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Research Article

Genetic Diversity among Sugarcane Genotypes Based on Qualitative Traits

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The study was conducted during 2012/2013 at Wonji Sugar Estate, Ethiopia, to estimate the extent of morphological diversity among sugarcane germplasm based on 16 qualitative traits. Four hundred sugarcane genotypes grouped in 20 locations were considered. Phenotypic frequency distributions of the characters were analyzed and Shannon-Weaver diversity index (H') was computed using the phenotypic frequencies. Results indicated that the variation in H' within locations was larger than the diversity observed between locations. The value of H' for all sample genotypes ranged from 0.43 to 0.98 with a mean of 0.87. Considerable phenotypic diversity was observed among the germplasm studied. This information can be used for establishing proper identity of the accessions, strategic conservation of these germplasm resources, and future improvement work of the sugarcane crop. This is the first study to report phenotypic diversity of local and exotic sugarcane genotypes in Ethiopia.

1. Introduction

Sugarcane (Saccharum spp.) is an important food crop of the tropics and subtropics [1]. It is cultivated in many countries between 40°N and 32.5°S [2] and cane sugar constitutes about 60% of the total sugar produced in the world [3]. Sugarcane plays a significant role in the Ethiopian socioeconomy. Sugar and its by-product are used for local consumption and export. The industry created job opportunity for a large number of people. The government of Ethiopia has an ambition in the second growth and transformation (2015/2016–2020) plan (GTP) to make the total sugarcane plantation area reach 386000 ha [4]. Therefore at the end of the GTP sugar production will be boosted from the current level of 0.3 to 3.9 million tons, ethanol production will be 31,341 m³, and the factories will contribute 448-megawatt electric power to the national grid. For this big dream to become realized the contribution of improved sugarcane varieties is immense.

Perfect assessment of genetic diversity is vital in crop breeding as it helps in the selection of desirable genotypes and introgressing desirable genes from diverse germplasm

into the available genetic base. Genetically diverse germplasm is therefore needed in breeding programs to enhance the productivity and diversity of cultivars. Since the start of the sugar industry, Ethiopia has been relying on importation of sugarcane varieties from many source countries to satisfy the varietal requirements of the sugarcane plantations. In spite of a long history of introduction, no systematic effort has been made so far to characterize and understand the phenotypic diversity of these cultivars. Utilization of introduced germplasm and estimation of the available genetic diversity are vital for their manipulation in crop improvement program [5]. Collection of germplasm is always the first step in any breeding program as it provides plant breeders with sources of useful traits. In particular collecting local germplasm and land races would be crucial as they provide locally adapted genes for better crop improvement. Accordingly, collection of local sugarcane germplasm in different geographic regions of Ethiopia has been conducted and more than 300 materials were collected and preserved [6]. Documented in a history of the monastery in Northern Ethiopia, it was learnt during this survey that sugarcane has been growing in the country

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since the 16th century [6]. It is presumed that sugarcane was introduced into Ethiopia by the Portuguese with other food crops like rice, banana, lime, mandarin, and ginger [7]. Information about the amount and distribution of genetic diversity in these germplasm collections is important for their efficient management and effective utilization in the breeding program.

When population structure in a collection is unknown, categorizing germplasm resources into morphologically similar and most likely genetically similar groups is most useful [8–10]. The local and exotic sugarcane genotypes in Ethiopia should be characterized to estimate the genetic diversity available for strategic conservation and further improvement of the crop. In this study, qualitative traits were used to estimate the levels of variation among the sugarcane germplasm. The main objectives of the study were to (1) estimate the extent of morphological diversity among sugarcane germplasm based on 16 qualitative traits and (2) assess the location-wise patterns of phenotypic diversity.

