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Research Article

Cluster analysis and genetic variability of sweet sorghum (*Sorghum bicolor* L. Moench) genotypes using agro-morphological and juice quality traits

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Abstract

The present investigation was conducted at Giza Research Station, Egypt, to evaluate the mean performance of 30 sweet sorghum genotypes for stalk and juice yields during the 2021 and 2022 summer seasons. The experiment was laid out as a randomized complete block design with three replicates. The magnitude of genetic variability was estimated using broad sense heritability and genetic advance expressed as a percent of the grand mean. Also, cluster analysis was automated to identify the similarity and dissimilarities among the tested genotypes. The genotype by trait (GxT) biplot was graphically diagrammed to compare genotypes on the basis of multiple traits. Results revealed significant differences among sweet sorghum genotypes for all studied traits across the two seasons. There were three promise genotypes Willy, William, and Atlas that surpassed the other genotypes regarding juice extraction percentage and juice yield indicating their magnitude as breeding materials that may be successfully used in breeding programs of sweet sorghum. The highest genotypic and phenotypic coefficient of variation was recorded by leaf area index, stalk diameter, stalk length, juice extraction percentage, and juice yield. In the same context, high values of heritability accompanied by genetic advance percentage were observed in terms of leaf area index, stalk diameter, stalk length, and juice yield indicating that these traits were well heritable and can be improved through breeding programs. The results of cluster analysis exhibited the presence of considerable genetic diversity among the tested genotypes. Cluster analysis classified the sweet sorghum genotypes into five clusters where the 1st cluster consisted of four genotypes Willy, William, Rio, and Dall that were lately flowered but recorded the highest values of all studied traits except stalk length, sucrose percentage, and purity percentage giving considerable stalk and juice yields. According to the GxT biplot graph, it is clear that genotypes; William, Rio, Tracy, and Atlas recorded the best values in the case of juice extraction percentage, juice yield, stripped stalk yield, stalk diameter, days to 50% flowering, and leaf area index. Information obtained from this research may be helpful to select the best sorghum genotypes to share in breeding programs to improve the characteristics of stalk and juice yields.

Keywords: Genetic variability, *Sorghum bicolor* L. Moench, juice yield, Cluster analysis, GxT biplot graph

INTRODUCTION

Sweet sorghum (*Sorghum bicolor* L. Moench) is a multiple-purpose crop used as a source of food and fodder. Additionally, due to its easily fermented sugar, it is a valuable source of bioethanol and lignocellulose feedstock production (Cifuentes *et al.*, 2014). Despite

its extreme importance as an agricultural, industrial, and economic crop that is used for many purposes, sweet sorghum has received little attention in Egypt so far. Sweet sorghum, a specific type of *Sorghum bicolor* L. Moench, has been considered a potentially valuable

source for biofuel production because of its high energy conversion efficiency (Zou *et al.*, 2011). It is predominantly grown for sorghum syrup where its stalks are harvested and crushed like sugarcane to produce syrup. Sweet sorghum is currently used as a safe alternative sweetener to produce biofuel, alcohol products, and other chemical productions. While farmers cultivate essential food crops on arable land, bioenergy crops such as sweet sorghum can be cultivated in poorly fertile soils or marginal soils as well as it requires low nitrogen fertilizer compared to maize and sugar cane. This low production cost of sweet sorghum encourages the state and farmers to expand its cultivated area.

Estimation of heritability and genetic advance is a pivotal point to identify the traits amenable to improvement through visual selection. Singh (2001), Zou *et al.*, (2011), Tomar *et al.*, (2012), Mulima *et al.*, (2018), Umakanthm *et al.*, (2019) and Naoura *et al.*, (2020) reported that the heritability estimates would not be practically useful without considering genetic advance. The presence of genetic variability among aimed genotypes is the cornerstone of any targeted genetic improvement of the breeding program. Since knowledge about the nature and degree of genetic variability supports the plant breeder in detecting diverse parents for successful hybridization. Cluster analysis is an effective statistical procedure used to quantify the degree of genetic divergence among some genotypes depending on their contributing traits' performance. Umakanthm *et al.*, (2019) demonstrated that the clustering pattern observed from the present study revealed that genetic diversity was not necessarily parallel to geographic diversity. Wide variability in 2834 accessions of sorghum germplasm in agriomorphological traits (Maruthamuthu *et al.*, 2022). Genotypes that evolved in the same area were grouped into different clusters. Genetic divergence among sweet sorghum genotypes using cluster analysis was reported by (Zhan *et al.*, 2012; Jain and Patel, 2016 and Mulima *et al.*, 2018 and Naoura *et al.*, 2020).

Graphical presentation using a GxT biplot diagram gives information on the usefulness of promising genotypes as well as information that helps to detect less important (redundant) traits. GxT biplot graph was used by Yan and Rajcan (2002) and Yan and Tinker (2005) to visualize the interrelationships among genotypes and traits. Guden *et al.* (2020) used principal components analysis (PCA) to discriminate some sweet sorghum germplasm based on the phenotypic traits. They confirmed that PCA is a vital breeding procedure commonly used by breeders to detect traits that discriminated against tested genotypes. Despite the recent interest shown in the GT biplot graph to interpret the two-way table of genotype and traits, however, it is rarely used in sweet sorghum trials in Egypt where few references were found concerning this technique. The present work was planned to investigate

the estimates of heritability (h^2), phenotypic and genotypic variances, and genetic advance (% mean) using ten morphological and biochemical trait data of 30 sweet sorghum genotypes and classify these genotypes using a cluster analysis procedure. Also, the research aimed to identify the genotype and trait relationships using the GxT biplot graph. The resulting conclusions may be helpful to plan an appropriate breeding program for improving sweet sorghum crops in Egypt.

