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Research Article

Constructing and comparing selection indices for early growth traits in *Saccharum spontaneum*

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Abstract
Saccharum spontaneum is the major donor of important traits like vigour, hardiness and ratooning potential to modern sugarcane cultivars. Identifying S. *spontaneum* clones with high early vigour and tillering ability is essential to include them in hybridization program. Forty three *Saccharum spontaneum* accessions were evaluated for number of tillers per clump, stalk length, stalk diameter, number of leaves on the main stem, leaf length and leaf lamina width at 90 days after planting. Variance components for these traits indicated high heritability coupled with genetic advance for leaf width and stalk length indicating the preponderance of additive gene action for these traits. The comprehensive index C_i value, Smith-Hazel's selection index (SHI) and rank sums of all the traits indicated six clones *viz*., IND 99-848, IND 99-881, IND 99-849, IND 99-850, IND 99-984 and IND 99-847 were superior clones and can be utilised in pre breeding programmes as potential donors in identification of bioenergy canes. Among the methods studied, DTOPSIS was comparatively effective in selecting the genotypes.

Keywords: Comprehensive index, *Saccharum spontaneum*, early vigour, Rank sums, Smith Hazel selection index.

INTRODUCTION

Saccharum spontaneum constituting the primary gene pool of sugarcane have contributed largely to sugarcane varietal improvement. The first interspecific hybrid variety of sugarcane, Co 205 was derived from the cross between *S. officinarum* clone Vellai and *S. spontaneum* clone Coimbatore local and lead to the stabilization of sugarcane agriculture worldwide. Modern sugarcane cultivars are complex aneupolyploids derived mainly from the crosses involving *S. officinarum* and *S. spontaneum*. *S. spontaneum* imparted genes for vigour, ratooning ability, resistance to pests and diseases and adaptability for growth under different stress conditions in modern sugarcane varieties (Manjunatha *et al.,* 2018). It is widely distributed in India, from the sub-Himalayan regions to the peninsular region and around 30 cytotypes are reported from Indian subcontinent. Its chromosome number varies from 2n= 40 to 128 (Sreenivasan *et al.,* 1987). Considering its importance in sugarcane improvement programs, explorations for *S. spontaneum* in India was started in the year 1933 (Amalraj and Balasundaram, 2006). At present a total of 1451 *S. spontaneum* accessions collected from different geographical regions of India and from different countries are conserved at the field gene bank of ICAR-Sugarcane Breeding Institute, Coimbatore. Extensive morphological variations in the *S. spontaneum* collection were reported by many sugarcane breeders (Kandasami *et al.,* 1983; Rao and Vijayalakshmi 1963; Sreenivasan *et al.,* 2001; Govindaraj *et al.,* 2014).

Even though large numbers of *S. spontaneum* accessions are available only a few have actually been exploited to develop new cultivars. To safeguard from the genetic vulnerability and to cope with the adverse effects of climate change, efforts need to be taken to broaden the genetic base of cultivated sugarcane. Hence, identification of diverse germplasm resources and utilization of these genotypes in the varietal development programs are required in the present situation.

A superior genotype can be identified only through the evaluation of multiple parameters. Dynamic Technique for Order Preference by Similarity to Ideal Solution (DTOPSIS) is used to compare the quality of various varieties based on multiple traits. In this method a comprehensive index (C_i) is calculated based on the traits studied and higher the C_i, the genotype is more close to the ideal. This technique helps to identify the elite genotypes through a comprehensive multi trait analysis. DTOPSIS method was developed by Yao *et al.* (1994) and it was first used to evaluate the regional economic developments. Plant researchers have used DTOPSIS method to evaluate varieties in many crops like tomato (Shen and Dai, 2005), rice (Yan *et al.,* 2008), tobacco (Li *et al.,* 2012) etc. Many sugarcane breeders have used this method (Zhao *et al.,* 2007; Zhao *et al.,* 2008; Ma *et al.,* 2013; Yang *et al.,* 2014; Yu *et al.,* 2013) and proved its efficiency in selection of genotypes.

Selection for an index which gives proper weight to each trait is more efficient than selection for a single trait or for several traits independently (Smith, 1936). Smith Hazel selection index is one of the best known indices in crop plants (Venmuhil *et al.,* 2020) as they consider heritability, genotypic correlations and phenotypic correlations into account In the present study, 43 *S. spontaneum* clones were evaluated using DTOPSIS, rank sums (RS) and Smith Hazel index (SHI) methods to identify the best method and superior clones among them for traits governing early vigour and biomass.

