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Metroglyph and D^2 Analysis for Estimation of Potential for Improvement in (*Saccharum officinarum* L.) Accessions

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ABSTRACT

Twelve sugarcane accessions were sown in a randomized complete block design to study the pattern of morphological variation among cultivars, which would be helpful for selection of important yield influencing characters. Data collected on various plant characters were analysed to evaluate various genotypes by metroglyph and D^2 analysis. Sucrose and purity per cent were found to be the best variable with maximum potential for selection.

Key Words: Sugarcane; Metroglyph; D^2 Analysis; Sucrose; Purity

INTRODUCTION

Sugarcane (*Saccharum officinarum* L.) belongs to the family Poaceae. It possesses a matchless attribute of sugar accumulation which attracted the attention of primitive man and his sweet tooth put him on the long avenue of cane domestication and improvement. It is cultivated on an area of 1,155,000 hectares with total annual production of 55,191,000 tones of cane (Anonymous, 1989-99). The national sucrose recovery had been far below, when compared with major sugarcane growing countries of the globe. Among sugarcane producing countries of the world, Pakistan ranks 5th in terms of overall production, but occupies 57th position for yield per hectare (Anonymous, 2000). The purpose of present study was to evaluate the genetic potential of the accessions for cane yield to develop a selection criterion.

MATERIALS AND METHODS

Present study was conducted in the Experimental Area, University of Agriculture, Faisalabad. Twelve sugarcane accessions namely SPF-232, SPF-234, CP-43-33, CPF-235, CP-72-2086, Coj-84, RB-82-5336, TCP-81-10, Triton, BF-129, SPSG-26 and CP-77-400 (standard) were planted in the field. The experiment was laid out in RCBD with three replications. Each genotype was accommodated in a plot having four rows of 15.75 m length with row to row spacing 0.75 m. The data were collected on the characters: cane height (cm), number of tillers plant^{-1}, internodal length (cm), number of leaves plant^{-1}, leaf area (cm^2), cane diameter (cm), cane weight (kg), juice content (l), brix value (%), commercial cane sugar (%), fibre contents (%), purity (%) and sucrose content (%). The data collected were subjected to statistical analysis by using Fisher's method (1958) analysis of variance technique, and Anderson's Metroglyph and Divergence analysis Technique according to Mahalanobis (1928).

RESULTS AND DISCUSSION

There were significant differences among various characters except fibre content which was non-significant (Table I).

Table I. Mean squares for the analysis of variance to indicated palnt characters among twelve genotypes of *Saccharum officinarum* L.

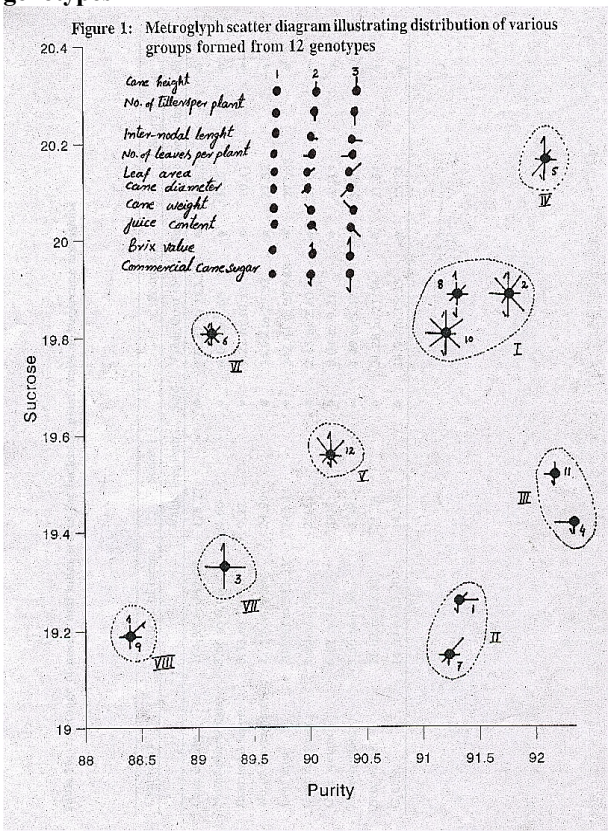
Characters	Replications Mean square	Genotypes Mean square	Error Mean square	F. Value
Cane height	80.028	177.604	65.210	2.723*
Number of tillers plant^{-1}	0.361	3.202	0.937	3.417**
Internodal length	2.083	1.765	0.598	2.949*
Number of leaves plant^{-1}	3.111	9.444	2.566	3.681**
Leaf area	72.250	3465.765	540.492	6.412**
Cane diameter	0.067	0.161	0.031	5.097**
Cane weight	0.952	3.577	0.327	10.941**
Juice content	0.014	2.345	0.018	131.284**
Brix value	0.049	0.291	0.032	9.206**
C.C.S.	0.005	0.360	0.005	65.540**
Purity	0.004	5.221	0.011	476.155**
Fibre	0.000035	0.00012	0.000055	2.222^{NS}
Sucrose	0.008	0.321	0.001	323.445**
Degree of	2	11	22	

Metroglyph analysis. Aderson's (1957) Metroglyph is a relatively simple technique used for preliminary grouping of genotypes (Bhadra & Akhtar, 1991). According to this technique 12 genotypes of sugarcane formed eight distinct clusters (Fig. 1).

