protein concentration (r=0.225, p=0.026).Starch concentration had a weaknegatively significant association with mean kernel diameter (r=-0.200, p=0.048). However, starch concentration showed a negative weakcorrelation with all studied parameters.This finding impliesthataskernel weight increases, there is lower possibility of existence of a relationshipwith the increase in kernel hardness; likewise,the increase in kernel hardnesshas lower likelihood of existence of arelationshipwith the increasein protein content of the genotypes.The weak correlations observed in the present study necessitatesthe need for further research to confirm these findings. However,Kumari & Chandrashekar (1994)found greater levels of protein content in corneous portion of the endosperm than floury endosperm in sorghum. The hard sorghum kernel is critical in resistance against fungal and insect attacksuch as *Sitophilus oryzae*(Zunjare *et al.,* 2015); due to presence of prolamins(War *et al.,* 2012).Hardness is also a good determinant of grain quality relating to cooking qualities such as stiffness and the milling qualities(Kumari & Chandrashekar, 1994).

Principal component analysis

Principle component analysis (PCA) grouped five traits into five components. Retention of PCs were based onproportion of variance criterion described by Hair *et al.,*(1998).Four components can be retained based on adequate cumulative amount of variance explained(>80%). About85.9%of the variances contained in the dataset were retained by the first four principal components. The first component explained 32.7% of the total variation.The high contributing factor loading are 100 seed weight, kernel hardness, mean kernel diameter (MKD), and protein content (Table 3). The second principle component (PC2)accounted 20.1% of the total variation; mainly a function of starch concentration and kernel hardness with negative loadings.With similar logic,in the third component (PC3) protein content have higher positive loading and 100Swt with the largest negative loading.PC4 accounted 15.8% of the total variation with high negative loadings from starch concentration and the mean kernel diameter.According toHair *et al.* (1998)loading greater than ±0.40 were considered to best represent the corresponding PC axis.The first and second components accounted over fifty percent of the variation demonstrating existence of relationship among traits.Sinha and Kumaravadivel (2016) reported large contribution of the first two components using forty sorghum accessions.Similar findings has been reported by Gerrano *et al.* (2014) using 22 sorghum accessions.

Table 3: Principle component analysisof quantitative physiochemical traits in 98 sorghum genotypes

Variable	PC1	PC2	PC3	PC4	PC5
MKD	0.452	0.386	0.256	-0.761	0.042
100Swt	0.492	-0.051	-0.657	0.076	0.563
Hardness	0.484	-0.485	-0.205	-0.066	-0.697
Protein	0.425	-0.394	0.677	0.300	0.342
Starch	-0.373	-0.677	-0.051	-0.567	0.281
Eigenvalue	1.6346	1.0060	0.8639	0.7907	0.7048
% variance	32.7	20.1	17.3	15.8	14.1
Cumulative % variance	32.7	52.8	70.1	85.9	100

PC= principal component, MKD = mean kernel diameter, 100Swt =100 seed weight;

Further, the score plot for the first two components(Figure 2) indicate existence of genetic variation among sorghum genotypesin terms of studied physiochemical traits. The scattered genotypes across all quadrantsindicate a high genetic variability among them. Genotypes from different origin and or type were scattered. The closer genotypes in the PC axes indicatetheclose genetic relationship, which can be explained by the shared traits. Genotypes ICSx152002-SB-4-1, IESH 22023, and ICSA75 x ICSR38 were the extremely genotypes; therefore some of these lines can be selected for hybridizationof traits of interest to improve sorghum cultivars.