MATERIALS AND METHODS

A set of 43 accessions of *S. spontaneum* were planted in the month of March 2017 in randomised complete block design with two replications at ICAR-Sugarcane Breeding Institute, Coimbatore. Each clone was planted in single row of 6 m length and spacing of 1.2 m between rows. A few of these are exotic clones and majority were collected from different states of India including Kerala, Tamil Nadu, Andhra Pradesh, Telangana, Rajasthan and Karnataka. The data on six traits *viz.,* number of tillers per clump, stalk length (cm), stalk diameter (mm), number of leaves on the main stem, leaf length (cm) and leaf lamina width (cm) were recorded in these accessions at 90 days after planting. Data was recorded in three clumps per replication and arithmetic mean was calculated over the replications. The clones were subjected to individual trait wise Analysis of Variance (ANOVA) and Multivariate Analysis of Variance (MANOVA) (Bray and Maxwell, 1985) for all traits at a time. These analyses were performed in R-studio. Estimates of variability such as Phenotypic coefficient of variation (PCV), Genotypic coefficient of variation (GCV), heritability (h^2), Genetic advance (GA), genetic advance as per cent of mean (GAM) were estimated from OP stat online (Sheoran *et al.,* 1998). The mean values of these traits were used to calculate Comprehensive index value (C_i) through DTOPSIS method as described by Yao *et al.* (1994). Ranks of clones for individual trait were calculated; their sums were taken and ranked to obtain rank sums (RS) for the individual clone over all traits. The best clones are those having lowest rank sums. The calculations of C_i and RS were performed in Microsoft Excel 2013. In DTOPSIS method, traits are classified into positive, neutral and negative depending on the breeding objective. High values are preferred for positive, neutral values for neutral and lower values for negative parameters. In this study, all the traits studied were considered as positive. No neutral and negative parameters were considered in this study. As units of the traits are different, C_i can be calculated only if these values are transformed. The Y_{ij} (mean value of i^{th} clone for j^{th} trait) was transformed to Z_{ij}, which ranges between 0 and 1. Here *i* refers to number of accessions i=1, 2, ….43 and *j* to number of traits *j*=1,2,…6. The positive parameters were transformed by dividing the mean value as numerator with maximum value of that trait. Based on Z_{ij}, a decision matrix R_{ij} is calculated by multiplying Z_{ij} with respective weights W_{ij} given for individual traits according to our breeding objectives. Weightage should be given such that sum of them should be equal to 1. In the present study, weights coefficients of 0.25, 0.25, 0.15, 0.15, 0.1 and 0.1 were given to tiller number per clump, stalk length, stalk diameter, number of leaves on main stem, leaf length and leaf lamina width respectively. From R_{ij} matrix, maximum values for all traits were taken as X^+_j and minimum value is taken as X^-_j. The Euclidean distance of each R_{ij} from corresponding X^+_j and X^-_j is calculated and these are referred to as distance from ideal solution (S^+_i) and distance from negative ideal solution (S^-_i) respectively. Then the comprehensive index *Ci* is calculated as $S^-_i/(S^-_i + S^+_i)$. The value of C_i also ranged between 0 and 1. The higher the value of index, the closer the clone is to ideal solution.

Smith Hazel index was constructed by assigning weights to different traits on the basis of the weighing coefficient (b_i) values. Smith (1936) defined genetic worth of an individual as

$$H = a_1\ G_1 + a_2\ G_2 + \cdots \ldots\ldots\ldots. + a_n\ G_n$$

Where G_1, G_2,…..G_n are the genotypic values of individual characters and a_1, a_2,…..a_n signify their relative economic importance. Another function (I), based on phenotypic performance of various characters, is defined as

$$I = b_1\ p_1 + b_2\ p_2 + \cdots \ldots\ldots\ldots. + b_n\ p_n$$

Smith Hazel index was constructed by assigning weights to different traits on the basis of the index coefficient (b_i) values. These b_is are calculated such that correlations between H and I are maximized. The index coefficients were calculated as

$$B = V_p^{-1}.V_g.a$$

Where, B is the vector of b_is, Vp is the phenotypic variance covariance matrix, Vg is genotypic variance covariance matrix, a is the vector of relative economic values. SHIs of clones were calculated in R studio (R core development team, 2020). Estimates of Spearman's rank correlation coefficient among Ci, RS and SHI were also calculated and their significance was tested in R-studio.

RESULTS AND DISCUSSION

Broadening the genetic base is one of the main objectives in sugarcane improvement programmes. Large collection of genetic resources including the different species in *Saccharum* genera and related genera like *Erianthus*, *Narenga*, *Mischanthus* and *Sclerostachya* are available in sugarcane. Being a crop where wide hybridisation lead to the revolution in the crop production, evaluation and utilization of genetic resources is a key factor in the breeding programmes. In this study we evaluated a set of 43 *S. spontaneum* clones for six quantitative traits in their early stages of growth using DTOPSIS, rank sums (RS) and Smith Hazel index (SHI) methods were used to identify the superior clones among them. Analysis of variance for individual trait showed significant differences among the clones at 1% level of significance (data not included). Multivariate analysis of variance (MANOVA) of these traits also indicated significant difference at 1% level of significance among these clones (**Table 1**). These results suggested significant differences among the clones indicating that the clones are sufficiently divergent for the traits under study. The most important yield (or biomass in this case) contributing traits like total number of tillers and stem length at 90 days ranged from 9.50 - 47.50 tillers/ plant and 31 - 120.5 cm, respectively. Among the *S. spontaneum* accessions, IND 99-848 had the highest mean values for stalk length (120.50 cm) and the number of tillers were the highest for IND 99-881 (47.50 tillers/ plant). The highest mean number of leaves on main stem (9.5) was reported in IND 99-848 and IND 99-850. IND 99-847 had the highest mean values for cane diameter (7.96 mm) and leaf length (149.25 cm), whereas highest leaf lamina width (0.8 cm) was recorded in three genotypes *viz.,* IND 02-1214, Ponape 1 and Taiwan 96. 43 (**Table 2**)