MATERIALS AND METHODS

The current investigation was carried out at Giza Agricultural Research Station (Latitude and longitude coordinates being 29.98 and 31.13, respectively and 19 m above sea level), to study the genotypic diversity for 30 sweet sorghum genotypes regarding ten morphological and biochemical traits during the 15th June 2021, and 2022 summer seasons. The name and origin of the thirty tested sweet sorghum genotypes were summarized in **Table 1**. Soil samples were taken from the study site of depth 0-30 cm then some soil properties were determined according to methods described in Black (1965) and Page *et al.* (1982). Based on the soil analysis result of the experimental site, the pH and CEC of the experimental soil were 7.3 and 31.80 meq/100g, respectively. Whereas available nitrogen and phosphorus were found at 76.13 and 10.59 mg/kg, respectively. The electrical conductivity (EC value) was about (2.14 dSm⁻¹) and it is good for sweet sorghum plants growing. On the other hand, the organic matter percentage was found 1.37%. The texture of the experimental site was 48.27% clay, 20.45% silt, and 31.28% sand; which is classified as clay based on the texture triangle classification system this type of soil is conducive for crop production since clay soils absorb and hold more water and exchangeable nutrients or cations than silty or sandy soils. Generally, the weather of Giza governorate is characterized by a long, hot, humid, arid, and clear summer season while the winter is cool, dry, and mostly clear. Giza experiences a hot desert climate like an arid climate. Wind storms can be frequent across Egypt in spring, bringing Saharan dust into the city during the months of March and April. Temperatures in winter range from 16 to 20 °C, while nighttime lows drop to below 7 °C. In summer, the highs are 40 °C, and the lows can drop to about 20 °C. Rain is infrequent in Giza; snow is extremely rare (web site: <http://power.larc.nasa.gov> 2023). Randomized complete block design (RCBD) with three replications was used. The plot area was 21 m² consisting of (5 rows, 7 m long and 0.6 m apart). The spacing between hills was 25 cm. All recommended cultural practices were followed to raise a healthy crop.

Morphological characters: Harvest time was detected for each genotype after complete maturity (90 to 120 days from sowing). To avoid border effect, ten stalks selected as sample from the three middle rows of each plot were used to determine:

Table 1. Name and origin of 30 sweet sorghum genotypes evaluated under the study.

No.	Name	Origin	No.	Name	Origin
1	Willy	Mississippi	16	Honey	Mississippi
2	William	Kentucky/Georgia	17	Sugar drip	Oklahoma
3	AGSC3	unknown	18	Rex	Mississippi
4	Rio	Texas	19	Rona	unknown
5	Dall	Mississippi	20	SS405	Nigeria
6	Tracy	Texas	21	Cukorciro	unknown
7	Atlas	South Africa	22	Roma	South Africa
8	MN405	Mississippi	23	MN2756	Mississippi
9	MN4508	Mississippi	24	MN4080	Mississippi
10	MN3556	Mississippi	25	Ramada	Mississippi
11	MN1383	Mississippi	26	AGSC2	unknown
12	MN4423	Mississippi	27	SS301-1	Nigeria
13	GK Ahron	unknown	28	Sudangrass	Sudan
14	Brands	Mississippi	29	Umbrella	Mississippi
15	GK Gaba	unknown	30	MN1054	Mississippi

1. Days to 50 percent flowering
2. Stalk length (cm): was measured from the land level till visible dewlap.
3. Stalk diameter (cm): was measured at mid stalk.
4. Leaf area index: estimate leaf areas from the measured length x width x 0.89 formulae to estimate the total leaf area per Sq. M of the land. 0.89 is a correction factor for the shape of the sweet sorghum leaf.
5. Stripped-stalks yield per ton/fed, was calculated on a plot basis kg/fed then converted to ton/fed (Feddan = 4200 m²).

Juice quality characters: Stalks free from leaves and husks were crushed through a three roller mill to extract the juice. Raw juice was filtered, weighed, and the following traits were measured for each genotype:

1. Brix (percent soluble solids) was determined with a hand refractometer.
2. Sucrose percentage of clarified juice was determined by using automated saccharimeter according to A. O. A. C. (2005).
3. Purity was calculated as: (Sucrose/Brix) x 100.
4. Juice extraction % (JEP) =
(Juice weight/stalk weight) x 100.
5. Juice yield (ton/fed) =
(Stripped stalk yield x JEP)/100

Combined analysis of the variance of randomized complete block design was automated across the two seasons (Gomez and Gomez, 1984). The homogeneity of error terms was tested prior to the combined analysis as described by the Levene test (1960) was run to satisfy. The mean comparison was done using the least significant

difference (LSD) at a 0.05 probability level. The genotypes factor was considered fixed while the season term was judged to be random that attributed to the environmental effects. Genotypic and phenotypic coefficient of variation and their corresponding coefficient of variations were estimated using variance components as suggested by Johnson *et al.* (1955 a and b). Estimates of broad sense heritability (h²) and genetic advance in terms of the percentage of means (with 5 % selection intensity) were parameterized according to the method outlined by Allard (1999). Hierarchical cluster analysis was performed on the standardized data using a measure of Euclidean distance and Ward minimum variance method as described by Ward (1963). Yan and Rajcan (2002) used a genotype by trait (GxT) biplot, which is a modified form of the GGE biplot graph to study the interrelationships among genotypes regarding trait data. Because the traits were measured in different units, the biplot graph was sketched using standardized values.

