

Full Length Research Paper

Genetic divergence among sugarcane genotypes (*Saccharum* spp.) for cane yield attributes and quality determinants

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The investigation was carried out at the Sugarcane Research Centre – Guneid (14, 48 -15.00° N) during the seasons 2003 - 04 and 2004 - 05. Twelve exotic sugarcane genotypes from Barbados, Guyana, Argentina and South India were tested in a randomized complete block design with four replicates. The objective was to quantify the genetic diversity among these genotypes regarding eleven cane yield and quality characters namely: stalk height, stalk diameter, internodal number per stalk; juice brix, juice pol, sugar recovery, juice purity, cane fiber and cane maturity percent, and yield of cane and sugar in Ton/hac. The results indicated that, the genotypes were grouped into six clusters based on the genetic distance using Mahalanobis's statistics. Higher inter-cluster distance was noticed between cluster IV and V (83.546) indicating high genetic diversity among two clusters. Thus, exploitation of genotypes within these two clusters as parents for crossing could produce good sugarcane segregants. The intra-cluster distance within cluster VI (7.226) and II (6.666) was very low indicating a close relationship of genotypes within each of these clusters. High cluster mean value for juice quality was recorded by cluster I whereas for cane and sugar yields, cluster VI was the best. It is suggested that genotypes within these two clusters could show greater potentiality for breeding purpose by virtue of their desirable characters.

Key words: Sugarcane, *Saccharum* spp., genetic divergence, Mahalanobis's D2 statistics, cluster distance, hybridization.

INTRODUCTION

Sugarcane (*Saccharum* spp) is an important cash crop grown in Sudan. The country has the potential to become one of the leading sugar producers in Africa due to the availability of land and irrigation water. Today's commercially grown sugarcane cultivars developed through interspecific and intervarietal hybridization programs with the crop known to carry the highest and variable number of chromosomes (usually an octaploid with $x = 10$ and aneuploidy) among the commonly grown crop plants (Prasanna et al., 2005). Sugarcane breeding in Sudan was aimed since 1986 at varieties with high cane and sugar yield following different breeding methods namely:

{1} direct introduction of varieties from foreign countries such as Barbados and France {2} Introduction of sugarcane true seeds (Fuzz) from Barbados and {3} local crossing programs to produce indigenous sugarcane true seeds for the local selection program.

Due to insufficient good sugarcane parents needed for local crossing program, the introduced varieties from different geo-graphical localities such as India, Barbados and France are routinely utilized in the hybridization process at the Sugarcane Research Centre at Gunied, presuming ample genetic diversity among these clones and greater likely-hood to receive promising segregants on hybridization. Studies of genetic divergence using one or more multivariate technique such as cluster and principal component analysis have been conducted over the last 20 years for several crops and with different objectives (Singh, 1981). The technique most often utilized in

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these studies is cluster analysis, which is employed to group sampling units such as varieties, lines and clones so as to obtain groups having the highest degree of within-group homogeneity and consequently heterogeneous in relation to one another (Johnson and Wickern, 1982). In studies of genetic divergence using cluster analysis, Mahalanobis' generalized distance (D^2) is commonly used as measurement of proximity due to the fact that characteristics with different measurements units which are normally correlated are being considered. Divergence studies are also useful for selection of parents in hybridization program (Arunachalam, 1981).

One of the most important problems in sugarcane breeding is its narrow genetic base of the parents, that is, the high frequency of common ancestors in their genealogy which has led to a high degree of progeny inbreeding and reduces variability. In order to stimulate progress in sugarcane breeding programs, the use of new technique in hybridization programs is suggested including evaluation of exploitable variability. This could be done by means of studies of genetic divergence (Peixota et al., 1984). Selection of parents using genetic diversity has been successfully utilized in sugarcane crops earlier by many workers in other crops such as cotton by Miller and Mariani (1963) and wheat by Somayajulu et al. (1970). Although the problem of discrimination may further be simplified if one could identify the yield characters that are responsible in discriminating between the utilization of such sugarcane parents. Since no report is available on genetic diversity of sugarcane varieties utilized in sugarcane breeding programs in Sudan, the objective of the present investigation is to quantify the genetic diversity among introduced sugarcane genotypes for further utilization of them in the breeding program using Mahalanobis's D^2 statistic.

