Peruvian Journal of Agronomy
http://revistas.lamolina.edu.pe/index.php/jpagronomy/index

RESEARCH ARTICLE
https://doi.org/10.21704/pja.v9i1.2215

Received for publication: 09 January 2025
Accepted for publication: 15 March 2025
Published: 15 April 2025
ISSN: 2616-4477

Morphological and nutritional characterization of sorghum (*Sorghum bicolor* L. Moench) accession collected in a typical guinea savanna ecology

Caracterización morfológica y nutricional de accesiónes de sorgo (*Sorghum bicolor* L. Moench) colectadas en una ecología típica de la savana guinea

Folusho Anuoluwapo BANKOLE[1], Olawale Serifdeen ABODERIN[1*], Kehinde Shukurat IBIYINKA[1], Olasunkanmi OLAJIDE[1], Mobolaji Omolabake MUSA[2]

[1] University of Ilorin, Faculty of Agriculture, Nigeria Department of Agronomy
[2] University of Ilorin, Faculty of Agriculture, Department of Agricultural Extension and Rural Development, Nigeria

*Corresponding author: olawaleaboderin@yahoo.com
*https://orcid.org/0009-0003-7435-1022

Abstract

Germplasm collection and characterization are crucial for crop improvement. Twenty different sorghum accessions collected from Kwara State, Nigeria, were evaluated over two years (2021 and 2022) at the University of Ilorin Research field to assess their morphological and nutritional diversity. Morphological traits such as plant structure, leaf orientation, panicle characteristics, seed attributes, and nutritional components such as carbohydrates, proteins, fats, and anti-nutritional factors (oxalate, phytate, HCN, phenolics, tannins) were evaluated. Analysis of variance revealed that weight at harvest and grain weight had high genotypic (GCV) and phenotypic (PCV) coefficients of variation (> 20 %), while other morphological traits exhibited low to moderate GCV and PCV values (10 % – 20 %). Nutritional traits such as phytate, moisture, ash content, carbohydrates, lipids, and fiber showed moderate GCV and PCV, while oxalate, HCN, phenolics, tannins, and protein content exhibited high variability. Principal Component Analysis identified days to flowering, leaf orientation, and plant height as important selection criteria in sorghum breeding programs, while fiber, carbohydrates, lipids, and phytate were key nutritional traits influencing the dietary value and quality of sorghum grains. Hierarchical clustering based on morphological traits grouped the accessions into four distinct clusters, while clustering by nutritional attributes classified them into three groups, each varying in levels of antinutrients, bioactive compounds, and macronutrients. Sorghum accessions identified in each cluster with superior traits offer opportunities for targeted breeding programs aimed at enhancing sorghum productivity, resilience, and nutritional value.

Keywords*: Nutritional traits, antinutritional traits, variation, accessions, Principal component analysis.*

Resumen

La recolección y caracterización del germoplasma son cruciales para la mejora de los cultivos. Veinte accesiones diferentes de sorgo recolectadas en el estado de Kwara, Nigeria, se evaluaron durante dos años (2021 y 2022) en el campo de investigación de la Universidad de Ilorin para determinar su diversidad morfológica y nutricional. Se evaluaron rasgos morfológicos como la estructura de la planta, la orientación

How to cite this article:
BANKOLE, F.A., ABODERIN, O.S., IBIYINKA, K.S., OLAJIDE, O., MUSA, M.O. (2025). Morphological and nutritional characterization of sorghum (*Sorghum bicolor* L. Moench) accession collected in a typical guinea savanna ecology.. *Peruvian Journal of Agronomy, 9*(1), 16-30. https://doi.org/10.21704/pja.v9i1.2215

de las hojas, las características de la panícula, los atributos de las semillas y componentes nutricionales como carbohidratos, proteínas, grasas y factores antinutricionales (oxalato, fitato, HCN, fenólicos, taninos). El análisis de la varianza reveló que el peso en el momento de la cosecha y el peso del grano presentaban altos coeficientes de variación genotípica (GCV) y fenotípica (PCV) (> 20 %), mientras que otros rasgos morfológicos mostraban valores bajos a moderados de GCV y PCV (10 % - 20 %). Los rasgos nutricionales como el fitato, la humedad, el contenido de cenizas, los carbohidratos, los lípidos y la fibra mostraron un GCV y un PCV moderados, mientras que el oxalato, el HCN, los fenólicos, los taninos y el contenido de proteínas mostraron una alta variabilidad. El análisis de componentes principales identificó los días hasta la floración, la orientación de las hojas y la altura de la planta como criterios de selección importantes en los programas de mejora del sorgo, mientras que la fibra, los carbohidratos, los lípidos y el fitato eran rasgos nutricionales clave que influían en el valor dietético y la calidad de los granos de sorgo. La agrupación jerárquica basada en rasgos morfológicos generó cuatro grupos distintos, mientras que la agrupación por atributos nutricionales las clasificó en tres grupos, cada uno de los cuales variaba en niveles de antinutrientes, compuestos bioactivos y macronutrientes. Las accesiones de sorgo identificadas en cada grupo con rasgos superiores ofrecen oportunidades para programas de mejora dirigidos a mejorar la productividad, la resistencia y el valor nutricional del sorgo.

Palabras clave: *Rasgos nutricionales, rasgos antinutricionales, variación, accesiones, análisis de componentes principales.*

Introduction

Sorghum (*Sorghum bicolor* L. Moench) holds significant agricultural and socioeconomic importance as a staple crop in many parts of sub-Saharan Africa, particularly in Nigeria (Kavithamani et al., 2019). Its resilience to harsh environmental conditions, adaptability to diverse agroecological zones, and versatility in end-use applications make it a crucial component of food security and livelihoods in the region (Food and Agriculture Organization [FAO], 2020; Tasie & Gabreyes, 2020; Stagnati et al., 2021).

Germplasm collection and characterization are fundamental in establishing a gene pool for crop improvement (Chakrabarty et al., 2022). Characterization of genotypes serves as the cornerstone of plant breeding, facilitating the identification, evaluation, and utilization of desirable traits in crop improvement (Motlhaodi et al., 2017). It provides breeders with a deeper understanding of genetic diversity within plant populations, enabling informed decisions in selecting parental lines and designing breeding strategies (Perazzo et al., 2014; Boyles et al., 2017; Stagnati et al., 2021). The International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), a global center for improving mandate crops including sorghum, millet, and groundnut, has made substantial achievements in germplasm collection, maintenance, and characterization. However, there is a lack of information regarding the characterization of sorghum germplasm in the Guinea Savanna of Nigeria. This region, with a Sudano-Sahelian climate and distinct wet and dry seasons, is a crucial hub for sorghum production, supporting the agrarian economy and traditional human and livestock feed systems. Its agroecological diversity, spanning from the southern forest-savanna transition zone to the northern semi-arid savanna, harbours a rich genetic reservoir of sorghum germplasm adapted to varied environmental conditions and farming practices (Ajeigbe et al., 2018; Yahaya et al., 2022).

Various methods, including morphological, biochemical, molecular, and nutritional approaches, are employed in characterizing germplasms. Morphological characterization involves evaluating phenotypic traits useful for identifying variations and similarities among genotypes, particularly in early breeding stages (Boyles et al., 2017; Fracasso et al., 2017; Perazzo et al., 2014). Nutritional characterization, on the other hand, analyzes key nutritional components influencing dietary value and health-promoting properties, aiding in identifying sorghum varieties with superior nutritional profiles and developing value-added products (Rhodes et al., 2017; Boyles et al., 2017; Xiong et al., 2019).