The PCV was higher than GCV for all the traits. GCV was the highest for leaf width followed by stalk length, while the lowest was recorded by stalk diameter. Almost all the traits except for tiller number, had high broad sense heritability, which ranged from 0.30 to 0.80. High heritability coupled with high genetic advance as per cent of mean (GAM) was manifested by stalk length and leaf width. Inclusion of genotypes from different geographical areas in India and two exotic clones contributed significantly to this variation. Extensive variations for morphological traits in *S. spontaneum* were reported by many researchers (Kandasamy *et al*., 1983; Govindaraj *et al*., 2014). Higher PCV than GCV indicates the role of environment in inheritance of these traits. Heritability indicates the index of transmission of traits from parent to offsprings, which is also reflects the proportion of phenotype that is accounted by genotype. Moderate to high heritability of all the traits indicates the involvement of genetic component in their expression, thereby emphasising the importance of selection in their improvement. High heritability with high GAM for stalk length and leaf width indicates involvement of additive gene action, which respond to simple selection (**Table 3**)

S. spontaneum accessions were evaluated based on six phenotypic traits using three different methods like DTOPSIS method, RS and SHI to identify the best genotypes. For evaluating these 43 clones, weight coefficients were given to each trait like 0.25, 0.25, 0.15, 0.15, 0.1 and 0.1 to tiller number, stalk length, stalk diameter, no. of leaves on main the stem, leaf lamina width and leaf length, respectively (**Table 4**). For calculating comprehensive index in DTOPSIS method and SH index in SHI method, weight coefficients are used and weightage can be assigned to each trait according to the breeding objectives. This is one of the main advantages of these two methods. High yielding commercial variety requires satisfactory stalk number, stalk diameter, and stalk length (Chang and Milligan, 1992) and hence these traits were given prime importance in this study. In addition, leaf characters like number of leaves on the main stem, leaf length and lamina width were also considered but with relatively less importance. Stalk number is the most important component of cane yield (James, 1971; Milligan *et al.,* 1990) and stalk diameter is a reliable trait for selection at seedling stage (James and Miller, 1971; Tai and Miller, 1989) and it is also important for manual harvesting practiced by farmers in some sugarcane growing regions (Zhao *et al.,* 2014). These are the traits that can contribute immensely to cane yield at harvest. Therefore, the decision matrix for six traits *viz.*,number of tillers per clump, stalk length (cm), stalk diameter (mm), number of leaves on the main stem, leaf length (cm) and leaf lamina width (cm) was obtained by multiplying the transformed values with weights and are presented in **Table 5**.

In DTOPSIS method, superior clones can be selected by considering multiple traits at a time and it is possible to give weightage to each trait according to the breeding objectives. This is one of the main advantages for a plant breeder because this will help the breeder to do a preliminary screening of large germplasm collections

Table 1. Multivariate analysis of variance for 43 Saccharum spontaneum accessions

Source of variation	DF	F approx.	p-value
Clone	42	2.44	<0.01
Replication	1	0.770	0.64
Residuals	42		

Table 2. The mean values (Y_{ij}), and the ideal family for different traits of Saccharum spontaneum accessions

