Characterization and Estimation of Diversity of Sugarcane (Saccharum officinarum) Genotypes Based on Qualitative Morphological Traits.

Melaku Tesfa (melakutesfa2015@gmail.com)
Ethiopian sugar Industry Group,
Esayas Tena
Ethiopian sugar Industry Group,
Mulugeta Kebede
Addis Ababa University

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Abstract

An accurate and extensive study of the qualitative morphological diversity of sugarcane genotypes would allow their identification, conservation and utilization in the sugarcane breeding program. The objectives of the study were to characterize and estimate the morphological diversity of sugarcane genotypes using qualitative traits. Data collected for 16 qualitative characters were analyzed using descriptive statistics and multivariate analysis to assess the overall patterns of morphological variation. Shannon diversity index (H') was calculated to estimate morphological diversity. The result indicated that the qualitative traits revealed high variability among 144 sugarcane genotypes. The most polymorphic character with the highest Shannon diversity index (H') was stalk corky patchs. The H' averaged across all countries for different characters was found to vary from 0.50 to 0.76 with an average of 0.61. The H' pooled across characters by country of collection ranged from 0.00 to 0.83, with a general average of 0.62. Multivariate cluster analysis has grouped the genotypes into four distinct clusters based on the relatedness and variation for all considered characters. Genotypes with close genetic relationships are grouped in a single cluster. The clustering pattern of the genotypes elucidated that genotypes originating from the same geographic locations did not form a single cluster. This shows that geographic diversity has not associated with genetic diversity, which may be due to the continuous exchange of genetic material among countries. Finally, we concluded that the qualitative morphological traits evaluated in this study could be used for varietal identification, maintaining genetic diversity and managing sugarcane germplasm.

Introduction

Sugarcane (*Saccharum officinarium* L.) belongs to a family *Poaceae*, subfamily *Poacoideae*, and tribe *Andropogoneae*. It possesses a complex genome, highly polyploidy (octoploid) and aneuploidy with 2n = 80 and ten basic chromosome numbers (8x). Current sugarcane varieties are hybrids of *S.officinarum* and *S.spontaneum* species (D'Hont et al. 1998; Casu et al. 2005). This crop is usually propagated by stem-cutting immature cane, known as the sett, for commercial production, while true seed (fuzz) is used for breeding purposes. Sugarcane is the most industrious agricultural crop globally, capable of accumulating high sucrose in its internode stem and dry matter (biomass) production capacity (Pierre et al. 2014). It is cultivated extensively in more than 100 countries between 40°N and 32° 5´S in the tropical and subtropical regions of the world, mainly for sugar and biofuel (daCosta et al. 2011).

Sugarcane crop has an important place in the economy of Ethiopia, cultivated not only for plantation white sugar production but also for sugar-related products such as ethanol. It is an exclusively raw material for economic white sugar production in Ethiopia. Because of the versatile nature of this crop, its contribution to the agricultural, industrial, and medicinal areas is significantly increasing. However, even though the commercial cane production area of the country expanded to more than 100 thousand hectares, the national total cane production shows a declining trend and currently becoming an area of concern in the sugar estates. For example, the cane yield per hectare in Fincha sugar esate has declined by about 26.63% from 1997 to 2008, by 49.03% at Metahara (1969–2008) and by 48.63% decrease at Wonji Shoa from 1954 to 2008 (Alemayehu & Lantinga 2016; Tesfaye 2021). As a result, the country is lower in sugar production and consumption globally. Among the factors responsible for its lower sugar production, the most important are the non-availability of high-yielding varieties and lack of capacity in cultivation of potential areas and relatively low practice in using recommended agronomic practices and technologies that reduce cost. Since sugarcane varieties are the lifeblood of the Ethiopian sugarcane industry, having variable locally adapted varities that suits production ecologies and can tolerate biotic and abiotic stress of great importance in attaining sustainable high production. Hence, efforts are needed to develop high-yielding varieties that adapt to the dissimilar agroecologies of the country (Esayas et al. 2016).

From the establishment of the sugar industry in Ethiopia to the present day, the sugarcane breeding program is exclusively dependent on importing exotic varieties and fuzz-seed of sugarcane varieties without keeping varietal character in view. Currently, the sugar industry has planned to establish its breeding station to develop varieties that are apt for different agro-ecologies of the country. To this end, for emerging breeding programs, morphological characterization of the germplasms is of a tremendous importance for identification of genotypes, protection of newly developed sugarcane varieties, avoiding duplication in the germplasm collection, and effective management and conservation of collection. It also helps to construct genotypes relationship through classifying the genotypes into similar or separate groups (Smith and Smith 1989) and provide member countries an exchangeable data of germplasm for the efficient use in breeding program. Accordingly, many researchers have carried out characterization and genetic diversity of sugarcane genotypes in Ethiopia using qualitative morphological traits. Esayas et al (2016) characterized and evaluated the genetic diversity of 400 (226 exotic and 174 local) sugarcane genotypes with 16 qualitative phenotypic traits. Khan et al (2017) evaluated sixteen sugarcane varieties for morphological characteristics using 11 discrete, 18 continuous and 12 combined characters. Esaya et al (2018) also characterized and categorized 211 (15 exotic & 196 landrace) sugarcane genotypes using 16 morphological qualitative traits. The present study was intended to strengthen the previous results and enrich the information by considering some still remain uncharacterized old collection of sugarcane genotypes introduced in different time from various part of the world.

Morphological evaluation and characterization using qualitative traits is the most direct method of identifying genotype identity and studying genetic diversity among sugarcane genotypes (Smith & Smith 1989; Hartatik et al. 2001; Brown et al. 2002). This technique is also easy, simple, cost-effective, and time-efficient, and finally, it does not require complicated equipment and a high level of specialists' knowledge for scoring (Khalid et al. 2016). On the contrary, qualitative morphological characters involve epistatic interaction and are affected by genotype and environment interaction. However, characters with high heritability and location stability can be used as genetic markers in variety identification and classification (Erskine and Williams 1980).

Previous researchers have reported that morphological traits showed nearly the same result with some molecular markers, like RAPDs in common beans (Johns et al. 1997) and wild rose (Deneber et al. 1996) crops. Similarly, many researchers have studied the characterization and genetic diversity of sugarcane germplasm using heritable and stable morphological qualitative traits to identify diverse genotypes used for variety improvement (Altoveros et al. 2003; Esayas et al. 2016; Khalid et al. 2016; Shahzad et al. 2016; Karpagam & Alarmelu 2017; Khan et al. 2017). Therefore, the main objectives of the

study were to morphologically characterize sugarcane genotypes and estimate the extent of diversity among sugarcane genotypes using the qualitative traits for identification and better conservation of germplasm.