The number to each cluster was alloted on the basis of net index score of the cluster in ascending order (Table II). The check variety CP-77-400 fell into cluster number V. The cluster numbers IV, V, VI, VII and VIII were formed by individual genotypes, e.g. genotype number 5 (CP-72-2086), 12 (CP-77-400), 6 (Coj-84), 3 (CP-43-33) and 9 (Triton), respectively. The index scores alloted to each

character of the genotypes indicated the worth of that genotype regarding that character (Tables III & IV). The same thing is represented as rays on the glyphs in Fig. 1. Among genotypes, genotype number BF-129 had the highest index score as total and as well as for individual characters except for internodal length and sucrose content for which it scored 2 for each of these trait (Table IV). From these results, it appears that the genotypes which have high index score and fell into different clusters may be crossed to have maximum variability for good combinations of characters. The information is useful for the breeders interested creating desired level of variability for a specific

Fig. 1. Metroglyph scatter diagram illustrating distribution of various groups formed from 12 genotypes



character and thus would be helpful in identifying and engineering the crosses.

D^2 analysis. From Divergence analysis technique, the analysis of covariance was performed for the 12 characters recorded from the 12 genotypes to obtain the error and genotype mean products. The error mean square and mean product matrix and error + genotype mean square and mean product matrix were inverted to pivotal condensation method. The pivotal elements (determinants) were used to conduct the analysis of dispersion (Singh & Chaudhary, 1977) for the differences among genotypes in respect to the pooled effects of all the 12 characters (Table V). The results were highly significant which highlighted the significance of using D^2-statistics. The pivotal elements from error matrix were used to convert the correlated means to uncorrelated means. On the basis of these uncorrelated means, the D^2-distance between each genotype was calculated. In total 66 values (Table VI) of D^2, which were calculated to know the genetic distance between the 12 genotypes. In all combinations, each character was counted for the number of times it appeared first in ranking (Table VII). This was used as a criterion for the contribution of each character to the total genetic divergence. The highest contribution was from sucrose content (53.03%) followed by commercial cane sugar (28.78%) but no contribution was made by cane height, internodal length and brix value (0.00%) to the total genetic divergence. Rao *et al.* (1985) concluded that genetic divergence was greatest for clump weight, followed by brix per cent and stem height at nine months. Raman *et al.* (1988) found that sucrose content and leaf width made the greatest contribution to divergence. This disagreement may be attributed to differences in the environmental condition as well as plant germplasm used in the experiment.

The clusters of the genotypes were obtained by using Tocher's method (Rao, 1952). Thereafter seven clusters were formed. Cluster I (RB-82-5336, SPSG-26, CP-77-400) and II (CP-43-33, CPF-235, BF-129) number being the largest having three sugarcane genotypes each and cluster III (Coj-84, TCP-81-10) had two genotypes, the clusters IV (Triton), V (CP-72-2086), VI (SPF-234) and VII (SPF-232) had only single genotype. Table VIII also indicated that standard variety (CP-77-400) fell in cluster I.

Table IX revealed the average intra-cluster and inter-cluster distances. Cluster number IV, V, VI and VII had 0 (zero) intra-cluster distance because each cluster was formed by single accession. The highest intra-cluster average D^2 value (280.79) was of the cluster number II. The lowest average inter-cluster distance was between cluster number I and IV e.g. 315.19. The highest average inter-cluster distance was between cluster VI and VII e.g. 10766.08. On the basis of their average intra and inter-cluster distances one can easily predict the genetic diversity that exist within and among clusters. A cluster diagram (Fig.

Table II. Cluster number, index scores and sugarcane genotypes included in each cluster following metroglyph technique

Cluster No.	Genotypes	Cluster index
I	2, 8, 10	77
II	1, 7	30
III	11, 4	27
IV	5	21
V	12	21
VI	6	20
VII	3	18
VIII	9	18

Table III. Range of means and index scores for indicated plant traits of sugarcane accessions

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Table IV. Scores of the twelve indicated traits of twelve genotypes of *Saccharum officinarum* L.

