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Evaluation and Characterization of *Saccharum* Germplasm for Sugarcane Breeding in Sri Lanka

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ABSTRACT

Genetically-variable sugarcane progenies are generated through the crossing of parents. The commercial varieties with high cane and sugar yields, moderate fibre content, pest and disease resistance, and high adaptability to growing conditions are selected from these progenies. This study was conducted to identify parents with high combining ability of most of these characteristics into the progenies for efficient variety selection in sugarcane breeding. In this regard, 508 accessions from the *Saccharum* germplasm were assessed for their commercial attributes. Data on cane and sugar yield components were collected from each accession. Phenotypic correlations were estimated for each pair of characteristics. Principal component analysis was performed, and subsequently, cluster analysis was done based on the first three principal components. Phenotypic relationships revealed that the plot yield of an accession is mainly determined by the number of stalks and stalk length, suggesting that accessions with a higher number of stalks and longer stalk lengths can be taken as promising parents for breeding for cane yield. The strong positive relationships of brix to other components of sugar content proved that the parents with high sugar can be classified by hand brix. The selected PCs clustered the accessions into four groups. Group 1 comprises the parental core collection for generating progenies with moderate cane yield, high sugar yield, and moderate fibre content, whilst accessions in group 3 can be used for breeding energy cane. The accessions SLC 91 46 and S 2003-US-247 were identified as the most promising parents in the simultaneous improvement of cane and sugar yields with moderate fibre content.

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INTRODUCTION

Sugarcane is an important crop cultivated in tropical and sub-tropical countries, including Sri Lanka. A significant improvement in sugarcane production is required to cope with the increasing demand for sugar and bio-ethanol due to population growth. Therefore, sugarcane crop improvement plays an important role in producing improved sugarcane varieties with high agronomic performance.

Currently, Sri Lanka produces 59,869 Mt of sugar, meeting only 9% of the domestic requirement (CBSL, 2020), with the balance being imported. There is a necessity to expand cultivation, use improved sugarcane varieties, adopt better management practices (OECD/FAO, 2019), and modern technologies (Sugarcane Research Institute, 2013) to achieve the targets of 40% self-sufficiency in sugar by 2020 and 100% by 2030. Cultivation of high-yielding sugarcane varieties, access to irrigation systems, an increase in sugarcane cultivation by means of an out-grower system, and achieving a high sugar recovery rate could contribute to the increase in sugar production (CBSL, 2018, 2019, 2020).
Sugarcane has a long crop cycle, and its cultivation requires costly inputs, including machinery, labour and agrochemicals. Therefore, to prevent farmers from converting sugarcane to other economically viable crops such as maize and banana (Keerthipala, 2016; De Silva et al., 2019), it is important to provide them with high cane and sugar-yielding varieties with optimal fibre contents that are resistant to different abiotic and biotic stress conditions.

The genus *Saccharum* includes six species, namely, *S. officinarum*, *S. sinense*, *S. barberi*, *S. robustum*, *S. spontaneum* and *S. edule* (Roach, 1972) that are perennial grasses belonging to the family Poaceae. The modern sugarcane varieties have been derived from introgression of the genomes of *S. officinarum* and *S. spontaneum* clones and subsequently by inter-varietal hybridization (Price, 1963). The success of the development of superior sugarcane varieties depends on the ability to select parents after the evaluation of the germplasm collections for economically important traits. Hence, germplasm evaluation, parental selection for hybridization, and progeny selection are important steps that determine the efficiency of sugarcane improvement programs. Sugarcane breeders contemplating the use of new germplasm in breeding programs need to know the characteristics of the many classes and clones of materials available and how a logical selection of parents could be made from them (Mbuma et al., 2019). Several authors have reported that the characterization of sugarcane germplasm in different parts of the world is done merely by giving a detailed description of the morphological characters that each variety possesses (Akhtar et al., 2006; Nosheen and Ashraf, 2001; Ekpélikpézé et al., 2016). Specifically, two useful traits are indicative of high sugar yield; viz. cane yield and sucrose content. Superior genotypes can be developed from the interactions of these characteristics (Papini-Terzi et al., 2009; Alvarez et al., 2009). Producing sugarcane seedlings from genetically diverse parents is essential for developing high-yielding and disease- and insect-resistant sugarcane cultivars for commercial planting by the sugar industry or by local cane farmers (Olaoye, 2005).