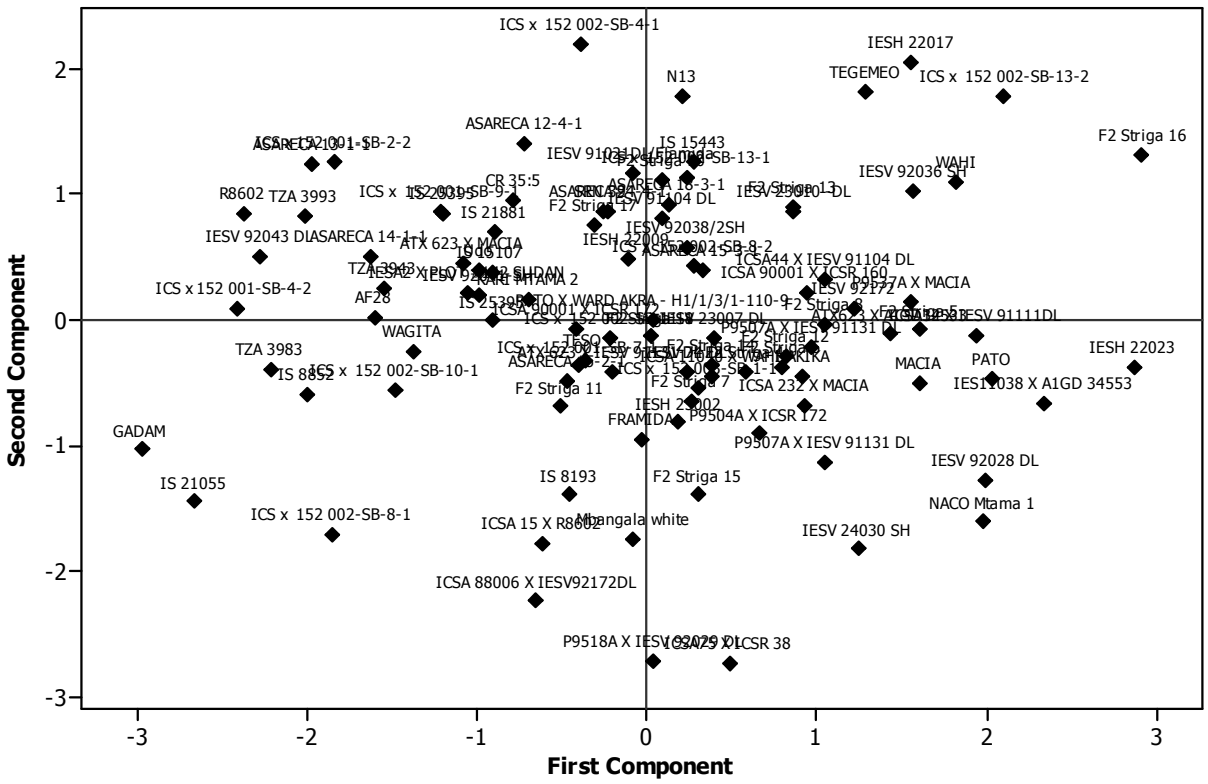

Figure 2: Score plotof first and second principle components explaining kernel phenotypic and biochemical variation among the evaluated sorghum genotypes.

Cluster analysis

Cluster analysis for the phenotypic kernel traits and biochemical parameters indicated a clear separation of the evaluated sorghum genotypes (Figure 3). Four main clusters was observed namely; cluster I, II, III and IV formed at 59.68% similarity level.(Table 4) indicates cluster means, explaining the differences among groupsof the evaluated genotypes. Cluster I grouped twenty (20)sorghum genotypesformed based on the lowest concentration of starch and small mean kernel diameter, and highest hundred seed weight, kernel hardness and protein content.