Entry No.	Cane height	No.of tillers/plant	Inter-nodal length	No.of leaves/ plant	Leaf area	Cane diameter	Cane weight	Juice content	Brix value	C.C.S.	Purity	Sucrose	Total
SPF-232	1	1	3	1	2	1	1	1	1	2	3	1	14
SPF-234	3	3	2	3	3	2	3	3	3	3	3	3	28
CP-43-33	1	3	3	3	1	1	1	1	3	1	1	1	18
CPF-235	1	2	1	3	1	1	1	1	1	2	3	1	14
CP-72-2086	1	3	2	2	2	3	1	1	3	3	3	3	21
Coj-84	2	2	2	2	2	2	2	2	2	2	1	2	20
RB-82-5336	1	2	2	2	3	2	1	1	1	1	3	1	16
TCP-81-10	2	2	2	2	2	2	1	1	3	3	3	3	20
Triton	2	2	2	2	3	1	1	1	3	1	1	1	18
BF-129	3	3	2	3	3	3	3	3	3	3	3	2	29
SPSG-26	2	1	1	2	1	1	1	1	1	2	3	2	13
CP-77-400	1	1	2	2	3	2	3	2	3	2	2	2	21

**= Significant at 0.01 probability level.

Table V. Analysis of dispersion

Source of variation	Degree of freedom	Sum of squares	Mean squares	F. calculated
Genotypes	q 11 (S-W)	83.77844419	7.6162222	2.695749^{10**}
Error	n-q 24 W	6.780560882^{-9}	2.8252712^{-10}	
Total	n 35 S	83.7784442		

Table VI. Contribution of each character to divergence

Characters	1	2	3	4	5	6	7	8	9	10	11	12	Total
Number of times appearing first in ranking	0	1	0	1	1	1	2	3	0	19	3	35	66
Percent contribution	0	1.52	0	1.52	1.52	1.52	3.03	4.54	0	28.78	4.54	53.03	100.00

Table VII. D^2 values in matrix form

Parents	2	3	4	5	6	7	8	9	10	11	12
1	10766.08	7002.30	6591.05	5109.55	2654.51	1669.62	1541.07	2508.55	5309.12	1801.12	1346.13
2		898.70	768.21	2373.72	2959.61	4258.71	4660.15	3645.30	998.28	4262.51	4516.73
3			149.39	845.26	1179.08	2448.09	2372.75	2319.78	434.10	2497.70	2411.79
4				766.93	981.05	1961.94	2009.27	1792.06	258.89	1890.20	2126.40
5					582.63	2000.76	1120.24	2482.38	723.02	1772.34	1710.56
6						473.53	225.29	797.39	552.68	461.18	314.42
7							335.23	156.20	1311.35	100.16	148.69
8								921.93	1400.68	287.04	209.09
9									1227.38	307.56	481.83
10										1350.06	1326.70
11											266.21

Table VIII. Grouping of varieties in to various clusters

Cluster No.	Populations
I	7, 11, 12
II	3, 4, 10
III	6, 8
IV	9
V	5
V1	2
VII	1

Table X. Average intra and inter-cluster distance (D) = D^2 values

Clusters	I	II	III	IV	V	VI	VII
I	13.10	43.87	18.62	17.75	42.75	65.92	40.07
II		16.75	37.62	42.18	27.89	29.80	79.37
III			15.00	29.31	29.17	61.72	45.80
IV				0.00	49.82	60.37	50.08
V					0.00	48.72	71.48
VI						0.00	103.75
VII							0.00

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

Clusters	I	II	III	IV	V	VI	VII
I	171.68	1924.91	346.74	315.19	1827.88	4345.98	1605.52
II		280.79	1415.91	1779.74	778.40	888.39	6300.82
III			225.29	859.66	851.43	3809.88	2097.79
IV				0.00	2482.38	3645.30	2508.55
V					0.00	2373.72	5109.55
VI						0.00	10766.08
VII							0.00

Fig. 2. Clustering pattern of 12 sugarcane accessions based on intra and inter-cluster average D^2 values

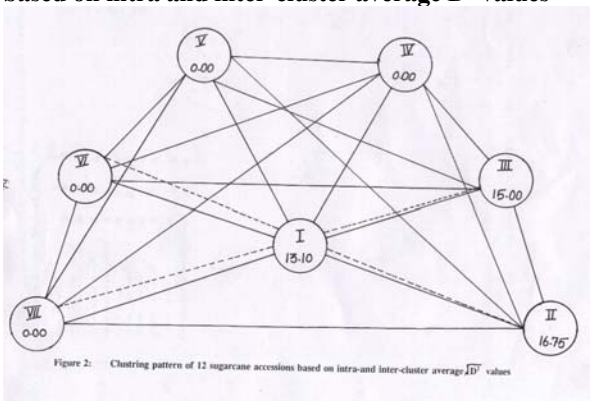

Figure 2: Clustring pattern of 12 sugarcane accessions based on intra-and inter-cluster average $\sqrt{D^2}$ values

CONCLUSIONS

It was concluded that the information obtained from these genotypes would facilitate the breeders to evaluate the genetic divergence among various populations, and to group the genotypes which are similar to each other into one group and those which are different into different groups. Then on the basis of this information one can plan and build up an effective breeding programme.

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