Material And Methods

Experimental site

The study was carried out at Metehara Sugar Estate. Metahara Sugar Estate is located in the East Shoa Zone, Oromia regional state, at a distance of 200 km to the southeast of Addis Ababa between the longitude of 8^{o}N and Latitude 39^{o}52`E at an elevation of 950 m.a.s.l. It receives an average of 554mm annual rainfall with minimum and maximum temperatures of 17.4^{o}C and 32.6^{o}C.

Plant materials

One hundred forty-four sugarcane genotypes were considered in this study. Of these, 134 genotypes were exotic and the rest 10 were landraces (locals). The materials were selected based on variation in country of origin and different time of introduction for exotic; and based on variation in geographic collection for landraces. The materials were obtained from the Ethiopian Sugar Corporation Research Centre and; Fincha sub-center, where the exotic and landrace materials are maintained for conservation of sugarcane germplasm. The plant materials used in this study and their country of origin are listed in supplementary Table 1.

Experimental design and management practice

The experiment followed a 12x12 partial balanced lattice design with two replications. The dimension of each experimental plot was four furrows of 5m spaced 1.45m. Spacing between plots, blocks, and replications was maintained at 1.5, 1.45 and 2.9m, respectively. Equal numbers of three budded setts were laid out along the furrow in an end-to-end fashion. All crop management practices were carried out uniformly according to the standard operating procedure of the Methara Sugar Estate.

Morphological characterization

The morphological traits were evaluated and characterized from randomly selected fully developed five cane stalks per genotypes. The observation data were recorded on 16 qualitative morphological traits at age of 10 months when varieties showed distinct morphological characteristics. The traits were evaluated and scored based on sugarcane descriptors (qualitative characters) given by USDA-ARS (GRIN 2004). For characterization, a range of morphological descriptors above-ground stem characters were recorded including bud cushion, degree of bud extension, relative bud shape, canopy structure, relative shape of dewlap, relative plant erectness, internode alignment, internode shape, color of the leaves, scarious leaf margins, type of auricle, the shape of ligule, stalk corky cracks, stalk corky patches, stalk growth cracks, color of the exposed rind, type of bud groove and leaf blade width. Descriptions of each qualitative morphological trait were listed in Table 1. Characters are chosen on criteria based on their ease of observation, availability and usefulness in classifying and identifying genotypes.

Statistical analysis

The phenotypic frequency data of the 16 characters were calculated by Shannon-Weaver diversity index H' (Shannon and Weaver 1949), which is given as:

$$\mathrm{H} = -\sum_{i=1}^{n} \mathrm{p_i ln p_i},$$

Where n is the number of phenotypic classes for a character and P_i is the relative frequency in the i^{th} class of the J^{th} trait. H was estimated for each trait, group of traits and country group. In order to keep the values of H' in the range between 0 and 1, each value of H' was divided by its maximum value ln(n). By grouping different characters across the locations (countries), the additive properties of H were used to evaluate diversity of locations and characters within the population. The average diversity H', over j traits was estimated as:$\mathrm{H\prime} = \frac{\mathrm{H_j}}{\mathrm{j}}$. To group the genotypes coefficient of dissimilarity was calculated in all of the pairwise comparisons of the sample germplasm and, hierarchal cluster analysis was performed through average linkage method with unweighted pair group method based on arithmetic average (UPGMA) using R studio (2020). The morphological traits frequencies were standardized to the mean of zero and variance of one by using R language prior to cluster analysis. Inter cluster distance was computed using Minitab ver.17 (Abolfazl Ghoodjani 2022).

Results And Discussions

Frequencies of phenotypic traits

Descriptive statistical analysis was carried out to elucidate the morphological character variability available across and within the region. The frequency distribution for 16 qualitative characters of genotypes by region is shown in table 2. All considered traits showed remarkable differences in their distribution and extent of variations within them. The characters are presented by grouping related traits together to enhance readability and avoid redundancy.

Bud cushion and relative degree of bud extension. Assessment of the presence or absence of bud cushion character showed that the character was polymorphic across all locations except for Demarara, Brazil, Mauritius and Mexico; they were monomorphic. The latter result may be because only a few genotypes were considered from these countries. The bud cushion was found at a higher frequency in all locations except in USA, Philippines and Demarara genotypes. Similarly, significant proportion (90%) of considered Ethiopian genotypes (landraces) contains bud cushion character. Contrary to the present result, Esaya et al (2018) reported that 70% of the landraces do not have bud cushion. Regarding the degree of bud extension character, the

phenotypic classes were observed in genotypes from all locations with different proportions. However, bud below growth ring class was expressed only in Indian and Philippines genotypes with less proportion, 11.1% and 9.1%, respectively. Seventy per cent of Ethiopian landraces exhibited bud extending above growth ring phenotypic class. Most of the genotypes in all locations expressed this phenotypic class except genotypes in France and Mauritius.

Relative Bud shape and Bud groove. Evaluationof this character revealed that bud shape had polymorphic distribution in genotypes of all locations except for genotypes from Brazil and Mauritius. Ovate bud shape was exhibited with the highest proportion in genotypes from Ethiopia (50%) and Sudan (62.5%). The result also showed that genotypes from Thailand exclusively exhibited a pentagonal bud shape. On the other hand, Obovate and rectangular bud shapes had the lowest distribution across the locations; they were recorded solely in genotypes from India and the Philippines, with less frequency, 5.6% and 9.1%, respectively. Concerning bud groove character, the genotypes from all locations had bud groove significantly. Eighty percent of landraces in Ethiopia were found to have bud grooves.

Canopy structure and relative plant erectness. In canopy structure character, the phenotypic classes were distributed fairly in the genotypes of fifty per cent of the locations. However, Brazil, Mauritius, and Porto Rico genotypes have only compact tip droopy and open semi-droopy phenotypic classes, respectively. The result also elucidated that only two phenotypic classes were distributed in fifty per cent of genotypes from Demarara, Australia, Thailand, and Mexico. For relative plant erectness, the phenotypic classes were polymorphic in some locations. On the other hand, the erect phenotypic class was less frequently distributed across the locations, exclusively recorded for germplasms of Cuba and South Africa at 6.3 % and 42.9%, respectively. Ethiopian landraces had semi-erect (grade 8) and fairly erect (grade 7) in equal proportion.

Color of the leaves and relative color of exposed rind. Among the three phenotypic classes for the color of the leaves, the green color was exhibited in the highest proportion in all locations except in genotypes from Demarara, where the whole genotypes expressed light green leaves color (monomorphic). Next to the green color, the light green color was distributed fairly in less proportion across the locations. At the same time, the greenish-yellow phenotypic class was observed in genotypes from three locations, namely the USA, France and Barbados, in an equal distribution. Green and light green phenotypic classes were found to have 90% and 10% proportion in Ethiopian landraces, respectively. Concerning the relative color of exposed rind, the phenotypic classes were distributed reasonably equally in 50% of the locations. In contrast, in the remaining locations, the character showed monomorphic distribution.