Genetic resources conserved and maintained by the Sugarcane Research Institute (SRI) of Sri Lanka comprise a rich collection of accessions representing pure *S. officinarum*, *S. spontaneum*, *Erianthus arundinaceous*, *Miscanthus japonica*, and commercial clones (*Saccharum* spp. hybrids). This is in addition to the first, second, and third generations of inter-generic and inter-specific hybrids and clones developed through the callus culture technique. Sugarcane crop improvement begins with the hybridization of these parental clones to create genetically variable seedling populations. At present, parents for hybridization are selected based on the results of germplasm evaluation and quantitative genetic experiments conducted by several research teams (Sunil, 1995; Sunil and Lawrence, 1996; Wijesuriya et al., 1997; Wijesuriya, 2012; Kiriwaththuduwa et al., 2021). The absence of a database on parents makes the selection of parents for the crosses more difficult. This results in the generation of a large proportion of inferior progenies in the seedling populations, eventually wasting funds and resources. The development and adoption of an appropriate methodology for parent selection and proven crossing systems for directional breeding of sugarcane, high sugar and cane yield, and pest and disease resistance are yet to be developed in Sri Lanka. Moreover, the limited number of accessions evaluated in previous experiments provides limited information for developing a proven mating system.

This research was therefore undertaken to determine the parental potential of the accessions of *S. officinarum*, *S. spontaneum*, *Erianthus arundinaceus*, and *Saccharum* spp. hybrids maintained in Sri Lanka for the components of cane and sugar yields and fibre content. The association between cane and sugar yield components and fibre content was also examined to identify parents for the development of core-collections to be used in directional breeding of sugarcane simultaneously for high cane yield, high sucrose, and optimum fibre contents. The parents selected through this study will be used for the development of core-collections for use in bi-parental and poly-crosses aiming at developing high cane and sugar yielding varieties with optimal fibre contents.

METHODOLOGY

Establishment of the field experiment

The field experiment was designed to evaluate 508 germplasm accessions that can be used as parental clones. It included 81 pure *S. officinarum* accessions, 25 *S. spontaneum* accessions, 26 *E. arundinaceus* accessions, and 376 *Saccharum* spp. hybrids. These clones were selected out of 1,460 accessions available at the *Saccharum* germplasm repository established at the Sugarcane Breeding Sub-station of the Sugarcane Research Institute (SRI) at Enselwatte, Deniyaya, Sri Lanka using a random number generator. The experiment was conducted at the Research Farm of SRI (6˚21' N Latitude and 80˚48' E Longitude).

The field experiment was established in the land that had been prepared using a ridge and furrow system to facilitate furrow irrigation. The furrow spacing of 1.37 m and the furrow depth of 25 cm were maintained throughout the field experiment. All treatments were tested in a Completely Randomized Design (CRD) with two replicates. The parental clones were planted in 1-meter-long plots, leaving a 0.5 m gap between two plots in the furrows. Five three-budded stem cuttings (setts) were planted in a plot. Crop management practices such as gap filling, fertilizer application, earthing up, weed management, and irrigation were done as recommended by SRI, Sri Lanka.

Harvesting and data collection

Only the matured stalks were used for the collection of data on yield and quality parameters. The number of millable stalks and plot weight were initially recorded at harvest, and then a sample of 12 randomly-selected mature stalks was obtained for recording data on stalk length, stalk diameter, number of internodes per stalk, rind hardness, and hand refractometer brix at the field, and ten stalks of the same sample were used for measuring / estimating laboratory brix, the % pol in juice, and purity at the laboratory. The remaining two stalks were used to measure the % of fibre on a fresh weight basis. Pure obtainable cane sugar (POCS) was calculated as POCS=3/2 pol {1-(fibre+5/100)} × brix {1-(5+3/100)}. Sugar yield was calculated by multiplying plot weight by the amount of pure, obtainable cane sugar.

Analysis of data

Phenotypic correlations were estimated for each pair of characteristics using the phenotypic values of accessions. Sugar yield per plot was not considered in the correlation analysis since it is calculated using plot weight and POCS.

The phenotypic correlation is given in Equation 1;

$$r_p = \frac{COV_p}{\sigma_{px}+\sigma_{py}} \qquad \text{………… Equation 1}$$

where, COV_p is the phenotypic covariance, σ_{px} and σ_{py} are phenotypic standard deviations of characteristics X and Y, respectively (Falconer, 1989).

Hierarchical clustering on principal components (HCPC) has been used in many disciplines to classify individuals. The main advantage of this approach over the use of principal component analysis (PCA) alone is that it involves the application of objective clustering techniques to the PCA results, leading to a better cluster solution (Argüelles *et al.,* 2014). Therefore, this method was used in this study to identify the principal components (PCs) and their PC scores for the clustering process.