Statistical methods like cluster analysis, including hierarchical clustering, K-means clustering, and model-based clustering, are valuable tools for characterizing germplasm

collections based on genetic or phenotypic similarities (Cruz et al., 2014; Kavithamani, et al., 2019; Ni et al., 2019). These methods help classify germplasms into distinct groups, aiding in maintaining diversity within breeding programs and identifying valuable genetic traits for future efforts (Jain & Patel, 2016). Ward's Minimum Variance Cluster Analysis, commonly known as Ward's method, is often used for hierarchical clustering, providing quantitative measures of relatedness and dissimilarity between clusters (Murtagh & Legendre, 2014). Principal Component Analysis (PCA), another statistical tool commonly employed by breeders, serves as a dimensionality reduction technique, effectively transforming complex datasets into uncorrelated variables known as principal components (Jain & Patel, 2016; Ni et al., 2019; Kavithamani et al., 2019). Principal Component Analysis identifies key descriptors or traits explaining the majority of observed diversity among samples, enabling more efficient and targeted characterization efforts. It also helps in identifying important agronomic traits correlated with yield, thus aiding breeders in prioritizing these traits in their breeding programs (Jain & Patel, 2016; Ni et al., 2019). This study was therefore carried out to assess the phenotypic variability among sorghum accessions and characterize them based on morphological and nutritional qualities, with the main aim of identifying accessions with desirable traits suitable for future breeding programs.

Materials and methods

Germplasm Collection

A five-stage sampling procedure was employed for germplasm collection. The first stage involved a purposive selection of four Local Government Areas (LGAs) in Kwara State, Nigeria and they were Ilorin East, Ilorin South, Ifelodun, and Irepodun LGAs because of the significant diversity of sorghum morphs in the areas. The second stage involved a stratified random sampling of five towns from each of the selected LGAs to ensure a comprehensive coverage of the region's sorghum genetic diversity. In Ilorin East, collection sites included Oke-Ose, Oke-Oyi, Apata-Yakuba, Ile-Apa, and Sentu. Similarly, Ilorin South encompassed Agbabiaka, Tanke, Unilorin Environs, Fufu, and Akanbi. Ifelodun included Babanla, Sare, Omupo, Ganmu-Alheri, and Oke-Ode, while Irepodun's towns visited were Ajase, Omu Aran, Gaa Federal, and Ara Orin (Figure 1). The third stage was a purposive selection of collection sites known for diverse

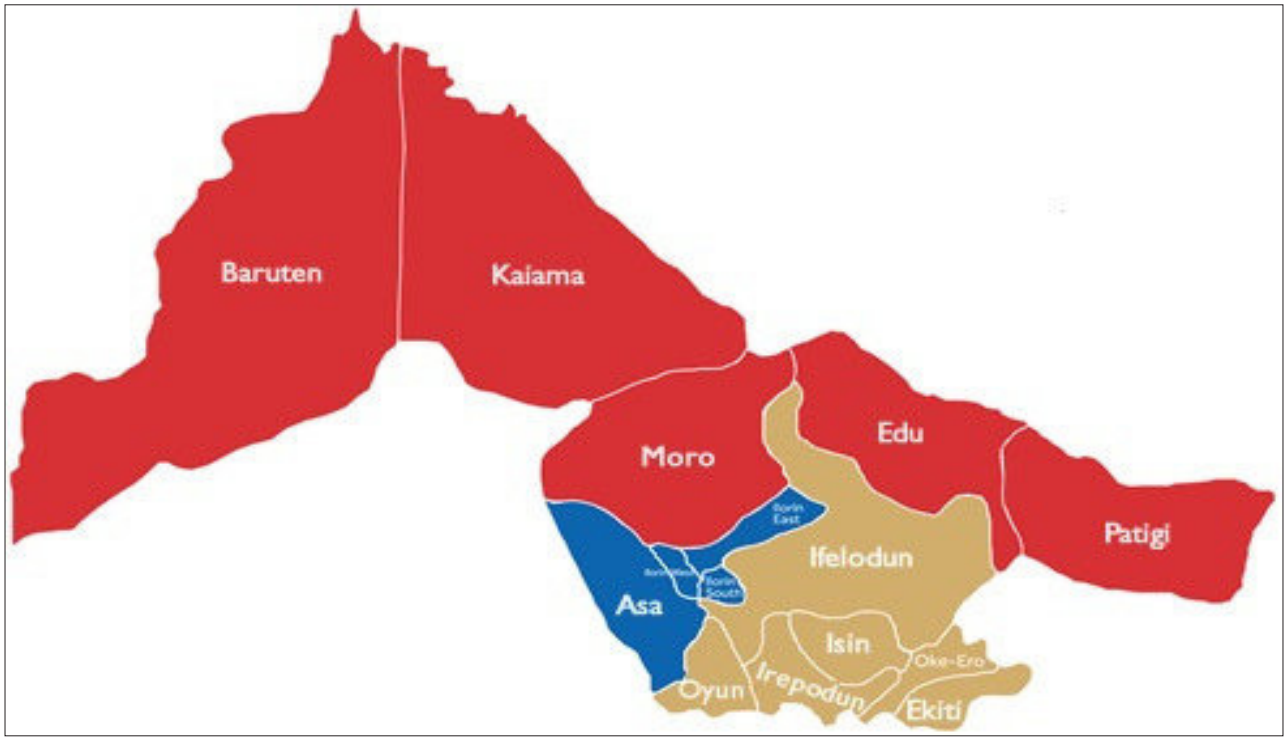

Figure 1. Map of Kwara State, Nigeria showing the Local Government Areas

sorghum morphs based on local knowledge and recommendations from agricultural experts. The fourth stage involved a random collection of 160 sorghum accessions from the selected LGAs from 10th December 2019 to 10th January 2020. Collections were carried out either during harvest or by selecting samples from farmers' stored stacks. The fifth was a purposive examination and narrowing down to twenty distinct accessions from the collected sorghum accessions, constituting the genetic materials used in this study for characterization and evaluation. These accessions were chosen based on observed differences in morphological traits, including shapes (peduncle, panicle, grain), orientation (leaf and panicle), compactness (panicle), color (glume and grain), and the presence of awns.

Field evaluation and management

The twenty sorghum accessions were evaluated at the Teaching and Research Farm of the University of Ilorin, Nigeria, over two successive years (2021 and 2022) under rainfed conditions. The University of Ilorin is a typical Southern Guinea Savanna (SGS) agroecology with latitude $8^0$30'N, longitude $4^0$32'60E, altitude 289 m and mean annual rainfall of 1318 mm. The experiment was laid out in a Randomized Complete Block Design with two replications. Two rows, each measuring 5 m in length, were utilized, with inter and intra-row spacings set at 0.75 m and 0.5 m, respectively. Initially, five seeds were planted per hole, subsequently thinned to two plants per hill at two weeks after planting (WAP) to achieve a population density of 53 333 plants per hectare. Urea fertilizer was applied at 6 weeks after planting at the rate of nitrogen of 50 $kg.ha^{-1}$, and all other agronomic practices, including weed control, were performed as needed.

Data collection

Data were collected on morphological, agronomic, and quality traits, either on a plot basis or from a representative sample. Morphological traits were measured from five randomly selected plants per plot in each replication. Plant height (cm) was measured from the base of the plant to the apex of the panicle using a measuring tape. The number of leaves per plant was recorded by counting. Leaf length (cm) and leaf width (cm) were measured using a ruler, with length taken from the base to the tip and width measured at the broadest point. Inflorescence (panicle) length (cm) and width (cm) were measured from the base to the tip and across the widest point of the sorghum panicle using a ruler for the length and caliper for the width. Grain Covering (%) was estimated visually as the proportion of the grain surface covered by glumes.

