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Full Length Research Paper

Genetic diversity and principal component analysis for agronomic and technological characterization of sweet sorghum germplasm under Egyptian conditions

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This genetic diversity is an essential prerequisite for improving the genetic makeup of any crop. So, an experiment was conducted to investigate the genetic diversity among thirty-six sweet sorghum germplasm with different origin imported by Sugar Crops Research Institute. They were evaluated for 13 agronomic and technological traits during the summer 2018 and 2019 seasons at Giza Agricultural Research Station, Giza Governorate, and Egypt. The experimental design used was a randomized complete block design with three replicates. The magnitude of genetic variability was estimated using broad sense heritability (h_b^2). Also, cluster analysis was automated to identify the interrelationships among the tested genotypes as well as principal component (PC) analysis that was used to explain the majority of the total variation. Our results showed significant differences among genotypes for most traits studied. High estimates of genotypic and phenotypic coefficients of variation (GCV and PCV) coupled with high h_b^2 were observed for ethanol yield, juice yield and stalk length in the two seasons indicating the presence of genetic variability and potential selection for these traits. Results of cluster analysis exhibited a considerable genetic diversity among the tested genotypes which gave a good chance to achieve sufficient scope for genotypic improvement of sweet sorghum through the hybridization among genotypes taken from divergent clusters. The dendrogram for the clustering pattern of germplasm was grouped into six major clusters according to hierarchical clustering analysis based on the relative dissimilarity among 36 germplasm. Considering the 4th sub-cluster, it comprised of six germplasm being Brands, Dale, Willy, Smith, Ramada, and Tracy, which had the best cluster. Also, these germplasms recorded the highest values of stalk diameter (cm), sucrose%, purity%, reducing sugars%, juice extraction%, Juice yield (t/fed), fermentable% and ethanol yield (L/fed) compared with other clusters, The PC analysis grouped the germplasm into groups and remained scattered in all four quadrants based on the phenotypic traits. The first four components of principal component (PC) analysis explained the majority of the total variation and contributed 81.30% of the total variation among the germplasm. Therefore, this germplasm can be used as parents in sweet sorghum breeding programs to develop superior sugar-rich cultivars for bioethanol production in Egypt.

Keywords: Genetic diversity, sweet sorghum, germplasm, cluster analysis, principal component analysis

INTRODUCTION

Sweet sorghum is promising as a multifunctional crop not only for its high economic value but also due to its high sustainable productivity (95 to 125 t/ha of green cane yield) and to the wide range of its products (grains, sucrose and lignocelluloses). Sweet sorghum thus can be considered as a cash crop (Umakanth *et al.*, 2019). Sweet sorghum accumulates fermentable sugars (10–20%) in the stalk and thus has an advantage for producing

grain for food and bioethanol from stalk juice without compromising food security (Reddy *et al.,* 2005).

A successful development of new cultivars relies in general on the availability of source germplasm with eligible traits such as biotic and abiotic tolerance and improved agronomic and quality traits. The important objective of the plant-breeding program is the diversification of the genetic base of cultivars, which is achieved by intercrossing the genetic sources of diverse origin. Sorghum is awarded high variability due to its wide range of adaptation in tropical and temperate climates and free gene exchange among various races (Elangovan *et al.,* 2014). For any progress in plant breeding, there is the need to study the genetic variability which cannot easily be quantified. Genetic improvement for quantitative traits depends on the nature and amount of variability present in any genetic stock and the extent to which the desirable traits are heritable. Sorghum, in general, possesses a wide range of genetic variability (Sharma *at al.,* 2006). Cluster analysis is a multivariate technique that groups genetically similar genotypes together through a repetitive process that results in cluster formation and the clustering algorithm aims to separate genetic material into homogenous groups, such that the within-group similarities are larger compared to the between-group similarities. (Bertan *et al.,* 2007). Also, Patankar *et al.* (2005) reported the genetic divergence in 41 sweet sorghum genotypes grouped the genotypes into ten clusters and observed that the clustering patterns of these genotypes did not follow the geographical distribution. Sujatha and Pushpavalli, (2015) also reported similar results in a genetic diversity study involving 62 sorghum genotypes. Maximum Heterosis is expected from crosses with parents belonging to most divergent clusters. Principal component analysis is a multivariate technique for examining the relationships among several quantitative variables (Johnson, 2012). It is the most common technique used in variability studies and numerical classification; it is useful in grouping varieties based on their similarities (Bello, 2004). Establishing suitable selection criteria for identifying genotypes with desirable traits is useful in developing improved varieties. Analysis of variability among traits and knowledge of associations among traits contributing to yield would be of great importance in planning a successful breeding program (Mary and Gopalan, 2006). Therefore, the objective of this study was to 1) determine the genetic diversity of sweet sorghum which would help enhance the efficiency of sorghum breeding program to develop better varieties and hybrids.

2) Evaluate the sweet sorghum germplasm and select superior genotypes that will be a potential source of feedstock for bioethanol production in Egypt.

MATERIALS AND METHODS

The present study was carried out to investigate the genetic diversity among thirty-six sweet sorghum germplasm with different origin (Table 1) and to evaluate for 13 agro-morphological and biochemical traits during 2018-2019 summer seasons at Giza Agricultural Research Station (The station is located at latitude 30º 02 N). A randomized complete block design (RCBD) with three replications was used. The area of each plot was 21 m^2 consisted of (5 rows, 7m long and 60cm apart). Spacing between hills was 25 cm. Other cultural practices such as hoeing, thinning, fertilization, irrigation, etc. were applied as recommended by the Ministry of Agriculture and Land Reclamation to assure optimum production.

