

Phylogenetic Analyses of Sugarcane Cultivars for Sugar Content and Early Maturation using Simple Sequence Repeat Markers

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Sugarcane (*Saccharum* sp.) is perhaps the world's most commercial crop that is extensively grown across globe as a source of sugar in Asian countries and fuel in some European countries. More than 75% of world sugar production is achieved from sugarcane which is grown across 100 countries [1]. The breeding of sugarcane is cornerstone of all advanced sugarcane industries including several research institutes and it is foremost important that such breeding is integrated with modern molecular techniques, so that maximum advantage can be achieved [2]. The success of sugarcane breeding program lies in the appropriate selection of genetically rich and diverse genotypes [3]. Research rationale of present study was to analyze genetic diversity among 24 promising flowering and non-flowering sugarcane cultivars. Twenty SSR primers were used to assess the genetic diversity among cultivars that are abundantly grown in Karnataka, India for sugar accumulation and early maturation. A genetic similarity index among cultivars was analyzed by using Unweighted pair group method with arithmetic mean (UPGMA). Thus, upon molecular analysis, study highlighted that among 24 sugarcane cultivars, some promising cultivars do exist which can be further subjected for future breeding program.

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