



GENETIC DIVERSITY AMONG SUGARCANE GENOTYPES (*Saccharum officinarum* L.)

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ABSTRACT

The assessment of the genetic diversity was done for 20 genotypes on the sixteen yield, yield components and quality characters. The results of D^2 analysis indicated that presence of considerable genetic divergence among the 20 genotypes studied. The 20 genotypes are grouped into five clusters based on the genetic distance using Mahalanobis's statistic. Out of 16 characters studied, cane yield, fibre per cent, cane volume/plot, CCS yield, germination per cent at 35 DAP, sucrose per cent, cane diameter contributed maximum towards divergence. Based on these studies crosses may be made between genotypes of cluster I (2000A225, 2009A288, 2009A399, 2007A81, 2009A252, 2009A377, 2008A120, 2009A107.) with cluster V (2006A223) followed by genotypes of cluster I and III (93A145, 2001A63, 2000A213, 87A298, CO6907) to obtain new desirable recombinants in sugarcane. The maximum intra cluster D^2 value of 198.738 was recorded for cluster III followed by 168.819 for cluster II, 117.486 for cluster I, while it was zero for clusters IV and V. The high intra cluster distance in cluster III indicated the presence of wide genetic diversity among the genotypes viz., 93A145, 2001A63, 2000A213, 87A298 and Co6907. Cluster mean values showed wide range among the genotypes studied, which indicates the presence of variation among the genotypes studied.

Key words: *Saccharum* spp., Genetic divergence, Mahalanobis's D^2 , statistics Cluster distance



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INTRODUCTION

Sugarcane (*Saccharum officinarum* L.) contributes about 60 percent to the world sugar production. It is the cheapest source of sweetening agent. Emphasis on future breeding programmes should be aimed at increasing the productivity per unit area which in turn will increase the total sugarcane production. Genetic diversity that arise

due to geographical separation or due to genetic barriers to cross ability or due to different patterns of evolution be measured following D^2 statistics that measure group distance based on multiple characters (Mahalanobis 1928) and it has become one of the important technique to assess genetic divergence on the basis of multiple traits. With the help of this technique, one can easily predict

genotypes which have high index scores and fell into different clusters can be crossed to have maximum variability of good combinations of characters. Rao (1952) suggested the application of these techniques for the assessment of genetic diversity in plant breeding. Divergence analysis is being a powerful tool in quantifying the degree of divergence at genotypic level based on phenotypic observations in different crops. An attempt was made in the present investigation of study the genetic diversity by using Tocher's method.

MATERIAL AND METHODS

The material for the present investigation comprised of twenty sugarcane genotypes *viz.*, of released and pre released clones was sugarcane grown in randomized block design with two replications at Regional Agricultural Research Station, Anakapalli were during 2015 - 16. were recorded for sixteen quantitative and qualitative characters, *viz.*, germination per cent at 35 DAP/plot, shoot population at 90 DAP/plot, shoot population at 120 DAP/plot, stalk population at 180 DAP/plot, number of millable canes/plot at harvest, brix per cent, sucrose per cent, purity per cent, cane length (cm), cane diameter (cm) single cane weight(kg), cane volume/plot cane yield (t/ha) and CCS yield (t/ha). The data was subjected to multivariate analysis given by Mahalanobis (1936). Grouping of the diversified genotypes into different clusters was done using Tocher's technique (Rao, 1952).

RESULTS AND DISCUSSION

The quantitative and quality assessment of genetic divergence was made by adopting Mahalanobis D^2 statistics for yield and its contributing characters. Genetic divergence was contributed for 16 characters of 20 genotypes revealed that the genetic divergence was high and 20 genotypes were grouped into five clusters.(Table-1& Figure-1). Out of five clusters, maximum number of 8 genotypes in cluster I.

Cluster II and Cluster III are the second largest with 5 genotypes. Cluster IV and V were included one genotype each. The pattern of distribution of genotypes into various clusters was at random indicating that geographical and genetic diversity were not related. The pattern of group constellations indicated significant variability among the genotypes. Similar results are furnished by Mohammad Tahir *et al.* (2013).

The percent contribution towards genetic divergence by all the 16 characters (Table-2) revealed that cane yield, fibre per cent, cane volume/plot, CCS yield, germination per cent at 35 DAP, sucrose per cent and cane diameter showed 80% towards total divergence suggested that these characters should be taken into consideration while selecting parents for hybridization. Similar results are reported by Ravishankaran *et al.* (2003), Muhammad and Ahmed (2009) and Sanghera *et al.* (2015). Average intra and inter cluster D^2 values (Table -3& Figure-2) indicated that maximum intra cluster D^2 value of 198.738 was recorded for cluster III followed by 168.819 for cluster II, 117.486 for cluster I, while it was zero for clusters IV and V. The high intra cluster distance in cluster III indicated the presence of wide genetic diversity among the genotypes *viz.*, 93A145, 2001A63 2000A213, 87A298 and Co6907

Cluster mean values (Table-4) showed wide range among the genotypes studied, which indicates the presence of variation among the genotypes studied. Cluster IV having highest mean value of germination per cent at 35DAP, purity per cent, fibre per cent; cluster III for shoot population at 90 DAP, stalk population at 120 DAP and 180 DAP; cluster II for cane length (cm); cluster I for NMC at harvest, cane diameter(cm), cane volume/plot, cane yield(t/ha), CCS yield(t/ha); cluster V for brix per cent, sucrose per cent, CCS

percent, single cane weight(kg) similar results are supported by Mali *et al.* (2009).