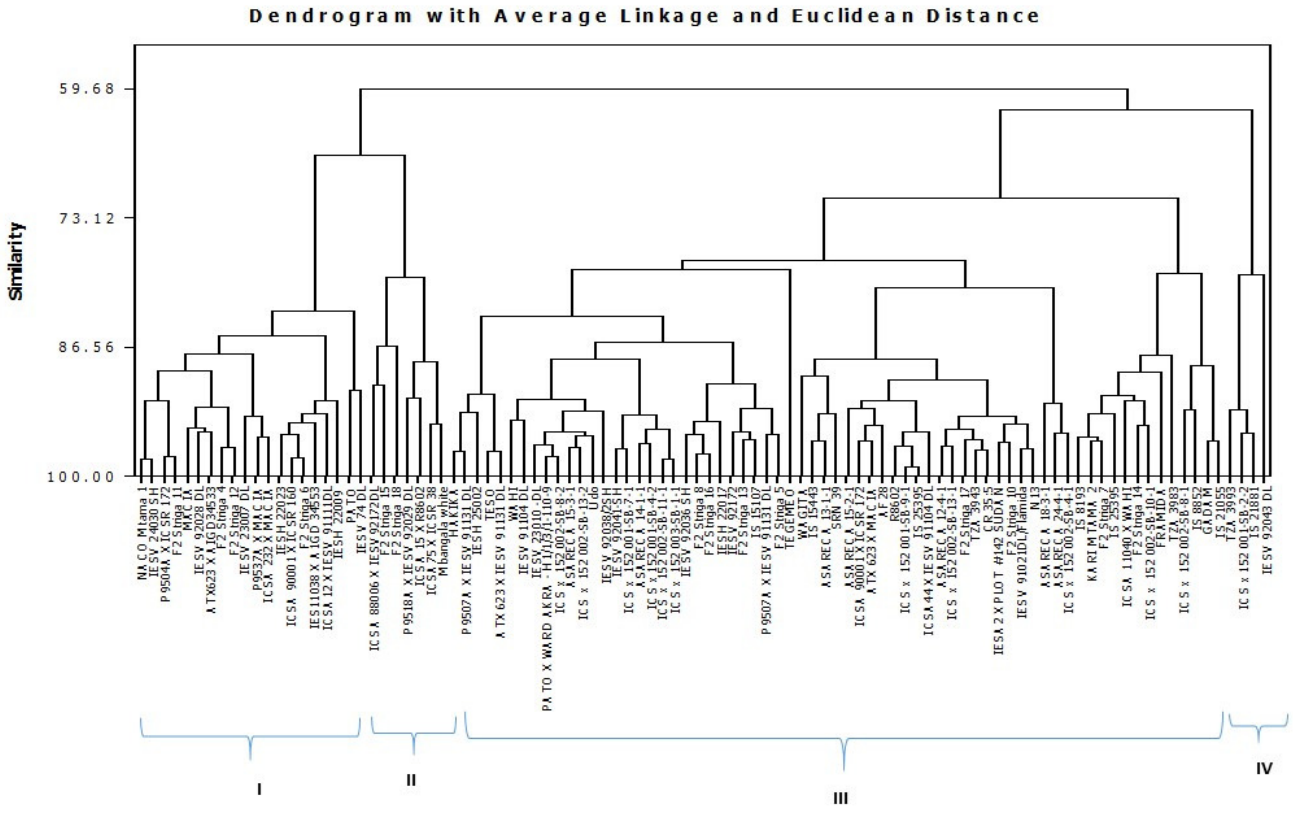

Figure 3: Dendrogram showing various clusters among 98 sorghum genotypes evaluated in terms of physiochemical properties.

Cluster II grouped seven (7) genotypes consisting of hybrids, breeding lines and a local cultivar (Mbangala white) with the average protein content, highest mean kernel diameter, and starch concentration.Cluster III grouped sixty seven (67) sorghum genotypes based on average mean kernel

diameter, 100 seed weight, kernel hardness, protein content and starch concentration. Cluster IV grouped four (4) sorghum genotypes originated from ICRISAT and Tanzania namely IESV92043DL, IS 21881, ICSx152001-SB-2-2 and TZA3993 these genotypes had the lowest mean kernel diameter, 100 seed weight, kernel hardness and protein content. Dendrogramshows that genotypes from the same origin and or the same type; were not necessarily assembled within similar clusters.

Table 4: Cluster means of the phenotypic and biochemical traits in the evaluated sorghum genotypes

Clusters	MKD	100Swt	Kernel hardness	Protein	Starch
1	3.0173	4.0499	96.0791	9.2978	39.4972
2	3.0571	3.6405	92.0763	8.9215	70.1171
3	3.0278	3.6451	62.4233	8.4778	44.9705
4	2.9163	3.2896	28.2581	7.9678	52.2067

MKD = mean kernel diameter, 100Swt =100 seed weight;

Identification of elite genotypes for breeding

Few sorghum genotypesperformed better In terms of 100 seed weight;these include genotype IES11038 X A1GD 34553 (6.20g), P9537A X MACIA (5.49g), F2Striga5 (5.30g), ICSA44 X IESV 91104 DL (5.30g) , ATX623 X AIGD34533 (5.12g), P9507A X IESV 91131 DL (5.12g) and F2 Striga 14 (5.03g).Lines F2Striga5 and F2Striga14 can be recommended for crop improvement in terms of yield. However, genotypes with highest average mean kernel diameter were ICS x 152 002-SB-13-2, F2 Striga 16, IESH 22017, IS 15443, F2 Striga 18, N13 and WAHI recorded 4.61, 4.54, 4.07, 3.82, 3.65, 3.62, and 3.60mm respectively.

