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DIVERGENCE IN SUGARCANE (*SACCHARUM OFFICINARUM* L.) BASED ON YIELD AND QUALITY TRAITS

MUHAMMAD KASHIF[*] AND FAROOQ AHMAD KHAN[1]

[*]*Plant Genetic Resources Program,*
National Agricultural Research Centre, Park Road, Islamabad, Pakistan.
Email: plantbreedergeneticist@yahoo.com
[1]*Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan*

Abstract

Fourteen genotypes of sugarcane, *Saccharum officinarum* L., were investigated for determining genetic diversity based on 12 quantitative traits using Meteroglyph and Divergence analysis based on pivotal elements. High variation was observed for most of the characters including sucrose recovery with high superiority of the genotypes, CP-43-33, CP-72-2086, COJ-84 and SPSG-26. Four clusters were observed with four genotypes in three clusters in each case, whereas cluster IV consisted two genotypes. The genotypes with high index scores can be crossed to have maximum variability of good combinations of characters. Though cluster analyses grouped genotypes with greater similarity for agronomic traits, they did not necessarily include the genotypes from the same source or origin.

Introduction

Sugarcane is an important food crop of the tropics and sub tropics that is cultivated in about 74 countries between 40°N and 32° 5´S, encompassing approximately half the globe (Anon., 1998). Its major use in primitive human societies was restricted to chewing or occasional manufacture of raw sugar by boiling the juice. A wide variety of sweet cane types existed from which the early people selected thick barreled, high sucrose soft sticks and this crude method of selection eventually produced better cane types. Sugarcane produces numerous valuable by-products like alcohol used by pharmaceutical industry, ethanol used as a fuel, bagasse used for manufacturing paper and chipboard and press mud used as a rich source of organic matter and nutrients for crop production.

Pakistan occupies an important position in cane producing countries of the world. It ranks at the fifth position in cane acreage and production and almost 15th position in sugar production and national average cane yield (~47 t ha^{-1}) is far below the existing potential (Anon., 1998). Through use of high yielding genetics resources, recovery of sugar has been increased from 8.5 to 11% (Anon., 1999). Degree of variance provide an estimate of genetic diversity and numerical taxonomic techniques have been successfully used to classify and measure genetic diversity in crop germplasm, in the country including cereals (Ashraf *et al*., 2003), legumes (Arshad *et al*., 2003; Iqbal, 2003; Ghafoor *et al*., 2005a; 2005b; Qureshi *et al*., 2004; Sultana *et al*., 2005) and oil seeds (Arshad *et al*., 2006). This type of study is not much reported on sugarcane in the country and few references are available (Mujahid *et al*., 2000). Therefore keeping in view the importance of sugarcane in the country and use of genetic diversity in crop improvement, 14 genotypes were investigated for determining genetic diversity based on quantitative traits for planning future germplasm management and utilization.

Materials and Methods

Fourteen sugarcane genotypes (SPF-232, SPF-234, CP-43-33, RB-82-5336, TCP-81-10, CPF-235, CP-72-2086, BF-129, Triton, COL-54, COJ-84, SPSG-26, COJ-64) alongwith one check (CP-77-400) were planted in a triplicate RCBD under field conditions. Each variety was accommodated in a plot having 4 rows of 52 meter lengths with row to row spacing 25cm and experiment was planted on September 15, 2000 and harvested on 25 meter during September, 2001. All the agronomic practices were kept normal for all the fourteen genotypes. Ten guarded plants from each replication (30 guarded plants from each in total variety) were randomly selected for recording data on plant height (cm), number of tillers/plant, inter-nodal length (cm), number of leaves per plant, leaf area (cm), cane diameter (cm), cane weight (kg), dry matter contents (g), juice content (L), brix value (%) and sucrose content (%). The data collected for various characters were analyzed by standard analysis of variance technique as given by Steel & Torrie, (1980).

Meteroglyph and Divergence analysis were also performed according to using pivotal elements to conduct the analysis of dispersion according to Wilk's criterion (Singh & Chaudhary, 1985). Clusters were made by Tocher's method using metroglyph, a technique being used for preliminary grouping of above accession (Rao, 1985). With the help of this technique 14 genotypes viz., SPF-232, SPF-234, CP-43-33, RB-85-5336, TCP-81-10, CPF-235, CP-72-2086, BF-129, Triton, COJ-84, SPSG-26, COJ-64, COL-54 and standard variety CP-77-400 (as a standard) were used to allot scores for each accession.