MATERIALS AND METHODS

Twelve sugarcane genotypes introduced to the Sudan from India (Co 6806, Co 527, Co 997 and CoC 671), Barbados (B 70531, B 79136, BJ 7451, BJ 7938, BJ 82105 and BT 74209), Argentina (TUC 75-3) and Republic of Guyana (DB 75159) were tested during the plant cane season of 2003 - 2004 and in the first ratoon during 2004 - 2005 in a randomized complete block design with four replicates at the Sugarcane Research Centre at Gunied (14,48 - 15.00°N) and (33,13 - 32,22°E). The soil is suliem series with clay content between 42 and 61% and calcareous and mildly to strongly alkaline in reaction. The experimental plot contained four rows each of 10 meters long with 155 cm as inter-row spacing with a net plot size of 60 m².

The standard cultural practices such as irrigation, fertilization and pesticide application were carried out as per recommendations. The plant cane was harvested manually at 14 months of age whereas the ratoon crop was reaped at eleven months. Cane yield per plot at harvest was weighed using digital weighing balance at plant cane and ratoon crops.

Estimation of cane yield attributes

Ten guarded plants were selected at random from each replication

(forty stalks per genotypes) to record observations on cane characters namely: stalk height (SHT), stalk diameter (STD) and number of internode (INN) and quality traits as per the method followed by Babu (2004) as given below.

Estimation of cane characters

Stalk height (cm) = (Total height of selected stalks) /10

Stalk diameter (mm) = (Total diameter readings values for selected stalks) /10

Number of internode = (Total number of internodes in stalks) /10

Estimation of quality determinates

The quality characters included are: juice brix (BRX%), juice pol (POL%), cane fiber (FIB%), juice purity (PUR%), sugar recovery (REC%) and cane maturity percent at harvest (MAT%) following the method suggested by Schneider (1979). This was followed at the sugarcane research centre laboratory at Gunied site.

Juice pol%

After cane crushing, the cane juice was clarified with lead sub acetate and the clear juice was polarized in. After adjusting the refracted light, the pole value was obtained and recorded.

Juice brix (%)

This was measured by using brix hydrometer calibrated at 27.5°C
Juice purity (%): This was calculated as per the following formula

$$= \frac{\text{Sucrose}}{\text{Brix}} \times 100$$

$$\text{Cane fiber (\%)} = \frac{\text{Oven dried weighed sample (250g)}}{\text{Respective fresh weight}} \times 100$$

$$\text{Sugar recovery (\%)} = (\text{Pol of juice\%} \times 0.75) - 3$$

$$\text{Cane maturity of (\%)} = \frac{\text{Top 1/3}^{\text{rd}} \text{ portion brix (\%)}}{\text{Bottom 1/3}^{\text{rd}} \text{ portion brix (\%)}} \times 100$$

Statistical analysis

Analysis of variance, estimation of standard error and critical difference were carried out as per Panse and Sukhatme (1946). Test of significance for difference between characters means was carried out by referring to the F- table given by Snedecor and Cochran (1967). Genetic divergence among the studied genotypes based on statistical differences was estimated by Mahalanobis's D^2 procedure using SPSS software (Statistical Package for Social Studies). Data obtained regarding genotypes classification in different clusters and results of inter and intra clusters D^2 values between clusters, as well as mean of intracusters D^2 values of different clusters were used for discussion and to draw conclusion.

RESULTS

Analysis of variance results for 12 sugarcane genotypes

Table 1. Analysis of variance for cane and quality characters.