Data on cane- and sugar yield components, namely, the number of internodes per stalk, stalk length, stalk diameter, number of stalks, laboratory brix, pol in juice, purity, and pure obtainable cane sugar, were used in the analysis excluding the cane yield and sugar yield of the accessions under consideration. The PCA was conducted on standardized variables, and the orthogonal rotation solution was obtained intending to load a smaller number of highly correlated variables onto each factor for easy interpretation. The data were checked for appropriateness for the PCA employing Kaiser-Maier-Olkin (KMO) and Bartlett's test of sphericity, which have been reported as the two most common techniques (Lattin et al., 2003).

This was followed by the Cluster Analysis (CA) of the PC scores that were retained from the rotated PCA. For the cluster analysis, the complete linkage hierarchical clustering method was applied. Genstat 20 software was employed in statistical analyses. To decide the optimum number of clusters to be retained, different methods have been reported in the literature. Among them, the elbow method (Marutho et al., 2018) is the simplest and most common and was used to decide the number of clusters in this analysis. The mean and standard deviation are computed for the variables in different clusters. An Analysis of Variance was performed for these variables, taking the clusters as the classificative variable. The comparison allows for identifying the differences in variances between clusters.

RESULTS AND DISCUSSION

Phenotypic correlations

The matrix of phenotypic correlations among the characteristics studied is presented in Table 1. The relationship between the characteristics that determine sugar content and cane yield is the most important concern of a sugarcane breeder in the selection of parents for directional breeding (Wijesuriya, 2012). The extent and direction of phenotypic correlation coefficients are important in deciding the characteristics on which selection of parents are to be carried out for directional breeding for the cane yield and sugar yield considering the optimum fibre content in cane. The number of millable stalks showed the highest phenotypic relationship with plot yield ($r=0.71$, $p<0.001$) followed by stalk length ($r=0.63$, $p<0.001$). Phenotypic correlations suggested that the accessions with a higher number of millable stalks per plot and higher stalk lengths can be taken as prospective parents for directional breeding for cane yield. The significant-negative relationship ($r=-0.24$. $p<0.001$) observed between the number of stalks per plot and stalk diameter, suggests that the accessions with a high number of stalks with moderate stalk diameters have to be considered in the parental selection for directional breeding for high cane yield as thin canes are not preferred by the growers. Manual cane harvesters, on the other hand, prefer thick-caned sugarcane varieties. The results indicated that thicker canes produced fewer millable canes, resulting in a decrease in cane yields. In this scenario, the selection of parents with acceptable diameters and high stalk lengths is required for directional breeding for cane yield.

Although a negative relationship ($r= -0.46$. $p<0.001$) was observed between the fibre content and POCS, the accessions with moderate fibre content should be considered in parental selection as they regulate the juice extraction efficiency in the sugar mills. Therefore, during sugarcane parental selection, breeders have to consider a longer cane and a higher number of stalks with an acceptable diameter and moderate fibre content for obtaining progenies with high cane yields and good milling qualities. The concept of developing *e*-canes (energy canes), i.e., canes with high fibre contents (17-18%) by sacrificing some amount of sucrose, is now favourably considered due to the economic and environmental benefits through the generation of renewable energy (van der Poel et al., 1998). Recent research has focused on power alcohol production by solid-state fermentation of bagasse technology involving enzymes (van der Poel et al., 1998). Hence, diversification of sugarcane products is more economical, and selection of parents with high fibre content has also become a necessity in breeding *e*-canes for use with factory modifications. The results indicated that there are strong or moderately significant and positive correlations between POCS and biochemical characteristics such as hand refractometer brix, laboratory brix and purity of juice. Strong, significant, and positive correlations of hand refractometer brix to laboratory brix (r= 0.74. p<0.001), pol in juice (r= 0.78. p<0.001), purity (r= 0.74. p<0.001) and pure obtainable cane sugar (r= 0.77. p<0.001) proved that the assessment of varieties for sugar content through hand brix is realistically accurate in the initial screening of high sugar parental clones, as well as high sugar clones in the initial populations of progeny selection. Parents with the highest sugar contents should be identified accurately through POCS for incorporation into the directional crosses of sugarcane for high sugar and cane yields.

All biochemical characteristics that determine sugar content in cane were positively associated phenotypically with plot cane yield, stalk length, and stalk diameter. All these results revealed that cane yield and sugar content are complex characteristics that can be improved independently and simultaneously by manipulating their components during variety selection and breeding through the choice of parental clones. Stalk diameter had a negative and significant correlation (r= -0.60. p<0.001) with the fibre content. This suggests that thinner canes in the population under study have high fibre contents, and thicker canes are associated with comparatively low fibre contents. Rind hardness reasonably assesses fibre content in cane (r= 0.24. p<0.001).

