

NOVEL PERSPECTIVES ON THE PATHOGENESIS OF *LONOMIA OBLIQUA* ENVENOMATION BASED ON ASSESSMENT OF HOST RESPONSE BY GENE EXPRESSION ANALYSIS

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Animal venoms are source of active substances on mammal hemostasis. These principles interfere with many physiologic pathways and have an enormous potential in the development of new drugs. The envenomation caused by *Lonomia obliqua* is characterized by a hemorrhagic clinical profile. Previous studies - based on isolation and characterization of active principles - have been focused on the pro-coagulant, fibrin(ogen)olytic, hemolytic, edematogenic and nociceptive activities. Recently, a significant advance was achieved through a transcriptome study, which generated a catalog of putative toxic proteins of the caterpillar venom, giving rise to hypotheses on the molecular basis of envenomation pathogenesis which could be explored. Here, using a microarray methodology, we analyzed the effects of the caterpillar venom on cultured cells gene expression profile and identified increased expression of genes possibly involved with the clinical manifestations. We also validated that in fact venom alteration of host gene expression profiles can contribute to the observed effects of envenomation. The direct action of *L. obliqua* venomous proteins and the change in the expression pattern of cells could synergistically be responsible for the profound symptoms observed during lonomism. Taken together, these data allow for a more complete understanding of the venom effects in hemostasis during lonomism.

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