RESULTS AND DISCUSSION

The homogeneity of individual error variances for all studied traits was satisfied which allows for running a combined analysis across two seasons. The genotypes were deliberately chosen, so it is considered fixed while season and replication terms were random. In addition, the genotype x season interaction effect was no sign for most studied traits. Therefore, only the genotypes averages were tabulated and discussed across the two seasons as summarized in **Tables (2 and 3)**. It is obvious that the coefficient of variation (CV%) was statistically acceptable for all traits under study ranging from 6.9 for stalk length to 18.58 for juice extraction %. This result indicated that, although the replication area was somewhat wide (630 m²), the randomized complete block design (RCBD) was

still valid. Results revealed the presence of significant differences among the thirty sweet sorghum genotypes regarding all morphological and juice characters indicating a wide genetic variability among them.

The mean values of five morphological traits for thirty sweet sorghum genotypes across the two seasons are summarized in **Table 2**. Results indicated that the earliest flowering genotypes were Rex (51.75 days) and Roma (50.50 days) while William (79.92 days) and Rona (74.67 days) were the latest flowering ones. The presence of a month difference in flowering between

early and late plants allows the possibility of selection and crossbreeding between them to convey the character of early flowering. Mulima *et al.* (2018) evaluated 26 sweet sorghum genotypes for determining the morphological characteristics that distinguish desirable breeding materials. They found that six genotypes were early mature while there were four late maturity genotypes. With respect to leaf area index (LAI), Dall and Atlas genotypes recorded the maximum values being 570.95 and 519.48 while the lowest LAI values (162.36 and 160.03) were obtained by MN1383 and Sudangrass, respectively. Leaf area index (LAI) during the growth process is an important

Table 2. Mean values of five morphological characters for thirty sweet sorghum genotypes across the two seasons of 2021 and 2022

Genotypes	Days to 50 percent flowering	Leaf area index (cm)	Stalk diameter (cm)	Stalk length (cm)	Stripped stalk yield (ton/fed)
Willy	70.92	378.67	2.28	177.83	13.93
William	79.92	356.60	1.95	232.50	12.97
AGSC3	68.25	354.86	2.45	142.17	9.42
Rio	69.42	444.45	2.19	190.42	11.71
Dall	63.75	570.95	2.82	123.08	15.07
Tracy	60.75	477.70	2.25	204.08	13.67
Atlas	64.92	519.48	1.94	225.58	12.56
MN405	70.58	406.50	2.04	239.25	8.72
MN4508	64.58	259.73	2.24	241.92	11.34
MN3556	63.58	204.44	2.58	185.58	13.85
MN1383	62.75	162.36	1.69	152.92	10.02
MN4423	67.08	299.95	1.76	183.58	12.32
GK Ahron	62.75	364.66	1.53	183.92	8.54
Brands	67.58	193.65	1.59	240.58	11.09
GK Gaba	59.58	232.07	2.42	184.42	8.93
Honey	67.08	252.73	1.49	154.08	12.90
Sugar drip	56.42	184.31	2.13	165.33	11.93
Rex	51.75	377.35	2.74	136.67	9.67
Rona	74.67	232.98	2.71	201.67	10.27
SS405	61.33	285.33	1.71	157.17	13.75
Cukorciro	57.33	301.35	1.24	167.17	15.08
Roma	50.50	381.10	1.27	216.00	13.19
MN2756	65.17	275.65	1.44	166.00	10.78
MN4080	70.17	179.14	1.72	228.33	10.72
Ramada	64.50	412.16	1.23	254.17	11.62
AGSC2	61.83	424.47	0.93	155.83	11.42
SS301-1	60.50	200.81	1.67	161.50	13.39
Sudangrass	71.08	160.03	1.92	250.67	14.53
Umbrella	69.08	200.12	1.18	133.67	13.96
MN1054	59.42	274.23	1.42	128.67	13.67
LSD _{0.05}	8.53	60.44	0.34	14.74	1.97
CV%	11.5	16.9	15.6	6.9	14.3

indicator for predicting high productivity provided it is accompanied by a good photosynthetic capacity of sweet sorghum leaves during growth periods. The highest stalk diameter (greater than 2.70 cm) was observed by Dall, Rex, and Rona while Cukorciro, Ramada, AGSC2, and Umbrella recorded the lowest stalk diameter (less than 1.25 cm). Meanwhile, the tallest stalk length (more than 250 cm) was produced by Ramada and Sudangrass but the shortest ones (less than 130 cm) were observed by Dall and MN1054. Regarding stripped stalk yield ton/fed, Dall and Ramada outperformed the remainder genotypes with stripped stalk yield productivity of more than 15 tons/fed while the lowest ones were MN405, GK Ahron, and

GK Gaba recording less than 9 tons/fed. Sweet sorghum researchers carried out field trials to evaluate many genotypes for different purposes, such as human food, animal feeding, ethanol content, and so on. Guden *et al.* (2020) found wide variability among 64 sweet sorghums for extractable stalk juice yield, bioethanol yield, and juice brix content that gives the chance to exploit in sweet sorghum breeding program for bioenergy production.

