

## Functional markers for gene mapping and genetic diversity studies in sugarcane

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The database of sugarcane expressed sequence tags (EST) offers a great opportunity for developing molecular markers that are directly associated with important agronomic traits. The development of new EST-SSR markers represents an important tool for genetic analysis. In sugarcane breeding programs, functional markers can be used to accelerate the process and select important agronomic traits, especially in the mapping of quantitative traits loci (QTL) and plant resistant pathogens or qualitative resistance loci (QRL). The aim of this work was to develop new simple sequence repeat (SSR) markers in sugarcane using the sugarcane expressed sequence tag (SUCEST database). A total of 365 EST-SSR molecular markers with trinucleotide motifs were developed and evaluated in a collection of 18 genotypes of sugarcane (15 varieties and 3 species). In total, 287 of the EST-SSRs markers amplified fragments of the expected size and were polymorphic in the analyzed sugarcane varieties. The number of alleles ranged from 2-18, with an average of 6 alleles per locus, while polymorphism information content values ranged from 0.21-0.92, with an average of 0.69. The discrimination power was high for the majority of the EST-SSRs, with an average value of 0.80. Among the markers characterized in this study some have particular interest, those that are related to bacterial defense responses, generation of precursor metabolites and energy and those involved in carbohydrate metabolic process. These EST-SSR markers presented in this work can be efficiently used for genetic mapping studies of segregating sugarcane populations. The high Polymorphism Information Content (PIC) and Discriminant Power (DP) presented facilitate the QTL identification and marker-assisted selection due the association with functional regions of the genome became an important tool for the sugarcane breeding program.

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