2. Materials and Methods

- 2.1. Description of the Study Area. The evaluation was conducted during the 2012/13 growing season at Wonji Sugar Estate of Sugar Corporation of Ethiopia. Wonji Sugar Factory is located in Oromia Regional Government State, Eastern Shewa Zone, Adama Woreda, about 110 km from Addis Ababa and about 10 km south of Adama town with latitude 8°31′N and longitude 39°12′E with elevation of 1550 masl. The average annual rainfall is 800 mm with maximum and minimum temperatures 26.9°C and 15.3°C, respectively [11].
- 2.2. Plant Materials. The plant materials for this study consisted of a total of 400 sugarcane genotypes of which 174 were local species-clones (Supplemental Table 1) (see Supplementary Material available online at http://dx.doi.org/10.1155/2016/8909506) collected from different regional states of Ethiopia and 226 were introduced varieties (Supplemental Table 2) maintained at conservation garden of Research and Training, Sugar Corporation of Ethiopia, found at Wonji. The local sample germplasm was chosen on representation basis, stratified systematic sampling method to a given range of geographic area and a range of morphological traits. Among introduced genotypes, selection was made taking into consideration the variation in place of origin, that is, source countries and different periods of introductions to the country and a range of morphological traits noted.
- 2.3. Experimental Design and Field Layout. The experiment was laid out in 20×20 partial balanced lattice design with two replications. Canes were cut into three budded sets and planted in single row plots of 5 m \times 1.45 m and 20 cm between plants within a row. Uniform crop management practices were applied to all entries in the trial as recommended for the area.
- 2.4. Data Collected. To categorize each accession morphologically, sugarcane descriptors adopted from USDA-ARS were

employed [12]. Table 1 lists the 16 qualitative traits, their descriptors, and the codes used in the analysis. Each accession was scored for the most frequent character state. Leaf color and color of the exposed rind were examined and scored using the Munsell color chart [13].

2.5. Data Analysis. Phenotypic frequency distributions of the characters were worked out for all the sample germplasm and locations. The Shannon-Weaver diversity index (H') was computed using the phenotypic frequencies to assess the phenotypic diversity for each character for all accessions.

The Shannon-Weaver diversity index as described by [14] is given as

$$H' = -\sum_{i=1}^{n} p_i \log_e(p_i),$$
 (1)

where p_i is the proportion of accessions in the ith class of an n-class character and n is the number of phenotypic classes of traits. Each H' value was divided by its maximum value ($\log_e n$) and normalized in order to keep the values between 0 and 1. By pooling various characters across the locations (regions and countries), the additive properties of H' were used to evaluate diversity of locations and characters within the population. The average diversity index (\overline{H}') over n traits was estimated as $\overline{H}' = \sum \overline{H}'/n$. Coefficient of dissimilarity was calculated in all of the pairwise comparisons of the sample germplasm and dendrogram created by cluster analysis with unweighted pair group method based on arithmetic averages (UPGMA) using the computer program SAS V9.

3. Results and Discussion

The frequency distribution for the 16 qualitative characters of germplasm samples is presented in Supplemental Table 3. Significant variation was observed for most morphological traits measured on the accessions with two to eleven character states found per trait as shown in Table 1. Significant differentiation of accessions from regions in Ethiopia and other countries was observed for bud cushion, bud shape, shape of dewlap, relative degree of internode alignment, internode shape, type of outer auricle, shape of ligule, bud groove, canopy structure, and leaf color.

Three-fourths of the sample germplasm did not have bud cushion; majorly this character was exhibited on accessions from Tigray region in Ethiopia and Brazil. A greater proportion of the accessions had tall deltoid bud shape followed by ovate, narrow ovate, pentagonal, round with central germ pore, flaring, squarish, and double crescent shape of dewlap and slightly zigzag and straight internode alignment. The relative internode shape showed a relatively high frequency for concave convex followed by cylindrical and conoidal. Other phenotypic classes were in similar proportion. Straight or nearly straight (slightly zigzag) internode alignment of cane stalks is a very important character for mechanized farming and postharvest handling in sugarcane. This is in agreement with the findings of [15].

Short and long lanceolate types of outer auricle were dominant followed by transitional type over all regions and

TABLE 1: Character, descriptor, and codes used for characterization of sugarcane germplasm.