Studied characters

Harvest time was carried out for each cultivar at the dough stage (90 to 120 days from sowing). The three middle guarded rows of each plot were used to determine yield per fedden of the millable stalks and stalk components (stalk length, diameter and weight). Then immediately crushed through 3 roller labs. Mill, and the obtained raw juice was filtered, weighed, and the following traits were measured for each genotype:

1. Net stripped-stalks yield per ton/fed, was calculated on a plot basis kg/ fed then converted to ton/fed.
2. Stalk length (cm): was measured from the land level till visible dewlap.
3. Stalk diameter (cm): was measured at mid stalk.
4. Brix (percent soluble solids) was determined with a hand refractometer.
5. Sucrose percentage of clarified juice was determined by using automated saccharimeter according to A. O. A. C. (2005).
6. Purity was calculated as: [(Sucrose / Brix) x 100].
7. Reducing sugar in juice: Determined by using Fehling solution according to the method described by Meade and Chen (1977).
8. Juice extraction % (JEP) = juice weight/stalk weight x 100.
9. Juice yield (ton/fed.) = stripped stalk yield × JEP /100
10. Syrup extraction percentage (SEP) calculated from the following equations: SEP = Syrup weight × 100 / Juice weight
11. Fermentable sugars% FSP = Sucrose % + Reducing sugars % according to the method described by of Meade and Chen, (1977).
12. Theoretical ethanol yield (EtOH) was calculated according to Smith and Buxton, (1993)

Statistical analysis

Collected data were subjected to the individual analysis of variance (ANOVA) of randomized complete block design for each one of the two seasons (Gomez and

Table 1. Origins of tested sweet sorghum germplasm in Egypt.

No.	Germplasm name	Origin	No.	Germplasm name	Origin
1	William	Kentucky/Georgia	19	SS405	Nigeria
2	MN1054	Mississippi	20	Ramada	Mississippi
3	MN1500	Mississippi	21	Leoti	Mississippi
4	MN4080	Mississippi	22	SS301-1	Nigeria
5	MN4508	Mississippi	23	Tracy	Texas
6	MN2756	Mississippi	24	Rona	unknown
7	MN1383	Mississippi	25	Rex	Mississippi
8	MN3556	Mississippi	26	Sugar drib	Oklahoma
9	MN4416	Mississippi	27	Roma	South Africa
10	MN3386	Mississippi	28	Planter	South Africa
11	Brands	Mississippi	29	E2	Ethiopia
12	Honey	Mississippi	30	Atlas	South Africa
13	Dale	Mississippi	31	AGSC2	unknown
14	Sudangrass	Sudan	32	AGSC3	unknown
15	Umbrella	Mississippi	33	GK Ahron	unknown
16	Willy	Mississippi	34	MN 4423	Mississippi
17	Smith	Texas	35	GK Gaba	unknown
18	Rio	Texas	36	Cukorciro	unknown

Gomez, 1984). Least significant difference (LSD) test was used to detect the significant differences among genotype means at the 0.05 probability level. The genotypic and phenotypic variances and their corresponding coefficient of variations were estimated using the pertinent mean square expectations according to the method suggested by Johnson *et al.* (1955):

Genotypic variance (σ^2 g) = gMS – EMS
Phenotypic variance (σ^2 p) = σ^2 g + EMS
Genotypic Coefficient of Variation (GCV) % was estimated as:

(GCV) % = (δg / general mean) x 100.
Phenotypic Coefficient of Variation (PCV) % was estimated as:

(PCV) % = (δp / general mean) x 100.

Where

δg = genotypic standard deviation

δp = phenotypic standard deviation

Heritability (H) in a broad sense was computed for each character as the ratio of genetic variance to the total variance as suggested by Hanson *et al* (1956):
H = σ^2 g / σ^2 p x 100

Where
σ^2g and σ^2p are genotypic and phenotypic variances respectively. Hierarchical cluster analysis was performed on the standardized data using a measure of Euclidean distance and Ward minimum variance method as outlined by Ward, (1963). While principal component analysis (PCA) was carried out as explained by Rao, (1964).

RESULTS AND DISCUSSIONS

Mean performance of 36 sweet sorghum germplasm

The present investigation revealed a considerable amount of variation for all genetic materials studied and for all studied characters (Tables 2 and 3). Large variation among genotypes was found for stalks yield/fed. It varied from (as an average of the two seasons) 7.55 t/fed for the genotype E2 to 19.71 t/fed for the genotype Rex. Nine genotypes (MN1383, Dale, Umbrella, Willy, Rona, Rex, Sugar drib, Roma and GK Ahron) were significantly the highest in stalks yield/fed as average of the two seasons compared with other genotypes. Rao *et al.* (2013) revealed variation among evaluated varieties ranged between 30.7 to 40.8 t/h. Whereas Rutto *et al.* (2013) evaluated Dale and Sugar drib varieties and they found that Dale variety exhibited stalk yield about 66.6% greater than sugar drib. For Stalk diameter (cm) three genotypes (Rona, Brands and Umbrella) were the tallest genotypes (331, 321.75 and 307.50 cm, respectively) as the average across the two seasons compared with other rival. Only the two germplasm (E2 and Leoti) were the shortest (125.50 and 152.50 cm respectively, as the average across the two seasons) compared with other studied genotypes. Moreover, the genotype Smith recorded the highest value for stalk diameter (3.32 cm as the average across the two seasons) conversely the

Table 2. Mean performance of 36 sweet sorghum germplasm.