Lines with the highest Kernel hardness include PATO,IESV 74 DL;IESV 92028 DL, Mbangala white and F2 Striga 11 which recorded 110.33, 108.43, 103.90, 101.11 and 100.72 N.The highest protein content were recorded in genotype NACO Mtama 1 (12.23),IESV 92174 DL (12.18), IESH 22023 (11.58),IESV 92028 DL (11.21) and ASARECA 15-3-1 (11.04).These genotypes can be potential source of hardness and protein

content in breeding programs. Hence, hardness and protein correlatedwith corneous portion in the endosperm; the laterplay significant role in resistance against pests including storage weevils. Improvement of these traits in commercial released varieties could benecessary for sustainablemanagement of storage insects. Nevertheless, more research is needed; a multi-location study is recommended to confirm potentiality of these genotypes.

Conclusion

The present study revealed a wide variability for the qualitative and quantitative parameters studied. Analysis of variance for the mean diameter, 100 seed weight, kernel hardness, protein and starch concentration showed a high significance difference ($p<0.001$). Crosses performed better in terms of yield possibly due to heterosis. The best genotypes in terms of 100 seed weight wereIES11038 X A1GD 34553 and P9537A X MACIA.However, lines F2Striga5 and F2Striga14 canbe recommendedto improve yield component. Promising genotypes in terms of mean kernel diameter were ICS x 152 002-SB-13-2, F2 Striga 16and IESH 22017. Lines with the uppermostkernel hardness include PATO, IESV 74 DL; IESV 92028 DL, and Mbangala white; representing potential sources of kernel hardness. Genotype NACO Mtama 1, IESV 92174 DL, IESH 22023 and IESV 92028 DL could be potential parental materials to improveprotein content in sorghum cultivars. However, weak correlation among these traits indicate the need for multi-location or multi-season study to confirm potentiality of these genotypes while accounting the effect of genetic environmental interaction. The studied materials were clustered into four main clusters at 59.68% similarity level; genotypes clustered together indicates the possibility of easy selection during hybridization. Physiochemical traits are useful in determination of food quality, processing and kernel protection against pests in sorghum. Variability identified in the present study could aid selection of useful traits for breeding precision.

Appendix

Table 5: Analysis of variance for the quantitative traits

Genotype	Origin	Type	100swt	MKD	hardness	Protein	Starch
NACO Mtama 1	Ilonga	Variety	4.3 A-F	3.07m-C	95.68H-K	12.229M	47.17 A-G
HAKIKA	Ilonga	Variety	4.2 Zab	3.275 x-I	76.8wxy	9.797 CDE	49.84 F-I
PATO	Ilonga	Variety	4.258z-E	3.16 r-E	110.33P	9.464 zA	33.41 e-h