The mean performance of thirty sweet sorghum genotypes regarding five juice quality traits (brix %, sucrose %, purity %, juice extraction %, and juice yield (ton/fed)) across the two seasons are presented in **Table 3**. Increasing the brix

Table 3. Mean values of five juice quality characters for thirty sweet sorghum genotypes across the two seasons of 2021 and 2022

Genotypes	Brix %	Sucrose %	Purity %	Juice extraction %	Juice yield (ton/fed)
Willy	18.90	8.68	45.86	34.28	4.87
William	19.43	9.58	49.79	39.82	5.24
AGSC3	17.07	9.33	55.88	26.93	2.56
Rio	18.27	10.01	54.93	34.23	3.96
Dall	17.17	8.35	49.33	30.80	4.64
Tracy	16.73	10.14	60.54	30.29	4.13
Atlas	16.23	10.57	65.52	36.90	4.69
MN405	14.63	10.82	74.48	22.21	1.97
MN4508	15.90	10.01	63.16	28.96	3.22
MN3556	14.93	10.50	71.52	26.87	3.71
MN1383	15.96	9.64	61.59	18.31	1.84
MN4423	14.33	9.77	67.94	27.01	3.29
GK Ahron	18.16	8.73	48.19	19.68	1.67
Brands	15.79	10.70	68.50	20.92	2.34
GK Gaba	15.89	9.53	59.96	25.24	2.18
Honey	16.07	9.10	58.73	31.42	4.04
Sugar drip	16.40	8.38	51.62	21.90	2.65
Rex	18.21	10.65	59.14	24.30	2.27
Rona	17.90	11.26	63.12	29.08	2.87
SS405	16.62	11.24	67.80	32.31	4.44
Cukorciro	17.84	10.03	56.42	22.00	3.32
Roma	18.71	11.03	59.19	22.56	2.98
MN2756	16.81	10.07	59.93	21.33	2.29
MN4080	17.03	9.81	57.76	23.11	2.44
Ramada	16.26	10.79	66.37	29.38	3.45
AGSC2	15.64	9.45	60.08	21.97	2.50
SS301-1	17.58	10.88	61.81	29.47	3.91
Sudangrass	15.90	10.26	64.27	19.35	2.81
Umbrella	16.22	10.11	62.44	20.95	2.92
MN1054	16.34	10.65	65.13	19.55	2.69
LSD _{0.05}	1.78	1.32	8.23	5.68	0.64
CV%	9.3	11.4	11.9	18.58	17.6

percentage is consequently followed by increasing the sugar content produced per cultivated area unit. Results deciphered that the maximum brix percent was obtained by William recording 19.43% followed by genotypes (Willy, AGSC3, GK Ahron, Rex, and Roma) that recorded values ranging between 18 and 19 %. However, the minimum brix % content obtained by MN405, Mn3556, and MN4423 genotypes that gave brix % values ranged from 14.33 to 14.99 %. The current results agreed with those obtained by Abd El-Raheem *et al.* (2010), Khidr *et al.* (2021), and Yücel *et al.* (2022) who found obvious differences among tested genotypes in brix percentage. With respect to sucrose % content, three genotypes (Rona, SS405, and Roma) were found to be outperformed the remainder of tested sweet sorghum genotypes in this study recording more than 11 % where the lowest sucrose % values (less than 9 %) were obtained by Willy, Dall, GK Ahron and Sugar drip genotypes showing the possibility of participation of these genotypes in the breeding program of sorghum crop to improve the sugar content (Rao *et al.*, 2013 and Erdurmus *et al.*, 2018). The highest purity % values were observed by MN405 genotype (74.48) followed by MN3556 (71.52) while Willy, William, Dall, and GK Ahron genotypes gave the lowest percentage of purity % where they were also the lowest in sugar % as previously mentioned. It is noteworthy that both juice extraction % and juice yield were widely varied amongst sweet sorghum genotypes under study. The values of juice extraction % ranged from 18.31 % for MN1383 genotype to 39.82 % for William while the produced juice yield fell between 1.67 ton/fed for GK Ahron and 5.24 ton/fed for William. Results in **Table 3** revealed that genotypes; Willy, William, and Atlas out yielded high values of juice extraction % (34.28, 39.82, and 4.69 %) and juice yield (4.87, 5.24 and 4.69 ton/fed), respectively indicating their magnitude as promising genotypes that may be used in breeding programs of sweet sorghum. The current results are harmonized with many previous investigations reported by Abd El-Raheem *et al.* (2010), Rao *et al.*

(2013), Erdurmus *et al.* (2018), Mulima *et al.* (2018), Khidr *et al.* (2021) and Yücel *et al.* (2022) who confirmed that the considerable variability among the assessed sweet sorghum genotypes considering the juice quality readings provides a real chance to improve the juice productivity of sweet sorghum crop and its extracts and other products.

Estimates of grand mean, range, genotypic (GCV%) and phenotypic (PCV%) coefficients of variation, broad sense heritability (h^2), and genetic advance (GA%) expressed as a percent of the grand mean (at 5 % selection intensity) are presented in **Table 4**. Genotypic components are important indicators that give the breeder an initial idea about the amount of genetic variation among the tested genotypes toward the studied traits. The results indicated that the values of (PCV%) were higher than their corresponding values of (GCV%) for all studied traits. The magnitude of this difference was low for leaf area index, stalk diameter, and stalk length indicating that the weak influence of environmental factors on the phenotype expression of genotypes was low and there is a higher chance to improve these traits through selection based on the phenotype performance. However, the differences between PCV% and GCV% values were high for the rest traits indicating the somewhat great influence of environmental factors which makes the selection process on the basis of the phenotype expression more complex. The highest estimates of genotypic (GCV%) and phenotypic (PCV%) coefficients of variation (more than 20) were obtained by leaf area index, stalk diameter, stalk length, juice extraction % and juice yield while the lowest values of GCV% and PCV% (lower than 20) were recorded by the remainder traits. These results are in agreement with the findings obtained by Zou *et al.* (2011) and Elangovan *et al.* (2014). Singh (2001) mentioned that heritability estimate is considered as high when its value equals 80 % or more and moderate when it ranged from 40-80 % and low if its value is less than 40 %. Accordingly, the highest heritability estimates