Character	Code	Description				
Presence or absence of bud cushion	BUDCUSHION	Present (1) and absent (2)				
Relative degree of bud extension	BUDEXTEND	Below growth ring (1), touching (2), and extending above growth ring (3)				
Relative bud shape	BUDSHAPE	Tall deltoid (1), ovate (3), narrow ovate (4), ovate with broad wing tip (5), ovate with emarginate basal wing (6), rhomboid (7), pentagonal (8), squarish pentagonal (9), round (10), round with central germ pore (11), obovate (12), and rectangular (13)				
Canopy structure	CANOPY	Open erect (1), open tip droopy (2), open semidroopy (3), open droopy (4), compact erect (5), compact tip droopy (6), and fan tip droopy (8)				
Relative shape of dewlap	DEWLAPSHAP	Deltoid (1), squarish (2), squarish deltoid (4), ascending (5), descending (6), flaring (7), tall (8), narrow (9), subcrescent (10), and double crescent (11)				
Relative plant erectness	ERECT	Prostrate (1), (4–8), and erect (9)				
Relative degree of internode alignment	INALIGN	Straight (1), slightly zigzag (2), and zigzag (3)				
Relative internode shape	INSHAPE	Cylindrical (1), conoidal (2), obconoidal (3), tumescent (4), Bobbin-shaped (5), and concave convex (6)				
Color of the leaves	LEAFCOLOR	Green (1), light green (2), and greenish yellow (7)				
Type of outer auricle	AURICLEOUT	Absent (1), transitional (2), dentoid (3), deltoid (4), falcate (5), unciform (6), calcariform (7), short lanceolate (8), and long lanceolate (9)				
Presence or absence of stalk corky cracks	STALKCORKC	Present (1) and absent (2)				
Presence or absence of stalk corky patches	STALKCORKP	Present (1) and absent (2)				
Relative shape of ligule	LIGSHAPE	Orbicular-crescent (1), flat-crescent (2), crescent with broad lozenge (3), crescent with narrow lozenge (4), crescent with lozenge (5), broad-crescent (6), deltoid (7), linear-crescent (8), and inverted crescent (11)				
Presence or absence of stalk growth cracks	STALKCRACK	Absent (1) and present (6)				
Presence or absence of bud groove	BUDGROOVE	Absent (1) and present (4)				
Color of the exposed rind RINDCOLE		Green (1), light green (2), dark green (3), yellow (4), light yellow (5), dark yellow (6), light purple (8), brown (10), light brown (11), dark brown (12), yellowish green (13), greenish yellow (14), brownish green (15), brownish yellow (16), and brownish purple (17)				

countries. Other phenotypic classes for this character had similar low frequency. The most frequent shape of ligule was crescent with lozenge followed by broad-crescent, deltoid, and linear-crescent with similar frequencies. Majority of the accessions had bud groove where mostly this character was exhibited in foreign genotypes of different source countries showing the peculiarity of the local accessions apart from exotic clones. Out of the eight phenotypic classes observed for canopy structure, compact tip droopy was the most frequent followed by open erect. Open tip droopy, open semidroopy, and open droopy classes had fairly equal distribution. Sample germplasm was found to belong only to three leaf color classes, namely, green, light green, and greenish yellow, where light green was the most frequent. Green and yellowish green were in equal proportion.

The results of this study indicated the wide distribution of phenotypic classes for the characters considered. This showed the presence of various genetically distinct genotypes in the local and exotic collections. The diversity of germplasm based on phenotypic markers can help sugarcane breeders

in strategic conservation of genetic diversity. However, this should be taken without excluding the fact that variability alone cannot be taken as a guarantee for improvement unless they possess traits of economic significance. Differences in morphological characters of different sugarcane varieties have been reported [16]. As described by [17], the most important morphological characters of sugarcane variety are the aerial organs. This is because qualitative characters are not influenced by environmental factors and thus can be used to properly identify the accessions and may also help in eliminating duplicates and closely related materials.

The amount of phenotypic diversity estimates based on the Shannon-Weaver diversity index (H') and its partitioning within and between locations are shown in Table 2. The 16 characters differed in their distribution as well as the amount of variation. Individual traits showed a different pattern of variation among accessions. Estimates of phenotypic diversity indices (H') for individual traits varied from 0.43 for presence or absence of stalk corky cracks to 0.98 for relative degree of internode alignment with an overall mean of 0.87.

Table 2: Estimates of H', partitioning into within and between locations (regions and countries) for 16 qualitative characters in 400 sugarcane germplasm samples.

