Evaluating sugarcane families by the method of Dynamic Technique for Order Preference by Similarity to Ideal Solution (DTOPSIS)

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Abstract

Enlarging the quantity of seedlings of elite families and discarding inferior sugarcane (*Saccharum* spp.) families could improve sugarcane breeding and selection efficiency. The feasibility of using the method Dynamic Technique for Order Preference by Similarity to Ideal Solution (DTOPSIS) method was explored to identify superior sugarcane families. Data on 5 traits: Brix, millable stalks per stool (MS), stalk diameter (SD), plant height (PH), and percent pith were collected from two family trials having 17 families and two check cultivars at two sites including plant-cane and first-ratoon crops. The rest of the seedlings were planted into field for routine selection in the regular program. The DTOPSIS method calculates a comprehensive index (C_i) which expresses the closeness of a solution to the ideal solution and was used in this study to test the distance of each family to the ideal family. The C_i of the families was compared to the family selection rate in the regular program by determining the selection rate at Stage 1 to Stage 4 for each family in the regular program. The result indicated that the C_i values calculated from family trials were significantly (p<0.01) correlated to the selection rate at Stage 2 (*r*=0.8059), Stage3 (*r*=0.7967), and Stage 4 (*r*=0.8202), and indicating that promising clones were selected from families with higher C_i values in the family trial. Thus, it could be feasible to use DTOPSIS to determine elite sugarcane families and to eliminate inferior families and thereby, increasing the variety selection efficiency.

Key words: Dynamic Technique for Order Preference by Similarity to Ideal Solution (DTOPSIS), family selection, *Saccharum officinarum* L.

Análise de famílias de cana-de-açúcar pelo método *Dynamic Technique for Order Preference by Similarity to Ideal Solution* (DTOPSIS)

Resumo

A elevação da quantidade de mudas de alta qualidade associada ao descarte das de baixa qualidade pode aprimorar os programas de seleção e melhoramento genético da cana-de-açúcar (*Saccharum* spp.). Este trabalho avaliou a capacidade do método *Dynamic Technique for Order Preference by Similarity to Ideal Solution* (DTOPSIS) de identificar famílias da cana-de-açúcar com elevada qualidade. As características avaliadas foram: Brix, aptidão para moagem, diâmetro do caule, altura e porcentagem de tecido parenquimatoso. Os dados foram coletados em dois experimentos com 17 famílias e duas cultivares incluindo cana soca e brota. O DTOPSIS estima o índice Ci que expressa a proximidade de uma solução particular à ideal. O Ci foi utilizado para avaliar a distância de cada família à família ideal. As demais mudas foram utilizadas em um programa tradicional de seleção. Os valores de Ci de cada família foram comparados às taxas de seleção de famílias obtidas pelo programa tradicional de seleção por meio da estimação das taxas de seleção nos estágios 1 a 4. Os resultados indicaram que os valores de Ci calculados a partir dos experimentos foram significativamente correlacionados (p<0,01) às taxas de seleção do estágio 2 (*r*=0,8059), estágio 3 (*r*=0,7967) e estágio 4 (*r*=0,8202). Os resultados também indicaram que clones com promissor uso apresentam elevados valores de Ci. Conclui-se, portanto, que o método DTOPSIS é apropriado para selecionar e descartar mudas de alta e baixa qualidade, respectivamente, podendo elevar a eficiência dos programas de seleção.

Palavras-chave: Dynamic Technique for Order Preference by Similarity to Ideal Solution (DTOPSIS), seleção de famílias, *Saccharum officinarum* L.