Table 1. The coefficients of phenotypic correlations among the components of cane and sugar yields and fibre content in cane

Variable	HB	RH	LEN	DM	PY	NST	LB	POL	PUR	POCS
RH	0.10 ***									
LEN	0.24 ***	0.52 ***								
DM	0.68 ***	-0.01 NS	0.08 ***							
PY	0.36 ***	0.43 ***	**0.63** ***	0.28 ***						
NST	-0.09 NS	0.37 ***	0.44 ***	**-0.24** ***	**0.71** ***					
LB	**0.74** ***	0.12 ***	0.30 ***	0.36 ***	0.36 ***	0.28 ***				
POL	**0.78** ***	0.13 ***	0.33 ***	0.45 ***	0.41 ***	-0.24 ***	0.71 ***			
PUR	**0.74** ***	0.10 ***	0.30 ***	0.51 ***	0.38 ***	0.36 ***	0.36 ***	0.91 ***		
POCS	**0.77** ***	0.10 ***	0.32 ***	0.44 ***	0.40 ***	0.45 ***	**0.41** ***	0.10 ***	**0.90** ***	
FIB	-0.58 ***	0.24 ***	0.02 NS	**-0.60** ***	-0.10 ***	0.51 ***	0.38 ***	-0.46 ***	-0.57 ***	**-0.46** ***

Stalk length (LEN), Stalk diameter (DM), Number of stalks (NST), Laboratory Brix (LB), Pol (POL), Purity (PUR), Pure obtainable cane sugar (POCS), Fibre (FIB) content, Rind hardness (RH), Plot yield (PY), Hand refractometer brix (HB). ***Significant at P≤0.001; Not significant (NS)

Hierarchical clustering on principal components

In total, nine variables were included in the PCA (Table 2) and three PCs were retained. The 1st and 2nd components, respectively, explain 52% and 21% of the total variability, while the 3rd explains 11%. The respective eigenvalues were 4.63, 1.90, and 0.97 for the 1st, 2nd, and 3rd components, respectively. It was decided to retain the 3rd component for further analysis, although the eigenvalue was less than one (Table 2). All three components were retained and explained 84% of the total variability of the data. Each component could be defined according to the variables with which it is most correlated. Relatively large loadings (above 0.33) are shown in boldface (Table 2). The first component (PC1), which explains 52% of the variance, was positively correlated with all sugar yield components, and therefore named a PC for sugar yield. The PC2, which explains 21% of the total variation, was negatively correlated with two of the cane yield components; the number of internodes and stalk length. Stalk diameter, number of stalks, and fiber content in cane were found to be important in PC3, with fiber content and number of stalks being positively related, whereas stalk diameter was negatively related. The correlation analysis revealed that the stalk diameter and number of stalks are negatively related, indicating that a higher number of stalks would result in a lower diameter of the cane in most instances. For the Cluster Analysis (CA), the first three PC scores that explained 84% of the variability of the data were used. The dendrogram illustrated the sequence in which the varieties were included in the four clusters (Figure 1). The best cluster partition was based on the elbow method (Marutho et al., 2018) which resulted in four clusters and was also agreeable with the dendrogram. The amalgamation of clusters at a 75% similarity level is given in Tables 4 to 7.

Cluster group 1, which was the largest cluster, consisted of 337 accessions. Out of these, 286 were *Saccharum* spp. hybrids, 44 were locally collected accessions, and seven were wild accessions, including six *S. spontaneum* and one *Erianthus* species. The standard variety Co 775 introduced from Coimbatore in India, the locally bred popular variety SL 96 128 that covered more than 75% of the sugarcane plantations in Sri Lanka, and all other varieties recommended for commercial cultivation in Sri Lanka were included in this group. This cluster group had varieties with moderate cane-yield components; stalk length above 200 cm, cane thickness about 22 mm, and nearly 18 stalks per plot (Table 3). However, this group comprised high sugar-yielding varieties with higher POCS values of

Table 2: The components (after rotation) resulting from principal component analysis with loadings of variables and cumulative variance (%) of components

Name of variable	Principal Component (PC)		
	PC1	PC2	PC3
Cane yield components			
Number of internodes	-0.0286	**-0.6624**	-0.1162
Stalk length	-0.0003	**-0.6540**	0.0838
Stalk diameter	-0.0087	-0.1864	**-0.6442**
Number of stalks	0.1017	-0.3064	**0.4823**
Sugar yield components			
Brix	**0.5213**	0.0502	0.0882
Pol	**0.5149**	-0.0024	0.0048
Purity	**0.4237**	-0.0461	-0.1256
Pure obtainable cane sugar	**0.5131**	0.0083	-0.0006
Milling quality parameter			
Fibre content	-0.0952	-0.0083	**0.5552**
Variance explained by each PC	52%	21%	11%
Cumulative variance explained	52%	73%	84%

