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A STUDY ON THE DIVERSITY OF *SACCHARUM OFFICINARUM* L. GERMPLASM

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ABSTRACT

A representative sample of *Saccharum officinarum* L. germplasm comprising 94 clones, drawn from different geographic sources, was evaluated for its diversity using nonhierarchical Euclidian cluster analysis. All the clones were grouped into nine clusters, which showed considerable diversity for yield and quality traits. There was no relationship between geographic origin of the clones and their clustering pattern.

Key words: *Saccharum officinarum*, diversity, Euclidian cluster analysis, geographic origin.

The *Saccharum officinarum* germplasm available today is large, diverse and represents many geographical groups. To facilitate effective utilization of this collection, a study of its diversity was considered appropriate.

MATERIALS AND METHODS

From 750 *Saccharum officinarum* clones maintained in the world collection of sugarcane germplasm at the Sugarcane Breeding Institute, Research Centre, Cannanore, 94 clones were randomly selected for this study. They were planted in randomized block design with three replications. The plot size was a single row of 3 m length. Data on number of germinants on 30th day, number of tillers on 90th day and millable stalk number (MSN) and stalk yield in 10th month were recorded on per plot basis. Early shoot height was recorded on five stalks in each replication on 90th day while stalk diameter, stalk height, stalk weight, and number of internodes were recorded in the 10th month. Hand refractometer brix was recorded on five stalks in each replication in the 7th, 8th, 9th and 10th months. Hydrometer brix, sucrose content, and purity percentage were determined in 10th month by analysing the juice from five stalks in each replication. Sucrose content was estimated by the Horne's method [1]. Sugar yield or commercial cane sugar/plot (CCS/plot) was worked out as CCS/plot = CCS % x stalk yield/plot; where CCS % = (sucrose x 1.022)–(brix x 0.292). The leaf length, leaf width, leaf angle and leaf flagging point (LFP) were recorded on 3rd leaf in

five plants in each replication and averaged. The LFP was obtained by dividing the distance from dewlap to the point at which the leaf starts drooping by the total leaf length.

Analyses of variance and covariance were done on individual characters as per standard procedures. For classifying the population, the nonhierarchical Euclidian cluster analysis was done using the computer programme developed at IASRI, New Delhi [2, 3]. Different cluster solutions were compared using a sequential F ratio test.

RESULTS AND DISCUSSION

Analysis of variance showed significant differences among the genotypes for all characters, implying that these characters could be effectively used for classifying the population. Cluster analysis was initiated with ten clusters and by reducing one cluster each at every subsequent stage, thus, six cluster solutions with 10, 9, 8, 7, 6 and 5 clusters were obtained. Sequential F ratio test showed that the solution with nine clusters aptly described the available data.

Cluster membership varied from six in clusters IV and IX to 14 in cluster VII. The intracluster distances were of lower magnitude compared to intercluster distances (Table 2). The intercluster distance between clusters III and IV was highest (Table 2). High level of divergence was observed whenever cluster IV was involved, especially with clusters I, II, III and V. This cluster had the highest phenotypic expression for all the economic attributes

Table 1 Cluster analysis in sugarcane: distribution of genotypes in different clusters

	Cluster I		Cluster II		Cluster III	
	genotype	source	genotype	source	genotype	source
1.	H.M. Black	*	Arrowed Pundia	Fiji	H.O. 39	Hawaii
2.	Langi	*	Java Hebbal	India	Kajla	India
3.	Luzon White	Guam	Pynmana Ribbon	Burma	Lajai	Thailand
4.	Mani	*	Vae vae ula	Puerto Rico	Mia do	Indonesia
5.	Ohia-1	*	White Cane	*	Vellai	India
6.	Witmanila	Indonesia	28 NG 80	New Guinea	28 NG 210	New Guinea
7.	96 NG 14A	New Guinea	51 NG 18	"	28 NG 212	"
8.	28 NG 21	"	57 NG 57	"	51 NG 22	"
9.	51 NG 32	"	57 NG 73	"	51 NG 58	"
10	57 NG 114	"	57 NG 78 red	"	51 NG 90	"
11.	57 NG 68	"	57 NG 259	"	51 NG 161	"
12.	57 NG 77	"				
13.	57 NG 185	"				

(Contd.)

Table 1 (Contd.)

	Cluster IV		Cluster V		Cluster VI	
	genotype	source	genotype	source	genotype	source
1.	B.L. Groen	*	Bamboo Blanca	*	Ashy Mauritius	Mauritius
2.	Chittan	India	Fiji 28	Fiji	Badila Fiji	Fiji
3.	Chrystalina	Australia	Fiji 30	Fiji	Bamboo Morada	*
4.	K. Boothan	India	Governor	Jamaica	Manjri Red	India
5.	Poona	India	Kabirya	*	Preanger Striped	*
6.	57 NG 179	New Guinea	Otamite	Australia	Yellow Bamboo	Hawaii
7.			21 NG 37	New Guinea	Zopilota	Costa Rica
8.			28 NG 11	"	21 NG 5	New Guinea
9.			28 NG 37	"	28 NG 54	"
10.			51 NG 98	"	57 NG 51	"
11.					57 NG 58	"
12.					57 NG 238	"