Table 4. Genetic variability of the studied characters computed from thirty sweet sorghum genotypes evaluated across the two seasons of 2021 and 2022

Characters	Grand mean	Range		Genetic parameters			
		Min.	Max.	GCV%	PCV%	h^2	GA %
Days to 50% flowering (DF)	64.58	41.0	89.50	8.81	13.65	41.67	11.71
Leaf area index (cm) (LAI)	312.26	128.25	675.0	35.10	38.28	84.05	66.28
Stalk diameter (cm) (SD)	1.88	0.60	3.64	26.24	30.93	71.96	45.85
Stalk length (cm) (SL)	186.16	110.0	280.0	20.96	21.92	91.43	41.28
Brix % (B%)	16.76	9.9	22.7	6.20	12.05	26.48	6.57
Sucrose % (S%)	10.00	6.95	13.23	6.41	13.83	21.47	6.12
Purity % (P%)	60.37	38.54	87.68	10.07	16.51	37.18	12.65
Juice extraction % (JE%)	26.37	13.40	47.79	20.47	26.60	59.21	32.45
Stripped stalk yield (ton/fed) (SSY)	12.03	6.94	17.18	14.99	19.99	56.20	23.15
Juice yield (ton/fed) (JY)	3.20	1.38	6.30	29.62	33.88	76.42	53.34

were obtained by leaf area index and stalk length. This result suggested the trait improvement is possible using selection strategy if the genetic advance % was also high. Meanwhile, moderate heritability estimates were appeared with five traits *i.e.* days to 50 % flowering, stalk diameter, juice extraction %, stripped stalk yield and juice yield indicating that selection should be delayed to more advanced generations. Low heritability estimates were recorded for three traits being Brix %, sucrose % and purity %. These results are confirmed by the findings obtained by Guden *et al.* (2020).

Genetic advance as percent mean (GA %) ranged from 6.12 % for sucrose % to 66.28 % for leaf area index. This result showed that selecting the top 5 % of the genotypes could result in an improvement being 6.12 % and 66.28 % for the aforementioned two traits, respectively. Six characters (LAI, SD, SL, JE %, SSY and SY) had high GA% values more than 20 in the current study. The highest genetic advance value of these characteristics may be attributed to the wide range among genotype means and also to their high heritability estimates. Moderate GA % values ($10 > GA \% > 20$) were obtained for two traits (days to 50% flowering and Purity %) while Brix % and sucrose % recorded low GA % which refers to improvement of these two characters may be less profitable. Johnson *et al.* (1955 a and b) reported that heritability estimates in conjunction with genetic advance would give more accurate index of selection value. Accordingly, it can be concluded that, without considering genetic advance (GA %), the heritability would be practically low important in the selection depends on phenotypic appearance.

In the current study, high heritability and genetic advance % estimates were observed in the case of leaf area index, stalk diameter, stalk length and juice yield indicating

that these traits were good heritable and selection of high performing genotypes is possible to improve these characters due to their additive gene effects which make the selection would be effective in early generations. On the other hand, all genetic parameters recorded their lowest estimates in terms of days to 50 % flowering, Brix %, sucrose % and purity % indicating that the selection process among tested genotypes would be useless to improve these traits. The current conclusions are supported by Tomar *et al.* (2012), and Umakanthm *et al.* (2019) who confirmed that plant breeders must be make their selection when they take in consideration high values of h^2 and GA %.

Cluster analysis is a statistical way of classifying objects into groups. The cluster analysis is considered an efficient procedure to reflect the structural relationships among tested genotypes and provides a hierarchical classification of them. In the present work, based on Euclidean distance, the sweet sorghum genotypes were classified using stalk and juice characters across the two seasons and were grouped as shown in the dendrogram graph (Fig. 1). It could be seen from Table 5 and the dendrogram (Fig. 1), that the cluster analysis discriminated the aimed genotypes into five clusters coded from 1 to 5. The five cluster averages as a percent of the grand mean for each morphological and juice characters across the two seasons are presented in Table 5 and Fig. 2. Cluster number 1st consisted of four genotypes (Willy, William, Rio, and Dall). The genotypes in this cluster were late in flowering and recorded the highest values over the grand mean of all studied traits except stalk length, sucrose %, and purity % (Table 5 and Fig. 2). In other words, their stalk and juice yields were high, but juice quality was low. It is clear that the 2nd cluster included five genotypes (AGSC3, GK Ahron, GK Gaba, Sugar drip, and Rex) that

Table 5. Summary of cluster analysis showed the included genotypes and cluster means of for the studied characters across the two seasons of 2021 and 2022