1. INTRODUCTION

Sugarcane (*Saccharum officinarum* L.) breeding starts with the hybridization of parental clones, followed by selection from a large population of seedlings. Even though large numbers of crosses have been used for producing seedlings for selection, the promising clones (assuming that the clones advanced to Stage 5 are promising clones) are only selected from several of these families. The families used for selection could be of great importance because poor families are a waste of time and funds (Tai and Miller, 1989) not only for the seedling stage but also for all subsequent stages of clonal selection. Thus, an effective method for selecting superior and discarding inferior families would help to improve the breeding efficiency, because selection of the best seedlings from the best families should increase the probability of selecting superior individuals in the later clonal selection stages (Kimbeng and Cox, 2003). Since the superiority of family selection was first identified by Hogarth (1971), it has been used in sugarcane breeding in Australia, India, Brazil, Columbia, Argentina, Indonesia, Cuba, South Africa, and the United States of America (Stringer et al., 2011) and was adapted to mainland China in 2006 (Wu, 2007).

The superiority of a family is determined by a range of parameters according to the breeding aims. These parameters include Brix, the estimate of tons of cane per hectare (TCH), the tons of sugar per hectare (TSH), disease reactions and so on. In other words, the ranking of a set of families could be by multiple objectives or parameters, and breeders are unlikely to simply judge the superiority or inferiority by only one or two parameters. The Dynamic Technique for Order Preference by Similarity to Ideal Solution (DTOPSIS) method described Yao et al. (1994) was first used for evaluating rural economies by several parameters. In plant breeding, the ideal clone or ideal family is represented by the best value for each trait or parameter involved, and a comprehensive index (C_i) is given by the DTOPSIS method to describe how close each evaluated clone or family is to the ideal. DTOPSIS has been widely used in evaluating other crops: tomato (Shen and Dai, 2005), silage corn (Chen and Ma, 2006), rice (Yan et al., 2008), tobacco (Li et al., 2012) and so on. In sugarcane, it was first adapted for evaluating chewing cane cultivars (Zhao et al., 2007), and then used for sugarcane clones (Ma et al., 2013; Yang et al., 2014; Yu et al., 2013; Zhao et al., 2008) and also for staling (post-harvest deterioration) resistance (Zhao et al., 2012).

The potential of a cross to produce elite progeny for a trait could be accurately predicted by the cross mean of that trait (Chang and Milligan, 1992), and there are several traits such as Brix, millable stalks per stool (MS), stalk diameter (SD), plant height (PH), and percent pith which could be used to determine the superiority of sugarcane families. The objectives of this study were to determine the potential of the DTOPSIS method for the evaluation of sugarcane families by comparing the C_i to the selection rate at later clonal selection stages. If DTOPSIS successfully predicts family quality, then it can be useful for evaluating sugarcane families based on the five traits measured.

2. MATERIAL AND METHODS

Origin of parental clones and seedlings

During October 2007 and February 2008, a total of 17 cross combinations from 32 parental clones (Table 1) were planned. The fuzz was produced by the Yacheng

Table 1. Sugarcane parental clones and their sources

Parental clones	Source	Parental clones	Source
Co1001	Sugarcane Breeding Institute, Coimbatore	YT00-236	GSIRI[c]
Co419	Sugarcane Breeding Institute, Coimbatore	YT85-177	GSIRI
CP72-1210	USDA ARS Sugarcane Field Station at Canal Point	YT93-159	GSIRI
CP84-1198	USDA ARS[a] Sugarcane Field Station at Canal Point	ZZ74-141	GSIRI
L75-20	Louisiana State University Agricultural Center at St.Gabriel,LA	ZZ92-126	GSIRI
Q121	BSES[b] Limited	YC97-48	GSIRI
Q141	BSES Limited	YR05-458	YSRI[d]
Q165	BSES Limited	YR05-612	YSRI
ROC1	Taiwan Sugar Research Institute	YR05-782	YSRI
ROC10	Taiwan Sugar Research Institute	YR05-785	YSRI
ROC24	Taiwan Sugar Research Institute	YR06-100	YSRI
ROC25	Taiwan Sugar Research Institute	YR95-105	YSRI
ROC26	Taiwan Sugar Research Institute	YR99-155	YSRI
RB45	Unknown	YZ89-151	YSRI
GT73-167	Sugarcane Research Institute, Guangxi Academy of Agricultural Sciences	YZ94-343	YSRI
NJ57-416	Sichuan Sugarcane Industry Research Institute	YZ94-375	YSRI

[a]ARS United States Department of Agriculture, Agricultural Research Service; [b]Bureau of Sugarcane Experimental Station, Australia; [c]Guangzhou Sugar Industry Research Institute; [d]Yunnan Sugarcane Research Institute.

