



Genetic diversity studies in sweet sorghum [*Sorghum bicolor* (L.) Moench] based on quantitative traits

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Abstract : From the genetic diversity studies based on 17 morphological characters of 52 sweet sorghum genotypes it could be inferred that, the that the maximum contribution to the genetic divergence was accounted by sucrose per cent followed by plant height, juice weight, stay green trait, fresh cane weight, days to fifty per cent flowering, sucrose yield, brix per cent, millable cane weight, stem girth and juice volume. The constellation pattern of the fifty two genotypes was grouped into ten clusters indicated that the distribution of genotypes into different groups did not follow any defined pattern with regard to their origin. Clusters IV, V, VI, VII, VIII, and X may be useful for exploitation of hybrid vigour for traits like plant height, millable cane weight, juice yield and sucrose yield. The genotypes from these clusters may serve as potential genotypes to improve these traits. The genotypes from the selected clusters having outstanding mean performance may serve as potential genotypes for future breeding programme.

Key Words : Sweet sorghum, Diversity, Cluster, Dendrogram

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INTRODUCTION

Sweet sorghum [*Sorghum bicolor* (L.) Moench] is a diploid species ($2n = 20$) that is closely related to sugarcane, a polyploid species. An important crop in many parts of the world is grown for food, feed and industrial purposes. The first step in any plant breeding program is the study of genetic variability. Knowledge of the existing phenotypic and genetic variation and the association between such components and their heritability is of interest, not only from a theoretical point of quantitative inheritance of characters, but also of practical value for simultaneous selection of two or more traits and developing appropriate selection strategies (Kenga *et al.*, 2006). Therefore, under present investigation, effort was made to understand the quantum and nature of genetic variability present in a set of 52 elite sweet sorghum accessions.

MATERIALS AND METHODS

For this study 52 accessions of sweet sorghum were

selected from sorghum gene bank at Department of Millets, Tamil Nadu Agricultural University, India. All the genotypes were evaluated during summer 2011. The experiment was laid out in a randomized block design (RBD) with two replications. The list of accessions taken for study is appended in Table A. Each genotype was sown in single row of 4m length with a spacing of 60 cm x 15 cm. The data were recorded on five random plants from each genotype in each replication for seventeen characters *viz.*, days to fifty per cent flowering, days to physiological maturity, plant height, stem girth, internode length, number of leaves, brix per cent, stay green trait fresh cane weight, millable cane weight, juice weight, juice volume, sucrose percentage, juice extractability percentage, cane yield, juice yield, sucrose yield. D^2 analysis was carried out using all the twelve characters and generalized distance (D^2) was calculated for each pair of genotypes. A method suggested by Tocher (Rao, 1952) was used to group the genotypes into different clusters based on the D^2 values.

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