Relative shape of Dewlap. Squarish deltoid dewlap shape was the most widely distributed phenotypic class with the highest proportion across the locations. Tall, narrow, and subcrescent classes were rare phenotypes found solely in genotypes from one location, tall class in India, narrow class in France, and subcrescent in Barbados.

Relative internode alignment and internode shape. It was remarkably noticed that slightly zigzag phenotypic class was exhibited in the highest frequency in genotypes from all regions, followed by straight internode alignment. The zigzag phenotypic class was poorly distributed across the location and found only in germplasms from India (5.6%), France (21%), Barbados (11.5%) and Porto Rico (50%) region. Similarly, all genotypes of the Sudan region exclusively possess straight internode alignment, while Ethiopian landraces fall in straight and slightly straight classes with 40% and 60% frequency, respectively. Regarding the internode shape character, the cylindrical shape was the most commonly distributed class across the regions, followed by the conoidal internode shape. Obconoidal shape was found only in Ethiopian landraces. On the other hand, the concave-convex phenotypic class had a great proportion (60%) in the Ethiopia region.

Type of Auricle and Relative Shape of Ligule. The evaluation result indicated that the transitional type of auricle is the most distributed phenotypic class across the regions with high frequency, followed by the long lanceolate class. On the contrary, unciform and calcariform auricle types were found to reside solely in one region. The unciform auricle was observed in Cuban genotypes, while calcariform in the Philippines. Significant proportions (60%) of Ethiopian landraces have a transitional type of auricle. Concerning the shape of Ligule, Crescent with lozenge was predominant in almost all regions except in Demarara, Brazil and Mauritius. Linear-crescent and Arcuate ligule shapes had poor distribution and occurred only in one region. The transitional phenotypic class was predominantly (90%) recorded for Ethiopian landraces.

Stalk Corky Cracks, Corky Patchs, Growth Cracks. Genotypes in all regions predominantly had no stalk corky cracks. Demarara, Australia, Thailand, and Mauritius genotypes had no stalk corky patches. Eighty per cent of Ethiopian landraces have no stalk corky cracks but have corky patches. The majority of genotypes in whole locations had no stalk growth crack character. Similarly, genotypes in the Philippines, Demarara, Australia, Thailand, Brazil, and Mauritius have no corky growth crack.

In general, the results of the present study showed the wide distribution of phenotypic classes for most characters considered within and among the regions. It also implies the presence of different races and a combination of races in genotypes of these regions. The distribution pattern may also be attributed to the diverse genetic background of the accessions studied (Geleta et al. 2005). This study also observed that various phenotypic classes of some characters were distributed commonly in all regions with relatively equal frequencies. This may be because qualitative characters are not influenced by environmental factors (stable) and thus can be used to identify the accessions properly and may also help eliminate duplicates and closely related materials (Kalyan *et al.* 2017). The implications of these findings for genetic material collection and maintenance are immense. Differences in morphological characters of different sugarcane varieties have been reported (Esayas et al. 2016). The present result agrees with Esayas et al (2018), who revealed wide distributions of phenotypic classes of the character of sugarcane genotypes within and across the regions. Polignano et al (1999) reported the difference in qualitative traits of Faba bean among geographic regions in their phenotypic proportion and range of variation. Negash (2015) also elucidated the distribution of phenotypic classes among and within the regions in16 qualitative traits of wheat crop.

Overall phenotypic frequency and distribution of character classes

The overall frequency distribution for the qualitative characters is depicted in supplementary Table 2. All characters under study showed a wide range of frequency distribution in the genotypes considered, except scarious leaf margin, which was monomorphic. A total of ninety-two (63.9%) genotypes were found with bud cushion, whereas the rest (36.1%) was without bud cushion. Concerning the degree of bud extension (BUDEXTEND), significant proportions (61.8%) of the genotypes contained extending bud above the growth ring**,** followed by touching character (36.1%). On contrary to this result, Altoveros et al (2003) found most genotypes (46.7%) having bud tip position below growth ring and sixteen percent above the growth ring.

At the node, a single bud is positioned which may differ in shape, size and color according to the genotypes. In this study, out of 144 genotypes evaluated, 34 genotypes (23.6%) exhibited ovate bud shape, while 22.2 % of the genotypes showed squarish pentagonal character (Supp. Table 2). However, almost all types of bud shape were observed in the collection. Altoveros et al (2003) reported that roundish bud shape was dominantly observed almost in 50% of the sugarcane genotypes considered in their study.

The canopy structure (CANOPY) of genotypes also showed a wide variation among the genotypes ranging from 32.6% (open semi-droopy) to 6.3% (open erect, fan erect, and compact erect). According to Altoveros et al (2003) erect leaves are more efficient in photosynthesis. For the character relative shape of a dewlap (DEWLAPSHAP), 47.2%, 22.9% and 13.9% of genotypes exhibited squarish, squarish deltoid and descending dewlap shape respectively. From studied genotypes, majorities (40%) of them showed moderate plant erectness (70^o) (ERECT), and less percentage (0.7%) of them had erect orientation (90^o). Cuenya and Mariotti (1984) considered canes that diverge from erectness by greater than 60 degrees unsuitable for commercial cultivation. This study also observed that 12.5%, 80.6%, and 6.9% of the genotypes had straight, slightly zig zag, and zigzag internode alignment (INALIGN), respectively.

Relative internode shape (INSHAPE) was another diverse character among the genotypes, in which concave-convex shape showed relatively high frequency (29.9%), followed by cylindrical (28.5%) and conoidal (19.4%). A similar result has been reported by Esayas et al (2016). The color of the leaves (LEAFCOLOR) was varied as green (65.3%), light green (27.8%), and greenish-yellow (6.9%). Concerning auricle type, 39 (27.1%) genotypes were found with long lanceolate, while a significant proportion (44.4%) showed transitional auricle type. In the shape of the legule variable, the genotypes showed the highest frequency (58.3%) for crescent with lozenge character, followed by broad-crescent (21.5%). This finding is in agreement with Esayas et al (2016) and Altoveros et al (2003).