Agronomic traits were assessed on a plot basis. Days to 50 % flowering (DF) was recorded as the number of days for 50 % of the plants per plot to flower. Weight at harvest (g) and grain weight (g) were determined using a weighing scale. The 100-seed weight (g) and 1000-seed weight (g) were measured by counting and weighing the respective number of seeds.

Qualitative traits, including grain color, grain luster, and endosperm texture, were assessed from a representative sample of five plants per row using standardized visual evaluation methods. The grain color was categorized into four groups: dark red, light red, red, and white. This was visually assessed and recorded during the harvest period. Grain luster, indicating the shininess or glossiness of the grain surface, was classified as lustrous or non-lustrous. To determine endosperm texture, grains from each accession were broken and assessed visually and manually. Grains that were opaque, white or pale in color, with a floury texture that crumbled easily into a fine powder, were classified as having completely starchy endosperm. Grains that had a combination of opaque and translucent areas, with mixtures of floury and vitreous textures, which partially crumbled into powder but also had harder fragments resistant to breaking, were classified as having mostly starchy endosperm

Additionally, a representative sample of the sorghum accessions was carefully selected and sent to the laboratory for comprehensive nutritional analysis. The analysis included the determination of various nutritional and antinutritional components, including oxalate, phytate, hydrocyanic acid (HCN), phenolics, tannin, moisture content, ash content, carbohydrates (CHO), caloric content, lipid

content, dietary fiber, and protein content. Each component was meticulously quantified using appropriate laboratory techniques (Association of Official Analytical Collaboration [AOAC] 2019) to provide a detailed nutritional profile of the sorghum accessions under investigation.

Data analysis

The data collected on both morphological and nutritional data were subjected to Analysis of Variance (ANOVA) using the General Linear Model (GLM) procedure of Statistical Analysis System (SAS) version 9.2 (SAS Institute, 2008). The descriptive statistics parameters of the sorghum accessions were computed and the calculated least square means were separated using the Fisher's least significant difference (LSD) test at 0.05 probability level.

Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) were calculated from the ANOVA.

$$GCV = (\sigma_g / \mathcal{X}) \times 100$$

$$PCV = (\sigma_p / \mathcal{X}) \times 100$$

Where σ_g = Genotypic standard deviation = $\sqrt{(\sigma_g^2)}$

σ_p = Phenotypic standard deviation = $\sqrt{(\sigma_p^2)}$

σ_g^2 = Genotypic Variance = (MSG - MSGEI)/re

σ_p^2 = Phenotypic Variance = $\sigma_g^2 + (MSGEI-MSE)/r + MSE$

X = Mean

MSG = Mean sum of squares for genotypes

MSGEI = Mean sum of squares for genotype x environment interaction

MSE = Mean sum of squares for environment

r = Number of replications

e = Number of environments

PCV and GCV were classified as low (< 10 %), Moderate (10 % – 20 %) and high (> 20 %) (Sivasubramanian & Madhavamenon, 1973).

Principal Component Analysis (PCA) and cluster analysis were performed using Statistical Analysis System (SAS Institute, 2008) software version 9.2. PCA was applied to identify the most influential variables contributing to the observed variation in sorghum morphological or nutritional traits. Cluster analysis was conducted separately for the standardized datasets of morphological traits and nutritional qualities. Standardization ensured that all variables were on a comparable scale.

Results

Mean Performance and variability of Morphological and nutritional traits in sorghum accessions

The mean performance for morphological and nutritional traits of the sorghum accessions, along with the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for each trait, are presented in Table 1. For all morphological traits, the PCV was higher than the GCV. Days to flowering (DF), number of leaves (NL), leaf dimensions (length and width), and inflorescence traits (length and width) exhibited low GCV (< 10 %) and moderate PCV (10 % – 20 %). Plant height (PHT), grain covering % (GC), number of panicles harvested (PH), 100-seed weight (HSW), and 1000-seed weight (TSW) displayed low to moderate GCV and high PCV (> 10 %). Among the morphological traits, weight at harvest (WH) and grain weight (GW) exhibited the highest GCV and PCV values.

For nutritional traits, PCV ranged from 9.48 % for calories to 51.20 % for HCN, while GCV ranged from 9.54% for calories to 51.21 % for HCN. Traits such as phytate, moisture, ash content, carbohydrate content, lipid, and fiber content exhibited moderate GCV and PCV values. In contrast, high GCV and PCV values were observed for oxalate, HCN, phenolics, tannin, and protein content.

Characterization of Sorghum Accessions by Qualitative Traits

The qualitative traits of the 20 sorghum accessions, including grain color, grain luster, and endosperm texture, are presented in Figure 2. The accessions were categorized into four

Table 1. Estimation of Mean and Variations for Morphological and Nutritional Traits in the evaluated Sorghum accessions

Variable	MIN	MAX	MEAN	GCV	PCV
Morphological Traits					
Days to flowering	81.00	86.00	83.70	7.67	15.68
Number of leaves	7.00	8.00	7.30	5.13	19.70
Leaf Length (cm)	14.30	14.80	14.60	3.87	8.55
Leaf Width (cm)	7.70	8.80	8.40	8.38	18.11
Plant Height (cm)	190.60	243.30	230.20	8.44	21.12
Inflorescence length (cm)	8.80	9.50	9.10	3.60	10.01
Inflorescence width (cm)	5.60	6.70	6.10	2.32	14.57
Grain covering (%)	46.30	66.30	57.40	9.81	34.14
Panicle Harvested	23.00	30.00	27.00	12.23	32.67
Weight at Harvest (g))	1081.00	1518.00	1131.00	27.18	54.56
Grain weight (g)	976.00	1455.00	1054.00	29.52	59.42
100 seed weight (g)	6.30	7.80	7.00	5.35	16.58
1000 Seed weight (g)	72.50	95.00	80.30	10.90	24.92
Nutritional Traits					
Oxalate	2.90	14.50	8.85	34.61	34.61
Phytate	0.20	0.40	0.37	14.79	14.79
Hydrocyanic acid (HCN)	1.50	9.40	3.21	51.20	51.21
Phenolics	9.55	32.30	20.87	28.25	28.25
Tanin	1.00	4.40	2.67	31.50	31.60
Moisture	5.20	7.90	6.04	13.18	14.67
Ash	1.40	2.15	1.77	11.79	15.21
Carbohydrate (CHO)	69.81	81.04	75.90	14.10	14.17
Lipid	3.25	6.05	4.33	16.03	18.82
Fibre	2.26	4.10	3.25	17.77	17.79
Protein	4.40	12.20	8.63	25.90	25.90
Calories	355.34	376.18	364.30	9.48	9.54

GCV: Genotypic Coefficient of Variation; PCV: Phenotypic Coefficient of Variation.