Results and Discussion

Analysis of variance results for 14 genotypes indicated significant differences for all the characters under study (Table 1). High variation was observed for most of the characters including sucrose contents. The genotypes, CP-43-33, CP-72-2086, COJ-84, SPSG-26 and Triton were observed better. Among these Triton is reported to be affected by red rot, hence only can be used in breeding program. The coefficient of variability was in the range from 0.51 to 7.79 that indicated the consistency in experimental conditions. Meteroglyph scatter diagram shows four groups from 14 genotypes of sugarcane (Fig. 1). The genotypes CP-72-2086, SPSG-26, Triton and CP-77-400 were indicated in cluster I while SPF-234, CPF-235, COJ-64 and COL-54 indicated cluster II. Cluster III indicated four genotypes (SPF-232, CP-43-33, BF-129 and COJ-84). Rest of the cluster had two genotypes. The standard accession CP-77-400 was in cluster I. The genotypes with high index scores and fell into different cluster can be crossed to have maximum variability of good combinations of characters. Similarly, if one is interested in improving a specific character which is undesirable or otherwise week on genotype. Though cluster analyses grouped genotypes with greater similarity for agronomic traits, they did not necessarily include the genotypes from the same source or origin. In most of the germplasm resources lack of association between agronomic traits and origin has been reported (Ghafoor *et al*., 2005a). This information will be helpful to use in crop breeding through identification of parents.

Table 2 revealed the average intra-cluster and inter-cluster distance. The highest intra-cluster average D^2 value (26.08) was of cluster number V. The highest average inter-cluster distance was between cluster number IV and V *i.e.*, 31.00, 176.00 on the basis of there average intra and inter-cluster distances one can early product the genetic diversity that exist within and between clusters. Since in Pakistan little information is available on sugarcane, therefore it could be used for further planning of experiments using huge genetic resources.

Table 1. Means and analysis of variance for 12 yield and quality traits among 14 genotypes of sugarcane.

Genotypes	Number of tillers	Internodal length	Number of leaves	Plant height (cm)	Leaf area (cm^2)	Cane diameter (cm)	Sucrose content (%)	Brix value (%)	Wet weight	Dry matter	Cane weight (kg)	Juice content (L)
CP-43-33	10.0	11.7	25.7	117.7	753.50	7.07	18.42	17.28	6.00	5.50	10.20	5.17
CP-72-2086	9.8	13.9	27.9	147.9	1147.00	8.42	19.34	17.14	7.00	6.50	8.20	4.50
SPF-232	9.7	9.0	27.5	124.9	812.10	7.16	18.77	16.23	5.00	4.50	9.40	4.40
RB-82-5336	9.5	11.5	24.8	93.9	817.70	7.23	18.35	17.58	6.00	5.00	8.43	3.20
COJ-84	9.5	13.9	25.3	136.3	789.80	7.15	19.01	17.36	7.00	6.00	7.46	4.05
COL-54	9.5	11.6	26.1	124.2	681.00	6.40	18.33	17.02	7.00	6.00	7.20	3.16
CP-77-400	9.4	13.8	22.0	121.9	931.30	7.43	10.10	20.20	7.33	6.50	9.60	4.60
SPF-234	9.3	13.3	26.9	140.3	983.50	7.59	18.52	18.15	6.00	5.50	8.26	6.20
SPSG-26	9.0	14.3	27.5	154.3	962.20	7.58	19.28	18.83	7.00	6.50	11.93	6.97
COJ-64	8.7	13.9	25.8	137.7	1048.00	7.75	18.55	15.34	6.00	5.00	6.83	3.31
TRITON	8.4	14.2	26.5	128.1	840.30	7.28	19.21	18.26	7.00	6.50	12.12	6.10
CPF-235	7.8	11.5	27.9	149.7	1006.00	7.60	18.24	19.12	7.00	5.50	9.23	3.53
TCP-81-10	7.4	11.4	26.9	98.6	845.00	7.29	18.18	17.41	6.33	5.00	10.23	4.13
BF-129	7.3	11.5	26.7	104.5	825.30	7.26	18.18	17.74	6.00	4.50	10.20	5.13
MS (R)	0.17	1.27	0.25	13.78	36983.97	0.86	0.01	0.01	0.04	0.05	0.15	0.01
MS (V)	2.36**	7.76**	9.43**	1064.28**	49055.04**	0.59**	0.49**	4.37**	1.32**	1.50**	8.07**	4.25**
MS (E)	0.330	0.497	0.278	84.720	4797.420	0.043	0.009	0.009	0.076	0.046	0.036	0.006
LSD 5%	0.96	1.183	0.8849	15.45	116.2	0.3480	0.1592	0.16	0.46	0.36	0.32	0.13
CV %	6.42	5.65	2.04	7.24	7.79	2.81	0.51	0.53	4.25	3.89	2.06	1.72