A wider variation was also observed for stalk corky crack (STALKCORKC) character. Only 19.4% of genotypes showed corky crack presence on the stalk, while 80.6% do not have this character in their stem. Similarly, 56.9% and 88.9% of the evaluated genotypes were devoid of stalk corky patch (STALKCORKP) and stalk growth crack (STALKCRACK), respectively. Color of exposed rind (LEAFCOLOR) was the most diverse character among studied genotypes, and brown color was found in a high proportion (17.4%) of genotypes, followed by brownish green (13.9%) and light green (11.8%). In agreement with this, Ekpélikpézé et al (2016) reported high variability for the external color of the sugarcane stem. The majority of the genotypes (77.8%) were with bud groove (BUDGROOVE), while 22.2% of the genotypes do not exhibit bud groove in their stalk. In general, the present study's results revealed the variation in the frequency distribution of qualitative characters in the sugarcane breeding population (Supp. Table 2). This showed the potential of these morphological characters to be used in sugarcane breeding programs for characterization, identification, and effective management of conserved germplasm. Genotypes with a wide variation for qualitative traits can determine the potential genotypes for diverse agro-ecologies (Tesfaye et al. 2021). As qualitative traits variation is not guarantee for crop improvement, one should consider whether the genotypes possess traits of economic importance. Almeida and Crocorno (1994a) elucidated that dewlap shape, ligule and sheath auricles are the outstanding descriptors of value for identifying diverse sugarcane genotypes. Similarly, Almeida and Crocorno (1994b) suggested bud shape as an outstanding character to assess variability in sugarcane genotypes.

Differences in qualitative morphological characteristics among sugarcane genotypes have also been reported by various previous studies (Akhtar et al. 2006; Arrey and Mih 2016; Esayas et al. 2016; Khan et al. 2016,Karpagam and Alarmelu 2017). In addition, morphological qualitative traits variability among accession was also reported for various crops, such as sesame (Tesfaye et al. 2021), rice (Ahmed et al. 2016), durum wheat (Ouaja et al. 2021), and sorghum (Geleta et al. 2005; Chavan et al. 2018).

Phenotypic Diversity Index

A total of 144 genotypes were characterized with 16 qualitative traits to determine the variability among them, thereby estimating the extent of diversity in the germplasm. Shannon diversity index (H¢) was calculated to compare phenotypic diversity among genotypes and locations (countries). The extent of phenotypic diversity estimates and its partitioning within and between countries are shown in Table 3. The diversity index value of 1 characterizes the highest diversity, while an index value 0 indicates there is no variation in distribution of phenotypic class (equal frequency) of a given character.

In the present study, the 16 characters differed in their distribution and extent of variation. The computed Shannon-Weaver indexes (H') of individual morphological characters ranged from 0.50 to 0.99, with an overall mean of 0.76 (Table 3). The most polymorphic characters were stalk corky patches (SCC; H' = 0.99), followed by bud cushion (BC; H' = 0.94), canopy structure (CS; H' = 0.91), color of the exposed rind (CER; H' = 0.88), the color of the leaves (CL; H' = 0.85), relative bud shape and internode shape (RBS & IS; 0.81) indicating that these descriptors are very variable in sugarcane germplasm. On the other hand, the character computed with the lowest diversity index value was the stalk growth crack character (SGC; H' = 0.50) (Table 3), indicating that there was less variability among the genotypes for this character and the character is chosen against in the development of varieties. The averaged diversity index for all the descriptors 0.76 is a high index value, showing that the evaluated genotypes were very diverse with these characters. The present result agrees with Altoveros et al (2003), who reported the diversity index (H¢) for various characters of sugarcane genotypes ranging from 0.18 to 1.00 with a mean diversity index of 0.79. They also revealed the highest H¢ values ranging from 0.90 to 1.00. In agreement with the present study result, Esayas et al (2016) reported the highest H¢ index (0.93) for relative bud shape, and Altoveros et al (2003) revealed the highest H¢ index for bud cushion and stalk corky patch. Contrary to the present findings, Balakrishnan et al (2000) obtained the lowest diversity index for stalk corky patches (0.25).

The Hç averaged across all countries for different characters varied from 0.39 for the stalk growth crack to 0.76 for canopy structure, with an overall average of 0.61 (Table 3). Esayas et al (2016) revealed Hç averaged over locations for different descriptors varying from 0.37 for the presence or absence of stalk corky cracks to 0.92 for the relative shape of dewlap and degree of internode alignment with an overall average of 0.80. The diversity of each character within countries varied from 0.59 for stalk corky patchs and color of the leaves to 0.99 for the degree of bud extension. Equal averaged diversity index was recorded for internode alignment and relative shape of ligule, bud cushion and internode shape, and stalk corky patchs and color of the leaves. On the other hand, the proportion of diversity of characters between countries in relation to total variation ranged from 0.01 for degree of bud extension to 0.41 for the color of leaves and stalk corky patch characters (Table 3).

Estimates were made for each character and pooled across characters and countries for qualitative characters (Table 4). The Hç pooled across characters by country of collection ranged from 0.00 to 0.83, with a general average of 0.62 (Table 4). The highest (0.83) diversity index (Hç) was recorded for India country followed by France and South Africa (0.82), and the lowest (0.44) value of Hç was obtained from Demarara and Thailand. No diversity was observed among genotypes for Mauritius (0.00), and Brazil (0.00) as solely single genotype was considered for each source country in this study. Hence, the diversity within a country varies based on the value of each character (Table 4). Esayas et al (2016) reported the Hç averaged across characters by region and country varied from 0.75 to 0.84 with an overall mean of 0.80. They also obtained the highest Hç for Benishangul-Gumuz and Harari and relatively lower values of Hç for Gambella, Barbados, Cuba, and India. Liu et al (2010) also revealed that a variety of populations from the USA, Taiwan of China, and Australia had high levels of genetic diversity in trait values.

In the present study, it was exhibited that the proportion of overall diversity computed within the country was greater than diversity among the countries. This is in agreement with Balakrishnan et al (2000) and Esayas et al (2016), who reported higher diversity within countries of collection than between countries. Furthermore, Geleta et al (2005) also revealed high diversity index within a locality than between localities in their study of qualitative trait variation in sorghum.

Cluster Analysis

The cluster analysis with the average linkage method grouped 144 sugarcane genotypes into four distinct clusters. Genotypes within a cluster are assumed to have more close relationships than others found in another cluster. The distribution of genotypes in different diversity classes was presented in table 5 and illustrated by the dendrogram as shown in figure 1. Each cluster comprises a different number of genotypes in such a way that genotypes having the least genetic distance were grouped in the same cluster and *vice versa*. Accordingly, cluster I comprised 83 genotypes (57.6%) in a group, cluster II had 5 genotypes (3.5%), cluster III had 51 genotypes (35.4 %), and cluster IV contained 5 genotypes (3.5 %) (Table 5, Figure 1). In agreement with the present result, Ekpélikpézé et al (2016) grouped the 89 cultivars into four morphological groups with different characteristics. Esayas et al (2016) divided 400 sugarcane genotypes into 20 clusters in which a maximum of 251 genotypes were grouped in one cluster, and four clusters were singleton, containing a single genotype in a cluster. Similarly, Khalid et al (2016) also clustered 16 sugarcane genotypes into four different clusters using qualitative traits.

