



# Analysis of genetic diversity among high sucrose genotypes of sugarcane (*Saccharum* spp.) derived from CoC 671 using morphological and sugarcane specific microsatellite markers

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**Abstract :** Twenty eight genotypes derived from a common donor parent for juice quality *viz.*, CoC 671 through crossing as male parent, as female parent, selfing, through somaclonal variation and induced mutagenesis were evaluated based on morphological markers and sugarcane specific STMS markers to estimate genetic diversity using Dice, Jaccard's and SM methods. The correlation between the mean similarity index values of molecular diversity and morphological diversity was +0.7506, showing strong relationship between the two characters. STMS markers were found to be suited to detect more differences among the clones of common descent as supported by the lower similarity index values. Mean genetic similarity among the somaclones (SI value = 0.72), mutants (SI value = 0.81), clones derived from CoC 671 as a female (SI value = 0.73) parent and male parent (SI value = 0.70) clearly showed that the clones with CoC 671 as the male parent were more diverse and indicated the role of male parent in creating a more segregating population than when used as female parent. Tissue culture based selection through somaclonal variation and induced mutations were less efficient in creating variability than the conventional methods. More diverse clones and combinations were identified to be used in hybridization for sucrose improvement in sugarcane.

**Key Words :** Genetic diversity, CoC 671 derivatives, Morphological markers, STMS markers, Breeding methods, Sugarcane

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## INTRODUCTION

A major objective of sugarcane improvement programmes worldwide is to produce more sugar per unit area. In spite of the diversity of sugarcane genetic resources and a long history of genetic improvement, the progress in varietal development during the past decade has been slow, especially in improving sucrose levels of commercial varieties. Genes concerned with high juice quality are almost entirely inherited from *Saccharum officinarum* ancestors. Successful efforts to improve sucrose content through the adoption of different selection strategies and choice of appropriate parents have been reported (Legendre, 1995). Building genetic stocks for sucrose content has been in progress in all the world sugarcane breeding

stations and donor parents identified have been extensively utilized in the progressive synthesis of several high sucrose derivatives. This repeated intercrossing necessitates an assessment of genetic base of such high sucrose parental clones to identify the more diverse clones in breeding for better gains. Molecular markers have been used in genetic improvement programmes to study genetic diversity and to select parents for planning crossing between parents from divergent backgrounds. Microsatellite repeats have the potential to be used in studies on genetic diversity (Selvi *et al.*, 2003; Cordeiro *et al.*, 2003; Hemaprabha *et al.*, 2005 and Hemaprabha *et al.*, 2006). In this study the derivatives of a common donor parent for juice quality *viz.*, CoC 671 bred

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