WAHI	Ilonga	Variety	4.242 z-D	3.595 IJK	65.08 nop	10.479I	27.43 bc
TEGEMEO	Ilonga	Variety	4.108 yzA	3.535 F-K	78.25 w-z	7.347i-m	21.88 a
TESO	ICRISAT	Line	3.85vwx	2.755 d-p	81.18 yzA	7.364 i-n	48.33C-H
MACIA	Ilonga	Variety	3.583 r-u	3.27 w-I	99.2 K-N	10.323 HI	37.81 j-q
IESV 92041-SH	ICRISAT	Line	3.533q-t	2.645 c-h	63.89 l-p	7.382 i-n	44.93 v-C
IESH 25002	ICRISAT	Line	3.858 vwx	3.025 j-A	72.27 s-v	9.762 BCD	55.15 JK
IS 8193	ICRISAT	Line	3.483p-s	2.69c-k	63.7l-p	10.777 J	59.76 LM
IESH 22023	ICRISAT	Line	4.983 NOP	3.485E-J	91.55E-H	11.582 L	35.21e-k
IESV 23010 -DL	ICRISAT	Line	4.633 H-L	3.205 s-G	66.69 n-r	8.344stu	34.7 e-j
WAGITA	ICRISAT	Line	3.075 j-n	2.49 a-d	42.96 c	9.832 C-F	49.13 D-I
IS 25395	ICRISAT	Line	2.9 g-k	3.035 j-A	65.51 nop	8.082 r	52.37 IJ
ASARECA 14-1-1	ICRISAT	Line	2.083 c	2.775 d-q	67.25 o-r	7.049 d-h	42.93 s-z
IESV 92038/2SH	ICRISAT	Line	3.85vwx	2.92 f-w	70.38 rstu	8.397 tuv	33.9 e-i
IESV 92174 DL	ICRISAT	Line	2.033 bc	3.195 s-F	108.43P	8.432uvw	41.62 q-v
PATO X WARD AKRA -	ICRISAT	Hybrid	3.692 r-w	2.625 b-h	64.33 m-p	9.832 C-F	35.62 f-l
ASARECA 15-2-1	ICRISAT	Line	3.667 r-v	2.805d-q	52.15efg	10.199 GH	52.56 IJ
IS 15443	ICRISAT	Line	2.442de	3.82 KL	47.42 d	10.462 I	39.01 l-r
ASARECA 18-3-1	ICRISAT	Line	2.85 f-j	2.805 d-q	53.91fgh	10.777 J	22.5a
IESV 24030 SH	ICRISAT	Line	3.633 r-v	2.705 c-l	96.12IJK	12.177 M	45.67 w-D
IESV 23007 DL	ICRISAT	Line	3.95wxy	3.19 s-F	90.07 D-G	7.399 j-n	48.17C-H
KARI MTAMA 2	ICRISAT	Variety	3.633r-v	3.29y-I	64.45 m-p	7.067 d-h	58.35 KL
R8602	ICRISAT	Line	2.258 cd	2.565 a-f	48.27 de	6.601 ab	43.69 t-A
ASARECA 12-4-1	ICRISAT	Line	2.8 f-i	3.4B-J	59.45 jkl	6.874 cde	40.45 n-u
IESV 92036 SH	ICRISAT	Line	4.583 G-K	3.55 G-K	81.35 yzA	8.082 r	32.01def
ASARECA 13-1-1	ICRISAT	Line	2.083 bc	2.82 d-r	47.37 d	7.032 d-h	39.15l-s
ASARECA 15-3-1	ICRISAT	Line	2.033abc	3.51 E-K	65.78n-q	11.039K	38.96l-r
ASARECA 24-4-1	ICRISAT	Line	2.85 f-j	2.775 d-q	48.3 de	10.549IJ	26.77 bc
IESV 92028 DL	ICRISAT	Line	4.35 A-G	2.92 f-w	103.9 O	11.214K	39.04 l-r
IESV 92172	ICRISAT	Line	3.308 n-q	3.58 H-K	78.12w-z	10.532 IJ	41.33p-v
P9507A X IESV 91131 DL	ICRISAT	Hybrid	5.117 PQ	2.76d-q	74.65 uvw	10.584 IJ	49.77E-I
ICSA 88006 X	ICRISAT	Hybrid	2.85 f-j	3.105o-D	81.96 zA	10.077	79.05 QR
P9518A X IESV 92029 DL	ICRISAT	Hybrid	4.033 xyz	2.625 b-h	99.38K-N	9.709 A-D	71.84 O
P9507A X IESV 91131 DL	ICRISAT	Hybrid	4.8 K-O	2.89 e-u	74.22 t-w	9.499zA	40.44 n-u
ICSA44 X IESV 91104 DL	ICRISAT	Hybrid	5.3QR	3.31 z-J	51.23 d-g	9.814 CDE	46.35 y-F
IESA2 X PLOT *#142*	ICRISAT	Hybrid	3.117k-n	2.305 ab	57.25 hij	8.869 xy	34.61 e-j
ICSA12 X IESV 91111DL	ICRISAT	Hybrid	3.7 r-w	3.245 v-H	87.26CDE	11.582 L	29.56 cd
IES11038 X A1GD 34553	ICRISAT	Hybrid	6.2 S	2.75 d-o	87.64 CDE	10.322 HI	34.38 e-j
ICSA 11040 X WAHI	ICRISAT	Hybrid	4.717 I-M	3.235 u-H	57.15 hij	9.622 ABC	58.6 L
P9504A X ICSR 172	ICRISAT	Hybrid	3.767 t-w	3.035 j-A	101.29	8.502 uvw	49.56 E-I
P9537A X MACIA	ICRISAT	Hybrid	5.492 R	3.29 y-I	86.34 BCD	7.802 opq	42.31 r-x
ICSA75 X ICSR 38	ICRISAT	Hybrid	3.517 q-t	2.69 c-k	97.56 KLM	11.617 L	65.23 N
ICSA 232 X MACIA	ICRISAT	Hybrid	3.715 s-w	3.055l-B	88.34 DEF	10.042	44 u-B
ICSA 15 X R8602	ICRISAT	Hybrid	2.85 f-j	3.375 A-J	101.5 MNO	7.399 j-n	79 QR
ATX623 X AIGD34533	ICRISAT	Hybrid	5.117 PQ	3.005 i-z	102.63 NO	7.277 h-l	37.56 i-p
ICSA 90001 X ICSR 172	ICRISAT	Hybrid	4.217 z-C	2.715d-m	57.09 hij	8.677 wx	47.54 B-G