Common traits for genotypes grouped in cluster I were present of bud cushion, bud extending above growth ring, ovate and squarish pentagonal bud shape, open semi-droopy canopy structure, squarish deltoid dewlap shape, moderately erect plant, slightly zig zag internode alignment, concave convex internode shape, green leaves color, transitional auricle shape, crescent with lozenge legule shape, no stalk corky crack, no stalk corky patch, no stalk growth crack, brownish green exposed rind color, and posses bud groove characters.

Most of the genotypes grouped in cluster II are characterized by the presence of bud cushion, bud touching the growth ring, pentagonal bud shape, open tip droopy canopy structure, squarish deltoid dewlap shape, moderately erect plant, straight and slightly zig zag internode alignment, cylindrical internode shape, green leaves color, transitional auricle shape, crescent with lozenge legule shape, no stalk corky crack, no stalk corky patch, no stalk growth crack, light green exposed rind color and has bud groove traits.

Predominant sugarcane genotypes grouped in Cluster III characterized by the presence of bud cushion, bud extending above growth ring, ovate bud shape, open semi-droopy canopy structure, squarish deltoid dewlap shape, moderately erect plant, slightly zig zag internode alignment, concave and convex internode shape, green leaves color, transitional auricle shape, crescent with lozenge legule shape, no stalk corky crack, no stalk corky patch, no stalk growth crack, brown exposed rind color, and presence of bud groove.

Similarly, presence of bud cushion, bud extending above growth ring, squarish pentagonal bud shape, open droopy canopy structure, squarish deltoid dewlap shape, slightly prostate to nearly erect plant, slightly zigzag internode alignment, cylindrical internode shape, green leaves color, transitional and short lanceolate auricle shape, crescent with lozenge legule shape, no stalk corky crack, posses stalk corky patch, no stalk growth crack, purple exposed rind color and presence of bud groove were the major characteristics among all the genotypes of Class IV.

In the present study, cluster I comprised 83 genotypes originating from fifteen countries or regions (Table4). In cluster II, genotypes originating from four countries were placed together; cluster III comprised fifty one genotypes obtained from thirteen geographic origins. Similarly, cluster IV encompassed five genotypes originated from four different countries. This clustering result revealed that genotypes from diverse geographic sources might have a similar genetic background. With the exception, genotypes obtained from Barbados were appeared in all four clusters (Table 4). The landraces collected from different regions of Ethiopia were grouped in three clusters with other exotic genotypes in different frequencies; clusters I, III and IV possessed three, five, and two landraces, respectively (Table 4). This indicated that these landraces have a close relationship with the exotic sugarcane genotypes in this group in terms of the characters considered. Clustering of geographically distant genotypes together indicating that the grouping of genotypes not associated with the geographic origin is rather mainly clustered due to their qualitative morphological traits. This finding was in agreement with the results of other researchers, Esayas et al (2016), Iqbal et al (2018), Mekonnen and Wakjira (2014) and Naznin *et al*(2015). They found an absence of association among

different clusters established with the origin of genotypes. Geographical segregation is not the only agent rendering genetic variability in sugarcane; rather, evolution driving forces such as genetic drift, mutation, natural and artificial selection, and exchange of germplasm might have played an essential role in assigning the genotypes to different clusters (Kandamoorthy and Govindarasu 2005; Senapati and Sarkar 2005).

The analysis of inter-cluster distance revealed that the inter-cluster distance varied from 5.252 to 9.695. The maximum inter-cluster distance was recorded between cluster II and IV, followed by cluster III and IV. While the minimum distance was observed between clusters I and III followed by clusters I and IV (Table 6). The distance among the clusters elucidates the extent to which the genotypes grouped in given cluster are differing from those genotypes placed in other clusters based on their qualitative morphological characters. Large inter cluster distance indicate high genetic divergence between the genotypes of the two cluster, hence crossing among them resulted in high heterosis. Minimum inter cluster distance conversely implies the close relationship between the clusters; hence crosses entailing the genotypes among the clusters may not be effective. On other hand, higher inter cluster distance enable ease identification and effective management of the genotypes by the breeders. Hence, the present result will helps breeders and researchers in identifying and maintainig germplasm used in breeding program for varietal improvement. Karpagam and Alarmelu (2017) also reported the maximum (14.08) inter cluster distance between cluster IV and VI and the least distance between cluster II and IV.

Conclusion

Morphological traits have been commonly used as a genetic marker for identification of varieties in sugarcane improvement program and germplasm management. The present study was undertaken to elucidate phenotypic relationships among the sugarcane genotypes using the morphological traits and the descriptive analysis indicated that all qualitative morphological traits revealed variability in 144 sugarcane genotypes. The highest Shannon diversity index (H') were recorded for stalk corky patches (H' = 0.99), while the lowest diversity is recorded by stalk growth crack (H' = 50). The H' pooled across characters by country of collection ranged from 0.00 to 0.83, with a general average of 0.62. The diversity analysis results indicated the polymorphic distribution pattern of the morphological characters among different series of sugarcane genotypes and across the locations and also their genetic potential of to reflect genetic diversity in sugarcane genotypes. The multivariate cluster analysis grouped 144 sugarcane genotypes into four main clusters elucidating the existence of genetic variability among the genotypes for further identification and selection of genotypes. However, the clustering pattern of the genotypes did not follow the geographical origin, revealing that geographical diversity could not necessarily be an index of genetic variability to group genotypes into different clusters. The highest inter cluster distance values were observed between cluster II and IV (9.695) indicating that genotypes in cluster II were far diverse from those of IV. Based on the present results we can conclude that the studied morphological traits can be utilized as a descriptor in maintainig proper identity of varieties and conservation of germplasms in breeding program. However, because morphological variation alone does not

reflect the total variation it is imperative to be complement with molecular markers to reach on the sound conclusion.

Declarations

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Competing Interest

The authors have no relevant financial or non-financial interests to disclose

Author Contributions

All authors contributed to the study conception and design. Field experiment implementation, data collection and analysis were undertaken by [Melaku Tesfa]. The first draft of manuscript was written by [Melaku Tesfa] and all authors commented on pervious versions of the manuscript. All authors read and approved the final manuscript.

Data Availability

The dataset collected and analyzed on the course of the present study are available from the corresponding author on reasonable request.