Characters of interest	MS genotype	MS error	Grand mean	SE±	C.V.%
Plant height (cm)	1240.5	293.1	247.60	6.05	6.91
Stalk diameter (mm)	0.17	0.05	2.30	0.08	9.72
Internode number	11.509	3.96	24.10	0.70	8.26
Juice brix (%)	1.69	0.27	17.31	0.18	3.00
Juice pole (%)	2.56	0.27	13.49	0.18	3.85
Sugar recovery (%)	2.97	0.322	11.45	0.20	4.95
Juice purity (%)	20.87	5.62	88.19	0.84	2.69
Cane yield (Ton/ha)	167.94	76.42	57.53	3.09	15.20
Sugar yield (Ton/ha)	1.99	0.86	6.53	0.33	14.21
Cane fiber (%)	0.215	0.399	17.22	0.22	3.67

Table 2. Grouping of genotypes into six clusters based on D² values.

Cluster No.	No. of genotypes	Genotypes	Origin
i	1	CoC 671	South India
ii	4	B70531, B79136, BJ 7938, TUC 75-3	Barbados(3), Argentina(1)
iii	1	BJ 7451	Barbados
iv	1	DB 75159	Guyana
v	1	BJ 82105	Barbados
vi	4	Co 6806, Co 997, Co 527, BT 74209	South India(3), Barbados(1)

Table 3. Intra-cluster (bold) and inter-cluster (light) D values based on 11 characters.

Cluster	I	II	III	IV	V	VI
I	00.00	17.837	61.647	12.755	77.107	33.786
II		6.666	45.399	22.676	61.466	16.513
III			00.00	67.561	18.587	31.009
IV				00.00	83.546	37.379
V					00.00	47.528
VI						7.226

indicated significant differences among genotypes for all recorded characters studied except for cane fiber percent (Table 1). This indicates sufficient genetic variability among the studied clones. Coefficient of variability was in the range of 2.69 to 15.20, which indicates the consistency of the experimental conditions. Based on the relative magnitude of D² values computed for all possible pairs of studied genotypes, the twelve genotypes were grouped into six clusters based on statistical differences. This was based on the fact that genotypes within a specific cluster usually have the smaller D² values among themselves when compared to those belonging to different clusters.

The results indicated that clusters I, III, IV and V were found to contain a single unique genotype each namely; CoC 671, BJ 7451, DB 75159 and BJ 82105 respectively (Table 2). On the contrary, clusters II and VI were the

largest groups, containing four genotypes each. The clustering pattern showed that varieties developed from same habitat (India) such as Co 527 (Co 349 x Co 312), Co 997 (Co 683 x Co P163I32), Co 6806 (Co 775 x Co 798) and CoC 671 (Q63 x Co 775) was noticed to have fell into two different clusters distanced by (33.786). The average of inter-cluster D² values (Table 3.) ranged from 12.755 (between cluster I and IV) to 83.546 (between cluster IV and V) and the maximum statistical value was found between cluster I and 1V. The lower inter-cluster value was noticed between cluster I and IV (12.755). The results indicated that the intra-cluster value was zero in cluster I (CoC 671), III (BJ7451), IV (DB 75159) and V (BJ 82105) since they contained only one genotype. The highest intra-cluster value was recorded by cluster VI at 7.226, followed by cluster II with 6.666 D² value.

Results of cluster's means with regard to different

Table 4. Mean intra-clusters values for cane yield attributes and quality determinates.

Character	Clusters					
	I	II	III	IV	V	VI
Stalk height (cm)	281.68	262.50	220.80	287.98	205.00	247.60
Stalk diameter (mm)	02.50	02.40	2.20	02.90	02.30	02.40
Internodes number	24.50	22.30	21.20	25.60	23.80	27.50
Cane yield (Ton/ha)	94.658	109.3925	114.7505	118.5575	101.6375	127.37
Juice brix (%)	18.31	17.38	18.02	14.60	16.00	18.11
Juice pol (%)	14.59	13.64	14.52	13.29	12.04	14.60
Cane fiber (%)	17.42	17.39	17.24	17.62	17.38	17.24
Juice Purity (%)	90.67	89.23	91.83	89.96	85.63	91.92
Sugar recovery (%)	12.64	11.61	12.55	11.24	09.91	12.67
Maturity (%)	86.15	93.77	89.02	85.82	89.41	87.09
Sugar yield (Ton/ha)	12.29	12.64	13.34	13.16	9.94	15.98

