## Transcriptome Analysis of Sugarcane Plants in Response to Herbivore Insects by DNA Macroarrays

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A DNA macroarray study was performed to monitor the expression of 3,840 sugar cane ESTs from leaf and bark tissues from SUCEST (Sugar cane EST Project, FAPESP) in response to the sugar cane borer (Diatraea saccharalis) treatment, the major insect pest of sugar cane in Brazil. Two sugar cane varieties with distinct levels of insect tolerance were analyzed. SP80-3280 is considered to be a susceptible genotype to borer damage, whereas SP81-3250 displays significant levels of insect tolerance. To screen differentially expressed transcripts in the libraries over time (0, 6h, 12h and 24 h after infestation), the macroarrays were treated with mRNAs of control and sugar cane borer-infested samples. We present a robust method of normalizing and analyzing the expression ration based on arbitrary thresholds and statistical criteria. Analyses were performed on log-transformed ratio values. We used an arbitrary twofold-difference criterion in at least one of the three time points to interpret macroarray data. On the basis of the signal intensities and expression ratios from two independent experiments with two replicates each, 24 ESTs showed differential gene expression levels in the tolerant genotype, whereas 12 ESTs were observed in the susceptible plants. Strikingly, 75% of the ESTs in the susceptible variety were repressed in at least one time point, whereas in the tolerant genotype nearly 75% of the ESTs were induced in at least one time point. Another interesting observation is that we identified early- and lateresponse genes that are affected by insect damage. These results are important not only because this is the first large-scale gene expression study of a monocot plant in response to insect attack, but also because it allows the comparison of the gene expression pattern between susceptible and tolerant genotypes, opening new insights in the understanding of the molecular basis of plant resistant to insect pests. Support: FAPESP, Pronex, CAPES