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Tables

Table 1. Descriptors, descriptor states and score codes used for characterization of sugarcane germplasm

Descriptor	Abbreviation	Score code and descriptor state
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), short deltoid (2) 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 germpore (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), fan erect (7), 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	INALIGN	Prostrate (1), (4–8), and erect (9)
Relative internode alignment	INSHAPE	Straight (1), slightly zigzag (2), and zigzag (3)
Relative internode shape	LEAFCOLOR	Cylindrical (1), conoidal (2), obconoidal (3), tumescent (4), Bobbin-shaped (5), and concave convex (6)
Color of the leaves	AURICLEOUT	Green (1), light green (2), purple(3), light purple(4), pink(5), light pink(6), and greenish yellow (7)
Type of auricle	LIGSHAPE	Absent (1), transitional (2), dentoid (3), deltoid (4), falcate (5), unciform (6), calcariform (7), short lanceolate (8), and long lanceolate (9)
Relative shape of ligule	STALKCORKC	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), broad subarcuate(9) and inverted crescent (11)
Presence or absence of stalk corky cracks	STALKCORKP	Present (1) and absent (2)
		Present (1) and absent (2)
		Absent (1) and present (6)
		Green (1), light green (2), dark green (3), yellow (4), light yellow (5), dark yellow (6), light purple (8), dark purple (9), brown (10), light brown (11), dark brown (12), yellowish green(13), greenish yellow (14), brownish green (15), brownish yellow (16), and brownish purple (17)
		Absent (1) and present (6)

Presence or absence of stalk corky patchs	STALKCRACK
Presence or absence of stalk growth cracks	RINDCOLE
Color of the exposed rind	
	BUDGROOVE
Presence or absence of bud groove	

Table 2. Frequency distribution of qualitative trait across the region or country

Trait	Scale	Country															
		Eth	Sud	USA	Cub	Ind	Fra	Phi	Bar	Dem	Aus	Tha	S.Af	Bra	PRi	Mau	Mex
BUDCUSHION	1	90	87.5	47	68.8	77.8	53	36.4	61.5	0	50	50	85.7	100	50	100	100
	2	10	12.5	53	31.2	22.2	47	63.6	38.5	100	50	50	14.3	0	50	0	0
	1	0	0	0	0	11.1	0	9.1	0	0	0	0	0	0	0	0	0
BUD EXTEND	2	30	25	29.4	37.5	44.4	53	63.6	19.2	0	50	50	28.6	0	0	100	50
	3	70	75	70.6	62.5	44.4	47	27.3	80.8	100	50	50	71.4	100	100	0	50
	1	20	0	17.6	0	22.2	15.8	0	7.7	0	0	0	14.3	0	50	0	0
	3	50	62.5	35.3	12.5	11.1	5.3	9.1	38.5	50	0	0	14.3	0	0	0	0
	4	0	0	0	0	5.6	0	0	3.8	0	0	0	0	100	0	0	0
	6	0	0	0	0	0	0	18.9	0	0	0	0	14.3	0	0	0	0
BUDSHAPE	7	10	12.5	11.8	6.3	5.6	5.3	0	0	0	0	0	0	0	0	0	0
	8	10	12.5	17.6	37.5	22.2	21	9.1	11.5	50	50	100	0	0	0	0	50
	9	10	0	0	25	16.7	26.3	27.3	30.8	0	50	0	57.1	0	50	100	50
	10	0	12.5	17.6	12.5	5.6	26.3	27.3	3.8	0	0	0	0	0	0	0	0
	11	0	0	0	6.3	5.6	0	0	0	0	0	0	0	0	0	0	0
	12	0	0	0	0	5.6	0	0	0	0	0	0	0	0	0	0	0
	13	0	0	0	0	0	0	9.1	0	0	0	0	0	0	0	0	0
	1	10	12.5	0	6.3	5.6	5.3	0	0	50	50	0	28.6	0	0	0	0
	2	30	12.5	5.9	6.3	38.9	15.8	9.1	23.1	0	0	0	14.2	0	0	0	0
	3	30	25	35.3	37.5	52.2	31.6	36.4	38.5	0	50	0	28.6	0	100	0	0
CANOPY	4	0	25	23.5	6.3	0	21	27.3	3.8	0	0	0	28.6	0	0	0	50
	5	0	12.5	5.9	6.3	5.6	10.5	9.1	7.7	0	0	0	0	0	0	0	0
	6	0	12.5	17.6	18.8	11.1	10.5	0	15.4	50	0	0	0	100	0	100	50
	7	20	0	5.9	12.5	5.6	5.3	9.1	0	0	0	50	0	0	0	0	0
	8	10	0	5.9	6.3	5.6	0	9.1	11.5	0	0	50	0	0	0	0	0
	2	10	75	17.6	25	18.8	5.3	36.4	23.1	0	0	50	28.6	0	50	0	50
	4	50	12.5	47.1	62.5	43.8	57.9	54.5	38.5	50	100	50	57.1	100	0	100	0
	5	0	0	5.9	0	0	5.3	0	0	0	0	0	0	0	0	0	0
	6	20	12.5	17.6	6.3	18.8	10.5	9.1	15.4	0	0	0	14.3	0	50	0	50
DEWLAPSHAPE	7	0	0	5.9	6.3	5.6	5.3	0	0	0	0	0	0	0	0	0	0
	8	0	0	0	0	5.6	0	0	0	0	0	0	0	0	0	0	0
	9	0	0	0	0	0	5.3	0	0	0	0	0	0	0	0	0	0
	10	10	0	0	0	0	0	0	0	50	0	0	0	0	0	0	0
	11	10	0	5.9	0	5.6	10.5	0	23.1	0	0	0	0	0	0	0	0
	5	0	0	0	12.5	18.8	5.3	0	11.5	0	0	0	0	0	50	0	0
	6	0	25	29.4	6.3	50	10.5	27.3	19.2	0	50	0	0	0	0	100	50
ERECT	7	50	50	35.3	43.8	31.3	42.1	36.4	46.2	100	0	0	14.3	0	50	0	50
	8	50	25	35.3	31.3	11.1	42.1	36.4	4.8	0	50	100	42.9	100	0	0	0
	9	0	0	0	6.3	0	0	0	0	0	0	0	42.9	0	0	0	0
	1	40	100	5.9	18.8	11.1	5.3	9.1	7.7	50	50	50	14.3	0	0	0	0
INALIGN	2	60	0	94.1	81.3	83.3	73.7	90.9	76.9	50	50	50	85.7	100	50	100	100
	3	0	0	0	0	5.6	21	0	11.5	0	0	0	0	0	50	0	0