Traits	Genotypes no.	Clusters and their included genotypes				
		Cluster (1)	Cluster (2)	Cluster (3)	Cluster (4)	Cluster (5)
		1, 2, 4 and 5	3, 13, 15, 17 and 18	11, 21, 22, 23, 26, 29 and 30	6, 7, 10, 12, 16, 20, 25 and 27	8, 9, 14, 19, 24 and 28
Days to 50% flowering		71.00	59.75	60.87	63.72	69.78
Leaf area index)cm(437.68	302.71	288.47	331.67	238.71
Stalk diameter)cm(2.31	2.25	1.31	1.83	2.04
Stalk length)cm (180.96	162.50	160.04	190.72	233.74
Brix%		18.44	17.15	16.79	16.09	16.19
Sucrose%		9.15	9.32	10.14	10.37	10.47
Purity%		49.98	54.96	60.68	65.03	65.22
Juice extraction%		34.78	23.61	20.95	30.46	23.94
Stripped stalk yield (ton/fed)		13.42	9.70	12.59	13.00	11.11
Juice yield (ton/fed)		4.68	2.27	2.65	3.96	2.61

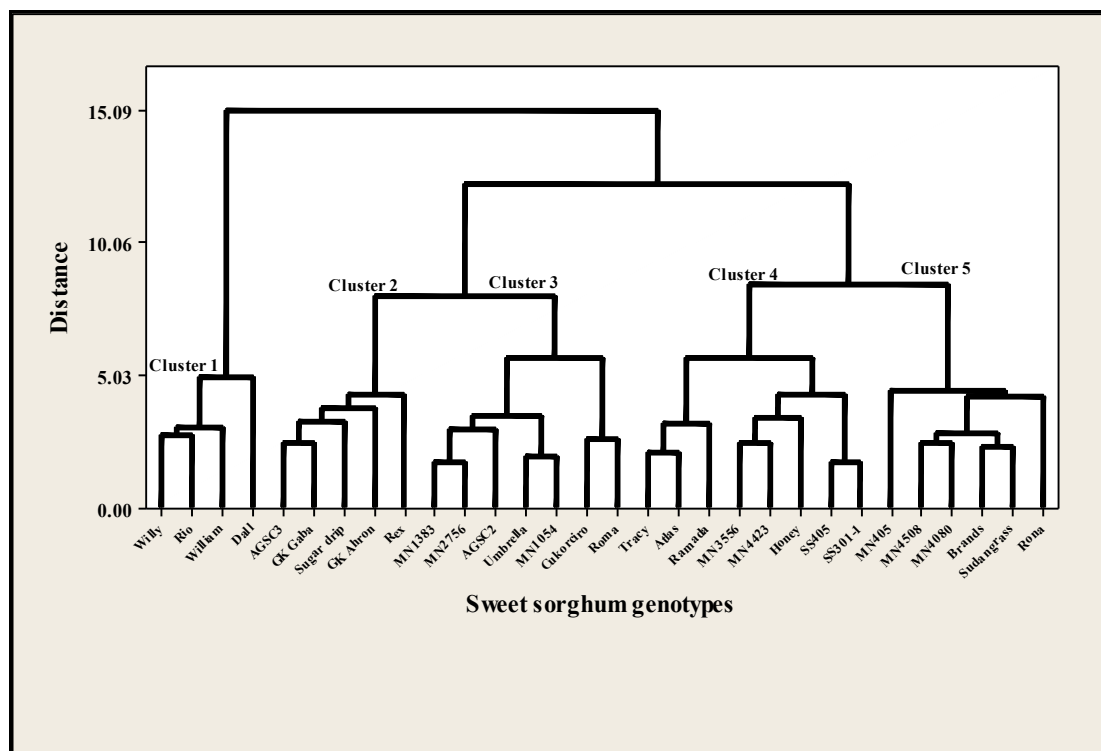


Fig. 1. Dendrogram displaying the distance among thirty sweet sorghum genotypes based on morphological and juice characters across the two seasons of 2021 and 2022

had early flowering plants and wide stalk diameter but they recorded the lowest mean values of stripped stalk yield and juice yield, compared to the other clusters. Therefore, this cluster contained the lowest genotypes with respect to stalk and juice productivity. Considering the 3rd cluster, it comprised seven genotypes MN1383, Cukorciro, Roma, MN2756, AGSC2, Umbrella, and MN1054. The plants of these genotypes were characterized by early flowering and their stalk traits were low where they recorded the minimum mean values of stalk diameter, stalk length, and juice extraction, over the rest clusters.

Cluster number 4 contained eight genotypes namely; Tracy, Atlas, MN3556, MN4423, Honey, SS405, Ramada, and SS301-1 as shown in **Fig. 2** and **Table 5**. These genotypes gave low values of stalk diameter and birch % content while they reflect good juice quality traits (Sucrose%, purity%, and juice extraction %). Finally, the last cluster number 5 included six genotypes i.e. MN405, MN4508, Brands, Rona, MN4080, and Sudangrass that were lately flowering and gave the tallest stalk and the lowest leaf area index. Also, they had good juice quality traits (sucrose % and purity %). In the light of current results, it is exhibited the presence of considerable genetic variability among the aimed sweet sorghum genotypes gives the ability to achieve sufficient improvement of sweet sorghum through the hybridization among genotypes

taken from different clusters to get desirable traits (Jain and Patel, 2016; Mulima *et al.*, 2018; Umakanth *et al.*, 2019 and Naoura *et al.*, 2020).