Character	H'	$H_{\rm cl}$	$H_{\rm cl}/H'$	$(H'-H_{\rm cl})/H'$
Presence or absence of bud cushion (BUDCUSHION)	0.93	0.82	0.88	0.12
Relative degree of bud extension (BUDEXTEND)	0.92	0.83	0.91	0.09
Relative bud shape (BUDSHAPE)	0.93	0.90	0.96	0.04
Canopy structure (CANOPY)	0.93	0.89	0.95	0.05
Relative shape of dewlap (DEWLAPSHAP)	0.94	0.92	0.97	0.03
Relative plant erectness (ERECT)	0.78	0.75	0.96	0.04
Relative degree of internode alignment (INALIGN)	0.98	0.92	0.93	0.07
Relative internode shape (INSHAPE)	0.89	0.83	0.93	0.07
Color of the leaves (<i>LEAFCOLOR</i>)	0.84	0.80	0.96	0.04
Type of outer auricle (<i>AURICLEOUT</i>)	0.91	0.87	0.96	0.04
Relative shape of ligule (<i>LIGSHAPE</i>)	0.90	0.89	0.99	0.01
Presence or absence of stalk corky cracks (STALKCORKC)	0.43	0.37	0.85	0.15
Presence or absence of stalk corky patches (STALKCORKP)	0.79	0.54	0.68	0.32
Presence or absence of stalk growth cracks (STALKCRACK)	0.88	0.69	0.78	0.22
Color of the exposed rind (<i>RINDCOLE</i>)	0.92	0.91	0.99	0.01
Presence or absence of bud groove (BUDGROOVE)	0.96	0.84	0.88	0.12
Average	0.87	0.80	0.91	0.09

H': diversity index for each character calculated from entire data set; H_{cl} : average diversity index of each character for the 20 locations and countries; H_{cl}/H' : proportion of diversity within localities and countries; and $H' - H_{cl}/H'$: proportion of diversity between localities and countries in relation to the total variation

Most of the characters were polymorphic except relative plant erectness and presence or absence of stalk corky patches which were relatively less polymorphic. Presence or absence of stalk corky cracks was monomorphic. The high diversity values for the characters showed wide variability among accessions.

The highest diversity computed on the descriptor relative degree of internode alignment indicates that this character is very variable in the sugarcane germplasm. On the other hand, the lowest H' value for stalk corky cracks may point out that this character is selected against during the development of the varieties. In agreement with the present study [8] working on S. officinarum accessions from the world collection of sugarcane germplasm obtained highest diversity for internode alignment with Shannon-Weaver index of 0.70, whereas a low index of 0.25 and 0.35 was found for stalk corky patches and cracks, respectively. They have also obtained high diversity index values for growth cracks, internode shape, bud cushion, bud extension, bud groove, and ligule shape. The H' value for bud shape in the present study was high (0.93) while their result indicated a medium value (0.68). Similarly, [9] experimenting on field collections of sugarcane accessions in Philippine reported high Shannon-Weaver diversity for stalk growth cracks, bud cushion, stalk corky patch, stalk corky cracks, bud extension, and auricle outer shape. Unlike the present study they have reported high index for stalk corky cracks. Medium index values were reported for stalk internode shape and low index values for ligule shape and bud shape. High variability of sugarcane varieties for dewlap shape was reported by [18].

The H' pooled across characters by region and country ranged from 0.75 to 0.84 with an overall average of 0.80 (Table 3). Most of the regions and countries showed high Shannon-Weaver diversity index. The locations that had the highest H' were Benishangul-Gumuz and Harari. Relatively lower values of H' were recorded from Gambella (0.75), Barbados (0.77), Cuba (0.78), and India (0.78) and exotic germplasm from unknown sources (0.78). Amhara, SNNP, Somali, Tigray, Brazil (Campos), Puerto Rico, and USA showed similar high H' (0.80) which is equal to the average over regions and countries. The H' averaged over locations for different characters was found to range from 0.37 for presence or absence of stalk corky cracks to 0.92 for relative shape of dewlap and relative degree of internode alignment with an overall average of 0.80 (Table 2).

Across regions in Ethiopia, the mean Shannon-Weaver diversity index of local sugarcane germplasm for 7 characters, namely, bud cushion, relative degree of bud extension, canopy structure, relative plant erectness, type of outer auricle, stalk growth cracks, and bud groove, was found to be greater than mean of the characters across countries for exotic accessions and the overall mean for the whole regions and countries (Table 3). On the other hand equal mean diversity index was observed for relative shape of ligule and color of the exposed rind. Similarly the mean diversities after being pooled across all the characters were equal for regions in Ethiopia and countries of sources of foreign clones.

