

Proteinase inhibitors and serine proteases are differently regulated by herbivory in sugarcane

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Plants respond to insect damage by induction and accumulation of a large set of defense proteins. An investigation was undertaken to study the sugarcane transcriptional changes following *Diatraea saccharalis* damage. The approach was the large-scale monitoring of transcripts, using DNA macroarrays containing sequences of sugarcane ESTs of serine proteases and serine proteinase inhibitors from the SUCEST (Sugarcane EST Project) database. The macroarray analyses revealed differently expressed sequences in response to herbivory. Transcript monitoring through Real-Time PCR confirmed that 10 proteinase inhibitors, such as 4 genes homologous to maize and rice Bowman-Birk inhibitors (BBI), 5 genes homologous to maize proteinase inhibitors (MPI) and 1 gene homologue to subtilisin inhibitor; and 3 genes homologous to serine proteases of the S1, S10 and S14 family were positively regulated by herbivory. While the protease inhibitor's function in defense is well established, the involvement of plant proteases in response to herbivory still remains to be elucidated. In this work we show that a sugarcane encoding S14 family protease member was upregulated in response to both *D. saccharalis* damage and wound treatment. Interestingly, homologous sequence from rice also responded to the same treatments, but not the *Arabidopsis thaliana* counterpart, suggesting a conserved role of this S14 protease in defense against herbivores in Poacea. One of the greatest applications of these results is the identification of genes for use in biotechnological strategies to improve sugarcane insect resistance.

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