TZA 3993	Gene	Local	3.258m-p	2.54 a-e	33.85 b	7.399 j-n	45.6 w-D
IESH 22009	ICRISAT	Line	3.083 j-n	2.75d-o	95.5 H-K	6.734 abc	29.8 cd
ICSA 90001 X ICSR 160	ICRISAT	Hybrid	3.667 r-v	3.055 l-B	91.96 F-I	8.642 vwx	31.93 def
ATX 623 X IESV 91131 DL	ICRISAT	Hybrid	4.217 z-C	2.785 d-q	82.28zAB	7.2 g-l	50.54GHI
IESH 22017	ICRISAT	Line	4.492 E-I	4.07 L	76.47 vwx	6.57 a	31.5 de
ATX 623 X MACIA	ICRISAT	Hybrid	4.442 B-H	2.545a-e	54.49 f-i	6.55 a	46.03 x-E
IESV 91021DL/Flamida	ICRISAT	Line	3.483 p-s	3.31 z-J	52.43 efg	8.484 uvw	38 j-q
F2 Striga 4	ICRISAT	Line	4.483 D-I	2.74 d-n	95.08 H-K	7.592 mno	41.3 p-v
F2 Striga 5	ICRISAT	Line	5.3QR	3.11 p-D	70.27 r-u	10.182 GH	39.54 m-s
F2 Striga 6	ICRISAT	Line	3.2mn	2.82 d-r	92.84 G-J	9.972 D-G	32.78d-g
F2 Striga 7	ICRISAT	Line	3.85 vwx	3.21 t-G	65.47 nop	10.094 GH	56.68 KL
F2 Striga 8	ICRISAT	Line	3.617 r-v	3.09 n-C	78.4 w-z	10.497 I	34.76 e-j
F2 Striga 11	ICRISAT	Line	3.033 i-m	2.77 d-q	100.72 L-O	6.892 c-f	49.8 F-I
F2 Striga 10	ICRISAT	Line	4.633 H-L	3.04 k-A	58.66 ijk	7.137 e-j	36.7 h-n
F2 Striga 12	ICRISAT	Line	4.45 C-H	2.835 d-r	96.71 JKL	7.784 op	38.88k-r
F2 Striga 13	ICRISAT	Line	4.767 J-N	3.505 E-K	79.52 x-A	6.515 a	42.18 r-w
F2 Striga 14	ICRISAT	Line	5.033 OP	3.445 D-J	64.62m-p	8.099 rs	64.56N
F2 Striga 15	ICRISAT	Line	4.85 L-O	3.165 r-E	79.45 x-A	8.537 uvw	70.4 O
F2 Striga 16	ICRISAT	Line	4.217 z-C	4.54 M	80 x-A	10.182GH	34.48e-j
F2 Striga 17	ICRISAT	Line	4.75 J-N	2.875 e-t	57.43 hij	6.839bcd	42.72 r-y
F2 Striga 18	ICRISAT	Line	3.617 r-v	3.65 JK	83.57 ABC	6.944 c-g	62.06MN
ICS x 152 001-SB-2-2	ICRISAT	Line	2.7 fg	3.235 u-H	30.16 b	7.434 lmn	51.89 HIJ
ICS x 152 001-SB-4-2	ICRISAT	Line	1.85 ab	2.36 abc	68.02 p-s	6.55 a	46.08 x-F
TZA 3943	Gene	Local	3.258m-p	2.295 ab	53.58 fgh	7.784 op	40.83 o-u
Udo	Ilonga	Local	2.667 fg	2.655 c-i	62.51 k-n	8.502 uvw	37.43 i-o
ICS x 152 001-SB-7-1	ICRISAT	Line	3.617 r-v	2.68 c-j	62.84k-o	9.464 zA	46.53 z-F
Mbangala white	Ilonga	local	3.767 t-w	2.79d-q	101.11MNO	8.169 rst	63.23 MN
ICS x 152 001-SB-9-1	ICRISAT	Line	2.675 fg	3.07 m-C	51.11 d-g	7.784 opq	44.75 v-C