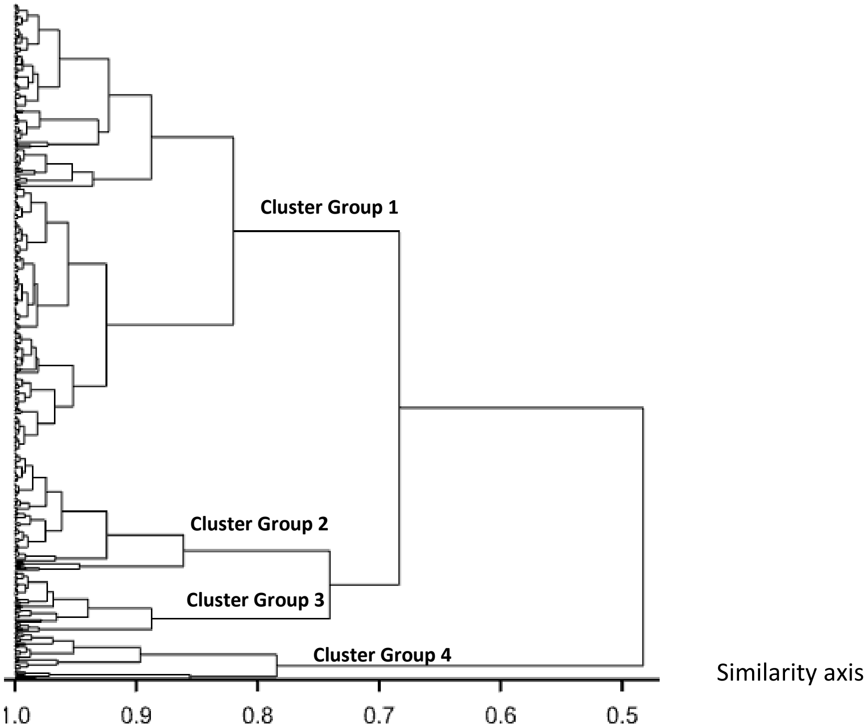

Figure 1: Dendrogram produced on rotated PC scores of cane and sugar yield components with fibre percentage

Table 3: The group mean comparison for cane yield and sugar yield components and milling quality parameter

Variables	Cluster Group 1 *N*=337	Cluster Group 2 *N*=89	Cluster Group 3 *N*=46	Cluster Group 4 *N*=36	Significance probability
Cane yield components					
Number of internodes	23.5 B	23.7 B	31.3 A	18.5 C	P<0.0001
Stalk length (cm)	215.3 B	211.2 B	271.1 A	198 C	P<0.0001
Stalk diameter (mm)	22.2 B	24.8 A	21.8 B	12.2 C	P<0.0001
Number of stalks	18.6 B	13.5 C	25.2 A	25.2 A	P<0.0001
Sugar yield components					
Brix (%)	**16.8 A**	**13.5 C**	**14.3 B**	**9.8 D**	P<0.0001
Pol (%)	14.0 A	10.1 B	10.9 B	4.1 C	P<0.0001
Purity (%)	82.3 A	72.7 B	74.1 B	42.5 C	P<0.0001
Pure obtainable cane sugar	9.9 A	6.5 B	7.2 B	1.5 C	P<0.0001
Milling quality parameter					
Fibre (%)	**15.1 C**	**14.1 D**	**16.6 B**	**24.3 A**	P<0.0001
Cane and sugar yields					
Plot yield (kg/1 m long plot)	**16.3 B**	**13.5 C**	**23.4 A**	**6.9 D**	P<0.0001
Sugar yield (kg/1 m long plot)	1.7 A	1.0 B	1.8 A	0.07 C	P<0.0001

Across columns, means with different letters are significantly different at the Alpha level, 0.05.

about 10% and an average of 16.8 brix. The varieties in this group had moderate fibre content, which is good for milling. Therefore, accessions in this group can be included in the parental core collection that is to be developed for use in breeding for high sugar yield with moderate fibre content (Table 4)