Sugarcane Breeding Station (YSBS) of Guangzhou Sugar Industry Research Institute (GSIRI), Hainan Province, and by the Ruili Sugarcane Breeding Station (RSBS) of YSRI, Yunnan Province (Table 2). The fuzz was received and sowed at the end of February 2008. For the seedling nursery, the temperature inside the greenhouse was kept within the 22 to 36 °C range. The leaves of seedlings were trimmed once a week after the age of 6-8 leaves. The seedlings of check cultivars ROC22 and ROC10 were obtained by planting single bud setts. Seedlings were then hardened for 15-20 days before transplanting them into the field.

Field experimental designs

Two identical family trials were conducted at two fields (E.103° 15',N.23°42',1050 m above sea level) at the beginning of May 2008 in a randomized complete block design (RCBD) with three replications for each trial, each containing seedlings derived from 17 families and two check cultivars (ROC22 and ROC10). The row length and row space was 6m and 1.2m, respectively with 18 seedlings per family-plot. Seedlings within a row were planted 33 cm apart. The average values of each trait for each family or cultivar were used in the method of DTOPSIS to determine C_i values. The regular selection stage was planted using the rest of seedlings (168-644 seedlings per family), and was used to determine the selection rate for each family for comparison to the C_i value of each family.

The selection in the regular program of seedling stage was conducted in February 2009 when the seedlings were about 9 months old. The selection criterion was primarily the stool size based on visible assessment and pith. The Brix was not measured in the regular program. All stalks of each selected stool were planted in 1 to 2 rows for each un-replicated clone as Stage 2. The row length and spacing was 4.5 m and 1.2 m, respectively. Selection within Stage 2 was conducted during February 2010 based on Brix (hand refractometer), plant height (PH), stalk diameter (SD), pith, and disease incidence. The clones selected from Stage 2 were advanced to Stage 3 and planted in a Randomized

Complete Block Design (RCBD) with two replications in February 2010. The first replication was in a 1 row block for each clone, and the second was in 2-4 rows depending upon the amount of seed cane of each clone. The row length and spacing was 6 m and 1.2 m, respectively (same as that in Stage 4). Selection in Stage 3 was done in February 2011 by comparing the superiority of the clones in plant height (measured from the ground surface to top visible dewlap from 10 plants), millable stalks (the number of stalks higher than 80 cm judged visually), stalk diameter (measured on the middle part of stalk from10 plants), sugar content (Li et al., 2009) and disease with that of the check cultivars. The selected clones were advanced to Stage 4 in March 2011 by planting in a RCBD with two replications: 2-3 rows for replication 1 and 2-5 rows for replication 2. Selection in Stage 4 was completed in February 2012 using the same criteria as in Stage 3. The selected clones were advanced to Stage 5 in February 2012.

Fertilizer was applied to entire field at an equivalent rate of 345 kg ha^{-1} N, 144 kg ha^{-1} P, and 90 kg ha^{-1} K to both the plant cane and ratoon crops. Clear polyethylene mulch was added to cover the field to maintain soil temperature and moisture. It was removed after the beginning of the grand growth period.

