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Studies on Genetic Diversity of *Saccharum* Complex

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ABSTRACT

Genetic diversity is essential for crop improvement. Therefore, it is necessary to maintain and further expand genetic variability to meet current and future breeding needs. N.I. Vavilov (1926, 1951) was the first to stress the need for a really broad genetic base for crop improvement. Sugarcane (Saccharum spp., hybrids) is an important agro industrial crop and knowledge on the genetic base of that material is important in breeding program worldwide. The genetic variability present in the sugarcane cultivars, cultivated by the producers, has hybrid origin, generally. The Saccharum officinarum L. has been contributing for genetic variability in sugarcane morethan Saccharum spontaneum, Saccharum sinense and Saccharum barberi. Intersspecific and intergeneric hybridization has provided the major break through in sugarcane breeding solving some of the disease problems but also providing additional and unexpectedly large increased yields, improved rationing ability and adaptability for growth and various stress condition. Hence in the present. Saccharum complex genotypes namely, Saccharum officinarum cv. Badila, S. spontaneum, Erianthus arundinaceus, Narenga porphyrocoma and Miscanthus sacchariflorus were subjected to divergence analysis. All the above five genotypes are having wider genetic base and can be utilized for sugarcane improvement programme and exploit its potential for increase sugar productivity. **Keywords:** Sugarcane, Genetic diversity.

INTRODUCTION

Sugarcane is widely grown in the tropical and subtropical areas of the world. Sugarcane is classified under the family of Poaceae, sub family Panicoideae and tripe Andropogoneae. Linnaeus named sugarcane as *Saccharum officinarum* L. *Saccharum* and related species are very promiscuous, readily inter cross with related genera and thought to have been evolved as a polyploid complex in Andropogoneae. Classification by various workers differed in the number of species included in the genus. Mukherjee [5] coined the term *Saccharum* complex to embrace the genus *Saccharum* L., *Erianthus micx, Salerostachya A. campus* and *Narenga* Bor. Heinz [2] reviewed the taxonomy of *Saccharum* thoroughly and include six species in the genus. All the genera and *Saccharum* species hybridize easily and form a large breeding pool and hence there is lot of scope for higher sugar productivity.

MATERIALS AND METHODS

Five genotypes namely *Saccharum officinarum* cv. Badila, *Saccharum spontaneum, Erianthus arundinaceus, Narenga porphyrocoma* and *Miscanthus sacchariflorus* were raised. The experiment was laidout in randomized block design with three replications. The genotypes were raised in plot of 5 rows with each row of 5 metre length and 0.8 metre distance between rows. The recommended agronomic practices were followed. They were evaluated for ten characters including cane yield and sugar yield attributing characters viz., cane length, internode length, number of millable cane per plot, cane thickness, single cane weight, brix per cent, sucrose percent, commercial cane sugar per cent (CCS %) cane yield per plot and sugar yield per plot. The genetic distance between the genotypes was worked out using Mahalanobis D² analysis [4] and grouping of genotypes into clusters was done following the Tochers method as detailed by Rao [6] and described by Singh and Chaudhary [7].

RESULTS AND DISCUSSION

Analysis of variance showed significant differences for all the ten characters studied among the genotypes. Based on the *per se* performance the genotype *Saccharum officinarum* cv. Badila recorded high mean values for eight characters mainly cane thickness, cane weight, brix per cent, sucrose per cent,

commercial cane sugar per cent, cane yield per plot and sugar yield per plot (Table 1). Genotype *Erianthus arundinaceus* recorded high mean values for cane length and internode length and the maximum number of millable cane per plot was recorded by the genotype *Miscanthus sacchariflorus*.

Based on D² values, five genotypes were grouped into four clusters (Table 2). The genotypes *Saccharum officinarum* cv. Badila was in cluster I. Cluster II consists of genotypes *Narenga porphyrocoma* and *Miscanthus sacchariflorus*. Genotype *Saccharum spontaneum* falls on cluster III and the genotype *Erianthus arundinaceus* falls on cluster IV. The overall composition of the clustering pattern showed that genotypes were distributed in different clusters. Similar results were observed by Jose Marcelo *et al.* [3] and Cornide *et al.* [1] [9].

The contribution of characters towards divergence showed that characters cane weight (5.26%), brix per cent (20.00%), commercial cane sugar per cent (4.21%), number of millabel cane per plot (4.21%), cane yield per plot (8.42%) and sugar yield per plot (50.00%) played a major role. Hence these characters should be given importance during hybridization and selection in the segregating population.

From the foregoing discussion, all the above five genotypes, have wide genetic base and can be exploited for hybrid vigour to increase the cane yield and sugar yield potential in sugarcane.

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Genotypes	Cane length (cm)	Internode length (cm)	Number of millable cane per plot	Cane thickness (cm)	Cane weight (kg)	Brix per cent	Sucrose per cent	Commercial cane sugar per cent	Cane yield per pot	Sugar yield per plot
Saccharum officinarum cv. Badila	147	7.80	148	2.7	2.08	22.90	19.10	13.20	307.80	40.63
Saccharum spontaneum	102	13.8	257	0.8	0.26	5.68	2.10	0.65	66.82	0.43
Erianthus arundinaceus	398	22.9	230	2.0	0.48	6.32	2.29	0.60	110.40	0.66
Narenga porphyrocoma	64	12.9	285	0.4	0.04	5.90	2.20	0.60	11.40	0.07
Miscanthus sacchariflorus	82	12.4	325	0.5	0.06	6.40	2.20	0.38	19.50	0.07

Table 1. Mean performance of genotypes

Table 2. Distribution of sugarcane genotypes in different clusters

Cluster No.	No. of genotypes	Name of the genotype				
Ι	1	Saccharum officinarum cv. Badila				
II	2	Narenga porphyrocoma, Miscanthus sacchariflorus				
III	1	Saccharum spontaneum				
IV	1	Erianthus arundinaceus				

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