Germplasm	Stripped Stalks Yield (t/fed)		Stalk length (cm)		Stalk diameter (cm)		Brix%		Sucrose%		Purity%	
	2018	2019	2018	2019	2018	2019	2018	2019	2018	2019	2018	2019
William	15.68	15.50	234.50	225.00	2.02	1.89	17.65	17.95	8.18	8.16	46.36	45.47
MN1054	14.25	14.37	205.00	205.00	1.69	2.15	20.30	20.80	8.48	8.49	41.81	40.82
MN1500	15.29	14.94	227.50	231.00	1.89	2.28	20.81	19.78	8.31	8.37	39.97	42.31
MN4080	17.02	17.25	205.00	194.50	2.02	1.95	19.03	19.08	9.18	9.14	48.23	47.88
MN4508	16.86	16.65	205.00	199.00	2.34	2.54	19.20	19.52	8.64	8.65	45.02	44.30
MN2756	18.34	18.18	207.50	215.00	1.95	2.47	18.00	18.17	9.15	9.20	50.81	50.61
MN1383	18.23	18.37	180.00	184.50	2.73	2.93	20.57	20.24	9.54	9.57	46.41	47.30
MN3556	16.05	16.69	210.00	221.00	1.56	1.56	17.24	17.30	8.14	8.18	47.19	47.29
MN4416	17.06	17.12	236.50	242.50	1.68	1.63	18.14	18.26	8.55	8.50	47.15	46.54
MN3386	18.20	17.57	246.50	253.50	1.85	2.13	18.51	18.50	8.47	8.55	45.77	46.22
Brands	17.25	17.66	317.50	326.00	2.57	2.48	21.34	21.38	10.38	10.44	48.65	48.83
Honey	16.18	16.06	220.50	245.00	2.80	2.73	19.50	20.30	8.75	8.76	44.85	43.34
Dale	19.17	18.86	289.00	252.00	2.08	2.41	18.36	19.10	9.36	9.32	50.81	50.56
Sudangrass	14.44	14.55	160.00	182.00	1.56	1.69	17.43	17.58	8.86	8.89	50.98	48.79
Umbrella	18.39	16.92	310.00	305.00	2.28	2.21	21.50	21.20	9.07	8.98	42.18	42.34
Willy	18.74	19.37	271.50	263.50	2.54	2.60	16.74	16.85	9.44	9.46	56.36	56.15
Smith	15.73	15.94	290.00	299.50	3.45	3.19	16.80	17.00	9.65	9.64	57.44	56.70
Rio	16.81	16.36	225.00	222.00	2.08	2.54	18.43	18.70	9.29	9.26	50.51	49.71
SS405	16.91	17.16	167.00	165.00	1.66	1.74	16.75	16.68	7.20	7.27	42.97	43.59
Ramada	16.48	16.69	260.00	245.00	1.89	2.80	20.30	20.50	10.04	10.05	49.43	49.00
Leoti	15.61	15.33	149.00	156.00	1.95	2.28	18.55	18.10	10.17	10.12	54.86	55.89
SS301-1	16.80	17.53	305.00	294.00	2.80	3.32	20.10	18.00	8.64	8.03	42.99	44.62
Tracy	17.94	18.01	230.00	257.50	1.95	2.41	18.83	18.32	9.12	9.03	48.43	49.28
Rona	19.24	18.52	322.00	340.00	2.08	2.28	18.11	19.25	8.07	8.07	44.58	41.97
Rex	19.79	19.64	279.50	290.50	2.15	1.76	20.30	20.10	8.74	8.73	43.07	43.49
Sugar drib	19.02	17.71	235.00	229.00	2.80	2.15	18.50	19.85	8.49	8.36	45.90	42.13
Roma	18.76	19.00	252.00	246.50	1.82	1.76	20.40	20.25	8.26	8.22	40.51	40.57
Planter	17.31	17.40	197.50	192.50	1.63	1.65	17.17	17.32	8.14	8.20	47.38	47.36
E2	7.82	7.29	130.00	120.00	0.98	1.43	9.07	9.00	4.84	4.84	26.66	26.86
Atlas	15.14	14.15	174.00	174.50	1.69	1.83	16.87	16.85	7.06	6.66	41.84	39.53
AGSC2	15.77	15.95	161.50	168.00	1.79	1.73	16.57	16.46	7.85	7.78	47.36	47.24
AGSC3	15.00	14.75	176.50	174.00	1.86	1.81	16.14	16.23	7.07	7.14	43.82	43.98
GK Ahron	18.69	18.55	171.50	177.50	1.55	1.60	16.94	16.85	8.15	8.15	48.11	48.37
MN 4423	18.01	16.85	189.50	187.50	1.78	1.83	17.05	17.10	8.33	8.32	48.85	48.63
GK Gaba	17.78	17.99	183.50	181.00	1.68	1.71	16.80	16.74	8.04	8.35	47.86	49.87
Cukorciro	16.50	16.58	152.50	148.50	2.06	2.16	16.44	16.50	6.89	6.97	41.90	42.22
LSD 0.05	3.93	3.54	70.02	62.17	0.57	0.88	4.35	4.39	2.32	2.34	13.00	13.28

genotype E2 recorded the lowest value for stalk diameter (1.20 cm) as average across the two seasons. These results are by following findings of Rono *et al.* (2018) where revealed variation among evaluated varieties. Regarding the brix per cent, there were significant variations among the genotypes. High brix is essential for maximizing the amount of sucrose and ethanol produced per unit area cultivated. Brix of cane juice at the fourth internode varied significantly with genotypes Umbrella registered highest brix of 21.5% making it sweeter and hence, more palatable amongst all genotypes tested. The lowest brix value was determined in E2 (9.07%) genotype. The above results harmonize with many researchers such as Reddy *et al.* (2005), Almodares and

Table 3. Mean performance of 36 sweet sorghum germplasm.