	Cluster VII		Cluster VIII		Cluster IX	
	genotype	source	genotype	source	genotype	source
1.	Blanche Reunion	Reunion	Green Sport	*	Pattapatti	India
2.	Brazilian	Virgin Islands	Negros Purple	*	57 NG 110	New Guinea
3.	Caira	*	Poovan	India	57 NG 114	"
4.	Desi Pounda	India	Vespertina	Brazil	57 NG 147	"
5.	Javari Kabbu	India	21 Ng 7	New Guinea	57 NG 188	"
6.	Mauritius 131	Mauritius	28 NG 59	"	57 NG 243	"
7.	Sepaya No. 4	*	28 NG 87	"		
8.	Yellow tip	Hawaii	28 NG 280	"		
9.	21 NG 57	New Guinea	51 NG 22	"		
10.	28 NG 209	"	51 NG 138	"		
11.	57 NG 67 Yellow	"	57 NG 17	"		
12	57 NG 182	"				
13.	57 NG 187	"				
14.	57 NG 236	"				

*Source of collection not available.

and was further characterized by highest leaf length and lowest leaf width, leaf angle and LFP (Table 3). Conversely, clusters I and III, which showed maximum divergence from it, had lowest cluster means for most economic traits and relatively high leaf angle and LFP.

Table 2. Intra- (in bold) and intercluster distance matrix in principal component units

Clusters	I	II	III	IV	V	VI	VII	VIII	IX
I	**3.00**								
II	4.12	**2.93**							
III	3.91	6.07	**3.16**						
IV	8.05	6.23	8.05	**3.18**					
V	4.42	5.97	5.24	6.43	**2.80**				
VI	4.85	3.60	6.23	3.96	3.92	**2.46**			
VII	3.53	4.27	3.54	5.60	3.83	3.30	**3.05**		
VIII	4.92	5.53	4.19	4.90	3.14	3.74	3.18	**2.87**	
IX	5.24	3.68	6.27	6.02	6.10	4.59	5.39	4.93	**2.98**

Table 3. Character means in different clusters of sugarcane (original values)

Character	Cluster mean									Overall mean
	I	II	III	IV	V	VI	VII	VIII	IX	
No. of germinants	32.6	32.9	27.6	41.9	33.7	33.6	33.0	33.5	32.8	33.5
Number of tillers	43.4	50.2	40.4	45.1	44.3	44.3	53.4	45.9	54.1	46.7
MSN	24.7	27.4	20.9	29.9	27.5	27.3	27.9	27.7	30.8	27.1
Stalk diameter (cm)	1.9	2.1	1.9	2.3	2.1	2.1	2.1	2.1	2.1	2.1
Early shoot height (cm)	27.9	39.1	25.9	46.3	31.3	40.4	35.0	36.8	41.4	36.0
Stalk weight (kg)	0.6	0.8	0.5	0.9	0.7	0.8	0.8	0.7	0.8	0.8
Stalk height (m)	1.7	1.8	1.7	2.0	1.7	2.0	1.9	1.9	2.0	1.8
No. of internodes	27.9	29.7	27.9	30.8	26.4	30.9	29.1	29.6	29.7	29.1
Stalk yield (kg)	15.6	22.0	11.7	25.5	19.9	22.4	21.4	19.9	24.1	20.3
Sugar yield (kg)	1.5	2.8	1.2	3.1	1.9	2.5	2.1	2.0	2.6	2.2
HR. Brix (7th month)	14.5	15.4	14.2	18.0	14.3	16.8	14.5	16.1	15.3	15.5
HR. Brix (8th month)	16.2	17.4	16.6	20.4	16.5	19.1	16.4	17.9	17.6	17.6
HR. Brix (9th month)	16.3	17.4	16.4	19.8	17.0	19.0	16.5	18.0	17.4	17.5
HR. Brix (10th month)	16.7	17.9	16.8	19.6	17.9	18.1	17.3	17.8	17.8	17.8
Sucrose %	13.9	15.6	14.0	18.2	15.4	16.2	14.9	15.0	15.6	15.4
Purity %	83.2	87.1	83.0	92.6	85.6	89.6	86.2	84.3	88.0	86.9
Leaf length (cm)	113.4	122.2	114.9	123.6	116.9	118.3	118.7	116.9	107.1	116.9
Leaf width (cm)	4.1	4.5	4.2	4.0	4.3	4.3	4.4	4.1	4.2	4.2
Leaf angle	16.4	15.6	17.0	13.8	15.3	15.2	15.6	16.0	14.7	15.5
LFP	0.5	0.4	0.5	0.3	0.4	0.4	0.5	0.4	0.5	0.5

The clustering pattern did not show any apparent relationship with geographic origin of the clones. The clones belonging to the same geographic area were included in different clusters (Table 1). Clones from New Guinea were distributed in all clusters, while clones of Indian origin were present in all clusters except clusters I and V. Clusters II, V and VI included clones from Fiji. Thus, phenotypic differences in these clones was independent of their geographic origin. Lack of parallelism between geographic diversity and genetic diversity had been reported in sugarcane [4, 5] and in other crops, viz. sorghum [6], cotton [7], linseed [8] and tomato [9]. Upadhyay and Murty [10] reported lack of correspondence between genetic diversity and geographical diversity in pearl millet and suggested that genetic drift and selection under different environments may cause greater divergence than the geographic distance.

The extensive diversity in the *S. officinarum* germplasm is evident from the present study. This diversity is manifest even within specific geographical groups, with the individual members distributed in diverse clusters. The single largest geographic group was the New Guinea group, which was also the most diverse, being distributed in all the clusters. This is indicative of the presence of considerable diversity in the region where the species is believed to have originated.

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