Generally, it was found that the proportion of total diversity obtained within locations (regions and countries) was larger than between locations. This is supported by the

Table 3: Estimates of the Shannon-Weaver diversity index (H'), for 16 qualitative characters in 400 sugarcane genotypes by location of collection of local and country of introduction of exotic genotypes.

Location	A	В	С	D	Е	F	G	Н	I	J	K	L	M	N	О	P	Mean ± SE
Amhara	0.83	0.77	0.78	0.89	0.87	0.80	0.96	0.86	0.87	0.80	0.86	0.44	0.66	0.66	0.85	0.95	0.80 ± 0.03
Benishangul-Gumuz	0.88	0.97	0.97	0.88	0.90	0.94	0.86	0.88	0.58	0.97	0.92	0.72	0.00	0.97	0.97	1.00	0.84 ± 0.06
Gambella	1.00	0.92	1.00	0.92	0.97	0.65	0.65	0.00	1.00	0.96	0.96	0.00	0.00	0.92	1.00	1.00	0.75 ± 0.10
Harari	1.00	0.81	0.81	0.95	0.95	0.95	1.00	0.81	0.81	0.95	0.95	0.00	0.81	0.81	1.00	0.81	0.84 ± 0.06
Oromia	0.89	0.74	0.81	0.81	0.90	0.67	0.97	0.77	0.64	0.79	0.85	0.55	0.79	0.62	0.84	1.00	0.79 ± 0.03
SNNP	0.82	0.72	0.85	0.78	0.82	0.71	0.98	0.83	0.74	0.83	0.90	0.51	0.59	0.88	0.86	1.00	0.80 ± 0.03
Somali	0.92	0.92	0.96	0.97	0.96	0.92	0.79	0.92	0.92	0.79	0.96	0.00	0.92	0.00	0.92	1.00	0.80 ± 0.08
Tigray	0.99	0.89	0.80	0.98	0.89	0.92	0.97	0.87	0.69	0.97	0.75	0.37	0.00	0.86	0.86	0.94	0.80 ± 0.07
Australia (Queensland)	0.81	1.00	0.95	1.00	1.00	0.95	0.81	0.95	0.81	0.95	0.95	0.00	0.81	0.00	0.95	1.00	0.81 ± 0.08
Barbados	0.70	0.85	0.88	0.92	0.86	0.55	0.93	0.82	0.84	0.85	0.85	0.26	0.54	0.73	0.86	0.87	0.77 ± 0.04
Brazil (Campos)	0.98	0.81	0.95	0.88	0.92	0.84	0.92	0.86	0.52	0.95	0.86	0.41	0.41	0.65	0.87	0.92	0.80 ± 0.05
Cuba	0.88	0.82	0.88	0.95	0.88	0.72	0.82	0.91	0.58	0.93	0.93	0.00	0.72	0.47	0.97	0.97	0.78 ± 0.06
Guyana (Demerara)	0.90	0.76	0.89	0.91	0.92	0.42	0.99	0.98	0.95	0.92	0.93	0.54	0.54	0.70	0.96	0.81	0.82 ± 0.04
India	0.90	0.84	0.94	0.92	0.90	0.50	0.95	0.88	0.84	0.80	0.81	0.30	0.59	0.80	0.89	0.68	0.78 ± 0.05
Mauritius	0.81	0.93	0.95	0.83	0.89	0.89	0.95	0.89	0.90	0.94	0.88	0.34	0.54	0.70	0.88	0.90	0.82 ± 0.04
Mexico	0.41	0.87	0.94	0.83	0.97	0.81	0.94	0.81	0.92	0.71	0.89	0.81	0.81	1.00	0.94	0.00	0.79 ± 0.06
Puerto Rico	0.37	0.72	0.86	0.71	0.93	0.81	1.00	0.89	0.90	0.89	0.91	0.59	0.37	0.99	0.97	0.90	0.80 ± 0.05
South A. Natal	0.75	0.70	0.92	0.83	0.92	0.81	0.97	0.90	0.82	0.79	0.87	0.68	0.68	0.68	0.89	0.49	0.79 ± 0.03
Unknown	0.69	0.77	0.92	0.92	0.92	0.51	1.00	0.88	0.82	0.89	0.92	0.30	0.49	0.69	0.91	0.83	0.78 ± 0.05
USA	0.94	0.84	0.88	0.88	0.94	0.65	0.88	0.86	0.90	0.82	0.84	0.47	0.51	0.69	0.85	0.82	0.80 ± 0.04
EL	0.82	0.83	0.90	0.89	0.92	0.75	0.92	0.83	0.80	0.87	0.89	0.37	0.54	0.69	0.91	0.84	0.80 ± 0.04