Over the last two decades, biplot graphs have been used extensively to explain the stability concept of such crops cultivated in multi-environments. Recently, the method has been modified and adapted to be used for genotype comparison in terms of multiple traits i.e. as described by Yan and Rajcan (2002) and Yan and Tinker (2005). In this diagram, the genotypes that are farthest from the origin point (namely vertex genotypes) are connected by lines forming a polygon shape where the other genotypes were located within this polygon. Also, the perpendicular lines from the original point to the polygon sides divided the figure into some sectors that facilitate the comparison among neighboring vertex genotypes. Subsequently, genotypes that came together in one section with one or more specific traits showed relatively good performance toward these traits. Also, genotypes close to the origin of the graph do not respond well to trait changes or had moderate mean values for most traits. In this investigation, the genotype x trait (GxT) biplot graph was exploited to identify the superior genotypes for certain traits that can be selected to become part of the sweet sorghum breeding program. Which-won-where or polygon diagram is an important and famous genotype by trait (GxT) biplot

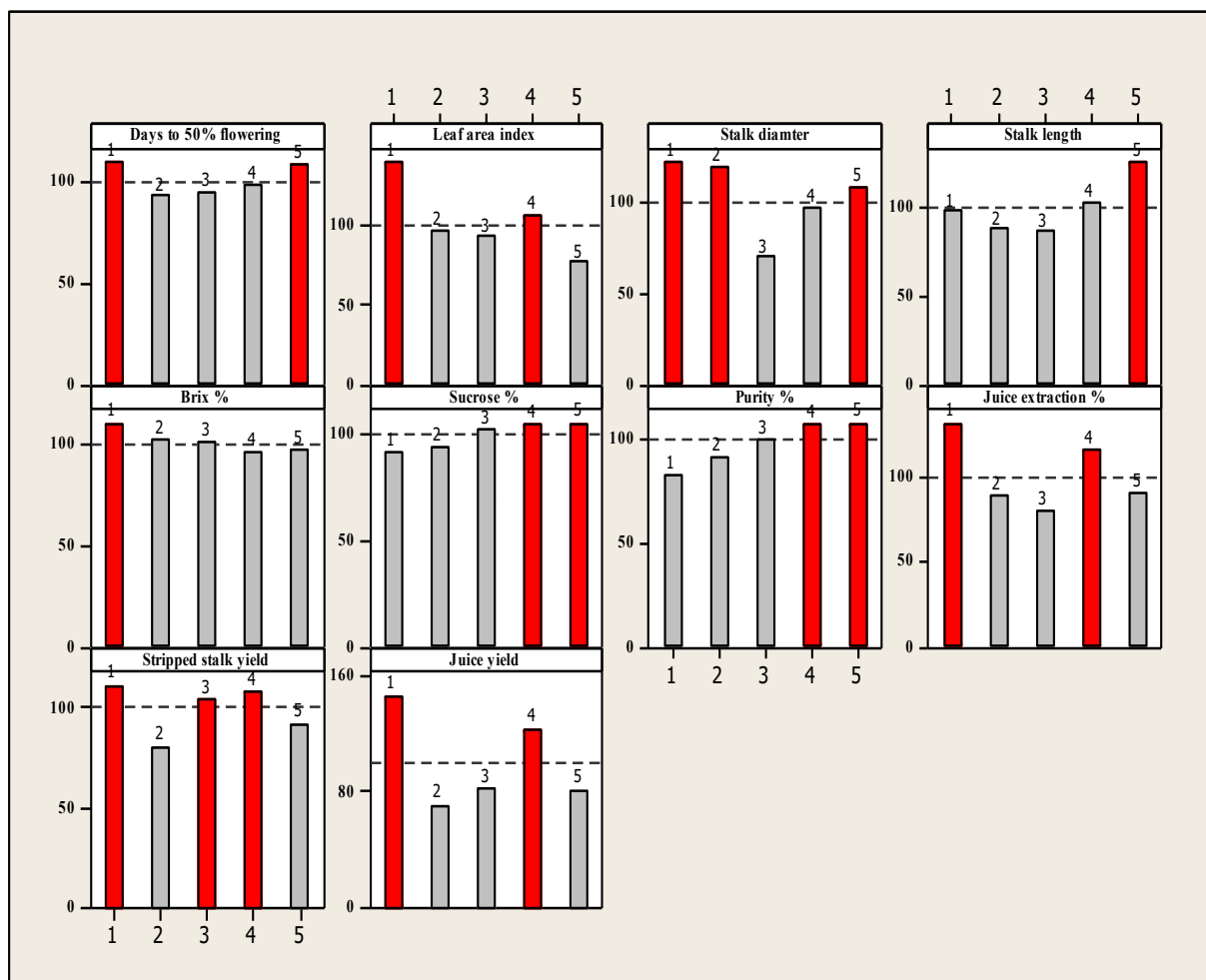


Fig. 2. Bar chart displaying the five cluster averages as percent of the grand mean for each morphological and juice characters across the two seasons of 2021 and 2022

graph that is considered a simplified and fast procedure to visualize the patterns of interrelationships among genotypes and their traits.