S.No.	Clone	Number of tillers	Stalk length (cm)	Stalk diameter (cm)	Leaves on main stem	Lamina width (cm)	Leaf length (cm)
1	IND 08 - 1491	30.00	66.50	3.91	6.00	0.50	113.50
2	IND 08 - 1492	25.50	44.00	4.03	5.00	0.45	76.25
3	IND 08 - 1500	32.00	79.00	4.14	5.00	0.45	119.25
4	IND 99 - 847	26.00	100.50	7.96	9.00	0.45	149.25
5	IND 99 - 848	41.00	120.50	4.24	9.50	0.40	73.50
6	IND 99 - 849	31.50	112.50	6.90	8.50	0.50	134.75
7	IND 99 - 850	33.00	107.50	6.16	9.50	0.35	139.25
8	IND 99 - 851	45.00	44.00	5.52	5.00	0.50	117.75
9	IND 99 - 853	16.00	64.00	5.87	6.00	0.60	85.25
10	IND 99 - 861	27.50	51.00	5.29	6.00	0.30	102.75
11	IND 99 - 862	30.50	52.00	6.65	4.50	0.35	105.50
12	IND 99 - 863	26.50	52.00	5.91	4.00	0.20	125.00
13	IND 99 - 864	35.00	51.00	6.48	5.00	0.55	109.00
14	IND 99 - 879	30.00	65.50	6.05	5.00	0.40	105.75
15	IND 99 - 881	47.50	82.00	7.65	7.50	0.55	84.75
16	IND 99 - 882	34.00	60.00	6.16	5.50	0.60	122.25
17	IND 99 - 917	33.00	53.00	7.71	5.00	0.55	94.50
18	IND 99 - 918	25.00	45.50	6.91	6.00	0.40	93.75
19	IND 99 - 982	31.00	78.00	7.57	6.00	0.40	142.25
20	IND 99 - 983	40.00	68.00	7.11	5.50	0.15	142.50
21	IND 99 - 984	36.00	88.00	7.41	7.00	0.50	139.00
22	IND 02- 1166	13.50	66.00	6.10	5.00	0.45	112.00
23	IND 02- 1176	15.00	43.00	4.36	4.00	0.15	93.50
24	IND 02- 1186	21.50	42.00	7.22	2.50	0.06	123.75
25	IND 02- 1192	26.50	73.50	5.51	5.00	0.10	118.75
26	IND 02- 1194	32.50	64.00	6.83	5.50	0.50	87.00
27	IND 02- 1214	38.00	38.50	6.12	6.00	0.80	106.00
28	IND 03- 1220	20.00	33.00	5.58	4.50	0.50	93.25
29	IND 03- 1221	40.00	48.00	7.15	5.50	0.40	109.75
30	IND 03- 1224	27.00	54.00	5.51	6.00	0.15	105.75
31	IND 03- 1226	20.00	56.50	5.05	5.00	0.10	107.25
32	IND 03- 1227	27.00	59.50	5.12	5.50	0.12	98.75
33	IND 03- 1232	13.50	58.00	5.08	5.00	0.45	88.00
34	IND 03- 1247	13.00	33.00	6.43	3.50	0.50	89.75
35	IND 03- 1249	24.00	32.00	5.18	4.00	0.35	94.75
36	IND 03- 1250	26.00	31.00	5.37	3.00	0.30	102.75
37	IND 03 - 1299	9.50	48.00	6.00	3.50	0.40	97.50
38	IND 03 - 1301	25.50	33.00	5.16	4.50	0.40	90.25
39	SES 121A	11.50	34.50	6.97	4.00	0.55	100.00
40	SES 515/7	19.00	36.00	6.37	4.00	0.65	89.25
41	Ponape 1	29.50	63.70	6.02	8.40	0.80	93.40
42	Pampa	15.00	57.50	5.45	7.00	0.55	90.00
43	Taiwan 96	19.00	78.00	6.72	8.00	0.80	101.50
	SEm	1.21	4.31	0.13	0.20	0.03	2.11
	Ideal family	47.50	120.50	7.96	9.50	0.80	149.25

Table 3. Variability parameters of 43 *Saccharum spontaneum* accessions for early vigour traits

Trait	MSS	Mean	Range	PCV (%)	GCV (%)	Heritability (%)	GA	GAM (%)
Tiller number	170.46*	27.03	9.50 - 47.50	42.47	23.26	30.28	7.07	26.23
Stalk length (cm)	976.50*	59.70	31.00 - 120.50	40.14	33.60	70.54	34.60	57.95
Stalk diameter (cm)	2.21**	6.02	3.91 -7.96	19.82	14.85	56.84	1.38	22.94
Leaves on main stem	5.79**	5.58	2.50 - 9.50	34.09	26.26	59.71	2.33	41.66
Leaf width (cm)	0.07**	0.42	0.06 - 0.80	48.11	38.11	63.94	0.26	62.19
Leaf length (cm)	700.57**	106.25	73.50 - 149.25	18.59	16.59	80.06	32.41	30.50

Table 4. The standardized transformed values (Z_{ij}) of different traits of *Saccharum spontaneum* accessions and the weight coefficient (W_j)

