

ANALYSIS OF GENETIC SIMILARITY FROM THE BRAZILIAN PANEL OF SUGARCANE GENOTYPES (BPSG) AS AN IMPORTANT STEP FOR ASSOCIATION MAPPING

Barreto, FZ¹; Balsalobre, TWA²; Mollinari, M³; Rosa, JRBF³; Garcia, AAF³; Souza, AP²; Carneiro, MS¹

Email: monalisa@cca.ufscar.br

¹*Departamento de Biotecnologia Vegetal, Universidade Federal de São Carlos;*

²*Centro de Biologia Molecular e Engenharia Genética, Universidade Estadual de Campinas;* ³*Departamento de Genética, Escola Superior de Agricultura Luiz de Queiroz.*

The Sugarcane breeding programs to obtain new varieties higher than those currently in cultivation has concentrated efforts to reduce costs and time involved, which usually exceeds 10 years. Molecular markers may be an important strategy in that reduced. The objective of this work was to evaluate the genetic diversity of 133 sugarcane genotypes belonging to Brazilian Panel of Sugarcane Genotypes (BPSG) by microsatellite markers. This panel brings together genotypes from different geographic regions of the world, which represent the genetic basis of Brazilian breeding programs, and also aims association mapping studies in sugarcane. For construction this panel, were adopted the following criteria: most planted varieties, most used varieties as progenitors, important ancestral species, genotypes from the genetic mapping programs, and newly released varieties by breeding programs in Brazil. Genetic diversity among all the genotypes, 2 to 2, was estimated by Jaccard coefficient within the software R. 100 SSR markers (86 derived from EST-SSRs and 14 genomic) generated a total of 1483 bands, of which 1082 were polymorphic (81,1%). Owing to the high ploidy level of sugarcane, most of analyzed SSRs produced more than two alleles, ranging from 4 to 36, with an average of 15 alleles per marker. The polymorphism information content (PIC) ranged from 0.50 to 0.96, with an average of 0.88. The power of discrimination (PD) ranged from 1 to 0.62, with an average of 0.97. Molecular data allowed to obtain a dendrogram composed of various correlation groups, contained into two large subdivisions originated from the *Saccharum barberi*. Bootstrap analysis (1000 estimates) were performed for each pair of genotypes in random samples of SSRs. Based on the dendrogram and the genetic diversity matrix, it was observed that, in general, genotypes from the same crossing (full-sib genotypes) presented superior genetic similarity when compared to those from only one joint parental (half-sib genotypes). These results are preliminary, since other data will also be used to analyze the extent of linkage disequilibrium and to perform subsequently the association mapping in genotypes of interest for genetic improvement in Brazil.

This document was created with Win2PDF available at <http://www.win2pdf.com>.
The unregistered version of Win2PDF is for evaluation or non-commercial use only.
This page will not be added after purchasing Win2PDF.