characters showed considerable differences among all clusters (Table 4). Cluster I had the genotype CoC 671 characterized with higher stalk diameter, juice quality (in terms of cane juice brix) and percent juice pole. Cluster II on the other hand contained genotypes (B7 0531, B7 9136, BJ 7938, and TUC 75-3) with better maturity percent at harvest compared to those in other clusters. Cluster III (BJ 7451) exhibited maximum value for juice purity percent among different genotypes; whereas cluster IV (DB 75159) was better for stalk height, stalk diameter, number of internodes and cane fiber percent. Cluster VI that included the national commercial varieties in Sudan, Co 6806 and Co 997, exhibited maximum values for cane yield and sugar ton/ha.

DISCUSSION

The constellation pattern of the 12 genotypes into six different clusters insured significant genetic variability among the materials studied. The results also indicated that distribution of genotypes into different groups did not follow any defined pattern with regard to their country of origin. This might be due to the free exchange of genetic stocks among the different regions world wide. Though the cluster analysis grouped the genotypes with greater similarity for agronomic characters, they did not necessarily include the genotypes from the same source of origin. Ghafoor et al. (2005) reported that in most of the germplasm resources, lack of association between agronomic traits and origin has been reported.

It is noticed that the six genotypes which developed from Barbados (B70531, B79136, BJ7938 and B7451, BT82105 and BT74209) were found to mingle into four different clusters indicating that the sugarcane genotypes from one geographical region could exhibit considerable diversity from each other and be dispersed into different clusters (Table 2). Therefore, it is clear that free clustering of sugarcane genotypes into different groups

might reflect the dependence on the pressure and direction of selection exerted on genotypes at the various regions for realizing maximum cane and sugar yields. Clustering pattern of Indian genotypes of the same habitat into different clusters could be due to different genetic nature of the parents from which they were derived or due to the selection pressure applied on some characters to evolve these varieties. Singh and Bains (1968) reported that characters constellation that might be associated with a particular region in nature could lose their individuality under selection and human interference.

Higher estimate of inter-cluster between cluster V and IV indicated wide genetic diversity between these two groups. Thus, genotypes with high index for specific character that fall into different clusters could be intercrossed to have maximum hybrid vigor and good number of useful segregants. Lower intercluster distance was noticed between cluster I and IV. This might indicate the close relationship and likelihood between genotypes groups within these clusters. Cluster VI is the most desirable group having variety Co 6806, which is the commercial variety across all sugar estates in the Sudan. It possessed most of the desirable traits with regard to cane yield and sugar content such as higher number of millable cane with good juice quality at harvest and better ratooning ability (Ahmed Obeid, 2005). This cluster also contained variety Co 997, the second national commercial variety in the Sudan having better juice quality and acceptable cane yield at harvest. A critical study of clusters means for different traits indicated that cluster I was desirable for good juice quality in terms of juice brix and juice pol percent, cluster II was better for early maturity character, cluster III for better juice purity percent and cluster IV for better cane characters namely: stalk height, stalk diameter and internodes number as well as percent fiber in cane (Table 4). Cluster VI was the best source for genotypes with good cane and sugar yield. It is therefore suggested that genotype in clusters I

(CoC 671), II (B70531, B79136, BJ 7938 and TUC 75-3), III (BJ 7451), IV (DB 75159) and V (Co 6806, Co 997, Co 527 and BT 74209) will show greater potentiality as breeding stocks by virtue of the corresponding desirable characters and the inter-cluster distance.