Data collection and analysis

Plant height (PH, ground surface to top visible dewlap), number of millable stalks per stool (MS, PH>80 cm, visual judgment), stalk diameter of primary stalk (SD, 5-6 internodes from the ground), and pith percentage (middle to top part of stem) data were recorded for plant and ratoon crops from family trials at the two fields. The plant cane was measured on 20-22 December 2008 and ratoon crops were measured on 18-22 December 2009. For each replication, ten seedlings were randomly chosen for each measurement. The average values of the two family trials at plant and ratoon crops for each trait (Y_{ij} in Table 3) were used as 5 parameters in the DTOPSIS method described by Yao et al. (1994) for calculating a comprehensive index (C_i) for each family and

Table 2. The 17 sugarcane crosses and the crossing site, and their Identification number (ID No.) for DTOPSIS

Crosses	ID No.	Crossing site	Crosses	ID No.	Crossing site
ZZ92-126×L75-20	1	1	RB45×YC97-48	11	1
YZ94-375×RB45	2	1	ROC26×YR05-782	12	2
YZ94-343×ROC24	3	1	ROC25×GT73-167	13	1
YR99-155×CP72-1210	4	1	ROC1×Co1001	14	1
YR06-100×ROC10	5	2	Q141×YR05-458	15	2
YR05-785×YT00-236	6	2	CP84-1198×ZZ74-141	16	1
YR05-612×Q165	7	2	Co419×YR95-105	17	2
YT93-159×Q121	8	2	ROC10	18	check
YT85-177×YZ89-151	9	1	ROC22	19	check
NJ57-416×ROC10	10	1			

Crossing site 1: Yacheng Sugarcane Breeding Station, Guangzhou Sugar Industry Research Institute, Yacheng, Hainan Province, China; Crossing site 2: Ruili Sugarcane Breeding Station, Yunnan Sugarcane Research Institute, Ruili, Yunnan Province, China.

Table 3. The mean values (Y_{ij}) , and the ideal family for 5 evaluated traits from Sugarcane families and checks

ID No.	Brix (%)	MS(no. stalks)	SD (cm)	PH (cm)	Pith (%)
1	19.58	3.57	2.68	172.93	40.00
2	18.63	3.96	2.39	191.50	40.00
3	18.58	3.35	2.37	153.89	18.33
4	18.95	3.48	2.57	174.03	35.71
5	19.42	3.49	2.40	173.77	41.67
6	19.17	4.13	2.44	157.22	45.00
7	19.93	3.68	2.29	184.00	45.00
8	19.97	4.18	2.51	176.92	33.33
9	19.18	2.79	2.26	160.30	45.00
10	18.75	3.76	2.46	173.82	35.00
11	20.04	3.20	2.48	169.39	55.00
12	18.48	3.17	2.40	176.48	35.00
13	19.52	3.81	2.56	183.87	38.33
14	19.43	3.30	2.46	190.92	35.00
15	17.63	3.73	2.49	193.70	48.33
16	19.71	2.73	2.30	178.45	40.00
17	17.44	3.80	2.70	192.69	22.86
18	19.41	3.02	2.57	164.83	32.14
19	18.10	3.28	2.84	206.50	25.45
Idea family	20.04	4.18	2.84	206.50	18.33

MS, millbale stalks per stool; SD, stalk diameter; PH, plant height.

two check cultivars ROC22 and ROC10. The calculation of C_i value was processed in Microsoft office excel 2010. The selection rate (SR) for each stage was calculated by the number of selected clones × 100 divided by the number of seedlings in the seedlings stage. They were SR1 for Stage 1, SR2 for Stage 2, SR3 for Stage 3 and SR4 for Stage 4. Spearman rank correlations of C_i with SR1, SR2, SR3 and SR4 were processed in software StatistixV8 (Statistix, 2014).

In DTOPSIS, the parameters involved could be grouped as positive, neutral or negative depending upon the breeding aim. High values are favored for positive parameters, and neutral values for neutral parameters, and low values for negative parameters. In this study, Brix, MS, SD and PH were used as positive because they were Brix yield components, and pith was used as a negative because clones with pith may be linked to low juice rate. Some traits could be treated as neutral parameters when extremes of that trait are not favored. There was no neutral parameter in this study.