	1	30	37.5	17.6	50	27.8	10.5	9.1	30.8	100	0	100	28.6	0	50	0	50
	2	10	37.5	52.9	18.8	22.2	42.1	27.3	19.2	0	0	0	14.3	0	0	0	0
INSHAPE	3	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	4	0	0	0	18.8	16.7	5.3	9.1	23.1	0	0	0	28.6	100	0	100	0
	5	0	0	0	0	5.6	0	9.1	3.8	0	0	0	0	0	0	0	0
	6	40	25	29.4	12.5	27.8	42.1	45.5	23.1	0	100	0	28.6	0	50	0	50
	1	90	37.5	64.7	81.3	55.6	57.9	63.6	69.2	100	0	100	14.3	100	100	100	50
LEAFCOLOR	2	10	62.5	23.5	18.8)	44.4	31.6	36.4	19.2	0	100	0	85.7	0	0	0	50
	7	0	0	11.8	0	0	10.5	0	11.5	0	0	0	0	0	0	0	0
	2	60	25	58.8	56.3	27.8	42.1	54.5	34.6	50	0	50	42.8	0	100	100	50
	4	0	0	0	6.3	5.6	5.3	0	3.8	50	0	0	0	0	0	0	0
	5	0	12.5	5.9	6.3	0	5.3	0	3.8	0	0	0	0	0	0	0	0
AURICLEOUT	6	0	0	0	6.3	0	0	0	0	0	0	0	0	0	0	0	0
	7	0	0	0	0	0	0	9.1	0	0	0	0	0	0	0	0	0
	8	20	37.5	23.5	6.3	5.6	21.1	9.1	26.9	0	100	0	42.8	100	0	0	0
	9	20	25	11.8	18.8	61	26.3	27.3	30.8	0	0	50	14.3	0	0	0	50
	1	10	0	5.9	6.3	0	0	0	3.8	0	0	0	14.3	0	0	0	0
	3	0	0	0	0	0	10.5	0	0	50	50	0	0	0	0	0	0
	4	0	0	0	6.3	0	0	0	0	0	0	0	0	0	0	100	0
LIGSHAPE	5	90	75	41.2	37.5	72.2	57.9	63.6	46.2	0	50	100	71.4	0	100	0	100
	6	0	25	47	18.8	27.8	15.9	9.1	26.9	0	0	0	14.3	0	0	0	0
	8	0	0	0	0	0	0	9.1	0	0	0	0	0	100	0	0	0
	9	0	0	0	25	0	10.5	9.1	3.8	50	0	0	0	0	0	0	0
	10	0	0	5.9	6.3	0	5.3	9.1	3.8	0	0	0	0	0	0	0	0
	12	0	0	0	0	0	0	0	3.8	0	0	0	0	0	0	0	0
STALKCORKC	1	20	0	23.5	6.3	22.2	21.1	9.1	26.9	0	0	0	28.6	0	50	0	50
	2	80	100	76.5	93.7	77.8	78.9	90.9	73.1	100	100	100	71.4	100	50	100	50
STALKCORKP	1	80	37.5	47.1	31.3	44.4	31.6	27.3	57.7	0	0	0	42.9	100	50	0	50
	2	20	62.5	52.9	68.7	55.6	68.4	72.7	42.3	100	100	100	57.1	0	50	100	50
STALKCRACK	1	90	87.5	82.4	93.7	88.9	78.9	100	92.3	100	100	100	85.7	100	50	100	50
	6	10	12.5	17.6	6.3	11.1	21.1	0	7.7	0	0	0	14.3	0	50	0	50
	1	0	0	5.9	12.5	11.1	0	0	11.5	0	0	50	0	0	0	0	0
	2	0	0	17.6	0	11.1	21.1	18.2	11.5	50	0	0	14.3	0	50	0	0
	3	0	0	0	0	11.1	0	0	0	0	0	0	0	0	0	0	0
	4	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
RINDCOLE	5	0	0	0	0	0	5.3	9.1	0	0	0	0	0	0	0	0	0
	6	0	0	0	0	0	5.	0	0	0	0	0	0	0	0	0	0
	7	30	12.5	5.9	12.5	5.6	5.3	27.3	7.7	0	0	0	0	0	0	0	0
	8	30	0	17.6	37.5	22	10.5	18.2	7.7	50	0	0	14.3	0	0	100	0
	9	0	25	0	0	0	5.3	0	3.8	0	0	0	0	0	0	0	0
	10	10	12.5	0	0	5.6	5.3	9.1	3.8	0	0	0	0	100	0	0	0
	11	0	12.5	5.9	6.3	5.6	0	0	3.8	0	0	0	0	0	50	0	0
	12	0	0	5.9	0	0	5.3	9.1	3.8	0	0	0	0	0	0	0	0

	13	10	25	17.6	12.5	5.6	5.3	9.1	15.4	0	0	0	42.8	0	0	0	0
	14	0	0	5.9	12.5	5.6	21.1	0	11.5	0	100	50	14.3	0	0	0	0
	15	10	0	11.8	6.3	5.6	5.3	0	11.5	0	0	0	14.3	0	0	0	0
	16	0	12.5	5.9	0	0	0	0	3.8	0	0	0	0	0	0	0	0
	17	0	0	0	0	0	5.3	0	3.8	0	0	0	0	0	0	0	0
BUDGROOVE	1	20	25	11.8	31.3	38.9	10.2	27.3	19.2	0	50	0	28.6	0	50	0	50
	6	80	75	88.2	68.7	61.1	89.5	72.7	80.8	100	50	100	71.4	100	50	100	50

Eth=Ethiopia, Sud=Sudan, Cub=Cuba, Ind =India, Fra=France, Phi = Philippines, Bar = Barbadose, Dem=Demarara, Aus = Australia, Tha=Thailand, Bra= Brazil, SAf= South Africa, PRi= Porto Rico, Mau=Mauritius, Mex=Mexico

Table 3. Estimates of Shannon-weaver diversity index (H¢) for 16 characters partitioned into within and between countries

Character	Code	H¢	H_c	H_c/H¢	(H¢-H_c)/H¢
Presence or absence of bud cushion	BUDCUSHION	0.94	0.63	0.67	0.33
Relative degree of bud extension	BUD EXTEND	0.68	0.67	0.99	0.01
Relative bud shape	BUDSHAPE	0.81	0.74	0.91	0.09
Canopy structure	CANOPY	0.91	0.76	0.84	0.16
Relative shape of dewlap	DEWLAPSHAPE	0.67	0.64	0.95	0.03
Relative plant erectness	ERECT	0.79	0.71	0.89	0.11
Internode alignment	INALIGN	0.56	0.55	0.98	0.02
Relative internode shape	INSHAPE	0.81	0.63	0.78	0.22
Color of the leaves	LEAFCOLOR	0.85	0.50	0.59	0.41
Type of outer auricle	AURICLEOUT	0.69	0.65	0.94	0.06
Shape of ligule	LIGSHAPE	0.60	0.55	0.91	0.09
Stalk corky cracks	STALKCORKC	0.71	0.47	0.66	0.34
Stalk corky patchs	STALKCORKP	0.99	0.58	0.59	0.41
Stalk growth cracks	STALKCRACK	0.50	0.39	0.78	0.23
Color of the exposed rind	RINDCOLE	0.88	0.71	0.81	0.19
Type of bud groove	BUDGROOVE	0.76	0.61	0.80	0.20
Mean		0.76	0.61	0.82	0.18

H¢= Diversity index for each character calculated from entire data set; Hc = Average diversity index of each character for the 16 countries; Hc/H¢=Proportion of diversity within countries; and (H¢-Hc)/H¢= Proportion of diversity between countries in relation to the total variation.