From the above investigations, it is concluded that hybridization of genotypes from two distant clusters is likely to yield desirable recombinants. Hybridization between genetically distant genotypes for exploiting hybrid vigour was frequently suggested in other crops species by Vivekananda and Subramanian (1993). Therefore, two important considerations for future breeding are the selection of parents from genetically distant parents and selection of particular sugarcane genotypes based on higher variability among the progenies. Present investigation has brought out the following important considerations in the Sudan sugarcane varietal development programme. Maximum inter-cluster between cluster I and IV indicated higher genetic diversity between these two groups. Thus, hybridization of these two groups could result in transgressive recombinants for agronomically important traits. Intra-cluster D^2 value was found low at 6.666 in cluster II and 7.226 in cluster VI. This might indicate the close relationship between genotypes within these two clusters. Therefore, genotypes within these clusters should not be selected for further breeding program among themselves.

Distribution of genotypes of same geographical regions (Barbados and India) into different clusters might indicate no influence of geographical location on the genetic architecture of the variety. The best specific genotypes combinations suggested for hybridization to generate good sugarcane progeny are (DB 75159 x BJ 82105), (Co C 671 x BJ 82105) and (CoC 671 x BJ 7451).

REFERENCES

- Ahmed O (2005). Sudanese Sugar Company, A brief Overview. Paper presented in the International Training Course on Genetic Improvement of sugarcane for use as food, fuel and fiber. Sugarcane Breeding Institute, Coimbatore, India. Oct. 12th-27th.
- Arunachalam V, Ram J (1967). Geographical diversity in relation to genetic divergence in cultivated Sorghum. *Indian Sugar. J. Gene. Plant. Breeding*, 27: 369-70.
- Arunachalam V (1981). Genetic distance in plant breeding. *Indian. J. Gene. Plant. Breeding*. 41: 226-236.
- Babu C (2004). Family performance of sugarcane (*Saccharum spp*) for yield quality and red rot *Collitorichum facaltum* Went) resistance and its relationship with genetic diversity based on STMS markers and coancestry of crosses. Phd thesis, Tamil Nadu Agricultural University, Coimabtoe. India.
- Ghafoor AZ and Anwar R (2005) Genetic diversity in *Pistium sativun* and strategy for indigenous biodiversity conservation *Pak. J. Bot.*, 37(1): 71-77.
- Mahalanobis PC (19360. On the generalized distance in Statistics. *Proceeding Natural Institute Sci., India.*, 2: 49-55.
- Miller PA, A Mariani (1963). Heterosis and combining ability in diellect crosses of upland cotton *Gossypium horsutum* *Crop. Sci.*, pp. 442-44.
- Panse VG, Sukhatme PV (1946). *Statistical methods for agricultural workers* 2nd Edn. Indian Council of Agricultural Research. New Delhi. pp. 123-126.
- Parasanna K, Ashok M, Parasannajeit M (2005). Genetic divergence in sugarcane, *Indian. Sugar. J.*, 53(3): 33-38.
- Pande K, Ghori DP (1987) Genetic divergence in rice *Oriza*, 24: 353-57.
- Piexoto TC, Machado Jr eDeotti RC (1984). *Novas tecnicas de melhoramento*. In: *Seminario de Tecnologia Agronomica, Copersucar, Piracicaba*. pp. 119-149.
- Schneider (1979). *International Commission for Uniform Methods of Sugarcane Analysis (ICUMSA). Cane Sugar Handbook*, Published by British Sugar Corporation, London.
- Singh (1981). The relative importance affecting genetic divergence. *Ind. J. Gene. Plant. Breeding*, 41: 237-245.
- Singh RB, Bains SS (1986). Genetic divergence for ginning outturn and its component in upland cotton (*Gossypium hirsutum* L) varieties obtained from different geographical locations. *Indian. J. Gene. Plant. Breeding*, 26: 262-268.
- Singh P, Singh VP (2002). Genetic divergence in Sugarcane germplasm. *Indian. J. Agric. Sci.*, 72(4): 252-253.
- Snedecore GW, Cochran (1967). *Statistical Methods*. Oxford and IBH publication Co., New Delhi.
- Somayajulu PLN, Joshi AB (1974). Relative importance of some yield contributing characters in triple dwarf wheat. *Indian. J. Gene. Plant. Breeding*, 30: 47-58.
- Vivekananda P, Subramanian S (1993). Genetic divergence in rainfed rice. *Oryza*, 30: 60-62.