The C_i was calculated as following:

Each of the five traits had different units, but C_i is a comprehensive index that is calculated using all five traits. The data (Table 3) for each trait were transformed into the form of Z_{ij} (Table 4) which was within the range of 0.000 to 1.000. The positive, the neutral and the negative parameters were transformed according to (1), (2) and (3) respectively.

$$Z_{ij} = \begin{cases} Y_{ij}/Y_i\,max, \text{ where } Y_i\,max = max\,(Y_{ij}) & (1) \\ Z_{ij} = Y_{jo}\,/\,[Y_{jo} + abs\,(Y_{jo}-Y_{ij})] & (2) \\ Y_i\,min\,/\,Y_{ij}, \text{ where } Y_i\,min = min(Y_{ij}) & (3) \end{cases}$$

Where, 'i' means the number of families or check cultivars, i=1, 2, 3, ~ 19; 'j' is the number of traits, j=1 (Brix), 2 (MS), 3 (SD), 4 (PH), 5(Pith); Y_{ij} means the values of the ith cross for the jth trait; for each trait, Y_{jo} was the objective value if a neutral parameter like fiber content (Zhao et al., 2008) is involved and 'abs' is the absolute value. The result of calculation of Z_{ij} is given at table 4. Based on Z_{ij}, a decision matrix R_{ij} could be calculated by multiplying each Z_{ij} to weight coefficient (W_j) which is set by the breeders according to their breeding aims. According to our breeding aims, the present study gave 0.60 of the weight coefficient to the cane yield components MS(0.25), SD (0.25) and PH (0.10), and another 0.40 was given to Brix (0.30) and pith (0.10). W_j = {0.30, 0.25, 0.25, 0.10, 0.10} for Brix, MS, SD, PH and Pith, respectively (Table 4), $\left(W_j \in (0,1), \sum_{j=1}^{5} W_j = 1\right)$. The decision matrix of R_{ij} is calculated by formula (4)

$$R_{ij} = W_{ij} \times Z_{ij} \quad (4)$$

In the R_{ij} matrix (Table 5), the highest value X_j^+ for each trait was found by (5)

$$X_j^+ = max_i(R_{ij}) \quad (5)$$

They were $X_j^+ \cdot$ {0.3000, 0.2500, 0.2500, 0.1000, 0.1000}; the lowest value X_j^- for each trait was found by (6),

$$X_j^- = min_i(R_{ij}) \quad (6)$$

They were X_j^- {0.2612, 0.1629, 0.1992, 0.0745, 0.0333}. Based on the X_j^+ and X_j^-, and R_{ij}, the negative Euclidean distance S_j^+ and positive Euclidean distance S_j^-were calculated by (7) and (8), respectively.

$$S_i^+ = \sqrt{\sum_{j=1}^{19}(R_{ij} - X_j^+)^2}, \text{where } X_j^+ = (X_1^+, X_2^+, X_3^+, X_4^+, X_5^+) \quad (7)$$

$$S_i^- = \sqrt{\sum_{j=1}^{19}(R_{ij} - X_j^-)^2}, \text{where } X_j^- = (X_1^-, X_2^-, X_3^-, X_4^-, X_5^-) \quad (8)$$

The C_i (Table 6) is calculated by

$$C_i = S_i^- / (S_i^- + S_i^+), C_i \in (0, 1) \quad (9)$$

The higher the C_i is, the closer the family is to the ideal family.