S.No.	Clone	Number of tillers	Stalk length	Stalk diameter	Leaves on main stem	Lamina width	Leaf length
1	IND 08 - 1491	0.6316	0.5519	0.4906	0.6316	0.6250	0.7605
2	IND 08 - 1492	0.5368	0.3651	0.5063	0.5263	0.5625	0.5109
3	IND 08 - 1500	0.6737	0.6556	0.5195	0.5263	0.5625	0.7990
4	IND 99 - 847	0.5474	0.8340	1.0000	0.9474	0.5625	1.0000
5	IND 99 - 848	0.8632	1.0000	0.5320	1.0000	0.5000	0.4925
6	IND 99 - 849	0.6632	0.9336	0.8662	0.8947	0.6250	0.9028
7	IND 99 - 850	0.6947	0.8921	0.7732	1.0000	0.4375	0.9330
8	IND 99 - 851	0.9474	0.3651	0.6928	0.5263	0.6250	0.7889
9	IND 99 - 853	0.3368	0.5311	0.7368	0.6316	0.7500	0.5712
10	IND 99 - 861	0.5789	0.4232	0.6646	0.6316	0.3750	0.6884
11	IND 99 - 862	0.6421	0.4315	0.8354	0.4737	0.4375	0.7069
12	IND 99 - 863	0.5579	0.4315	0.7418	0.4211	0.2500	0.8375
13	IND 99 - 864	0.7368	0.4232	0.8134	0.5263	0.6875	0.7303
14	IND 99 - 879	0.6316	0.5436	0.7601	0.5263	0.5000	0.7085
15	IND 99 - 881	1.0000	0.6805	0.9611	0.7895	0.6875	0.5678
16	IND 99 - 882	0.7158	0.4979	0.7739	0.5789	0.7500	0.8191
17	IND 99 - 917	0.6947	0.4398	0.9680	0.5263	0.6875	0.6332
18	IND 99 - 918	0.5263	0.3776	0.8675	0.6316	0.5000	0.6281
19	IND 99 - 982	0.6526	0.6473	0.9510	0.6316	0.5000	0.9531
20	IND 99 - 983	0.8421	0.5643	0.8932	0.5789	0.1875	0.9548
21	IND 99 - 984	0.7579	0.7303	0.9309	0.7368	0.6250	0.9313
22	IND 02- 1166	0.2842	0.5477	0.7657	0.5263	0.5625	0.7504
23	IND 02- 1176	0.3158	0.3568	0.5477	0.4211	0.1875	0.6265
24	IND 02- 1186	0.4526	0.3485	0.9070	0.2632	0.0750	0.8291
25	IND 02- 1192	0.5579	0.6100	0.6916	0.5263	0.1250	0.7956
26	IND 02- 1194	0.6842	0.5311	0.8580	0.5789	0.6250	0.5829
27	IND 02- 1214	0.8000	0.3195	0.7682	0.6316	1.0000	0.7102
28	IND 03- 1220	0.4211	0.2739	0.7004	0.4737	0.6250	0.6248
29	IND 03- 1221	0.8421	0.3983	0.8982	0.5789	0.5000	0.7353
30	IND 03- 1224	0.5684	0.4481	0.6922	0.6316	0.1875	0.7085
31	IND 03- 1226	0.4211	0.4689	0.6344	0.5263	0.1250	0.7186
32	IND 03- 1227	0.5684	0.4938	0.6426	0.5789	0.1500	0.6616
33	IND 03- 1232	0.2842	0.4813	0.6376	0.5263	0.5625	0.5896
34	IND 03- 1247	0.2737	0.2739	0.8078	0.3684	0.6250	0.6013
35	IND 03- 1249	0.5053	0.2656	0.6501	0.4211	0.4375	0.6348
36	IND 03- 1250	0.5474	0.2573	0.6740	0.3158	0.3750	0.6884
37	IND 03 - 1299	0.2000	0.3983	0.7531	0.3684	0.5000	0.6533
38	IND 03 - 1301	0.5368	0.2739	0.6482	0.4737	0.5000	0.6047
39	SES 121A	0.2421	0.2863	0.8756	0.4211	0.6875	0.6700
40	SES 515/7	0.4000	0.2988	0.7996	0.4211	0.8125	0.5980
41	Ponape 1	0.6211	0.5286	0.7557	0.8842	1.0000	0.6258
42	Pampa	0.3158	0.4772	0.6847	0.7368	0.6875	0.6030
43	Taiwan 96	0.4000	0.6473	0.8442	0.8421	1.0000	0.6801
	Weight	0.2500	0.2500	0.1500	0.1500	0.1000	0.1000

within a short period of time. DTOPSIS method is a sorting method approximate to the ideal solution, which quantifies integrated traits of varieties (or clones) into relative approach degree, C_i to ideal solution and comprehensively evaluates crop varieties by comparing the relative approach degree C_i, thereby avoiding the defects in other analysis where main emphasize is on the yield but neglecting other important traits and achieving more scientific and reasonable analysis results with uniform evaluation method (Wu *et al*., 2013). The principal purpose of DTOPSIS is to determine how close the evaluated subject (e.g. an accession) is to the ideal solution (Yao *et al.,* 1994). The ideal solution is defined as comprehensive set having best values for all the traits in the population evaluated. As all the traits under consideration are positive or desirable traits, the ideal solution would be maximum value of the traits and *vice versa* for negative ideal solution. The C_i calculated by this

Table 5. The decision matrix (R_{ij}) for six traits of 43 *Saccharum spontaneum* accessions