Table 4. Estimates of standardized Shannon-Weaver diversity index (H¢) of sugarcane germplasm for the qualitative traits by country of origin

Country	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	Mean ±SE
Ethiopia	0.47	0.88	0.85	0.94	0.84	1.00	0.97	0.86	0.47	0.86	0.47	0.72	0.72	0.47	0.92	0.72	0.76±0.05
Sudan	0.54	0.81	0.77	0.97	0.67	0.95	0.00	0.99	0.95	0.95	0.81	0.00	0.95	0.54	0.97	0.81	0.73±0.08
USA	1.00	0.87	0.96	0.86	0.82	1.00	0.32	0.91	0.79	0.77	0.76	0.79	0.74	0.67	0.94	0.52	0.80±0.04
Cuba	0.90	0.96	0.88	0.87	0.71	0.83	0.76	0.89	0.70	0.74	0.80	0.34	0.90	0.34	0.90	0.90	0.78±0.05
India	0.76	0.88	0.92	0.83	0.88	0.91	0.51	0.94	0.99	0.61	0.85	0.77	0.99	0.50	0.95	0.96	0.83±0.04
France	1.00	1.00	0.91	0.91	0.73	0.81	0.64	0.81	0.90	0.84	0.77	0.74	0.90	0.74	0.92	0.49	0.82±0.03
Philippines	0.95	0.78	0.93	0.89	0.83	1.00	0.44	0.85	0.95	0.83	0.72	0.44	0.08	0.00	0.95	0.85	0.72±0.08
Barbados	0.96	0.71	0.80	0.87	0.96	0.91	0.59	0.92	0.71	0.83	0.75	0.84	0.98	0.39	0.95	0.71	0.81±0.04
Demarara	0.00	0.00	1.00	1.00	1.00	0.00	1.00	0.00	0.00	1.00	1.00	0.00	0.00	0.00	1.00	0.00	0.44±0.13
Australia	1.00	1.00	1.00	1.00	0.00	1.00	1.00	0.00	0.00	0.00	1.00	0.00	0.00	0.00	0.00	1.00	0.50±0.13
Thailand	1.00	1.00	0.00	1.00	1.00	0.00	1.00	0.00	0.00	1.00	0.00	0.00	0.00	0.00	1.00	0.00	0.44±0.13
South Africa	0.59	0.86	0.83	0.98	0.87	0.91	0.59	0.98	0.59	0.91	0.73	0.86	0.99	0.59	0.92	0.86	0.82±0.04
Brazil	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00±0.00
Puerto Rico	1.00	0.00	1.00	0.00	1.00	1.00	1.00	1.00	0.00	0.00	0.00	1.00	1.00	1.00	1.00	1.00	0.69±0.12
Mauritius	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00±0.00
Mexico	0.00	1.00	1.00	1.00	1.00	1.00	0.00	1.00	1.00	1.00	0.00	1.00	1.00	1.00	0.00	1.00	0.75±0.11

1= BUDCUSHION, 2 = BUD EXTEND, 3 = BUDSHAPE, 4 = CANOPY, 5 = DEWLAPSHAPE, 6 = ERECT, 7 =INALIGN, 8 = INSHAPE, 9 = LEAFCOLOR, 10 = AURICLEOUT, 11= LIGSHAPE, 12 = STALKCORKC, 13 = STALKCORKP, 14 =STALKCRACK, 15 = RINDCOLE, 16 = BUDGROOVE

Table 5. Cluster analysis of 144 sugarcane genotypes with 16 qualitative traits

Cluster group	Number of genotypes	Genotypes in cluster										Origin country
		44	80	71	88	28	38	37	47	54	67	Ethiopia, Sudan ,
		70	62	18	30	21	41	56	100	86	19	Cuba, India,
		81	102	112	66	133	123	98	105	64	127	France, Philippines
I	83	12	108	94	32	122	10	65	33	114	103	Barbados, Demarara
		143	39	7	25	128	138	31	1	106	110	Australia, south Africa
		5	135	142	83	129	6	72	73	140	120	Porto Rico, Mauritius
		69	4	96	126	77	58	45	99	113	60	Thailand, Mexico
		43	42	101	78	35	36	121	71	78	26	and USA
		36	121	71	78	26	136					
II	5	79	134	8	14	22						Barbadose, France,
												India and Demarara
III	51	144	74	104	141	48	124	85	111	109	9	Cuba, France, USA
		16	90	89	137	132	27	131	17	15	68	Barbados, India,Brazil
		40	55	49	130	91	76	11	24	97	46	Philippines, Ethiopia
		84	139	29	59	118	51	117	50	125	82	Mexico, Australia
		93	75	87	20	61	53	3	115	57	92	South Africa, Porto Rico, Thailand
IV	23	52	119	13	95							Barbados, Philippines,
												USA, Ethiopia

Table 6. Estimates of inter-cluster distances among the four clusters of 144 sugarcane genotypes

	Cluster I	Cluster II	Cluster III	Cluster IV
Cluster I	0.000	8.623	5.252	5.734
Cluster II	8.623	0.000	9.005	9.695
Cluster III	5.252	9.005	0.000	9.354
Cluster IV	5.734	9.695	9.354	0.000

Figures

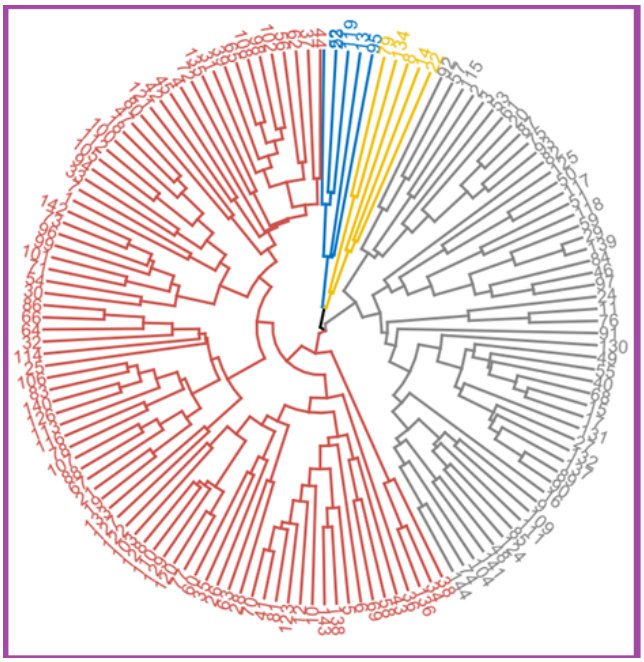

Figure 1

A dendrogram depicting the clustering pattern of sugarcane genotypes based on morphological qualitative triats. The clusters are colored with red, gray, yellow, and blue color. Each numbers represents sugarcane genotypes. See the respective genotypes on supplementary table 1.

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- SupplementaryTables.docx