3. RESULTS AND DISCUSSION

The C_i values

In the DTOPSIS method, the C_i values vary with the weight coefficient given to each trait. This is one of the advantages of DTOPSIS because it allows for selection based on multiple traits simultaneously. This gives breeders flexibility in determining weight coefficients for each trait

Table 4. The standardized transformed values $(Z_{ij})^{ab}$ of five traits from 17 sugarcane families and two check cultivars, and the weight coefficient (W_j)

ID No.	Brix[a]	MS[a]	SD[a]	PH[a]	Pith[b]
1	0.9771	0.8532	0.9435	0.8374	0.4583
2	0.9295	0.9467	0.8401	0.9274	0.4583
3	0.9270	0.7996	0.8347	0.7452	1.0000
4	0.9458	0.8309	0.9067	0.8428	0.5133
5	0.9691	0.8352	0.8459	0.8415	0.4400
6	0.9566	0.9863	0.8599	0.7613	0.4074
7	0.9945	0.8796	0.8054	0.8910	0.4074
8	0.9967	1.0000	0.8853	0.8567	0.5500
9	0.9570	0.6662	0.7966	0.7763	0.4074
10	0.9359	0.8976	0.8665	0.8417	0.5238
11	1.0000	0.7654	0.8723	0.8203	0.3333
12	0.9220	0.7579	0.8442	0.8546	0.5238
13	0.9741	0.9097	0.9005	0.8904	0.4783
14	0.9696	0.7894	0.8671	0.9245	0.5238
15	0.8799	0.8922	0.8770	0.9380	0.3793
16	0.9836	0.6516	0.8089	0.8642	0.4583
17	0.8705	0.9080	0.9510	0.9331	0.8021
18	0.9687	0.7216	0.9036	0.7982	0.5704
19	0.9035	0.7830	1.0000	1.0000	0.7202
W_j	0.30	0.25	0.25	0.10	0.10

MS, millbale stalks per stool; SD, stalk diameter; PH, plant height; [a]Equals the family and check mean divided by the highest value within the family or check varieties; [b]Equals the least value within 17 families and two checks divided by each mean of a family or a check.

Table 5. The decision matrix $(R_{ij})^a$ from five traits of 17 families of Sugarcane and two check cultivars

ID No.	Brix	MS	SD	PH	Pith
1	0.2931	0.2133	0.2359	0.0837	0.0458
2	0.2788	0.2367	0.2100	0.0927	0.0458
3	0.2781	0.1999	0.2087	0.0745	0.1000
4	0.2837	0.2077	0.2267	0.0843	0.0513
5	0.2907	0.2088	0.2115	0.0841	0.0440
6	0.2870	0.2466	0.2150	0.0761	0.0407
7	0.2984	0.2199	0.2014	0.0891	0.0407
8	0.2990	0.2500	0.2213	0.0857	0.0550
9	0.2871	0.1666	0.1992	0.0776	0.0407
10	0.2808	0.2244	0.2166	0.0842	0.0524
11	0.3000	0.1913	0.2181	0.0820	0.0333
12	0.2766	0.1895	0.2110	0.0855	0.0524
13	0.2922	0.2274	0.2251	0.0890	0.0478
14	0.2909	0.1973	0.2168	0.0925	0.0524
15	0.2640	0.2230	0.2193	0.0938	0.0379
16	0.2951	0.1629	0.2022	0.0864	0.0458
17	0.2612	0.2270	0.2378	0.0933	0.0802
18	0.2906	0.1804	0.2259	0.0798	0.0570
19	0.2710	0.1957	0.2500	0.1000	0.0720

MS, millbale stalks per stool; SD, stalk diameter; PH, plant height; [a]R_{ij} was calculated by standardized transformed values (Z_{ij}) multiplied by the weight coefficient W_j.