It is observed that no cluster contained at least one genotype with all the desirable traits,

which ruled out the possibility of selecting directly one genotype for immediate use. Therefore, hybridization between the selected genotypes from divergent clusters is essential to judiciously combine all the targeted traits.

Table 1 : Clustering pattern of 20 genotypes of Sugarcane (*Saccharum officinarum* L.) by Tocher's method

Cluster No.	No. of genotypes	Genotypes
I	8	2000A225,2009A288,2009A399,2007A81, 2009A252, 2009A377, 2008A120, 2009A107.
II	5	2008A124, 2009A385, 2003A255, CO7219, 2011A294.
III	5	93A145, 2001A63 ,2000A213,87A298, CO6907.
IV	1	97A85
V	1	2006A223

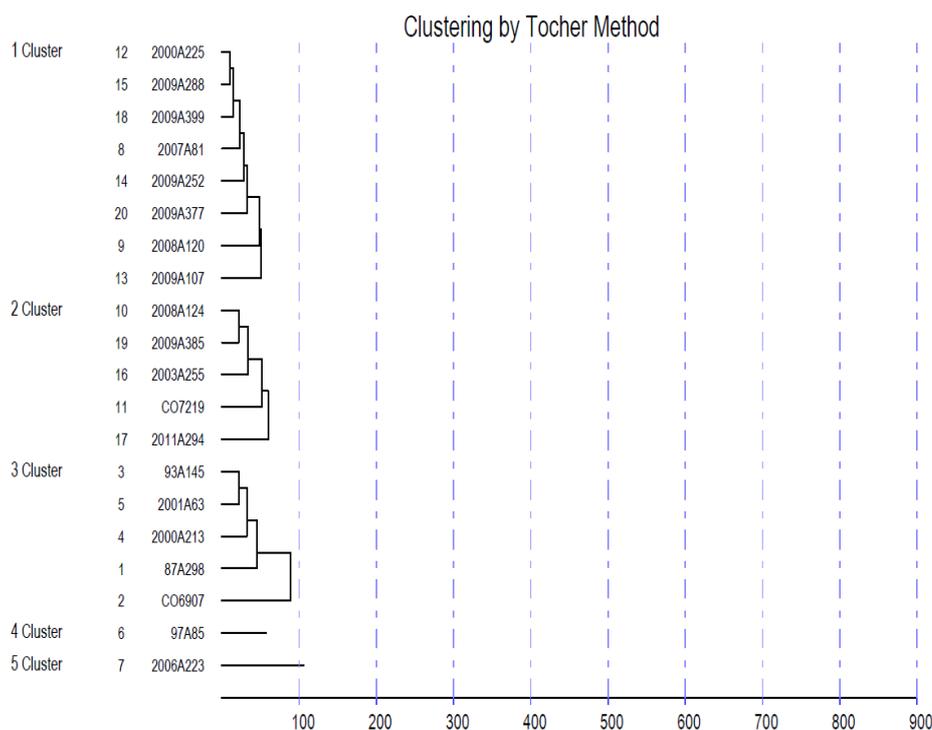


Figure 1: Dendrogram of 20 different sugarcane based upon mean of 16 cane yield and quality and morphological variables

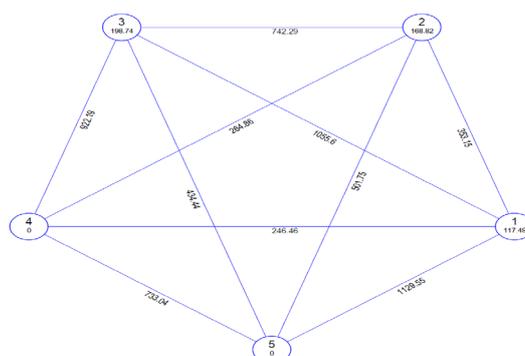
Table 2: Contribution of different characters towards genetic divergence among 20 genotypes of sugarcane (*Saccharum officinarum* L.).

Source	Times Ranked 1 st	Contribution %
Germination % at 35 DAP	2	1.05 %
Shoot population at 90DAP	0.01	0.00 %
Stalk population at 120DA	0.01	0.00 %
Stalk population at 180 D	0.01	0.00 %
NMC at harvest	0.01	0.00 %
Brix %	0.01	0.00 %
Sucrose %	1	0.53 %
Purity %	0.01	0.00 %
CCS %	0.01	0.00 %
Cane Length (cm)	0.01	0.00 %
Cane Diameter (cm)	1	0.53 %
Single Cane Weight (kg)	0.01	0.00 %
Cane Volume/ Plot	16	8.42 %
Fibre %	80	42.11 %
Cane Yield (t/ha)	85	44.74 %
CCS Yield (t/ha)	5	2.63 %

Table3 : Average intra (diagonal) and inter-cluster D₂ and D values (within parenthesis) values among five clusters in Sugarcane(*Saccharum officinarum* L.) genotypes.

Cluster No	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	117.486	353.151	1055.603	246.464	1129.549
Cluster II		168.819	742.289	264.860	501.754
Cluster III			198.738	922.189	434.444
Cluster IV				0.000	733.044
Cluster V					0.000

Diagonal bold values indicate intra cluster distances



Mahalanobis Euclidean Distance (Not to the Scale)

Fig.2. Intra-and Inter-cluster distances of 20 genotypes of Sugarcane(*Saccharumofficinarum* L.) in five clusters based on Euclidean² dist

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