Germplasm	Reducing sugar%		Juice Extraction %		Juice Yield (t/fed)		Syrup Extraction %		Syrup yield (t/fed)		Fermentable sugars%		Ethanol Yield (L/fed)	
	2018	2019	2018	2019	2018	2019	2018	2019	2018	2019	2018	2019	2018	2019
William	6.22	6.28	43.20	40.06	6.77	6.21	11.63	11.70	1.82	1.81	14.40	14.45	519.00	477.37
MN1054	5.52	5.61	31.16	34.46	4.44	4.95	13.54	13.64	1.93	1.96	14.00	14.10	330.88	371.45
MN1500	5.66	5.73	33.68	38.14	5.15	5.70	11.25	10.58	1.72	1.58	13.95	14.10	382.85	427.47
MN4080	5.60	5.62	38.41	36.18	6.54	6.24	10.68	10.29	1.82	1.77	14.75	14.75	513.94	490.41
MN4508	6.60	6.53	48.80	47.97	8.23	7.99	10.42	9.18	1.76	1.53	15.25	15.20	667.30	644.97
MN2756	6.85	6.85	41.67	44.80	7.64	8.15	13.66	11.26	2.51	2.05	15.95	16.05	650.24	695.76
MN1383	6.75	6.65	33.01	35.86	6.02	6.59	13.19	13.05	2.40	2.40	16.25	16.20	521.97	568.92
MN3556	6.07	6.15	35.27	33.15	5.66	5.54	10.88	10.14	1.75	1.70	14.25	14.35	428.09	422.24
MN4416	6.70	6.76	44.02	43.22	7.51	7.40	10.61	10.87	1.81	1.86	15.25	15.25	609.43	600.54
MN3386	7.34	7.31	33.92	31.79	6.17	5.59	9.83	9.28	1.79	1.63	15.85	15.90	519.45	471.53
Brands	8.13	8.20	44.20	45.93	7.62	8.11	12.76	12.84	2.20	2.27	18.55	18.65	751.13	804.94
Honey	5.74	6.25	46.18	41.82	7.48	6.72	9.89	10.01	1.60	1.61	14.50	15.00	575.75	536.49
Dale	6.37	6.20	47.18	45.23	9.04	8.53	13.40	11.41	2.57	2.15	15.20	15.10	732.96	684.88
Sudangrass	6.31	6.16	41.49	43.94	5.99	6.40	10.20	10.32	1.47	1.50	15.65	15.45	499.77	526.72
Umbrella	6.21	6.30	44.26	47.85	8.13	8.10	9.83	9.87	1.81	1.67	15.25	15.25	661.00	658.37
Willy	6.64	6.55	46.01	48.03	8.62	9.30	10.73	10.82	2.01	2.10	16.10	16.05	737.60	792.65
Smith	6.83	7.86	47.75	46.84	7.51	7.47	11.15	10.53	1.76	1.68	16.50	17.50	658.62	695.38
Rio	6.79	6.91	37.09	40.34	6.21	6.57	12.69	11.78	2.13	1.94	16.05	16.20	531.57	564.73
SS405	6.15	6.17	32.59	35.80	5.52	6.14	10.25	10.31	1.74	1.77	13.35	13.45	391.60	439.37
Ramada	6.94	6.75	45.21	46.80	7.45	7.81	12.30	12.14	2.03	2.03	16.95	16.80	672.83	698.43
Leoti	7.13	7.07	45.86	46.91	7.16	7.20	11.31	12.59	1.77	1.93	17.30	17.20	659.59	657.67
SS301-1	6.85	6.82	38.36	36.29	6.45	6.36	11.78	11.84	1.98	2.08	15.50	14.85	531.51	502.72
Tracy	7.25	7.47	46.90	46.12	8.42	8.31	11.57	11.63	2.08	2.09	16.40	16.50	733.05	729.49
Rona	6.39	6.42	37.04	34.96	7.13	6.48	10.91	13.23	2.10	2.45	14.45	14.50	548.44	499.22
Rex	6.75	6.52	38.28	39.91	7.58	7.84	11.76	11.27	2.33	2.22	15.50	15.25	624.69	636.01
Sugar drib	7.33	7.34	44.17	45.77	8.41	8.11	11.27	12.32	2.14	2.19	15.80	15.70	707.40	677.54
Roma	6.63	6.63	44.54	46.97	8.36	8.93	12.34	11.50	2.32	2.19	14.90	14.85	662.03	704.91
Planter	6.50	6.59	46.89	47.07	8.12	8.19	12.03	12.33	2.08	2.15	14.65	14.80	632.43	644.98
E2	3.43	3.44	20.61	22.61	3.22	3.30	5.18	5.57	0.81	0.81	8.25	8.30	283.50	290.46
Atlas	5.87	5.97	37.66	40.73	5.71	5.76	11.94	12.02	1.81	1.70	12.95	12.60	392.12	386.64
AGSC2	6.49	6.51	42.29	43.91	6.67	7.01	9.92	9.33	1.56	1.49	14.30	14.30	508.50	532.54
AGSC3	6.11	6.16	42.95	44.02	6.45	6.49	9.94	10.86	1.49	1.61	13.20	13.30	452.08	459.64
GK Ahron	7.27	7.13	35.19	36.86	6.58	6.84	10.73	10.84	2.01	2.01	15.40	15.30	539.61	556.14
MN 4423	7.14	7.20	41.22	42.86	7.43	7.22	10.40	9.87	1.88	1.66	15.45	15.50	610.98	596.53
GK Gaba	6.52	6.44	41.59	44.08	7.40	7.93	12.04	9.93	2.14	1.79	14.55	14.75	573.02	623.69
Cukorciro	5.40	5.36	44.01	44.19	7.26	7.33	10.73	10.84	1.77	1.80	12.30	12.35	474.83	480.66
LSD	1.66	1.72	10.11	11.05	1.66	1.63	3.00	3.33	0.53	0.56	3.96	4.02	145.40	144.54

