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Ciência, tecnologia e inovação no Brasil: desafios e transformações

Genomic and transcriptomic analysis of defensins in wild species and commercial sugarcane cultivars

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Saccharum spp. is a hybrid resulting from the crossing of wild species *Saccharum officinarum* and *Saccharum spontaneum*. The hybridization aimed to combine the adaptability to adverse environments from *S. spontaneum* with increased ability to accumulate sucrose from *S. officinarum*. The high demands for sugarcane products requires the generation of hybrids resistant to diseases caused by various microorganisms. However, the molecular mechanism underlying the different defense capacities observed in hybrids and wild species has not yet been fully elucidated. The antimicrobial peptides (AMPs) are the first line of defense in animals and plants. Among the AMPs, defensins are small peptides components of the host defense system. Seventeen defensins were already identified in EST libraries on the sugarcane SUCEST project, but no genomic information of these defensins was investigated. The main goal of this work is to characterize genomic and transcriptomic sequences of defensins in wild species and commercial sugarcane cultivars and their relationship with the predisposition to pathogens of the different genotype. The methodology involves analysis of sugarcane genomic and transcriptomic data and prediction of the tertiary structure of defensins by bioinformatics. The genomic DNA sequences available at (<http://lbmp.bioqmed.ufrj.br/genome/index>) were used to identify the genes of defensins through TBLASTN with the defensins predicted from sugarcane EST sequences. Fifteen proteins for defensins were used as reference. The alignment of defensins against genomic assembly of SP70-1143 cultivar identified 11 possible defensins genes in this sugarcane genome. The size of scaffolds containing the defensin's genes range from 314 to 5,793 bp. An alignment was also made against the transcriptome of the SP70 cultivar in order to corroborate the results obtained with the genomic scaffolds of defensins. This alignment identified 19 transcripts from five different *loci*, with the coverage ranged from 85% to 100% and the alignment identity of most transcripts close to 100%. It is expected that the characterization of defensins in sugarcane will allow a better understanding of the first line defense mechanisms of wild species and cultivars.

Palavras-chave: Defensins, Sugarcane, Plant defense.

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