S.No.	Clone	Number of tillers	Stalk length	Stalk diameter	Leaves on main stem	Lamina width	Leaf length (cm)
1	IND 08 - 1491	0.1579	0.1380	0.0736	0.0947	0.0625	0.0760
2	IND 08 - 1492	0.1342	0.0913	0.0759	0.0789	0.0563	0.0511
3	IND 08 - 1500	0.1684	0.1639	0.0779	0.0789	0.0563	0.0799
4	IND 99 - 847	0.1368	0.2085	0.1500	0.1421	0.0563	0.1000
5	IND 99 - 848	0.2158	0.2500	0.0798	0.1500	0.0500	0.0492
6	IND 99 - 849	0.1658	0.2334	0.1299	0.1342	0.0625	0.0903
7	IND 99 - 850	0.1737	0.2230	0.1160	0.1500	0.0438	0.0933
8	IND 99 - 851	0.2368	0.0913	0.1039	0.0789	0.0625	0.0789
9	IND 99 - 853	0.0842	0.1328	0.1105	0.0947	0.0750	0.0571
10	IND 99 - 861	0.1447	0.1058	0.0997	0.0947	0.0375	0.0688
11	IND 99 - 862	0.1605	0.1079	0.1253	0.0711	0.0438	0.0707
12	IND 99 - 863	0.1395	0.1079	0.1113	0.0632	0.0250	0.0838
13	IND 99 - 864	0.1842	0.1058	0.1220	0.0789	0.0688	0.0730
14	IND 99 - 879	0.1579	0.1359	0.1140	0.0789	0.0500	0.0709
15	IND 99 - 881	0.2500	0.1701	0.1442	0.1184	0.0688	0.0568
16	IND 99 - 882	0.1789	0.1245	0.1161	0.0868	0.0750	0.0819
17	IND 99 - 917	0.1737	0.1100	0.1452	0.0789	0.0688	0.0633
18	IND 99 - 918	0.1316	0.0944	0.1301	0.0947	0.0500	0.0628
19	IND 99 - 982	0.1632	0.1618	0.1427	0.0947	0.0500	0.0953
20	IND 99 - 983	0.2105	0.1411	0.1340	0.0868	0.0188	0.0955
21	IND 99 - 984	0.1895	0.1826	0.1396	0.1105	0.0625	0.0931
22	IND 02- 1166	0.0711	0.1369	0.1149	0.0789	0.0563	0.0750
23	IND 02- 1176	0.0789	0.0892	0.0822	0.0632	0.0188	0.0626
24	IND 02- 1186	0.1132	0.0871	0.1361	0.0395	0.0075	0.0829
25	IND 02- 1192	0.1395	0.1525	0.1037	0.0789	0.0125	0.0796
26	IND 02- 1194	0.1711	0.1328	0.1287	0.0868	0.0625	0.0583
27	IND 02- 1214	0.2000	0.0799	0.1152	0.0947	0.1000	0.0710
28	IND 03- 1220	0.1053	0.0685	0.1051	0.0711	0.0625	0.0625
29	IND 03- 1221	0.2105	0.0996	0.1347	0.0868	0.0500	0.0735
30	IND 03- 1224	0.1421	0.1120	0.1038	0.0947	0.0188	0.0709
31	IND 03- 1226	0.1053	0.1172	0.0952	0.0789	0.0125	0.0719
32	IND 03- 1227	0.1421	0.1234	0.0964	0.0868	0.0150	0.0662
33	IND 03- 1232	0.0711	0.1203	0.0956	0.0789	0.0563	0.0590
34	IND 03- 1247	0.0684	0.0685	0.1212	0.0553	0.0625	0.0601
35	IND 03- 1249	0.1263	0.0664	0.0975	0.0632	0.0438	0.0635
36	IND 03- 1250	0.1368	0.0643	0.1011	0.0474	0.0375	0.0688
37	IND 03 - 1299	0.0500	0.0996	0.1130	0.0553	0.0500	0.0653
38	IND 03 - 1301	0.1342	0.0685	0.0972	0.0711	0.0500	0.0605
39	SES 121A	0.0605	0.0716	0.1313	0.0632	0.0688	0.0670
40	SES 515/7	0.1000	0.0747	0.1199	0.0632	0.0813	0.0598
41	Ponape 1	0.1553	0.1322	0.1133	0.1326	0.1000	0.0626
42	Pampa	0.0789	0.1193	0.1027	0.1105	0.0688	0.0603
43	Taiwan 96	0.1000	0.1618	0.1266	0.1263	0.1000	0.0680

method indicated that six clones had C_i value greater than 0.6, with IND 99-848 topping the list followed by IND 99-881, IND 99-849, IND 99-850, IND 99-984 and IND 99-847 (**Table 5)**. The *Ci* values ranged from 0.15 to 0.72, indicating how close each clone is to the ideal solution (**Fig. 1**). In this method, while selecting the genotypes prime importance was given to those traits which were given more weightage. Here the genotypes in the top positions are with highest number of tillers/plant and stalk length.

Ranks of the clones for individual traits were calculated and ranks of their overall rank sum (RS) were obtained. The clones IND 99-984 had lowest RS followed by IND 99-849, IND 99-847, IND 99-881 and IND 99-850 (**Table 6**). The traits with different measurement units are not amenable for pooling to evaluate overall worth of the clone based on all the traits, therefore ranks of clones for individual trait were calculated and their overall rank sums (RS) were estimated. In this method all the six traits were considered equally for calculating the rank sum. So there was a chance to miss genotypes having high values for economically important traits. For instance, the accession IND 99-848 having third highest value (41 number/ plant) for tiller number and highest value for stalk length (120.5 cm) but its stalk diameter and leaf length are comparatively less and it ranked 17th in RS method. This disadvantage can be rectified in DTOPSIS and SHI method by assigning economic weights to each trait according to our breeding objectives.

Smith and Hazel selection index (SHI) was calculated for clones and these values ranged from 44.29 to 19.49 with a mean of 28.67 (**Table 6**). The economic coefficients were the same as given in DTOPSIS method. The bi values obtained were 0.049 for Tiller number, 0.195 for stalk length, -0.88 for stalk diameter, 0.232 for leaves on the main stem, 4.487 for lamina width and 0.167 for leaf length. The clone IND 99-850 had highest SHI value followed by IND 99-849, IND 99-847, IND 99-984, IND 99-848, IND 99-982. In SHI method the discriminant function is applied to differentiate the desirable genotypes from the undesirable ones based on the phenotypic performance of several traits. The discriminant function is developed based on the phenotypic performance of each trait and the economic weights assigned to it. The multiple regression (b_i) values are calculated by maximizing the genotypic and phenotypic covariance of each traits