Hadi, (2009), Atokple *et al.* (2014) and Erdurmus *et al.* (2018) they also found mighty variations in brix percentage among evaluated genotypes ranged between 11 to 23%. Sucrose percentage has insignificantly differed among the evaluated germplasm. The lowest sucrose value was determined in E2 genotype (4.84% as average across the two seasons).

However, the highest sucrose% value was determined by three germplasm; Brands, Leoti and Ramada (10.41%, 10.14% and 10.04%, respectively (as average across the two seasons). The above result concurrence with Besheit *et al.* (2019), who found insignificantly differences among the evaluated varieties for sucrose percentage. Besides, Audilakshmi *et al.* (2010) found a big variation among tested genotypes. Purity percentage did not differ between genotypes, by contrast, reducing sugar percentage had significant variations among the genotypes and ranged from 3.44 to 8.13% as average across the two seasons. There were significant differences among sweet sorghum germplasm for percent juice extraction and juice yield. The juice yield was influenced by sorghum genotype. Willy genotype had a greater juice yield (8.96 t/fad as average over the two seasons) than all other genotypes while E2 produced the least juice yield. Genotypic differences for juice yield have also been reported by Reddy *et al.* (2011), Reddy *et al.* (2013), Soleymani *et al.* (2013), El-Geddawy *et al.* (2014), Elangovan *et al.* (2014) and Reddy *et al.* (2014).

Syrup extraction % and syrup yield t/fad differed significantly among tested genotype, also Besheit *et al.* (2019) found differences among evaluated verities for syrup extraction %, rather fermentable sugars% did not show significant differences among tested germplasm. Highly significant differences among tested germplasm were noticed for ethanol yield. Genotype Brands produced the greatest ethanol yields in 2018 and 2019 seasons (751.13 and 804.94 L/fad, respectively). Nonetheless the genotype E2 recorded the lowest production of ethanol yield in 2018 and 2019 seasons (283.50 and 290.46 L/fad, respectively). Furthermore, the variation among sweet sorghum ability in ethanol production as detected in this work was affirmed by Allam *et al.* (2001), Al-Labbody *et al.* (2008), Besheit and Mekdad, (2016), Reddy *et al.* (2011), Reddy *et al.* (2013);

Table 4. Genetic variability and heritability (h_b^2) for studied traits during 2018 and 2019 seasons for 36 sweet sorghum germplasm.

Traits	Genotypic variance		Phenotypic variance		Broad sense heritability (h_b^2)	Genotypic coefficient of variation (G.C.V %)		Phenotypic coefficient of variation (P.C.V %)		
	2018	2019	2018	2019	2018	2019	2018	2019	2018	2019
Stripped Stalks Yield (t/fed)	2.59	3.11	4.48	4.64	57.89	67.02	9.57	10.56	12.57	12.89
Stalk length (cm)	1950.94	2287.67	2551.16	2760.85	76.47	82.86	20.13	21.62	23.02	23.75
Stalk diameter (cm)	0.18	0.13	0.22	0.23	81.94	57.97	21.09	16.78	23.31	22.07
Brix%	2.49	2.40	4.80	4.76	51.74	50.43	8.67	8.51	12.05	11.97
Sucrose%	0.44	0.45	1.10	1.12	40.17	40.13	7.81	7.89	12.32	12.46
Purity%	7.89	7.26	28.58	28.84	27.62	25.19	6.07	5.85	11.55	11.65
Reducing sugar%	0.28	0.28	0.62	0.65	45.42	43.86	8.19	8.20	12.15	12.38
Juice Extraction %	23.37	18.33	35.88	33.27	65.13	55.09	11.90	10.33	14.74	13.92
Juice Yield (t/fed)	1.19	1.17	1.53	1.49	77.93	78.31	15.71	15.40	17.81	17.40
Syrup Extraction %	1.18	0.83	2.28	2.19	51.88	37.91	9.73	8.29	13.52	13.45
Syrup yield(t/fed)	0.07	0.06	0.11	0.10	68.47	62.14	14.23	13.35	17.22	16.97
Fermentable sugars%	0.97	0.97	2.89	2.95	33.50	32.91	6.57	6.57	11.35	11.45
Ethanol Yield (L/fed)	11847.68	12474.58	14435.71	15031.99	82.07	82.99	19.31	19.56	21.32	21.48

Soleymani *et al.* (2013); Elangovan *et al.* (2014); Reddy *et al.* (2014). Also, huge variations among evaluated varieties for ethanol yield ranged between 738 and 3146 L/ha were found by Erdurmus *et al.* (2018).

It was noticed that the genotypes expressing significance in ethanol yield also had significant value for one or more characters i.e. stalk yield, brix%, and juice yield and stalk length. Rono *et al.* (2018) reported that ethanol yield, cane yield, juice yield and plant height were all positively correlated at $P<0.001$. Accordingly, the genotype; Brands, Dale, Willy and Tracy showed significantly high brix value, high stalk yield, high juice yield and tall stalks produced the highest ethanol yield/fed (gave more than 700L/fed) compared with other germplasm. Thus, the various genotypes which recorded outstanding mean performance for different traits may be used as potential parents and could be utilized in hybridizing program of sweet sorghum for improving the yield and performance of trait of interest.

