

FAPESP BIOENERGY PROGRAM

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DEVELOPMENT OF A DATABASE FOR MOLECULAR PROFILE MANAGEMENT OF COMMERCIAL CULTIVARS, PARENTS AND WILD ACCESSIONS OF SUGARCANE

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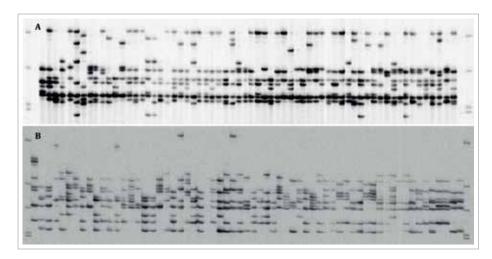


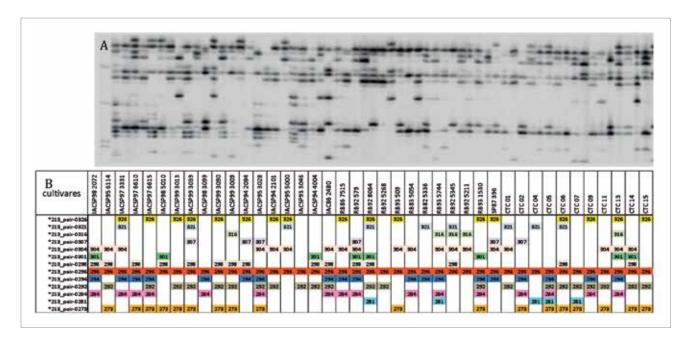
Figure 1. Molecular profile obtained by using SSRs genotyped at the 4300 DNA Analyser (LiCor) System. A: Sugarcane elite clones from the IAC Active Germplasm Bank. B: Saccharum officinarum clones

The efficient
management and utilization
of the germplasm of a
breeding program is critical
to the development of
new cultivars. In Brazil,
the sugarcane breeding
programs have used
molecular markers to
characterize the molecular
profile of their genotypes.
However, there is a lack of
a consolidated bank with
the molecular profile of
cultivars, elite clones and

wild accessions. This project has as main objective start the construction of a molecular profile database of sugarcane cultivars, wild accessions and elite clones used as parents in crosses. In addition, we intend to create a database of genomic DNA of these genotypes; identify a set of SSR primer pairs with high discriminatory power; estimate the genetic variability within and between the groups assessed and develop SCAR markers (Sequence Characterized Amplified Regions) derived from AFLP (Amplified Fragment Length Polymorphism) species-specific to S. spontaneum. The development of SCAR markers will allow the rapid identification of hybrids derived from crosses between sugarcane commercial cultivars and accessions of *S. spontaneum* assisting the Genetic Introgression Bioenergy Programs. We emphasize that, to our knowledge, until the present moment, in the case of public sugarcane breeding programs, in Brazil does not exist, a molecular profile database of such nature to sugarcane.



SUMMARY OF RESULTS TO DATE AND PERSPECTIVES



The molecular profile based on microsatellite markers of the sugarcane cultivars and elite clones have already been established. In addition, the molecular profile of the majority of the accessions from the Saccharum species (S. officinarum, S. spontaneum, S. baberi, S. robustum) and related genera (Erianthus and Miscanthus) which compose the IAC Sugarcane Germplasm Collection is near to be completed. All these molecular profiles are being deposited in a molecular profile data bank which will be used in the management of the germplasm collection and also in a genetic diversity study to define a core collection that can be used for association mapping and breeding purposes. The SSR primer set showed high PIC values (0.734 up to 0.926) and was suitable either to establish the molecular profiles or capture the genetic variability assessed through SSRs. Initial analysis conducted for each genotype category, i.e., varieties and elite clones, revealed a high degree of average genetic diversity, respectively, 0.887 and 0.860. Only 3.22% of the total SSR alleles were common among the variety category. Some alleles were variety exclusive (private), showing potential application for variety identification. In general, the dendrograms were in agreement with the pedigree information. In relation to the SCARs development, a preliminary screening for species-specific AFLP markers at the Saccharum Complex was conducted by using AFLP markers. This search allowed the identification of candidate species-specific and genera-specific AFLP derived markers. These candidate markers are being cloned and sequenced and will be validated to be used as SCARs.

Figure 2. A: Molecular profile of some sugarcane cultivars from different Brazilian sugarcane breeding programs obtained by using SSRs genotyped at the 4300 DNA Analyser (LiCor). B: Example of a graphic representation of the cultivars based on their allele types and sizes represented by different colors, stored at the allele panel of the Molecular Profile Data Bank

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