TZA 3983	Gene	Local	1.808 a	2.96 h-z	54 fgh	8.169 rst	64.85N
ICS x 152 002-SB-4-1	ICRISAT	Line	3.617 r-v	3.115 q-D	47.62 d	6.944 c-g	24.61 ab
ICS x 152 002-SB-8-1	ICRISAT	Line	3.517 q-t	2.585 a-g	59.49 jkl	8.344 stu	78.25 QR
ICS x 152 002-SB-8-2	ICRISAT	Line	3.85 vwx	2.855 e-s	63.85 l-p	9.359z	33.85 e-i
ICS x 152 002-SB-10-1	ICRISAT	Line	3.8 u-x	2.655c-i	60.16 j-m	7.154 f-k	62.52 MN
ICS x 152 002-SB-11-1	ICRISAT	Line	3.75 t-w	2.87 e-t	70.47 r-u	8.467 uvw	46.85 A-G
ICS x 152 002-SB-13-1	ICRISAT	Line	3.583 r-u	3.475 E-J	57.31 hij	8.484 uvw	39.26 l-s
ICS x 152 002-SB-13-2	ICRISAT	Line	3.8 u-x	4.605 M	65.19 nop	9.517 zAB	37.79 j-q
ICS x 152 003-SB-1-1	ICRISAT	Line	4.158 yzA	2.785 d-q	70 q-t	9.797 CDE	46.01 x-E
IS 8852	ICRISAT	Line	3.3n-q	2.925 g-x	55.61 g-j	6.731 abc	72.79 OP
IS 15107	ICRISAT	Line	3.187 lmn	2.68 c-j	76.97 wxy	6.594 ab	40.18 n-t
AF28	ICRISAT	Line	2.95 h-l	2.645 c-h	57.1 hij	7.627 no	51.28HI
CR 35:5	ICRISAT	Line	3.717 s-w	3.005 i-z	54.78 f-i	6.962 c-g	42.93 s-z
GADAM	ICRISAT	Line	2.633 ef	2.625 b-h	47.08 d	7.119 e-i	79 R
IS 25395	ICRISAT	Line	3.133k-n	2.955 h-y	50.5def	7.417 k-n	44.77 v-C
FRAMIDA	ICRISAT	Line	2.767 fgh	3.42 C-IJ	71.78stu	10.497 I	62.54 MN
SRN 39	ICRISAT	Line	4.533 F-IJ	2.91 f-v	41.91 c	8.467 uvw	40.76o-u

N13	ICRISAT	Line	3.85 vwx	3.615 IJK	54.31 f-i	7.294 h-l	36.37 g-m
IESV 91104 DL	ICRISAT	Line	4.9M-P	2.605 a-h	62.58 k-o	7.399 j-n	31.44 de
IESV 92043 DL	ICRISAT	Line	3.75 t-w	2.68 c-j	14.94 a	8.029 pr	59.81 LM
IS 21881	ICRISAT	Line	3.45 o-r	3.21 t-G	34.09 b	9.009 y	51.53 HI
IS 21055	ICRISAT	Line	3.217	2.285 a	47.09d	8.047 r	75.61 PQ
		Mean	3.02	3.713	70.02	8.656	45.95
		SE	0.1	0.075	1.377	0.08	1.116
		SED	0.14	0.106	1.948	0.114	1.578
		LSD	0.28	0.211	3.866	0.226	3.131
		CV	4.7	2.9	2.8	1.3	3.4
		F prob	<0.001	<0.001	<0.001	<0.001	<0.001

MKD = mean kernel diameter, 100Swt =100 seed weight;
SE= Standard error of mean, SED = Standard of error of differences of means, LSD = Least significance difference of means (5% level), CV= coefficient of variation,

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