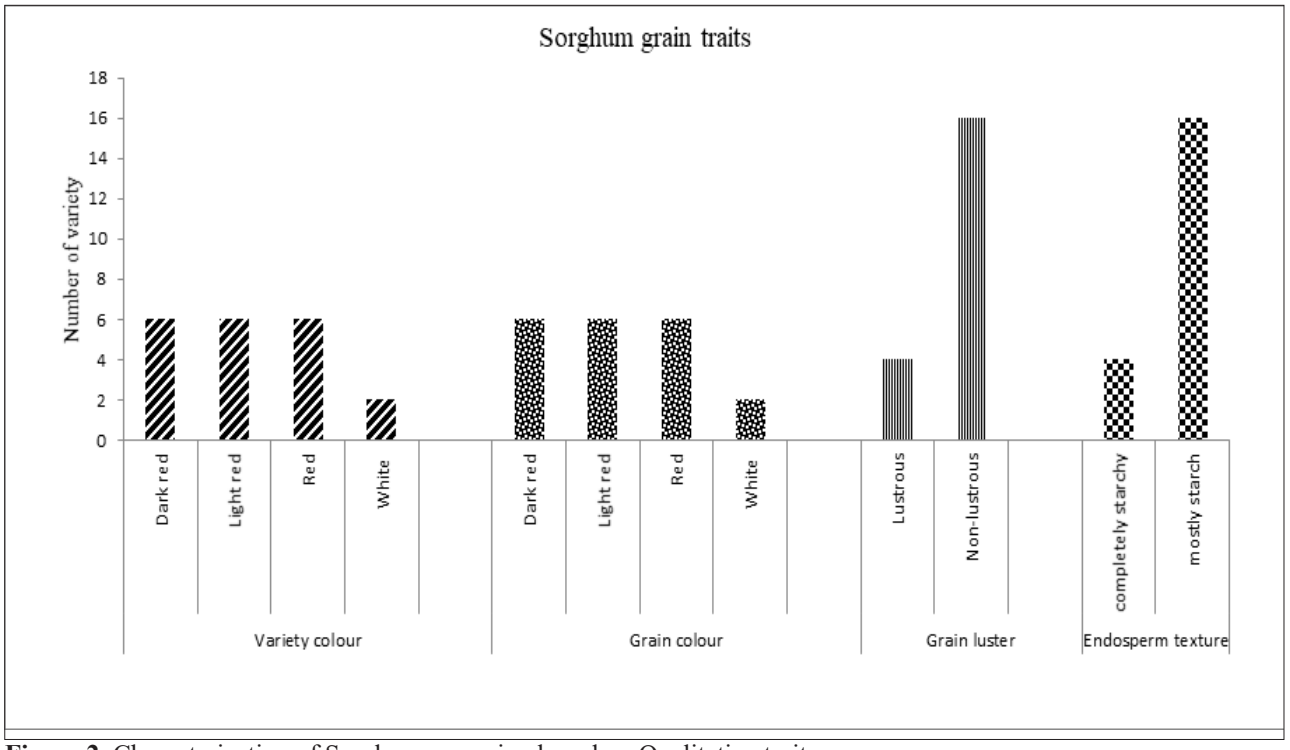

Figure 2. Characterization of Sorghum accession based on Qualitative traits

grain color groups: dark red (6 accessions), light red (6 accessions), red (6 accessions), and white (2 accessions). For grain luster, the accessions were classified into lustrous and non-lustrous categories. Only 4 accessions exhibited lustrous grains, while the majority (16 accessions) were non-lustrous. Endosperm texture was categorized into completely starchy and mostly starchy types. Four accessions were identified as having a completely starchy endosperm, whereas the remaining 16 accessions were mostly starchy.

Principal Component Analysis of Morphological and Nutritional Traits

Principal Component Analysis (PCA) conducted on the 12 morphological and 12 nutritional traits of the sorghum accessions revealed significant patterns of variability among the 24 traits. These traits were grouped into 24 principal components, collectively accounting for the total observed variation. Eigenvalues ranged from 0 to 5.06, with the proportion of variance explained varying from 0 to 20.2%. The first five principal components, which cumulatively accounted for 65 % of the total variation, were identified as significant and selected for further interpretation. The loadings of individual variables in each principal component were also calculated to understand their contribution to the PC. Principal Component 1 (PC1), with an eigenvalue of 5.06 and accounting for 20% of the variance, was strongly associated with HSW, TSW, and nutritional attributes such as fiber, calories, and carbohydrate content (CHO). PC2, which explained 16 % of the variation with an eigenvalue of 3.88, was dominated by DF, PHT, and lipid content. The third principal component (PC3), contributing 11 % of the variance, had GW, PHT, and leaf width (LW) as major contributors. PC4 and PC5, both explaining 9% of the total variation with eigenvalues of 2.26 and 2.24, respectively, were associated with traits such as weight at harvest, leaf number, and inflorescence length, as well as nutritional traits like moisture content and phytate (Table 2).

Table 2. Eigenvalues, total and cumulative variance of the first five principal components describing the variations in the sorghum accessions evaluated

Characters	Principal Component (PC)				
	PC1	PC2	PC3	PC4	PC5
Days to flowering	0.004	**0.34**	-0.25	0.05	-0.07
Number of leaves	-0.002	0.20	-0.16	0.01	**0.42**
Plant Height (cm)	-0.038	**0.31**	**0.40**	-0.03	-0.09
Leaf Length (cm)	0.004	0.09	-0.09	0.20	**-0.44**
Leaf Width (cm)	0.133	-0.21	**-0.35**	0.10	-0.07
Weight at Harvest (g)	0.130	-0.11	-0.07	**-0.56**	-0.04
Inflorescence length (cm)	0.160	-0.10	0.11	-0.20	**-0.38**
Inflorescence width (cm)	0.268	-0.09	0.12	0.18	0.23
Grain covering (%)	-0.113	0.04	0.18	-0.13	0.30
100 seed weight (g)	**0.356**	0.10	0.22	-0.01	0.04
Grain weight (g)	-0.151	-0.03	**0.40**	-0.03	0.10
1000 Seed weight (g)	**0.356**	0.10	0.22	-0.01	0.04
Oxalate	0.187	-0.06	0.07	0.08	0.13
Phytate	0.036	-0.30	0.17	**0.42**	0.00
Hydrocyanic acid (HCN)	0.076	0.08	-0.20	0.08	0.17
Phenolics	-0.109	0.29	-0.05	0.27	0.06
Tanin	0.104	0.10	-0.04	-0.28	0.20
Moist	0.067	0.22	-0.18	**-0.38**	0.08
Ash	-0.183	0.29	-0.04	0.00	-0.29
Carbohydrate (CHO)	**-0.349**	-0.23	0.08	-0.10	0.03
Protein	0.113	0.18	-0.05	0.20	0.28
Lipid	-0.213	**0.34**	-0.14	0.09	-0.04
Fibre	**0.379**	0.11	-0.03	0.08	-0.14
Calories	**-0.388**	-0.10	0.04	-0.01	0.13
Eigenvalue	5.06	3.88	2.73	2.26	2.24
Variance (%)	20.24	15.51	10.93	9.06	8.96
Cumulative Variance (%)	20.24	35.75	46.68	55.74	64.70

Cluster Analysis of Morphological Traits in Sorghum Accessions

The 20 sorghum accessions were grouped into four clusters based on morphological traits, with the dendrogram truncated at a 42 % genetic similarity level (Figure 3). Cluster 1 comprised eight accessions (DR1, LR24, LR2, DR25, LR6, W86, DR38, and LR11), characterized by a balanced combination of traits with moderate values across most attributes (Table 3). Cluster 2 included five accessions (DR15, R65, DR49, R88, and R73) at a 58% genetic similarity level. Accessions in this cluster exhibited similar morphological characteristics to Cluster 1, albeit with slight variations including higher trait values for the number of leaves and TSW. Cluster 3 contained six accessions (DR18, R20, R79, LR55, W60, and R57), also defined at a 42 % genetic similarity coefficient. While sharing some morphological similarities with Clusters 1 and 2, these accessions exhibited lower values for NL and grain covering percentage but higher inflorescence length. Cluster 4 was distinct, comprising a single accession (LR46) with unique morphological traits. LR46 demonstrated lower values for plant height (PH), inflorescence width, HSW, GW, TSW, and GC, but higher values for leaf width and weight at harvest.