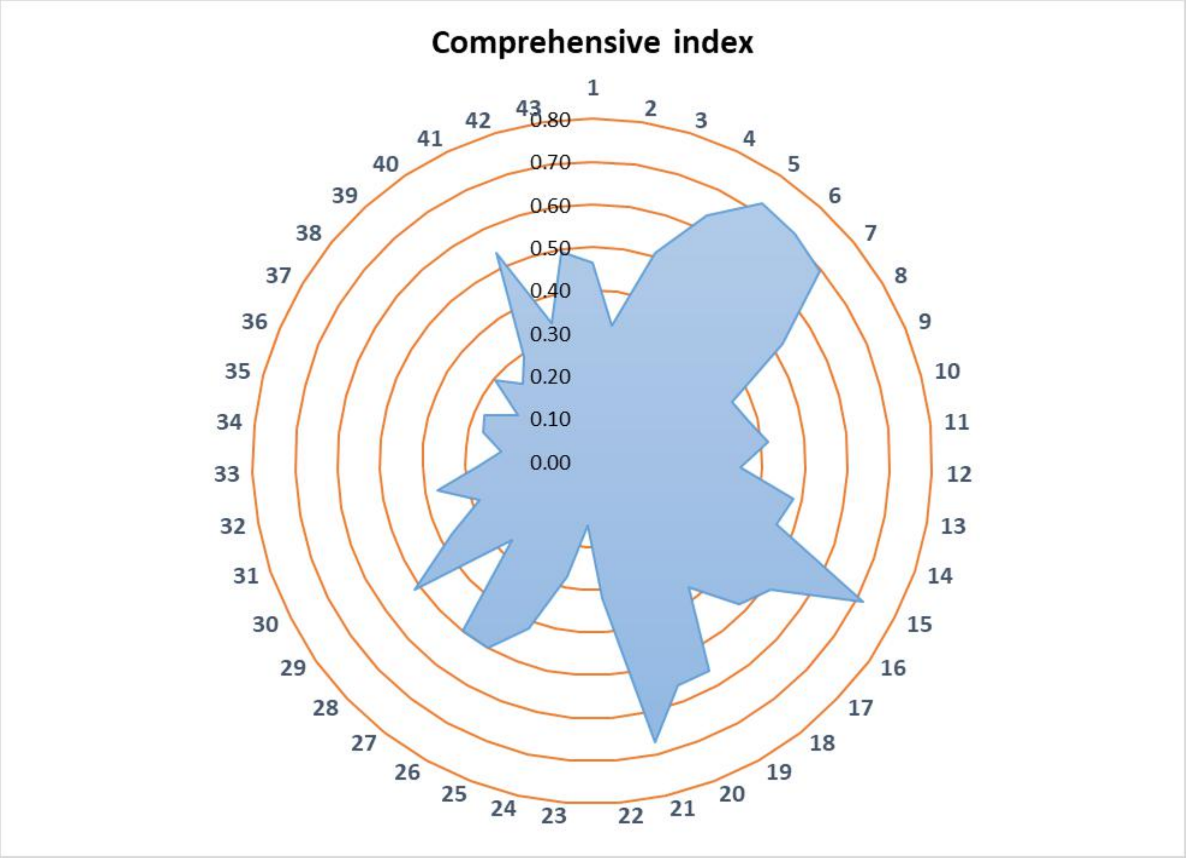

Fig. 1. Graph showing C_i values of 43 *Saccharum spontaneum* accessions evaluated for six quantitative traits

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Table 6. The positive Euclidean distance (S^{+}_{j}), negative Euclidean distance (S^{-}_{j}), and comprehensive index (C_i), rank sums and SHI values for each accession and checks