A: BUDCUSHION; B: BUDEXTEND; C: BUDSHAPE; D: CANOPY; E: DEWLAPSHAP; F: ERECT; G: INALIGN; H: INSHAPE; I: LEAFCOLOR; J: AURICLEOUT; K: LIGSHAPE; L: STALKCORKC; M: STALKCORKP; N: STALKCRACK; O: RINDCOLE; P: BUDGROOVE; EL: entire location. Character abbreviations are as defined in Table 2.

findings of [8] where they reported higher diversity in qualitative traits within locations of collection than between locations in world collection of *Saccharum officinarum*. Similar findings were reported by [19] in world collection of *Saccharum spontaneum*. With studies on sorghum germplasm from Ethiopia, [20] found similar results. Generally, highest (greater than 0.90) within locations diversity was recorded for most of the characters studied (Table 2). The lowest diversity within locations was observed for the character stalk corky patches. On the other hand, a relatively higher proportion of diversity between localities in relation to the total variation was observed for stalk corky patches followed by stalk growth cracks, stalk corky cracks, bud cushion, and bud groove.

Cluster analysis divided the accessions into nineteen main clusters and a singleton (Table 4). The first cluster included 251 genotypes out of which 85 were local clones from different regional states in Ethiopia while the rest were exotic clones from various source countries. This indicated that these local genotypes have close similarity in terms of the characters considered with the group of exotic sugarcane accessions belonging to this group. In cluster two, out of the twenty-three accessions only four were local clones, Moris and Ye Kenya Shenkora from SNNP Region, Shenkora

from Gambella, and Nech Shenkora (Wonji) from Oromia Regions. Cluster three and clusters five to eight contained local genotypes with only one, three, and two exotic clones in clusters six, seven, and eight, respectively.

This pattern of clustering in the local clones suggests that the genetic divergence and tendency to group separated from the introduced clones could be due to their original variability in farmers' field and further selection for adaptation. Two local clones Ye Kenya Ageda and Shekole from SNNP and Oromia Regions, respectively, and two exotic clones Mex52/29 and N53/216 from Mexico and Natal, South Africa, did not join any group and stood as separate clusters. This relationship might be because these genotypes were geographically diverse and evolved independently.

Generally, the results of the cluster analysis have shown that regardless of their origin sugarcane genotypes from different geographical regions tend to cluster together and likewise genotypes from the same foreign country or region in Ethiopia were often in different clusters disclosing the possibility of close similarity between their evolutionary courses (Table 4). Similar results were reported by [8, 19, 21] where they showed that sugarcane genotypes from different places of origin clustered together.

Table 4: Clustering of 400 sugarcane genotypes into twenty groups using 16 qualitative characters (numbers refer to code of genotypes * in Supplemental Tables 1 and 2).