Table 6. The positive Euclidean distance (S_j^+), negative Euclidean distance (S_j^-), and comprehensive index (C_i) for each family or check cultivars

ID No.	S_j^+	S_j^-	C_i	Rank of C_i
8	0.0553	0.1005	0.6452	1
17	0.0512	0.0903	0.6380	2
13	0.0635	0.0789	0.5541	3
6	0.0741	0.0893	0.5466	4
19	0.0676	0.0769	0.5321	5
2	0.0722	0.0798	0.5249	6
3	0.0731	0.0787	0.5184	7
1	0.0692	0.0718	0.5090	8
10	0.0683	0.0702	0.5070	9
7	0.0831	0.0700	0.4573	10
4	0.0722	0.0608	0.4572	11
15	0.0828	0.0665	0.4453	12
5	0.0816	0.0578	0.4147	13
14	0.0793	0.0554	0.4112	14
18	0.0881	0.0498	0.3610	15
11	0.0961	0.0523	0.3524	16
12	0.0906	0.0396	0.3042	17
16	0.1141	0.0382	0.2508	18
9	0.1172	0.0274	0.1896	19

according to how important each trait is for their breeding aims. In the present study, weight coefficients of 0.30, 25, 0.25, 0.10 and 0.10 were given to traits Brix, MS, SD, PH and pith, respectively (Table 4). A high-yielding commercial variety requires satisfactory stalk number, stalk diameter, and stalk length (Chang and Milligan, 1992). 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 hand harvesting practiced by farmers in some sugarcane regions. Because the crop was short on average (Table 3), the selection emphasized number of millable stalks and stalk diameter rather than plant height at seedling stage. Brix is highly associated with sugar content (Papini-Terzi et al., 2008), which is one of the most important sugarcane breeding aims. Improvement of sugar content is believed to be more beneficial than improvement of cane yield (Jackson, 2005); moreover, the selection for sugar content was found to be more accurate than other traits for cane yield within small plots (Jackson and McRae, 2001). The Brix was given a high weight coefficient even if it was not measured during the selection in seedling stage because the measurement of Brix is laborious and expensive; however, it was measured on clones judged superior to the check cultivars by visible or yield comparison at later selection stages. During the seedling stage selection, the pith was checked and some the seedlings judged as vigorous were selected even though they showed a slight amount of pith, and would be discarded at the later stages if the pith exists and lowered the juice percentage when compared to check cultivars.

The principle purpose of DTOPSIS is to determine how close the evaluated subject (e.g. a sugarcane family) is to the ideal solution (e.g. the ideal family in Table 3) (Yao et al., 1994). Among all the 17 families and two check cultivars, the families with the highest Brix and the largest MS were found in crosses RB45×YC97-48 (20.04%) and YT93-159×Q121 (4.18 stalks), respectively. The largest SD (2.84 cm) and PH (206.50 cm) were found in the check cultivar ROC22, and the lowest pith was found in cross YZ94-343×ROC24 (18.33%). So, the ideal family for this study was characterized with Brix, MS, SD, PH and pith of 20.04%, 4.18(stalks per stool), 2.84 cm, 206.50 cm and 18.33%, respectively. The C_i ranged from 0.1896 to 0.6452 (Table 7) and described how close each family was to the ideal family comprehensively. There were four families YT93-159×Q121, Co419×YR95-105, ROC25×GT73-167, YR05-785×YT00-236 that showed higher C_i values than ROC22 (C_i=0.5321). These four families also had clones advanced to Stage 5. There were nine families that showed C_i values between two check cultivars, and two of them had clones advanced to Stage 5. For the four families with C_i values lower than those of the two check cultivars, no clones were selected. Of the seven families that had higher C_i values than 0.5000, six of them have clones selected in Stage 4.

The SR and correlations with C_i values

For each cross evaluated in the family trials, at least 168 seedlings were planted for selection in Stage 1 (Table 7). The selection rate at Stage 1(SR1) varied from 1.71 to 6.52%, with an overall selection rate of 3.50% for Stage 1.