X1– Number of tillers, X2– internodal length, X3– number of leaves, X4– plant height (cm), X5– leaf area (cm^2), X6– cane diameter (cm), X7– sucrose content (%), X8– brix value (%), X9– wet weight, X10– dry matter, X11– cane weight (kg) and X12– juice content (Liter)

Table 2. Average intra- and inter-cluster D^2 values

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	7.91	23.34	57.34	41.71	43.18	39.08
Cluster II		22.72	64.81	45.09	63.38	38.73
Cluster III			9.85	31.75	176.84	118.49
Cluster IV				10.63	136.71	115.51
Cluster V					26.08	37.78
Cluster VI						0.00

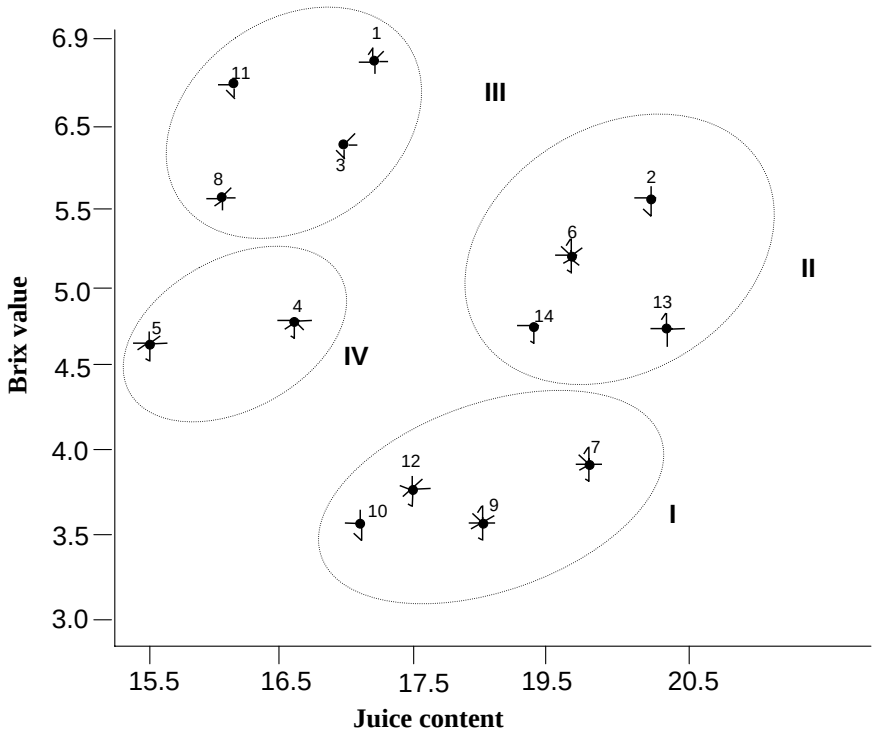

Fig. 1. Meteroglyph scattered diagram illustrating distribution of various groups formed from 14 genotypes of sugarcane.

This information helps to determine the genetic variability and contribution of some morphological traits in cane yield and sucrose recovery and could largely facilitate the formulation of appropriate selection strategies to develop the clones of best commercial merits, which are suitable for the cultivation in different climate zones (Mariotti *et al*., 1990; Li & Wang, 1991). Singh *et al*., (1996), Das *et al*., (1996) and Kumar & Ram (1996) derived information on genetic variability, heritability and genetic advance. Genetic divergence investigated for present research material would be helpful for selection of important yield influencing characters (Doule & Balasundaram, 1997; Kadian *et al*., 1997; Verma & Sachan, 2000).

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