The polygon biplot graph (**Fig. 3**), it is showing the interrelationships among the tested sweet sorghum genotypes using ten morphological and biochemical traits across the two seasons. GxT biplot explained 50.22 % of the total variation of the standardized data that reflected the linear relationships among the sweet sorghum genotypes regarding their measured traits. The first and two principal components (PC1 and PC2) explained 30.20 % and 20.02 %, respectively. This relatively moderate variability proportion explained by the GxT biplot graph (50.22 %) may be attributed to the complexity of the relationships among the genotypes with regard to the measured traits and to the absence of some traits that were not included in the study. Examining the graph, it is obvious that genotype No. 2 (William) recorded the best

values in terms of juice extraction%, juice yield, stripped stalk yield, stalk diameter, days to 50% flowering, and leaf area index. Also, genotypes; Rio, Tracy, and Atlas are located in the same sector and reflected similar performance for the same traits. It is shown that the points of these genotypes and traits were founded in one sector and the angles among them were acute indicating positive associations among them. Mulima *et al.* (2018) used cluster analysis and a GxT biplot graph to classify sweet sorghum genotypes according to their characters. Genotype (MN405) followed by genotypes; MN4508, MN3556, MN4423, Brands, Ramada, and MN4508 gave the best results in terms of juice quality being sucrose % and purity %, while they were the lowest in brix percentage because the obtuse angles between both of sucrose % and purity % and brix% indicating the negative association between them. Contrary to the abovementioned results, genotypes; (Dall) and (Willy) had high brix % content and low sucrose and purity percentages. On the other

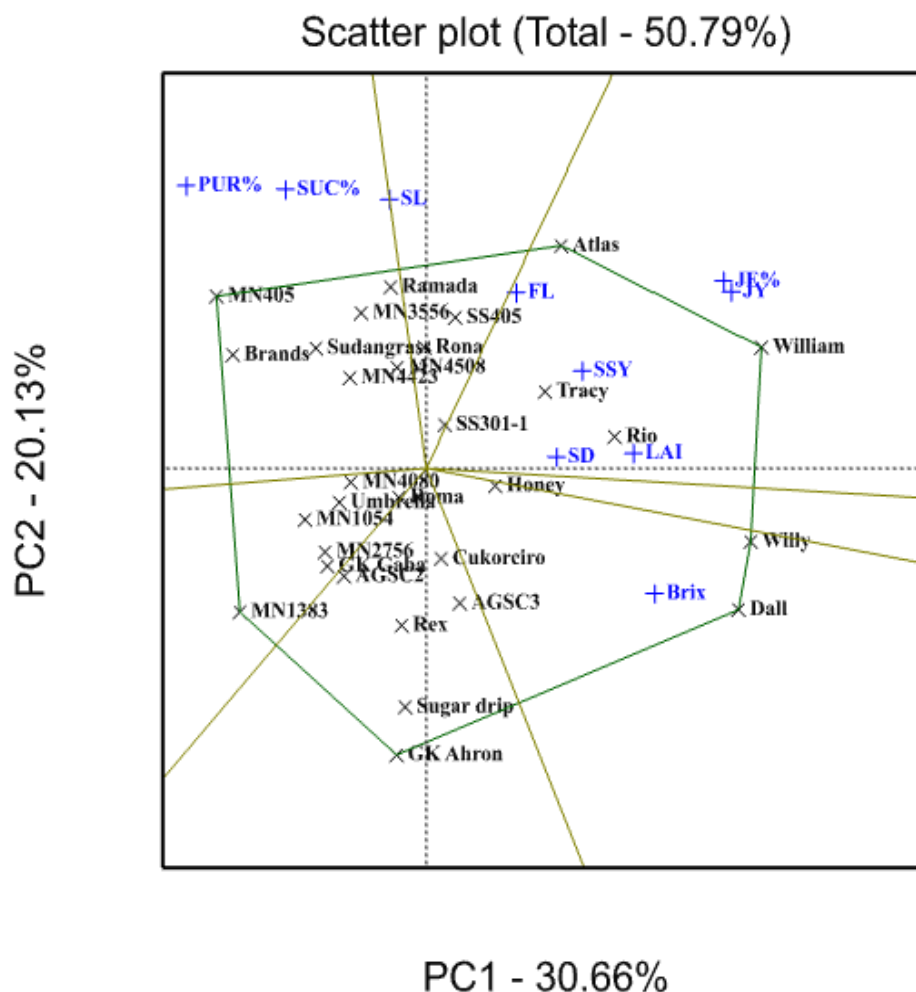


Fig. 3. Which-won-where or polygon of genotype by trait (GxT) biplot graph displaying which genotype is superior for which studied traits across the two seasons of 2021 and 2022

hand, the genotypes located around the original point are not considered distinctive for any of the studied traits. As for the genotypes that fall far from the studied traits, this expresses their poor performance towards these traits. Jain and Patel (2016) used a principal components method to compare the mean performance of sorghum varieties via nine quantitative traits. Al-Naggar *et al.* (2018) used GGE-biplot models to estimate G×E interaction in sorghum parental lines and to identify sorghum B-lines of stability and adaptability across different environments. Undoubtedly, Genotype × Trait (GxT) biplot graph is considered an easy and effective visualized technique to interpret and extrapolate results.

The present study showed a wide range of variability among the tested sweet sorghum genotypes in terms of all the measured stalk and juice traits. The maximum juice yield was produced by the elite three genotypes

Willy, William, and Atlas which indicate the possibility of their participation in the future breeding programs of sweet sorghum. Leaf area index, stalk diameter, stalk length, and juice yield gave the highest heritability and genetic advance % estimates indicating the possibility of improving them through selection on the basis of the phenotypic pattern of the plant. The aimed sweet sorghum genotypes were classified into five clusters using cluster analysis. The four genotypes (Willy, William, Rio, and Dall) that were included in the first cluster recorded the highest values of all studied traits except stalk length, sucrose %, and purity % giving good stalk and juice yields. With regard to GxT biplot graph, genotypes; William, Rio, Tracy, and Atlas recorded the best values of juice extraction %, juice yield, stripped stalk yield, stalk diameter, days to 50 % flowering, and leaf area index. The difference in results between cluster analysis and GxT biplot graph is expected due to the different mathematical basis of each.

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