Table 4: Accessions belong to cluster group 1

Ajawa	HOCP 93746	PS 36	SL 93 677	SLC 12 64 (O)
Ajex	Homer	PS 52	SL 93 697	SLC 12 68 (O)
B 45151	HoSG 1257	PS 55	SL 94 2917	SLC 12 71 (O)
BL 04	HoSG 315	PS 56	SL 94 3325	SLC 12 76 (O)
Co 1001	HoSG 529	Q 58	SL 94 3360	SLC 12 91 (O)
Co 1148	HoSG 795	Q 63	SL 95 2476	SLC 12 92 (O)
Co 245	HSF 240	Q 68	SL 95 4033	SLC 13 01 (O)
Co 321	HSF 242	Q 70	SL 95 4226	SLC 13 02 (O)
Co 540	IK 77 92 (S)	Q 73	SL 95 4421	SLC 13 19 (O)
Co 62175	Irritty3 (S)	Q 83	SL 95 4425	SLC 13 23 (O)
Co 622	IS 76 215 (S)	QSG 1741	SL 95 4426	SLC 13 24 (O)
Co 6304	ISD 20 (S)	Ragnar	SL 95 4430	SLC 13 25 (O)
Co 658	ISD 30 (S)	RB 70141	SL 95 4432	SLC 13 29 (O)
Co 7717	Kaba	RB 70194	SL 95 4443	SLC 13 41 (O)
Co 775	LF 5104	RB 705051	SL 95 4444	SLC 13 51 (O)
Co 789	LF 51204	ROC 09	SL 95 4514	SLC 13 53 (O)
Co 8106	LF 51239	ROC 6528	SL 96 061	SLC 13 68 (O)
Co 8232	LF 6362	ROC 69403	SL 96 128	SLC 91 39 (O)
Co 853	LF 6367	ROC 703065	SL 96 175	SLC 91 46 (O)
Co 8713	LF 6372	SES 356 (E)	SL 96 234	SLC 92 20 (O)
Co 975	LF 722246	SL 00 529	SL 96 236	SLC 92 47 (O)
COJ 84	LF 72940	SL 02 0061	SL 96 277	SLC 92 91 (O)
CP 4333	LF 742943	SL 71 03	SL 96 278	SLC 93 01 (S)
CP 48120	LF 743466	SL 71 16	SL 96 293	SLI 121
CP 63306	LF 7510021	SL 71 26	SL 96 328	SLT 1049
CP 63350	LF 7537	SL 71 30	SL 96 347	SLT 4818
CP 691052	LF 765285	SL 77 226	SL 96 385	SLT 4823
CP 70330	LF 765298	SL 77 85	SL 96 753	SLT 4830
CP 70414	LF 76621	SL 81 09	SL 96 771	SLT 4920
CP 721210	LF 781245	SL 83 02	SL 97 1118	SLT 4921
CP 722086	LF 78961	SL 83 03	SL 97 1164	SLT 8415
CP 77400	LF 811586	SL 83 04	SL 97 1239	SLT 8416
CPF 213	M 115666	SL 83 06	SL 97 1419	SLT 8418
CPF 235	M 115666	SL 85 01	SL 97 1442	SLT 8420
CPF 237	M 12459	SL 85 18	SL 98 2007	SLT 88 238
CPF 246	M 1358	SL 85 20	SL 98 2020	SP 07
CPSF 1353	M 1358	SL 86 02	SL 98 2087	SP 832847
CPSG 1607	M 155770	SL 86 12	SL 98 2524	SP 870396
CPSG 1663	M 33758	SL 86 13	SL 98 2535	SP 903723
CPSG 2423	M 33765	SL 86 14	SL 98 2549	SPF 213
CPSG 25	M 35157	SL 86 15	SL 98 2557	SPF 234