Genetic components

Genetic variance is important as it describes the amount of genetic variation present for the trait. Data in Table (4) revealed that the relative influences of genotypic variance ($\sigma^2 g$) in determining phenotypic variance was more important for most studied traits (study in the first and second seasons), whereas genotypic variance represented more than 50% from phenotypic variance for all traits expect sucrose, purity, reducing sugar and fermentable sugars%. These results indicate that a negligible role was played by the environmental factors in the inheritance of most studied characters in sweet sorghum genotypes under this study. The high genotypic variance in stalk height, diameter and brix were also reported by Elangovan *et al.* (2014). The estimates for the phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV) in all the traits, suggesting that the apparent variation is not only due to genetics but also due to environmental influences. However, the differences between PCV and GCV for most of the traits were small, indicating high prospects for genetic progress through selection under the conditions of this investigation which conformed with the findings of Sami *et al.* (2013). The genotypes exhibited varying degrees of ratios of heritability for most traits. Heritability estimates observed for the characters ranged from 25.19% (purity % in 2019 season) to 82.99 % (ethanol yield in 2019 season). High to moderate estimates of genotypic and phenotypic coefficients of variation (GCV and PCV) were coupled with high heritability recorded for stripped stalks yield, stalk length, stalk diameter, brix%, juice extraction %, juice yield, syrup yield and ethanol yield. The high level of heritability indicates the preponderance of genetic variation which is less affected by the environment. This result is in agreement with finding of Tomar et al (2012). Low to moderate estimates of genotypic of variation (GCV) were coupled with low heritability recorded for sucrose%, purity%, reducing sugar% and syrup extraction %. This result indicated that variations are attributed to high level of environmental effects and non- additive gene action was found and there was a limited role for selection Prabhakar, (2003).

Table 5. Summary of cluster analysis showed the 36 sweet sorghum germplasm.

Cluster no.	No. of Germplasm in each group	Included germplasm
1	5	William , MN1054, MN1500, MN4080 and MN2756
2	5	E2, Atlas, AGSC2, AGSC3 and Cukoriro
3	6	MN4508, MN3556, Honey , Umbrella, SS405 and Leoti
4	6	Brands, Willy, Smith, Ramada and Tracy
5	7	MN1383, Rio, SS301-1, Rex, Sugar drip and Roma
6	7	MN4416, MN3386, Sudan grass, Planter, GK Ahron, MN4423 and GK Gaba

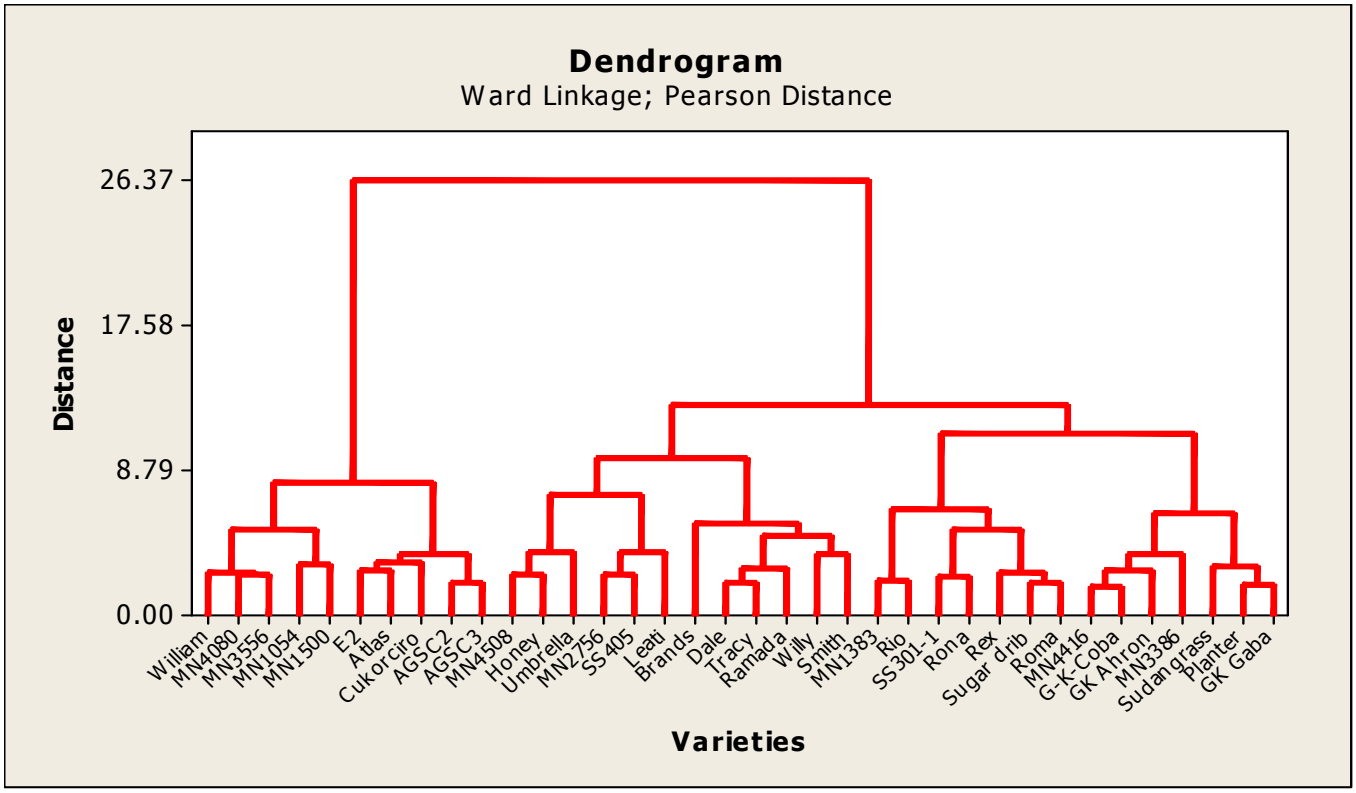

Figure 1. Dendrogram showing the distance among 36 sweet sorghum germplasm based on yield and its related attributes.