Cluster Analysis of Nutritional Traits in Sorghum Accessions

The sorghum accessions were classified into three distinct groups based on nutritional quality, determined by truncating the dendrogram at a 40 % genetic similarity level (Figure 4). These clusters exhibited varied profiles of antinutrients, bioactive compounds, and macronutrients, reflecting their diverse nutritional potential.

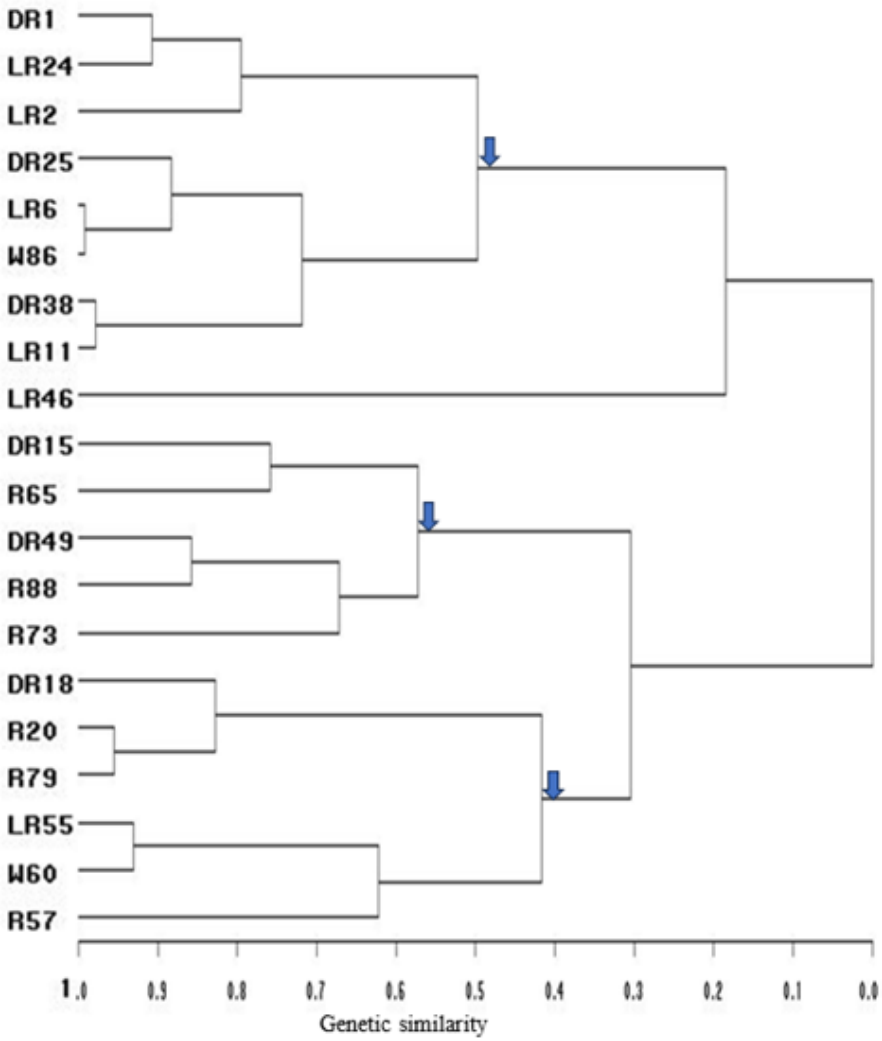

Figure 3. Dendrogram of Sorghum genotypes based on Morphological traits resulting from Ward's Minimum Variance Cluster Analysis

Table 3. Mean Performance of Sorghum Genotypes within each Cluster based on Morphological and Nutritional Attributes

Morphological Traits					Nutritional Attributes			
Characters	Group				Characters	Group		
	1	2	3	4		1	2	3
DF	83.61	84.72	83.13	82.80	Oxalate	8.70	11.19	7.25
NL	7.25	7.80	7.00	7.00	Phytate	0.27	0.40	0.38
LL	14.65	14.56	14.60	14.70	HCN	3.18	3.26	3.19
LW	8.20	8.48	8.37	8.80	Phenolics	23.03	19.84	20.94
PHT	234.83	228.70	231.92	190.60	Tanin	3.23	2.56	2.58
IL	9.00	8.90	9.32	9.20	Moist	7.83	5.81	5.66
IW	5.90	6.30	6.37	5.70	Ash	1.83	1.60	1.86
GC	58.64	58.28	55.45	53.80	CHO	72.05	75.87	77.07
PH	26.00	26.80	27.50	26.00	Protein	10.13	9.10	7.85
WH	1141.38	1088.00	1158.17	1094.00	Lipid	4.65	3.71	4.66
GW	1077.63	1004.20	1074.33	993.00	Fibre	3.38	3.80	2.83
HSW	6.65	7.18	7.27	6.30	Calories	357.53	358.47	370.50
TSW	78.75	81.50	84.17	72.50				

Days to flowering (DF); Number of leaves (NL); Leaf Length (LL); Leaf Width (LW); Plant Height (PHT); Inflorescence length (IL); Inflorescence width (IW); Grain covering % (GC); Number of Panicles Harvested (PH); Weight at Harvest (WH); Grain weight (GW); 100 seed weight (HSW); 1000 Seed weight (TSW).