Table 4: Continued

CPSG 26	M 43859	SL 86 16	SL 98 2790	SPF 237
CPSG 2713	M 44251	SL 86 19	SL 98 2792	SPF 238
CPSG 2875	Mahona	SL 86 21	SL 98 2827	SPF 245
CPSG 3453	MER 5905	SL 87 219	SLC 09 01	SPSH 35
CPSG 3481	MER 6010	SL 87 300	SLC 09 02	S 2003-US-114
CPSG 437	MSG 59	SL 87 360	SLC 10 04 (O)	S 2003-US-127
CPSS 437	MY 5565	SL 87 54	SLC 10 21 (O)	S 2002-US-133
CSSG 2007	N 115066	SL 88 116	SLC 10 22 (O)	S 2003-US-165
CSSG 212	N 12	SL 88 168	SLC 10 26 (O)	S 2003-US-247
CSSG 2402	Nanahu	SL 88 205	SLC 10 28 (O)	S 2002-US-312
CSSG 2453	NCO 310	SL 89 111	SLC 12 02 (O)	S 2005-US-54
CSSG2476	NCO 334	SL 89 1429	SLC 12 03 (O)	S 2003-US-618
CSSG 668	Ni 09	SL 89 1675	SLC 12 04 (O)	S 2003-US-623
CSSG 676	Ni 11	SL 89 2227	SLC 12 06 (O)	S 2002-US-628
F 146	NSG 59	SL 89 2518	SLC 12 09 (O)	S 2003-US-633
F 148	PH 1164	SL 89 309	SLC 12 11 (O)	S 2003-US-694
F 156	PH 37960	SL 90 5599	SLC 12 12 (O)	S 2003-US-718
F 166	PH 5333	SL 90 5695	SLC 12 15 (O)	S 2003-US-778
F 167	PH 7115	SL 90 6237	SLC 12 19 (O)	UCW 5463
F 7213	PH 7544	SL 92 4896	SLC 12 20 (O)	UCW 5465
Galoa	PH 8013	SL 92 4997	SLC 12 21 (O)	UT 03
H 382915	PH 821396	SL 92 5300	SLC 12 25 (O)	Vatu
H 442772	PH 831528	SL 92 5588	SLC 12 32 (O)	
H 443098	PH 841000	SL 93 305	SLC 12 34 (O)	
H 593775	PH 84450	SL 93 331	SLC 12 39 (O)	
H 700144	PH 84788	SL 93 3370	SLC 12 42 (O)	
Hellamulla	PH 85562	SL 93 4919	SLC 12 63 (O)	

E – *Erianthus* spp.; Variety name without brackets - *Saccharum* spp. hybrids; O – *Saccharum officinarum*; S – *Saccharum spontaneum*

Table 5: Accessions belong to cluster group 2

Akoki 22	SLC 12 35 (O)	SLC 12 96 (O)	SLC 13 21 (O)	SLC 91 37 (E)
BF 166	SLC 12 36 (O)	SLC 13 03 (O)	SLC 13 27 (O)	SLC 92 72 (O)
BN 415	CP 70310	SLC 13 09 (O)	SLC 13 31 (O)	SLT 4820
Co 1157	CP 70360	SLC 13 11 (O)	SLC 13 32 (O)	SLT 4825
Co 1287	CP 70383	Hina hina	SLC 13 40 (O)	SP 302
Co 290	CP 75308	Karanga	SLC 13 63 (O)	SP 853877
Co 421	CP 77414	Kodayana	LF 765287	SP 901638
Co 6415	CPSG 104	Korpi	LF 765300	SL 71 77
Co 896	Gampaha	LF 51753	LF 7696	SL 85 02
CP 701193	H 502036	LF 51887	M 186189	SL 85 06
SL 98 2118	H 681158	LF 6376	Mana	SL 86 03
SL 98 2528	H 821600	LF 701168	NSG 555	SL 86 04
SLC 12 07 (O)	SLC 12 37 (O)	LF 7126	PH 821370	SL 87 56
SLC 12 10 (O)	SLC 12 41 (O)	LF 74446	PH 861096	SL 89 2247

Table 5: Continued

SLC 12 14 (O)	SLC 12 67 (O)	SLC 13 15 (O)	SES 304 (E)	SL 89 2299
SLC 12 16 (O)	SLC 12 73 (O)	SLC 13 16 (O)	SL 63 01	SL 92 631
SLC 12 18 (O)	SLC 12 88 (O)	SLC 13 18 (O)	SLC 13 73 (O)	SL 95 4394
SLC 12 26 (O)	SLC 12 94 (O)	SLC 13 20 (O)	SLC 87 16 (O)	

E – *Erianthus* spp.; Variety name without brackets - *Saccharum* spp. hybrids; O – *Saccharum officinarum*; S – *Saccharum spontaneum*

Table 6: Accessions belong to cluster group 3

Co 1111	H 588255	N 11	SL 83 01	SLC 92 61 (E)
Co 453	H 624671	N 14	SL 85 16	SLC 92 77 (E)
Co 527	H 704646	NCO 339	SL 87 11	SP 911049
Co 740	H 781207	PH 3533	SL 87 35	LF 75 10025
Co 8720	IK 76 218 (E)	PH 85256	SL 89 1673	LF 75 10030
Co 8743	IK 76 62 (E)	PH 86108	SL 92 4918	Mindanao (E)
Co 977	IK 76 76 (E)	POJ 64	SL 93 945	
CP 701548	LF 653663	Q 101	SLC 10 08 (O)	
Fiji 56 (E)	LF 753395	RB 70151	SLC 12 46 (O)	
H 54775	N 07	SL 77 71	SLC 92 28 (O)	