Cluster analysis

Cluster analysis is a tool for classifying objects. The cluster analysis was used as an efficient procedure to emerge the structural relationships among tested germplasm and provides a hierarchical classification of them. The genetic divergence can provide a visual idea about variability presented in the thirty-six germplasm, also besides, to assure the continued genetic improvement. In the present work, based on Euclidean distance, the tested germplasm were estimated with stalk yield and its related characters and was achieved distance as shown in dendrogram graph (Figure 1). The Dendrogram for clustering pattern of germplasm was grouped into six major clusters according to hierarchical clustering analysis based on the relative dissimilarity among the 36 germplasm. The results of the cluster analysis were presented in groups of germplasm to infer relationships among germplasm (Table 5). The germplasm per cluster differed from 1 to 7. Clusters 1 and 2 contained 5 germplasm, Clusters 3 and 4 contained 6 germplasm, Clusters 5 and 6.

It could be seen from (Table 5) and dendrogram (Figure 1), that the cluster analysis discriminated the aimed germplasm into two major clusters namely; Cluster A and B. However, the first main cluster divided into two sub-clusters which could be named, 1and 2. The sub-cluster number one consisted of five germplasm

(William, MN1054, MN1500, MN4080 and MN2756). The 2nd sub cluster included five germplasm (E2, Atlas, AGSC2, AGSC3 and Cukorciro). The 2nd main cluster consisted of four sub-clusters (3, 4 and 5).

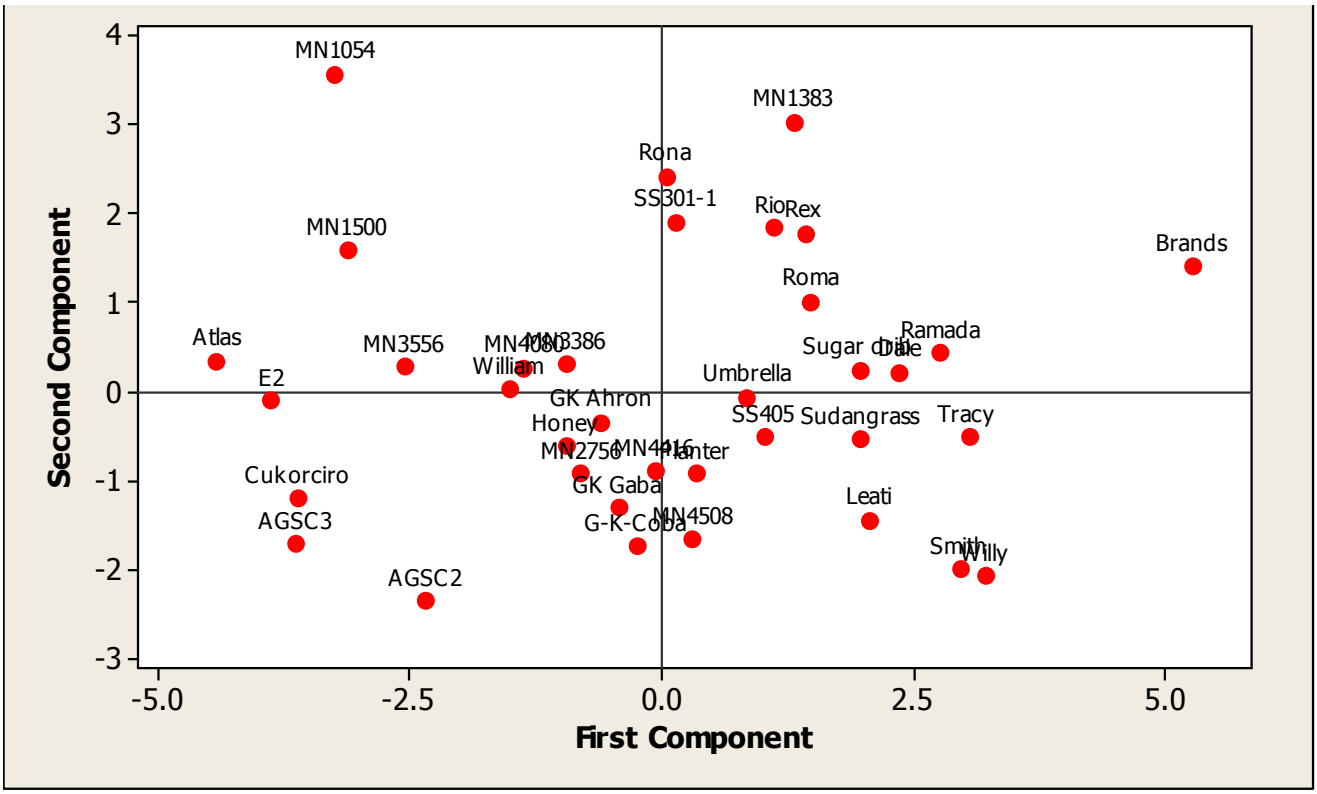

Figure 2. Principal component analysis of measured traits in the 36 sweet sorghum germplasm.