Cluster	Number of genotypes	Genotypes										
	· /1	305,	357,	89,	252,	213,	292,	16,	92,	107,	279	
		326,	350,	60,	131,	67,	339,	76,	202,	315,	404	
		91,	268,	206,	361,	245,	275,	197,	324,	355,	104	
		348,	71,	162,	340,	242,	440,	146,	356,	203,	372	
		301,	388,	207,	410,	136,	196,	267,	401,	40,	223	
		274,	428,	36,	349,	138,	191,	367,	78,	157,	323	
		338,	314,	407,	247,	332,	124,	158,	266,	288,	368	
		290,	429,	426,	427,	123,	439,	307,	405,	199,	436	
		309,	433,	231,	395,	99,	134,	263,	364,	257,	298	
		85,	246,	110,	282,	195,	164,	310,	192,	253,	313	
		331,	186,	198,	383,	423,	180,	325,	384,	222,	187,	
		243,	59,	51,	200,	347,	220,	362,	254,	287,	54,	
C_1	251	156,	218,	373,	239,	271,	97,	353,	133,	142,	366	
		425,	286,	57,	216,	406,	74,	370,	337,	159,	160	
		29,	259,	69,	260,	96,	299,	83,	114,	101,	437	
		365,	430,	56,	308,	165,	403,	87,	204,	393,	82,	
		343,	233,	412,	126,	113,	116,	359,	378,	81,	63,	
		441,	297,	79,	341,	122,	93,	371,	408,	214,	402	
		399,	117,	346,	269,	400,	351,	248,	391,	152,	209	
		240,	194,	392,	20,	143,	249,	115,	385,	58,	128	
		276,	379,	153,	354,	21,	66,	70,	208,	244,	221,	
		32,	228,	5,	61,	145,	177,	304,	238,	345,	328	
		435,	225,	241,	278,	394,	94,	141,	380,	311,	377,	
		289,	293,	281,	229,	317,	318,	265,	182,	344,	235	
		211,	193,	15,	397,	154,	119,	64,	189,	172,	334	
		237										
		303,	424,	219,	374,	201,	273,	422,	283,	418,	217,	
C_2	23	251,	163,	300,	80,	294,	295,	270,	327,	409,	234	
2		43,	396,	75	,	,	,	,	,	,		
		55,	84,	171,	184,	10,	25,	144,	178,	169,	47,	
C_3	15	111,	37,	183,	179,	185	20,	,	2, 0,	10,,	,	
		35,	382,	48,	173,	73,	140,	132,	431,	24,	42,	
		68,	230,	121,	363,	272,	417,	161,	255,	90,	100,	
C_4	48	129,	389,	212,	98,	333,	335,	26,	105,	174,	27,	
\mathcal{C}_4	10	127,	175,	381,	419,	415,	53,	360,	312,	151,	190,	
		49,	170,	150,	41,	72,	33,	434,	420	151,	170,	
<u> </u>	-	155,			45,		65	131,	120			
C ₅	6		166,	149,		167,		106	1.4	20		
C_6	20	19,	22,	8,	12,	28,	11,	106,	14,	30,	50,	
		9,	38,	46,	31,	34,	23,	1,	4,	3,	215	
C_7 C_8 C_9 C_{10}	8	7,	39,	13,	330,	139,	188,	302,	280			
C ₈	7	18,	103,	2,	6,	181,	210,	224				
C ₉	3	205,	296,	236								
C ₁₀	2	118,	386									
C ₁₁	2	321,	398									
C ₁₂	2	264,	432									
C ₁₃	3	291,	306,	320								

ח	r	n 4.	Continued	
	ARI	F 4.	Continued	

Cluster	Number of genotypes			Genotypes
C ₁₅	2	62,	226	
C ₁₆	2	232,	250	
C ₁₇	1	390		
C ₁₈	1	77		
C ₁₉	1	176		
C ₂₀	1	421		

^{*}Code numbers 1-191 and 192-441 are local and exotic genotypes, respectively.

4. Conclusions

Among the 16 qualitative traits measured in the 400 sugarcane germplasm samples, the highest diversity index (H')was obtained for relative degree of internode alignment and the lowest value was recorded for stalk corky crack. Furthermore, results showed that the proportion of total diversity obtained within locations (regions and countries) was larger than between locations. Pooled over characters within locations, the mean of H' ranged from 0.75 for Gambella to 0.84 for Benishangul-Gumuz and Harari. Moreover, the mean diversity indices pooled over locations showed high H' value for relative shape of dewlap and relative degree of internode alignment. The results of the study are noteworthy for characterization and identification as well as strategic conservation of the diversity of available sugarcane germplasm. However, care should be taken as variability alone cannot be taken as a guarantee for improvement unless they possess traits of economic significance. Future molecular markers diversity analysis when coupled with the phenotypic diversity estimates will give clear picture of the magnitude and distribution of the variability existing for further improvement of the crop.

Competing Interests

The authors declare that they have no conflict of interests.

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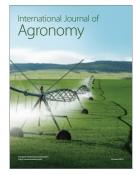
















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