S.No.	Clone	S+j	S−j	Ci	Rank of Ci	Rank sum (RS)	SHI
1	IND 08 - 1491	0.1786	0.1545	0.4637	19	16	33.67
2	IND 08 - 1492	0.2312	0.1085	0.3193	31	39	22.25
3	IND 08 - 1500	0.1632	0.1698	0.5099	13	19	36.51
4	IND 99 - 847	0.1285	0.2228	0.6343	6	3	43.00
5	IND 99 - 848	0.1057	0.2757	0.7229	1	17	38.16
6	IND 99 - 849	0.0976	0.2426	0.7132	3	2	44.24
7	IND 99 - 850	0.1045	0.2403	0.6970	4	5	44.30
8	IND 99 - 851	0.1854	0.2050	0.5250	10	18	29.07
9	IND 99 - 853	0.2198	0.1220	0.3570	27	22	26.48
10	IND 99 - 861	0.2058	0.1254	0.3786	23	28	26.60
11	IND 99 - 862	0.1977	0.1399	0.4144	22	24	26.08
12	IND 99 - 863	0.2176	0.1157	0.3471	28	29	29.01
13	IND 99 - 864	0.1807	0.1672	0.4806	17	13	27.86
14	IND 99 - 879	0.1766	0.1491	0.4577	20	20	29.60
15	IND 99 - 881	0.1013	0.2573	0.7176	2	4	30.03
16	IND 99 - 882	0.1640	0.1730	0.5133	12	7	32.40
17	IND 99 - 917	0.1812	0.1674	0.4802	18	12	24.64
18	IND 99 - 918	0.2135	0.1257	0.3706	26	23	22.92
19	IND 99 - 982	0.1447	0.1846	0.5605	8	6	37.10
20	IND 99 - 983	0.1559	0.1995	0.5615	7	8	34.79
21	IND 99 - 984	0.1064	0.2186	0.6726	5	1	39.58
22	IND 02- 1166	0.2316	0.1096	0.3213	30	21	30.12
23	IND 02- 1176	0.2743	0.0490	0.1515	43	43	22.55
24	IND 02- 1186	0.2579	0.0977	0.2748	36	32	24.46
25	IND 02- 1192	0.1923	0.1385	0.4187	21	26	32.30
26	IND 02- 1194	0.1660	0.1665	0.5008	14	15	26.18
27	IND 02- 1214	0.1912	0.1912	0.5001	15	10	26.73
28	IND 03- 1220	0.2549	0.0909	0.2628	39	35	21.41
29	IND 03- 1221	0.1778	0.1881	0.5141	11	13	26.49
30	IND 03- 1224	0.2081	0.1238	0.3730	24	27	26.79
31	IND 03- 1226	0.2347	0.0917	0.2810	34	34	27.14
32	IND 03- 1227	0.2071	0.1228	0.3723	25	31	26.80
33	IND 03- 1232	0.2458	0.0900	0.2679	37	36	25.44
34	IND 03- 1247	0.2806	0.0775	0.2165	41	37	19.50
35	IND 03- 1249	0.2526	0.0921	0.2672	38	42	21.23
36	IND 03- 1250	0.2551	0.0982	0.2780	35	41	21.85
37	IND 03 - 1299	0.2769	0.0715	0.2052	42	38	23.49
38	IND 03 - 1301	0.2438	0.1029	0.2969	32	40	21.10
39	SES 121A	0.2787	0.0902	0.2444	40	30	21.30
40	SES 515/7	0.2523	0.1042	0.2924	33	33	21.14
41	Ponape 1	0.1610	0.1862	0.5364	9	11	29.74
42	Pampa	0.2295	0.1168	0.3371	29	25	26.33
43	Taiwan 96	0.1800	0.1768	0.4956	16	9	32.70

Table 7. Spearman’s rank correlation coefficient among the three indices

Indices	Ci	RS	SHI
Ci	1		
RS	0.91**	1	
SHI	0.82**	0.80**	1

and using the economic weights assigned. Based on these b_i values the SHI index was calculated for each genotype. The b_i value depends on genetic variability of each trait, correlation between genotype and phenotypic performance for each trait and genotypic correlations between each pair of traits (Hazel, 1943). Here the stalk diameter had the lowest b_i value (-0.88) because of its lowest genetic coefficient of variation (14.85) compared to all other traits, similarly the leaf lamina width had highest value for b_i (4.48) and this trait had the highest genotypic coefficient of variation (38.11). In SHI method more weightage is given to those traits which are having more genetic variability and thus high genetic advance. The genotype IND 99-881 with highest number of tillers (47.5/ plant) had a SHI value of 30.02 and it was in 14th rank. This may be due to its highest number of tillers and stalk diameter (7.65 mm), the traits with lowest b_i values, and comparatively low stalk length value (82 cm). Even though SHI method is based on the genetic variability and the selection of genotypes is reliable there is a chance to miss rare genotypes which are extremely good in one or two economically important traits.

Pairwise spearman's rank correlations were estimated among C_i, RS and SHI and found significant (p=0.01) positive correlations of 0.91, 0.82 and 0.80 between Ci and RS, Ci and SHI and RS and SHI respectively (**Table 7**). Ranking order of clones based on RS, C_i and SHI are almost the same as evident by highly significant Spearman's rank correlations among them. But for a preliminary evaluation of large number of germplasm according to the breeding objective, DTOPSIS method seems to be the best because it selected the genotypes based on the economic weight assigned and did not lose the genotypes which are good according to our breeding objectives.

Alexander (1985) indicated that the vigour of early generation interspecific hybrids involving *S. spontaneum* could be exploited to develop high biomass canes. In recent years, *S. spontaneum* is used extensively as a donor for high yield and high fibre content for the development of high biomass energy canes (Burner and Legendre, 2000). Development of bioenergy canes have criteria different from that of commercial sugarcane cultivars. In the case of energy canes, biomass yield is of utmost importance and the components that contribute to dry biomass are no. of stalk/plot, fiber per cent and dry matter per cent (Mohanraj and Nair, 2014). In the present study the traits like tiller number, stalk height, stalk diameter and number of leaves on the main stem are the traits that can contribute more to biomass of the plant. Hence the clones with higher mean values for these traits can be used for developing bioenergy canes and these include IND 99-881, IND 99-847, IND 99-848 and IND 99-984. A set of 43 accessions of *S. spontaneum* were evaluated for their early vigour traits like tiller number, stalk length, stalk diameter, number of leaves on main the stem, leaf length and leaf lamina width. Based on the DTOPSIS index, rank sums and SHIs calculated including all the traits, the clones IND 99-848, IND 99-881, IND 99-849, IND 99-850, IND 99-984 and IND 99-847 are better and can be further utilized in breeding as potential parents for developing bioenergy types as well as commercial canes.

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