Cluster number 3 contained six germplasm namely; MN4508, MN3556, Honey, Umbrella, SS405 and Leoti as shown in (Figure 1 and Table 5). Considering the 4th sub-cluster, it comprised of six germplasm being Brands, Dale, Willy, Smith, Ramada and Tracy, that had the best cluster, Also, ,that recorded the highest values of Stalk diameter(cm), Sucrose%, Purity%, reducing sugars%, Juice Extraction%, Juice Yield (t/fed),Fermentable% and Ethanol yield(L/fed) compared with other clusters, Characters such as juice extraction, reducing sugar and non-reducing sugar plays prominent and direct role in ethanol production for biofuel Mandke and Kapoor (2004) and Almodares and Hadi, (2009). Characters such as cane yield, juice extractability, type and content of sugar in stalk have been proved to be major contributors to its economic superiority Bala *et al.* (1996) and Almodares *et al.* (2008). Genetic diversity instigated in the present study among these characters can be a base for genetic improvement in sweet sorghum. The 5th sub cluster included seven germplasm (MN1383, Rio, SS301-1, Rona, Rex, Sugar drib and Roma. These genotypes were characterized by the highest yield (t/fed), brix%, syrup extraction % and syrup yield (t/fed). On the other hand, the 6th sub cluster included seven germplasm (MN4416, MN3386, Sudangrass, Planter,GK Ahron, MN 4423 and GK Gaba. The results are in agreement with Patankar *et al.* (2005); Sujatha and Pushpavalli, (2015) and Umakanth *et al.* (2019) who reported that clustering pattern of the germplasm revealed that genetic diversity was not necessarily parallel to geographic distribution. Genotypes evolved in the same area were grouped into different clusters.

The PCA grouped the germplasm into groups and remained scattered in all four quadrants based on the phenotypic traits.

The germplasm MN1054, AGSC2 and Brand were placed at extreme positions from the origin in the PCA biplot whereas the germplasm E2, William and Umbrella were concentrated around the origin on PC2. The results of the PCA analysis were presented in groups of germplasm to infer relationships among germplasm (Figure 2).

Principal component analysis is an important breeding tool commonly used by breeders to identify traits that could be used to discriminate crop genotypes. Analysis of variability among traits contributing to yield would be of great importance in planning a successful breeding program (Das, 2000; Yan and Kang, 2003; Johnson, 2012; Mary and Gopalan, 2006).

Table 6 present principal component (PC) analysis that out of the seven components, the first four components explained the majority of the total variation and contributed

Table 6. Principal component analysis of measured characters in sweet sorghum germplasm under Egyptian conditions.

Variable	PC1	PC2	PC3	PC4	PC5	PC6	PC7
Stripped Stalks Yield (t/fed)	0.23	0.11	0.50	0.04	0.37	0.28	0.31
Stalk length (cm)	0.23	0.21	-0.04	-0.44	0.31	0.17	-0.74
Stalk diameter (cm)	0.24	0.13	-0.33	0.03	-0.22	0.77	0.09
brix%	0.16	0.45	-0.12	-0.50	-0.18	-0.22	0.36
Sucrose%	0.35	0.06	-0.36	-0.01	-0.07	-0.10	0.21
Purity%	0.25	-0.33	-0.29	0.42	0.09	0.11	-0.10
R.Sucrose %	0.32	-0.06	-0.06	0.12	0.44	-0.33	-0.04
Juice Extraction %	0.22	-0.43	0.11	-0.23	-0.48	-0.11	-0.17
Juice Yield (t/fed)	0.31	-0.27	0.38	-0.16	-0.19	0.07	0.03
Syrup Extraction %	0.15	0.43	0.07	0.42	-0.44	-0.23	-0.34
Syrup yield(t/fed)	0.25	0.36	0.37	0.32	-0.07	0.05	-0.02
Fermentable%	0.38	0.01	-0.27	0.05	0.16	-0.22	0.13
Ethanol Yield (L/fed)	0.39	-0.19	0.17	-0.10	-0.08	-0.06	0.05
Eigenvalue	5.46	2.17	1.83	1.11	0.93	0.58	0.51
Proportion	42.00	16.70	14.10	8.50	7.10	4.50	4.00
Cumulative	42.00	58.70	72.80	81.30	88.50	93.00	96.90

81.30% of the total variation among the germplasm. The principal component analysis aims to resolve the total variation of a set of traits into linear, independent composite traits, which successively maximize variability in the data (Johnson, 2012). Considering a minimum threshold eigenvalue of one, the four principal components (PCs) accounted for a cumulative of about 81.30% of the whole phenotypic diversity observed among the germplasm accessions. These results were in similar to those of different authors (Mujaju and Chakuya, 2008; Ali *et al.,* 2011; Abraha et al., 2015; Chikuta et al., 2015). Abraha et al. (2015) and Massaoudou et al. (2018) who reported four principal components with eigenvalues greater than one, which explained > 75% of the total variation for the traits.

Conclusion

Considering the fourth sub-group, it included six germplasm being Brands, Dale, Willy, Smith, Ramada and Tracy, that had the best cluster. Additionally, these germplasm recorded the most elevated estimations of most qualities contrasted and different groups. In this manner, these germplasm can be utilized as guardians in sweet sorghum rearing programs to create predominant sugar-rich cultivars for bioethanol generation in Egypt.

Authors' declaration

We declared that this study is an original research by our research team and we agree to publish it in the journal.

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