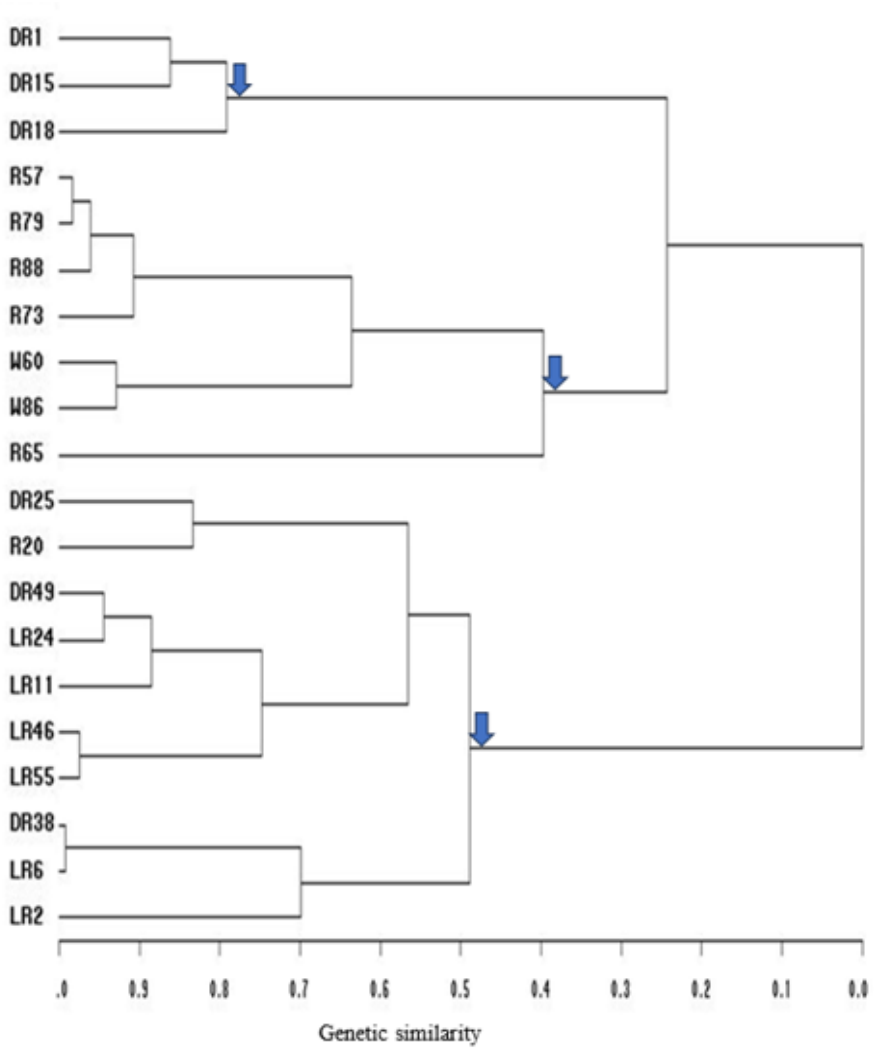

Figure 4. Dendrogram of Sorghum genotypes based on Nutritional attributes resulting from Ward's Minimum Variance Cluster Analysis

Cluster 1 comprised three accessions (DR1, DR15, and DR18) with a 79 % genetic similarity coefficient. These accessions were characterized by moderate levels of oxalate, phytate, and hydrocyanic acid (HCN), as well as high levels of phenolics and tannins (Table 3). They also demonstrated moderate moisture content, low ash content, and high fiber content, coupled with moderate protein and caloric levels. Cluster 2 included seven accessions (R57, R79, R88, R73, W60, W86, and R65), forming at a 40 % genetic similarity coefficient. This cluster had the highest levels of oxalate, phytate, and HCN among the groups, along with substantial amounts of phenolics and tannins. Accessions in this cluster showed lower moisture and ash content but retained high fiber levels. Cluster 3 consisted of the remaining ten accessions (DR25, R20, DR49, LR24, LR11, LR46, LR55, DR38, LR6, and LR2) with a 50 % genetic similarity coefficient. These accessions exhibited the lowest levels of oxalate, phytate, and HCN, paired with moderate levels of phenolics and tannins. Their nutritional profile included high carbohydrate and moderate lipid content, along with low levels of fiber and protein.

Discussion

The higher PCV compared to GCV across all morphological traits indicates a substantial influence of environmental factors on trait expression. For traits such as days to flowering, number of leaves, and inflorescence dimensions, the low GCV indicates limited genetic variability, making genetic improvement through direct selection more challenging (Stagnati et al., 2021). Conversely, traits such as weight at harvest and grain weight, which exhibited high GCV, show significant potential for genetic improvement through selection due to their strong genetic control. However, the corresponding high PCV values for these traits highlight the strong influence of environmental factors, which could complicate the selection process (Pranay et al., 2022). Breeding strategies for these traits should prioritize the identification of stable genotypes that are genetically superior across diverse environments, potentially through multi-environment trials (Aboderin et al., 2023). For nutritional traits, the high GCV values observed for oxalate, HCN, phenolics, tannin, and protein content indicate a strong genetic control, suggesting these traits are reliable targets for selection in breeding programs focused on nutritional quality (Queiroz et al., 2015; Tasie & Gebreyes, 2020).

The characterization of sorghum accessions based on qualitative traits such as grain color, grain luster, and endosperm texture provide valuable insights into their genetic diversity and potential for targeted utilization in breeding programs. Grain color significantly influences sorghum's suitability for various applications, including its nutritional quality, processing properties, pest and disease resistance and market appeal (Verma et al., 2017). Accessions with light-colored grains, such as white and light red, are particularly favored for food products like flours and porridges due to their ability to produce a lighter-colored final product, which is often preferred by consumers (Awika & Rooney, 2004). Additionally, these grains are ideal for malting purposes, owing to their lower tannin content and superior fermentability (Waniska et al., 2004). In contrast, accessions with darker-colored grains, such as red and dark red, demonstrated higher concentrations of phenolic compounds, tannins, and anthocyanins. These bioactive compounds are associated with antioxidant properties, which contribute to potential health benefits, such as reducing the risk of chronic diseases (Dykes & Rooney, 2006; Awika & Rooney, 2004). Moreover, the higher tannin content of these grains provides natural resistance against pests, fungal infections, and birds, offering an agronomic advantage by reducing field losses. This dual role of darker-colored grains in promoting health and enhancing field durability highlights their utility for both nutritional and agronomic purposes.

Grain luster, an attribute reflecting the shininess or glossiness of the grain surface, is another significant determinant of marketability and processing quality. Lustrous grains, although less common among the studied accessions, are often preferred for their visual appeal, higher milling yields, finer flour particles, and better resistance to spoilage during storage (Awika

& Rooney, 2004; Waniska et al., 2004). The predominance of non-lustrous grains among the accessions indicates a potential breeding target for enhancing grain luster, particularly for markets and industries where this trait is highly valued.

Endosperm texture also plays a crucial role in processing and end-use suitability. Accessions with completely starchy endosperm types, characterized by their hardness and vitreous nature, are advantageous for milling and brewing applications. These types are associated with higher yields of fine flour and increased fermentable sugar content, making them highly suitable for beer production and bioethanol manufacturing (Awika & Rooney, 2004). Conversely, mostly starchy varieties, which are softer and cook faster, are better suited for preparing traditional dishes and porridges where a tender and mushy texture is desired.

Principal Component Analysis was conducted on the morphological and nutritional traits of the sorghum accessions in the study. Principal Components with eigenvalues greater than 1 and with approximately 9% proportion of variance are typically considered significant, as they explain more variance than an average original variable and contribute substantially to the total variance in the dataset (Hair et al., 1998; Jain & Patel, 2016; Olakojo et al., 2021). Retaining these components ensures high information retention and effective dimensionality reduction, capturing meaningful patterns and relationships in the data with strong discriminatory power. Hence, in this study, only the first five principal components, which cumulatively accounted for 65 % of the total variation, satisfied both criteria and were retained. The loadings of individual variables in each principal component were also calculated to understand their contribution to the PC. Loadings indicate the strength and direction of the relationship between original variables and principal components, with component loadings greater than 0.3 or less than -0.3 considered meaningful (Jain & Patel, 2016). Among morphological traits, days to flowering, plant height, leaf number, and leaf length were identified as important contributors within the first five components. These traits are fundamental to sorghum's adaptability and agronomic performance, making them essential selection criteria for breeding programs aimed at improving yield and environmental resilience (Olakojo et al., 2021). Additionally, high contributions from weight-related traits like 100-seed weight and 1000-seed weight in PC1 underline their importance in determining grain yield, further highlighting their potential as targets for genetic improvement.

In terms of nutritional quality, fiber, carbohydrate content, and lipid content were identified as significant contributors to the variation among the accessions. These traits not only influence the nutritional profile of sorghum but also enhance its health-promoting properties, aligning with consumer and industrial demands for nutrient-dense grains (Awika et al., 2003; Chavan et al., 2017). The high loading of phytate underscores the importance of addressing anti-nutrient levels in sorghum breeding. Phytate is known to reduce the bioavailability of essential minerals, and breeding programs should aim to develop varieties with lower phytate content to improve the nutritional value of sorghum grains.

