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RAPD ANALYSIS OF SUGARCANE CULTIVARS FOR EARLY MATURATION AND YIELD IMPROVEMENT

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Abstract

Sugarcane (*Saccharum* sp.) is one of the world's most commercial crops as it is the main source of sucrose. Sugarcane breeding programs are concentrated to improve the sucrose content and cane yield. Sucrose content is important for sugar industries and cane yield is profitable concern for farmers. Selection of genetically rich and diverse genotypes is necessary to achieve both the improvements. In the present study, initially physicochemical analysis performed for 24 promising sugarcane cultivars, mainly for sucrose accumulation and cane yield. Among the 24 cultivars, 10 cultivars were selected for further RAPD molecular screening of potential genotypes. PCR analysis was done using 20 RAPD primers. The genetic similarity and UPGMA clustering were performed for all 10 sugarcane cultivars and compared the analysed data of both physicochemical and RAPD analysis. The study showed S1, S8, S11, S18 and S23 as closest ones and S2, S24, S15 as distant ones. This evaluation of genetic relatedness among 10 cultivars revealed primary information for the selection of high sucrose accumulative and cane yielding parental genotypes for further sugarcane breeding.

Key words: Cane yield, genetic similarity coefficients, RAPD markers, sucrose accumulation, Sugarcane.

Introduction

Sugarcane (*Saccharum* sp.) is the main source for sucrose production followed by sugar beet in the world (Zucchi *et al.,* 2002). The basic objective of the sugarcane breeding programs is to enlarge its genetic base by transferring traits of economic value from wild species (Burner and Legendre, 1993). Morphological distinction in *Saccharum* species is very lower due to high levels of genetic polymorphism and gene-environment interactions. Seasonally changing environmental factors affect variations in the phenotypic traits. Hence, morphological characters will not stand as reliable markers for genetic diversity and phylogenetic studies (Harvey and Botha, 1996; Burner *et al.,* 1997). Commercially important Sugarcane varieties are poly-aneuploid hybrid results of unequal composition from *S. officinarum* (80–90%) and *S. spontaneum* (10–20%) as parental genomes with minimum recombination (Jisen *et al.,* 2013). The large genomic size and more complexity have made sugarcane breeding attempts difficult (Cunff *et al.,* 2008). Use of molecular techniques from last two decades has made understanding of complexity in genome easier (Rossi *et al.,* 2003). Genes from *S. officinarum* are responsible for the high cane yield (cane weight) and sucrose production in the new varieties (Sreenivasan *et al.,* 1987). Genetic diversity information obtained by the molecular marker studies has considerable impact on selection of parent materials for crop improvement (Mohammadi and Prasanna, 2003). Molecular markers reveal complete information about genetic diversity, as they are independent of the effects of environmental factors. Use of PCR based DNA markers such as RAPD, SSR, ISSR and AFLP is advantageous than other methods in studying polymorphism and genotypic variability in plants (Rani *et al.,* 1995; Munthali *et al.,* 1996; Devarumath *et al.,* 2002). Development of RAPD markers was an important turning point regarding DNA marker technology based on the use of PCR to amplify

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