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Phylogenetic analyses of sugarcane cultivars using simple sequence repeat markers.

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Sugarcane (Saccharum sp.) is one of the world's most commercial and extensively grown crops. The breeding of sugarcane is keystone of all advanced sugarcane industries and several research institutes. The success of sugarcane breeding program lies in the appropriate selection of genetically rich and diverse genotypes. Research rationale of present study was to analyze genetic diversity among 24 promising flowering and non-flowering sugarcane cultivars. Molecular marker based screening was done with PCR analysis using 10 SSR primers. SCM-32 primer showed highest polymorphic bands. The genetic similarity and UPGMA clustering were analyzed for all 24 sugarcane cultivars. The similarity index values for S19, S21, S22 and S23 suggested them as closest ones and S17 as the most distant one. UPGMA clustering based dendrogram showed that the correlation between Jaccard coefficient and similarity index is high and significant. All 5 clusters showed a mixture of flowering and non-flowering cultivars, indicating that molecular marker can play a potential role in sugarcane breeding programs than morphology based analysis.