In this study, hierarchical clustering using Ward's minimum variance method was employed to classify sorghum accessions into distinct groups based on morphological traits, revealing valuable insights into their genetic diversity and potential applications (Ward, 1963; Mohammadi & Prasanna, 2003). Accessions were grouped into four clusters, each displaying unique characteristics. Cluster 1, characterized by balanced trait performance, includes accessions that could be targeted for general cultivation due to their moderate trait values, which suggest adaptability to diverse growing environments and consistent yield potential. Cluster 2 accessions exhibited superior performance in key traits such as the number of leaves, 1000- seed weight, and 100- seed weight, indicating better grain quality and canopy development. These attributes make them suitable for environments requiring high-yielding varieties or accessions with specific end-use purposes. In contrast, Cluster 3 accessions displayed unique traits, including higher inflorescence length and lower NL and grain covering percentage, suggesting a distinctive

plant architecture that could influence harvesting efficiency and grain exposure, particularly for mechanized farming. The uniqueness of LR46, the sole member of Cluster 4, highlights its distinct genetic makeup or environmental adaptation. Its traits, such as lower plant height and inflorescence width coupled with higher leaf width and weight at harvest, indicate potential for breeding dwarf varieties or addressing agronomic challenges like limited water availability or reduced lodging.

The clustering based on nutritional quality classified the accessions into three groups, each with distinct profiles of antinutrients, bioactive compounds, and macronutrients. Cluster 1 accessions, with moderate levels of antinutrients and high phenolic and tannin content, offer a balanced nutritional profile suitable for diverse applications (Queiroz et al., 2015). Their moderate moisture content and low ash content enhance their processing and storage characteristics, while their high fiber and moderate protein content contribute to health benefits such as improved digestive health and satiety (Rooney, 2004). These attributes, combined with relatively high caloric content, increase their utility for energy-dense food products. Cluster 2 accessions exhibited high levels of antinutrients such as oxalate, phytate, and hydrocyanic acid (HCN), posing challenges to digestibility and mineral bioavailability. However, their elevated phenolic and tannin levels present opportunities for antioxidant-rich food products, and their high fiber content makes them suitable for functional foods targeting gut health and cholesterol management (Belton & Taylor, 2004; Queiroz et al., 2015). Processing interventions like fermentation or thermal treatment could mitigate the effects of their high antinutrient content. Cluster 3 accessions, with the lowest levels of antinutrients, provide a balanced nutritional profile conducive to direct consumption. Their high carbohydrate and moderate lipid content make them suitable for energy-dense food products aimed at addressing dietary energy requirements (Dlamini et al., 2007; Hegde et al., 2023). However, their low fiber and protein content may limit their application in functional foods, suggesting the need for strategies such as blending with legume flours to enhance their nutritional value and expand their utility in health-focused products.

In conclusion, days to flowering, leaf number, leaf length, and plant height were identified as key morphological traits suitable for use as selection indices in sorghum breeding programs. Fiber content, carbohydrates and lipid levels were highlighted as important nutritional traits. Clustering based on morphological traits identified four distinct groups, each exhibiting unique combinations of traits, with accessions in cluster 2 showing superior characteristics such as balanced morphological traits and higher grain weight. Similarly, clustering based on nutritional attributes revealed three distinct groups, each exhibiting varying levels of antinutrients, bioactive compounds, and macronutrients, which could influence their potential usefulness in food and nutrition. Notably, sorghum accessions in cluster 3 possessed desirable nutritional qualities, suggesting their potential for further evaluation and utilization in breeding programs aimed at enhancing the nutritional value of sorghum-based foods.

Acknowledgements:

We sincerely thank the staff and members of the University of Ilorin Teaching and Research Farm for their invaluable assistance throughout the study.

Conflicts of Interest:

There was no conflict of interest.

Authors Contribution:

FAB, OSA, KSI, OO: Conceptualization and Methodology; FAB, KSI, OO, MOM: Investigation; FAB, OSA: Data Analysis: FAB, OSA: Data Curation; FAB, OSA: Writing – Original

Draft Preparation; Writing – Review and Editing: FAB, OSA, MOM; FAB: Supervision

All authors declare that they have read and approved the publication of the manuscript in this present form.

Funding Declaration:

The germplasm collection activity was carried out with funds received from the International Crop Institute for the Semi-Arid Tropics (ICRISAT).

ID ORCID and e-mails

Folusho Anuoluwapo BANKOLE
bankole.fa@unilorin.edu.ng
https://orcid.org/0000-0002-7825-4487

Olawale Serideen ABODERIN
olawaleaboderin@yahoo.com
https://orcid.org/0009-0003-7435-1022

Kehinde Shukurat IBIYINKA
shukrahibiyinka@gmail.com

Olasunkanmi OLAJIDE
olajide.sunkanmiolushola@gmail.com

Mobolaji Omolabake MUSA
musa.mo@unilorin.edu.ng
https://orcid.org/0009-0001-8393-8998

References

Aboderin, O. S., Bankole, F. A., Oyekunle, M., & Olaoye, G. (2023). Yield stability and inter-trait relationships of maize hybrids under low- and optimum-nitrogen conditions. *Agriculture (Poľnohospodárstvo), 69*(4), 171–185. https://doi.org/10.2478/agri-2023-0015

Ajeigbe, H. A., Akinseye, F. M., Jonah, J., & Kunihya, A. (2018). Sorghum yield and water use under phosphorus fertilization applications in the Sudan Savanna of Nigeria. *Global Advanced Research Journal of Agricultural Science, 7*(8), 245–257.

Association of Official Analytical Collaboration [AOAC] (2019). *Official Methods of Analysis of AOAC INTERNATIONAL (21st ed.)*. Washington, DC: AOAC International.

Awika, J. M., Rooney, L. W., Wu, X., Prior, R. L., & Cisneros-Zevallos, L. (2003). Screening methods to measure antioxidant activity of sorghum (Sorghum bicolor) and sorghum products. *Journal of Agricultural and Food Chemistry, 51*(23), 6657–6662. https://doi.org/10.1021/jf034790i

Awika, J. M., & Rooney, L. W. (2004). Sorghum phytochemicals and their potential impact on human health. *Phytochemistry, 65*(9), 1199–1221. https://doi.org/10.1016/j.phytochem.2004.04.001

Belton, P., & Taylor, J. (2004). Sorghum and millets: Protein sources for Africa. *Trends in Food Science and Technology, 15*(2), 94–98. https://doi.org/10.1016/j.tifs.2003.09.002

Boyles, R. E., Pfeiffer, B. K., Cooper, E. A., Rauh, B. L., Zielinski, K. J., Myers, M. T., Brenton, Z., Rooney, W. L., & Kresovich, S. (2017). Genetic dissection of sorghum grain quality traits using diverse and segregating populations. *Theoretical and Applied Genetics, 130*(4), 697–716. https://doi.org/10.1007/s00122-016-2844-6

Chakrabarty, S., Mufumbo, R., Windpassinger, S., Jordan, D., Mace, E., Snowdon, R., & Hathorn, A. (2022). Genetic and genomic diversity in the sorghum gene bank collection of Uganda. *BMC Plant Biology, 22*(378). https://doi.org/10.1186/s12870-022-03770-y

Chavan, U., Kajjidoni, S., Shinde, M., Dalvi, U., Nirmal, S., Patil, V., Awari, V. R., Pawar, G., & Jadhav, A. (2017). Regional effect on nutritional quality of sorghum genotypes. *International Journal of Current Microbiology and Applied Sciences, 6*(11), 75–85. https://doi.org/10.20546/ijcmas.2017.611.010

Cruz, C. D., Carneiro, P. C. S., & Regazzi, A. J. (2014). *Modelos Biométricos Aplicados ao Melhoramento Genético (3rd ed.)*. Viçosa, Brazil: UFV.