Table 7. The selection rate (SR) at Stage 1(SR1), Stage 2(SR2), Stage 3(SR3), and Stage 4(SR4), and the comprehensive index (C_i) value of 17 sugarcane families and two check cultivars

ID No.	NS	SR1	SR2	SR3	SR4	Stage [a]	C_i
8	182	3.30	2.75	1.65	1.65	5	0.6452
17	644	6.52	1.55	0.47	0.31	5	0.6380
13	210	6.19	1.90	1.43	0.48	5	0.5541
6	252	3.17	0.79	0.40	0.40	5	0.5466
19	/	/	/	/	/	/	0.5321
2	280	4.64	1.07	0.36	0.36	5	0.5249
3	392	4.85	0.26	0.00	0.00	3	0.5184
1	630	5.24	1.75	0.63	0.16	5	0.5090
10	602	1.66	0.33	0.00	0.00	3	0.5070
7	252	5.16	0.00	0.00	0.00	2	0.4573
4	574	1.92	0.17	0.00	0.00	3	0.4572
15	518	1.93	0.19	0.00	0.00	3	0.4453
5	308	1.62	0.00	0.00	0.00	2	0.4147
14	616	3.41	0.00	0.00	0.00	2	0.4112
18	/	/	/	/	/	/	0.3610
11	392	1.79	0.00	0.00	0.00	2	0.3524
12	168	2.98	0.00	0.00	0.00	2	0.3042
16	238	3.36	0.42	0.00	0.00	3	0.2508
9	350	1.71	0.00	0.00	0.00	2	0.1896
r	/	0.4507	0.7967**	0.8059**	0.8202**	/	/

NS, the number of seedlings planted in seedling Stage for selection; **the correlations of SR with C_i was significant at P=0.01. r Spearman correlation coefficient; [a]the final stage to which clones were advanced from each family.

In Stage 2, the SR2 ranged from 0.00 to 2.75%, and no clones were selected from 6 families. In Stage 3, the SR3 ranged from 0.00 to 1.65%, and no clone was selected from 11 families. In Stage 4, the SR4 ranged from 0.00 to 1.65%, and no clone was selected from 11 families. Judging from the clones advanced to Stage 5 that were selected from six families, around 64% (11 families out of 17) should not have been planted as seedlings for selection. During individual selection, if one family is superior to the check in one character but not in others, it can result in a lower selection rate (Wells and Kofoid, 1986). The low selection rate for YR06-100×ROC10 (1.62%) may be the result of a comparatively small stalk diameter and high pith percentage, even its mean Brix was comparatively high; however, the Brix was not measured during the selection at seedlings stage. Six families YT93-159×Q121, ROC25×GT73-167, YR05-785×YT00-236, YZ94-375×RB45, Co419×YR95-105 and ZZ92-126×L75-20 should be considered for use in selection.

The C_i values were significantly (P<0.01) correlated with SR2, SR3 and SR4 (Table 7). It showed a positive correlation (r=0.4507) with the SR1 but was not significant which could be the result of not measuring the Brix during seedling selection. If clones that have been advanced to Stage 5 (reflect by SR4>0.00) are considered as promising clones, then all 6 families showed higher C_i values than 0.5000, and 4 of them had higher C_i values than ROC22. In contrast, all the families with lower C_i values than both check cultivars had 0.00% of the SR3 and SR4, and three of them had no clones selected after Stage 2. This suggested that there was a higher possibility for selecting promising clones from families with higher C_i values.

4. CONCLUSION

Evaluating sugarcane families is multi-objective process, because the superiority of a family is composed of several traits. In this study, sugarcane families were evaluated based on five parameters, namely Brix, plant height, number of millable stalks per stool, stalk diameter and pith percentage at family trial. The C_i values calculated by the DTOPSIS method for family trials were significantly correlated with the selection rate at Stages 2, 3 and 4. The DTOPSIS method can be used in sugarcane family evaluation based on data collected from family trials and the weight coefficient set by the breeder. The C_i values and selection rate indicated six families (YT93-159×Q121, Co419×YR95-105, ROC25×GT73-167, YR05-785×YT00-236, YZ94-375×RB45 and ZZ92-126×L75-20) could be considered for further selection.

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