E – *Erianthus* spp.; Variety name without brackets - *Saccharum* spp. hybrids; O – *Saccharum officinarum*; S – *Saccharum spontaneum*

Table 7: Accessions belong to cluster group 4

IJ 76 395 (E)	IND 8180 (E)	NG 77 159 (S)	SLC 08 144 (S)	SLC 92 90(E)
IK 76 47 (S)	IS 76 220 (S)	NG 77 162 (S)	SLC 89 04 (E)	SLC 92 95(S)
IK 76 48 (E)	IS 76 73 (S)	NG 77 54 (S)	SLC 89 30 (E)	SLC 92 97(S)
IK 76 73 (S)	LF 65 3675	NG 77 94 (E)	SLC 89 51 (S)	SLC 92 99(S)
IK 76 74 (E)	LF 73 290	NG 77 95 (E)	SLC 90 04 (S)	
IK 76 78 (E)	Mandalay (S)	SES 03 (E)	SLC 92 64 (E)	
IK 76 88 (S)	MOL 4503 (E)	SES 07 (S)	SLC 92 76 (S)	
IND 81164 (S)	NG 51 162 (S)	SES 218 (E)	SLC 92 80 (E)	

E – *Erianthus* spp.; Variety name without brackets - *Saccharum* spp. hybrids; O – *Saccharum officinarum*; S – *Saccharum spontaneum*

Cluster group 2 consisted of eighty-nine accessions (Table 5). It consisted of 55 *Saccharum* spp. hybrids, 32 locally-collected sugarcane accessions, and two wild accessions. This group had thick canes with moderate lengths but fewer stalks (Table 3). These values are not acceptable, and they produced a low cane yield. These accessions had low sugar yields when considering laboratory brix. Therefore, they are not suitable to be used as a core-parental collection for high cane and sugar yields in breeding programs.

Groups, 3 and 4 included 46 and 36 accessions, respectively (Tables 6 and 7). Accessions in group 3 consisted of 37 *Saccharum* spp. hybrids, 6 *Erianthus* spp., and 3 locally-collected sugarcane accessions. This group had moderately thick but a higher number of lengthy canes (Table 3), the characteristics that are useful in obtaining a high cane yield (Wijesuriya et al., 1997). The varieties in this group had a moderate sugar content. The fibre content was higher in group 3. Therefore, accessions in this group can be utilized in the core-parental collection to be developed for use in breeding programs for high cane yield and moderate sugar yield with high fibre content. Moreover, sugarcane varieties with high fibre content are required for the co-generation of electricity (van der Poel et al., 1998), a specific area of study that sugarcane breeders should be encouraged to pursue. Hence, these 46 accessions can be included in the crosses directed for *e*-cane production. Selection of parental clones directed for simultaneous improvement of cane yield and sugar content should be performed, and these parental clones need to be crossed with the clones in the parental core collection with moderate fibre content. Therefore, varieties in this group can be used as a core-parental collection for breeding for high cane and sugar yields with moderate/high fibre content through inter-group crosses with varieties in group 1.

Out of the 36 accessions included in group 4, 34 are wild types (*S. spontaneum* and *Erianthus* spp.), and only 2 varieties; LF 65 3675 and LF 73 290, were *Saccharum* spp. hybrids imported from Fiji. This group consisted of thinner canes, which are shorter in length yet have a high number of stalks per plot. Thinner canes with a short length, but a higher number of stalks per plot also resulted in a low cane yield. These accessions had low brix and POCS values (Table 3) and a very high fiber content (about 24%). The accessions of *Erianthus* spp.; Fiji 56 and SLC 92 61 in group 3 and *S. spontaneum* accession IK 76 88 in group 4 had high cane yields with high fibre contents. Therefore, these accessions can be used for "nobilization" and not as parents in inter-varietal crosses for breeding for high cane yields.

CONCLUSIONS

The principal components: PC1, PC2, and PC3 described sugar yield, cane yield, and cane yield and fibre content, respectively. Of the four clusters, cluster group 1 consisted of 337 varieties, including all the recommended sugarcane varieties for commercial cultivation in Sri Lanka. The accessions in this group can be included in the parental core-collection to produce progenies with moderate cane yields and high sugar yields with moderate fibre content. The accessions in cluster group 2 are not suitable to be used as a core-parental collection. The accessions in cluster group 3 can be incorporated into the parental core collection for breeding for *e*-canes or energy canes. The wild accessions: Fiji 56, SLC 92 61, and IK 76 88 can be used for "nobilization". The accessions SLC 91 46 and S 2003-US-247 were identified for simultaneous improvement of cane and sugar yields with moderate fibre content, and the accession SLC 12 21 as an *e*-cane.

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