Dlamini, N. R., Taylor, R. N., & Rooney, L. W. (2007). The effect of sorghum type and processing on the antioxidant properties of African sorghum-based foods. *Food Chemistry, 105*(4), 1412–1419. https://doi.org/10.1016/j.foodchem.2007.05.017

Dykes, L., & Rooney, L.W. (2006). Sorghum and millet phenols and antioxidants. *Journal of Cereal Science, 44*(3), 236–251. https://doi.org/10.1016/j.jcs.2006.06.007

Food and Agriculture Organization [FAO] (2020). FAO Statistical Database (online). *Food and Agricultural Organization of the United Nations, Rome.* http://www.fao.org/faostat/en/#data/QC

Fracasso, A., Magnanini, E., Marocco, A., & Amaducci, S. (2017). Real-time determination of photosynthesis, transpiration, water-use efficiency, and gene expression of two Sorghum bicolor (Moench) genotypes subjected to dry-down. *Frontiers in Plant Science, 8*, 932. https://doi.org/10.3389/fpls.2017.00932

Hair, J. F., Tatham, R. L., Anderson, R. E., & Black, W. (1998). *Multivariate Data Analysis* (5th ed.). London, UK: Prentice-Hall International Inc. ISBN: 978-0138948580.

Hegde, S., Thangalakshmi, S., & Singh, R. (2023). A review of gluten and sorghum as a gluten-free substitute. *Trends in Horticulture, 6*(2), 1–17. https://doi.org/10.24294/th.v6i2.2840

Jain, S. K., & Patel, P. R. (2016). Principal component and cluster analysis in sorghum (Sorghum bicolor (L.) Moench). *Forage Research, 42*, 90–95.

Kavithamani, D., Yuvaraja, A., & Selvi, B. (2019). Principal component analysis and grouping of sorghum (Sorghum bicolor L. Moench) gene pool for genetic diversity. *Electronic Journal of Plant Breeding, 10*(4), 1426–1434.

Mohammadi, S. A., & Prasanna, B. M. (2003). Analysis of genetic diversity in crop plants: Salient statistical tools and considerations. *Crop Science*, *43*(4), 1235–1248. https://doi.org/10.2135/cropsci2003.1235

Motlhaodi, T., Geleta, M., Chite, S., Fatih, M., Ortiz, R., & Bryngelsson, T. (2017). Genetic diversity in sorghum (*Sorghum bicolor* (L.) Moench) germplasm from Southern Africa as revealed by microsatellite markers and agro-morphological traits. *Genetic Resources and Crop Evolution*, *64*, 599–610. https://doi.org/10.1007/s10722-016-0388-x

Murtagh, F., & Legendre, P. (2014). Ward's hierarchical agglomerative clustering method: Which algorithms implement Ward's criterion? *Journal of Classification*, *31*, 274–295. https://doi.org/10.1007/s00357-014-9161-z

Ni, C., Zhang, S., Gaopeng, Z., Jianjun, C., & Huanyu, Z. (2019). Evaluation of edible quality of sorghum based on principal component analysis. *Journal of Chemistry, 2019*(1), 2013109 https://doi.org/10.1155/2019/2013109

Olakojo, O., Bankole, F., & Ogunniyan, D. (2021). Correlation, regression, and cluster analyses on yield attributes and popping characteristics of popcorn (*Zea mays* L. everta) in derived savanna and rainforest agro-ecologies of Nigeria. *Acta Agriculturae Slovenica, 117*(3), 1–11. https://doi.org/10.14720/aas.2021.117.3.1625

Perazzo, A., Carvalho, G., Santos, E., Pinho, R., Campos, F., Macedo, C., Azevedo, J., & Tabosa, J. (2014). Agronomic evaluation of 32 sorghum cultivars in the Brazilian semi-arid region. *Revista Brasileira de Zootecnia, 43*(05), 232–237. https://doi.org/10.1590/S1516-35982014000500002

Pranay, G., Shashibhushan, D., Rani, K. J., Bhadru, D., & Kumar, C. V. (2022). Genotype and phenotype coefficient of variance in maize (Zea mays L.). *International Journal of Environment and Climate Change, 12*(12), 1119–1132. https://doi.org/10.9734/ijecc/2022/v12i121550

Queiroz, V., Silva, C., Menezes, C., Schaffert, R., Guimarães, F., Guimarães, L., Evaristo, P., & Tardin, F. (2015). Nutritional composition of sorghum (Sorghum bicolor (L.) Moench) genotypes cultivated without and with water stress. *Journal of Cereal Science, 65*, 103–111. https://doi.org/10.1016/j.jcs.2015.06.018

Rhodes, D. H., Hoffmann, L., Rooney, W. L., Herald, T., Bean, S., Boyles, R., Brenton, Z., & Kresovich, S. (2017). Genetic

architecture of kernel composition in global sorghum germplasm. *BMC Genomics, 18*(1), 15. https://doi.org/10.1186/s12864-016-3403-x

Rooney, W. L. (2004). Sorghum improvement: Integrating traditional and new technology to produce improved genotypes. *Advances in Agronomy, 83*, 37–109. https://doi.org/10.1016/s0065-2113(04)83002-5

SAS Institute Inc. (2008). *SAS/STAT Software 9.2*. Cary, NC, USA: SAS Institute.

Sivasubramanian, S., & Madhavamenon, P. (1973). Genotypic and phenotypic variability in rice. *Madras Agricultural Journal, 60*(9/12), 1093–1096.

Stagnati, L., Busconi, M., Soffritti, G., Martino, M., Lanubile, A., & Marocco, A. (2021). Molecular and phenotypic characterization of a collection of white grain sorghum (*Sorghum bicolor* (L.) Moench) for temperate climates. *Genetic Resources and Crop Evolution, 68*, 2931–2942. https://doi.org/10.1007/s10722-021-01166-9

Tasie, M. M., & Gebreyes, B. G. (2020). Characterization of nutritional, antinutritional, and mineral contents of thirty-five sorghum varieties grown in Ethiopia. *International Journal of Food Science, 2020* (1), 8243617 https://doi.org/10.1155/2020/8243617

Verma, R. J., Ranwah, B. R., Barti, B., Kumar, R., Kunwar, R., Diwaker, A., & Meena, M. (2017). Characterization of sorghum germplasm for various qualitative traits. *Journal of Applied and Natural Science, 9*(2), 1002–1007. https://doi.org/10.31018/jans.v9i2.1311

Waniska, R. D., Rooney, L. W., & McDonough, C. (2004). Sorghum utilization. *Encyclopedia of Grain Science* (pp. 126–136). Cambridge, MA, USA: Academic Press. https://doi.org/10.1016/B0-12-765490-9/00152-X

Ward, J. H. (1963). Hierarchical grouping to optimize an objective function. *Journal of the American Statistical Association, 58*(301), 236–244. https://doi.org/10.1080/01621459.1963.10500845

Xiong, Y., Zhang, P., Warner, R. D., & Fang, Z. (2019). Sorghum grain: From genotype, nutrition, and phenolic profile to its health benefits and food applications. *Comprehensive Reviews in Food Science and Food Safety, 18*(6), 2025–2046. https://doi.org/10.1111/1541-4337.12506

Yahaya, M., Shimelis, H., Nebié, B., Ojiewo, C., & Danso-Abbeam, G. (2022). Sorghum production in Nigeria: Opportunities, constraints, and recommendations. *Acta Agriculturae Scandinavica, Section B - Soil & Plant Science*, *72*(1), 660–672. https://doi.org/10.1080/09064710.2022.2047771